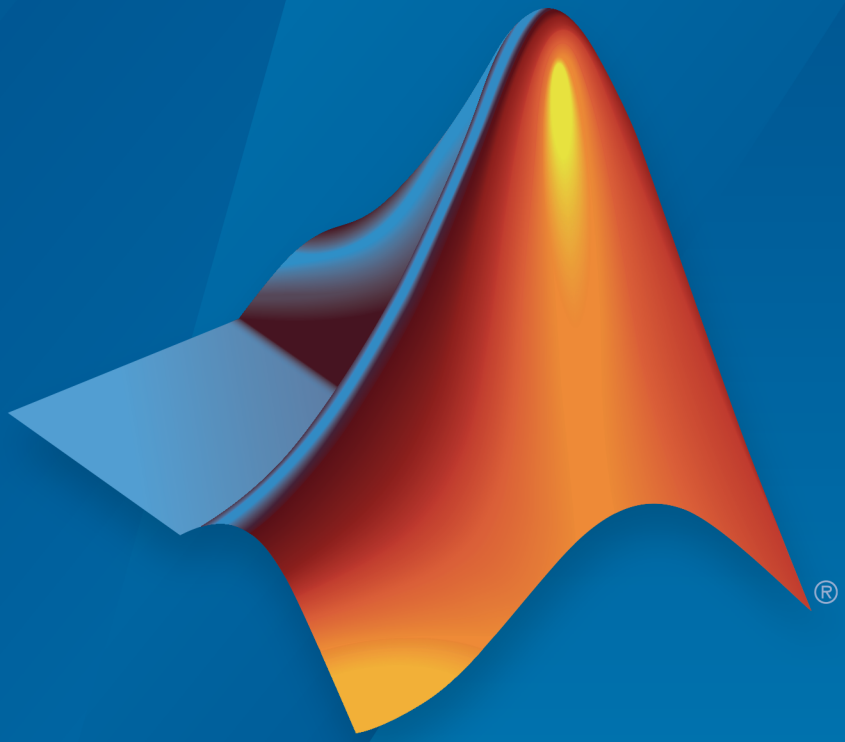
Statistics and Machine Learning Toolbox™

User's Guide



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Statistics and Machine Learning Toolbox™ User's Guide

Revision History

September 1993	First printing	Version 1.0
March 1996	Second printing	Version 2.0
January 1997	Third printing	Version 2.11
November 2000	Fourth printing	Revised for Version 3.0 (Release 12)
May 2001	Fifth printing	Minor revisions
July 2002	Sixth printing	Revised for Version 4.0 (Release 13)
February 2003	Online only	Revised for Version 4.1 (Release 13.0.1)
June 2004	Seventh printing	Revised for Version 5.0 (Release 14)
October 2004	Online only	Revised for Version 5.0.1 (Release 14SP1)
March 2005	Online only	Revised for Version 5.0.2 (Release 14SP2)
September 2005	Online only	Revised for Version 5.1 (Release 14SP3)
March 2006	Online only	Revised for Version 5.2 (Release 2006a)
September 2006	Online only	Revised for Version 5.3 (Release 2006b)
March 2007	Eighth printing	Revised for Version 6.0 (Release 2007a)
September 2007	Ninth printing	Revised for Version 6.1 (Release 2007b)
March 2008	Online only	Revised for Version 6.2 (Release 2008a)
October 2008	Online only	Revised for Version 7.0 (Release 2008b)
March 2009	Online only	Revised for Version 7.1 (Release 2009a)
September 2009	Online only	Revised for Version 7.2 (Release 2009b)
March 2010	Online only	Revised for Version 7.3 (Release 2010a)
September 2010	Online only	Revised for Version 7.4 (Release 2010b)
April 2011	Online only	Revised for Version 7.5 (Release 2011a)
September 2011	Online only	Revised for Version 7.6 (Release 2011b)
March 2012	Online only	Revised for Version 8.0 (Release 2012a)
September 2012	Online only	Revised for Version 8.1 (Release 2012b)
March 2013	Online only	Revised for Version 8.2 (Release 2013a)
September 2013	Online only	Revised for Version 8.3 (Release 2013b)
March 2014	Online only	Revised for Version 9.0 (Release 2014a)
October 2014	Online only	Revised for Version 9.1 (Release 2014b)
March 2015	Online only	Revised for Version 10.0 (Release 2015a)

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Getting Started

Statistics and Machine Learning Toolbox Product Description

Analyze and model data using statistics and machine learning

Statistics and Machine Learning Toolbox™ provides functions and apps to describe, analyze, and model data using statistics and machine learning. You can use descriptive statistics and plots for exploratory data analysis, fit probability distributions to data, generate random numbers for Monte Carlo simulations, and perform hypothesis tests. Regression and classification algorithms let you draw inferences from data and build predictive models.

For analyzing multidimensional data, Statistics and Machine Learning Toolbox lets you identify key variables or features that impact your model with sequential feature selection, stepwise regression, principal component analysis, regularization, and other dimensionality reduction methods. The toolbox provides supervised and unsupervised machine learning algorithms, including support vector machines (SVMs), boosted and bagged decision trees, k-nearest neighbor, k-means, k-medoids, hierarchical clustering, Gaussian mixture models, and hidden Markov models.

Key Features

- Regression techniques, including linear, generalized linear, nonlinear, robust, regularized, ANOVA, and mixed-effects models
- Repeated measures modeling for data with multiple measurements per subject
- Univariate and multivariate probability distributions, including copulas and Gaussian mixtures
- Random and quasi-random number generators and Markov chain samplers
- Hypothesis tests for distributions, dispersion, and location, and design of experiments (DOE) techniques for optimal, factorial, and response surface designs
- Classification Learner app and algorithms for supervised machine learning, including support vector machines (SVMs), boosted and bagged decision trees, k-nearest neighbor, Naïve Bayes, and discriminant analysis
- Unsupervised machine learning algorithms, including k-means, k-medoids, hierarchical clustering, Gaussian mixtures, and hidden Markov models

Supported Data Types

Statistics and Machine Learning Toolbox supports the following data types for input arguments:

- Numeric scalars, vectors, matrices, or arrays having single- or double-precision entries. These data forms have data type `single` or `double`. Examples include response variables, predictor variables, and numeric values.
- Cell vectors of strings; character, logical, or categorical arrays; or numeric vectors for categorical variables representing grouping data. These data forms have data types `cellstr`, `char`, `logical`, `categorical`, and `single` or `double`, respectively. An example is an array of class labels in machine learning.
    - You can also use nominal or ordinal arrays for categorical data. However, the `nominal` and `ordinal` data types might be removed in a future release. To work with nominal or ordinal categorical data, use the `categorical` data type instead.
    - You can use signed or unsigned integers, e.g., `int8` or `uint8`. However:
        - Estimation functions might not support signed or unsigned integer data types for nongrouping data.
        - If you recast a `single` or `double` numeric vector containing `NaN` values to a signed or unsigned integer, then the software converts the `NaN` elements to `0`.
- Some functions support tabular arrays for heterogeneous data (for details, see "Tables"). The `table` data type contains variables of any of the data types previously listed. An example is mixed categorical and numerical predictor data for regression analysis.
    - For some functions, you can also use dataset arrays for heterogeneous data. However, the `dataset` data type might be removed in a future release. To work with heterogeneous data, use the `table` data type if the estimation function supports it.
    - Functions that do not support the `table` data type support sample data of type `single` or `double`, e.g., matrices.

Statistics and Machine Learning Toolbox does not support the following data types:

- Complex numbers.
- Custom numeric data types, e.g., a variable that is double precision and an object.
- Numeric scalars, vectors, matrices, or arrays on a GPU.

- Signed or unsigned numeric integers for nongrouping data, e.g., `unint8` and `int16`.
- Sparse matrices, i.e., matrix `A` such that `issparse(A)` returns `1`. To use data that is of data type `sparse`, recast the data to a matrix using `full`.

Note: If you specify data of an unsupported type, then the software might return an error or unexpected results.

Organizing Data

Other MATLAB Functions Supporting Nominal and Ordinal Arrays

Notable functions that operate on nominal and ordinal arrays are listed in Using nominal Objects and Using ordinal Objects. In addition to these, many other functions in MATLAB® operate on nominal and ordinal arrays in much the same way that they operate on other arrays. A few functions might exhibit special behavior when operating on categorical arrays:

- If multiple input arguments are categorical arrays, the function often requires that they have the same set of categories, including order if ordinal.
- Relational functions, such as `max` and `gt`, require that the input arrays be `ordinal`.

The following table lists MATLAB functions that operate on nominal and ordinal arrays in addition to other arrays.

`size`	`isequal`	`intersect`	`histogram`	`double`
`length`	`isequaln`	`ismember`	`pietimes`	`single`
`ndims`		`setdiff`		`int8`
`numel`	`eq`	`setxor`	`sort`	`int16`
	`ne`	`unique`	`sortrows`	`int32`
`isrow`	`lt`	`union`	`issorted`	`int64`
`iscolumn`	`le`			`uint8`
	`ge`		`permute`	`uint16`
`cat`	`gt`		`reshape`	`uint32`
`horzcat`			`transpose`	`uint64`
`vertcat`	`min`		`ctranspose`	`char`
	`max`			`cellstr`
	`median`			
	`mode`			

See Also

Using nominal Objects | Using ordinal Objects

Create Nominal and Ordinal Arrays

In this section...

Create Nominal Arrays

This example shows how to create nominal arrays using `nominal`.

Load sample data.

The variable `species` is a 150-by-1 cell array of strings containing the species name for each observation. The unique species types are setosa, versicolor, and virginica.

```
load('fisheriris')
unique(species)
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'
```

Create a nominal array.

Convert `species` to a nominal array using the categories occurring in the data.

```
speciesNom = nominal(species);
class(speciesNom)
```

```
ans =

nominal
```

Explore category levels.

The nominal array, `speciesNom`, has three levels corresponding to the three unique species. The levels of a nominal array are the set of possible values that its elements can take.

```
getlevels(speciesNom)
```

```
ans =

     setosa      versicolor      virginica
```

A nominal array can have more levels than actually appear in the data. For example, a nominal array named `AllSizes` might have levels `small`, `medium`, and `large`, but you might only have observations that are `medium` and `large` in your data. To see which levels of a nominal array are actually present in the data, use `unique`, for instance, `unique(AllSizes)`.

Explore category labels.

Each level has a label, which is a string used to name the level. By default, `nominal` labels the category levels with the values occurring in the data. For `speciesNom`, these labels are the species types.

```
getlabels(speciesNom)
```

```
ans =

    'setosa'    'versicolor'    'virginica'
```

Specify your own category labels.

You can specify your own labels for each category level. You can specify labels when you create the nominal array.

```
speciesNom2 = nominal(species,{'seto','vers','virg'});
getlabels(speciesNom2)
```

```
ans =

    'seto'    'vers'    'virg'
```

You can also change category labels on an existing nominal array using `setlabels`

Verify new category labels.

Verify that the new labels correspond to the original labels in `speciesNom`.

```
isequal(speciesNom=='setosa',speciesNom2=='seto')
```

```
ans =

     1
```

The logical value 1 indicates that the two labels, `'setosa'` and `'seto'`, correspond to the same observations.

Create Ordinal Arrays

This example shows how to create ordinal arrays using `ordinal`.

Load sample data.

```
AllSizes = {'medium','large','small','small','medium',...
            'large','medium','small'};
```

The created variable, `AllSizes`, is a cell array of strings containing size measurements on eight objects.

Create an ordinal array.

Create an ordinal array with category levels and labels corresponding to the values in the cell array (the default levels and labels).

```
sizeOrd = ordinal(AllSizes);
getlevels(sizeOrd)
```

```
ans =

     large      medium      small
```

Explore category labels.

By default, `ordinal` uses the original strings as category labels. The default order of the categories is ascending alphabetical order.

```
getlabels(sizeOrd)
```

```
ans =

    'large'    'medium'    'small'
```

Add additional categories.

Suppose that you want to include additional levels for the ordinal array, `xsmall` and `xlarge`, even though they do not occur in the original data. To specify additional levels, use the third input argument to `ordinal`.

```
sizeOrd2 = ordinal(AllSizes,{},...
                   {'xsmall','small','medium','large','xlarge'});
getlevels(sizeOrd2)

ans =

     xsmall      small      medium      large      xlarge
```

Explore category labels.

To see which levels are actually present in the data, use `unique`.

```
unique(sizeOrd2)

ans =

     small      medium      large
```

Specify the category order.

Convert `AllSizes` to an ordinal array with categories `small` < `medium` < `large`. Generally, an ordinal array is distinct from a nominal array because there is a natural ordering for levels of an ordinal array. You can use the third input argument to `ordinal` to specify the ascending order of the levels. Here, the order of the levels is smallest to largest.

```
sizeOrd = ordinal(AllSizes,{},{'small','medium','large'});
getlevels(sizeOrd)

ans =

     small      medium      large
```

The second input argument for `ordinal` is a list of labels for the category levels. When you use braces `{}` for the level labels, `ordinal` uses the labels specified in the third input argument (the labels come from the levels present in the data if only one input argument is used).

Compare elements.

Verify that the first object (with size `medium`) is smaller than the second object (with size `large`).

```
sizeOrd(1) < sizeOrd(2)
```

```
ans =

     1
```

The logical value `1` indicates that the inequality holds.

See Also

`getlabels` | `getlevels` | `nominal` | `ordinal`

Related Examples

- “Change Category Labels” on page 2-9
- “Reorder Category Levels” on page 2-11
- “Merge Category Levels” on page 2-19
- “Index and Search Using Categorical Arrays” on page 2-47

More About

- “Categorical Arrays” on page 2-42
- “Advantages of Using Categorical Arrays” on page 2-44

Change Category Labels

This example shows how to change the labels for category levels in categorical arrays using `setlabels`. You also have the option to specify labels when creating a categorical array.

Load sample data.

The variable `Cylinders` contains the number of cylinders in 100 sample cars.

```
load('carsmall')
unique(Cylinders)
```

```
ans =

     4
     6
     8
```

The sample has 4-, 6-, and 8-cylinder cars.

Create an ordinal array.

Convert `Cylinders` to a nominal array with the default category labels (taken from the values in the data).

```
cyl  = ordinal(Cylinders);
getlabels(cyl)
```

```
ans =

    '4'    '6'    '8'
```

`ordinal` created labels using the integer values in `Cylinders`, but you should provide labels for numeric data.

Change category labels.

Relabel the categories in `cyl` to `Four`, `Six`, and `Eight`.

```
cyl = setlabels(cyl ,{'Four','Six','Eight'});
getlabels(cyl)
```

```
ans =
```

```
    'Four'    'Six'    'Eight'
```

Alternatively, you can specify category labels when you create a nominal or ordinal array using the second input argument, for example by specifying `ordinal(Cylinders, {'Four','Six','Eight'})`.

See Also

`getlabels` | `nominal` | `ordinal` | `setlabels`

Related Examples

- "Reorder Category Levels" on page 2-11
- "Add and Drop Category Levels" on page 2-21
- "Index and Search Using Categorical Arrays" on page 2-47

More About

- "Categorical Arrays" on page 2-42
- "Advantages of Using Categorical Arrays" on page 2-44

Reorder Category Levels

In this section...

Reorder Category Levels in Ordinal Arrays

This example shows how to reorder the category levels in an ordinal array using `reorderlevels`.

Load sample data.

```
AllSizes = {'medium','large','small','small','medium',...
            'large','medium','small'};
```

The created variable, `AllSizes`, is a cell array of strings containing size measurements on eight objects.

Create an ordinal array.

Convert `AllSizes` to an ordinal array without specifying the order of the category levels.

```
size  = ordinal(size);
getlevels(size)
```

```
ans =

     large      medium      small
```

By default, the categories are ordered by their labels in ascending alphabetical order, `large` < `medium` < `small`.

Compare elements.

Check whether or not the first object (which has size `medium`) is smaller than the second object (which has size `large`).

```
size(1) < size(2)
```

```
ans =
```

```
     0
```

The logical value `0` indicates that the medium object is not smaller than the large object.

Reorder category levels.

Reorder the category levels so that `small` < `medium` < `large`.

```
size = reorderlevels(size,{'small','medium','large'});
getlevels(size)
```

```
ans =

     small      medium      large
```

Compare elements.

Verify that the first object is now smaller than the second object.

```
size(1) < size(2)
```

```
ans =

     1
```

The logical value `1` indicates that the expected inequality now holds.

Reorder Category Levels in Nominal Arrays

This example shows how to reorder the category levels in nominal arrays using `reorderlevels`. By definition, nominal array categories have no natural ordering. However, you might want to change the order of levels for display or analysis purposes. For example, when fitting a regression model with categorical covariates, `fitlm` uses the first level of a nominal independent variable as the reference category.

Load sample data.

The dataset array, `hospital`, contains variables measured on 100 sample patients. The variable `Weight` contains the weight of each patient. The variable `Sex` is a nominal variable containing the gender, `Male` or `Female`, for each patient.

```
load('hospital')
getlevels(hospital.Sex)
```

```
ans =
```

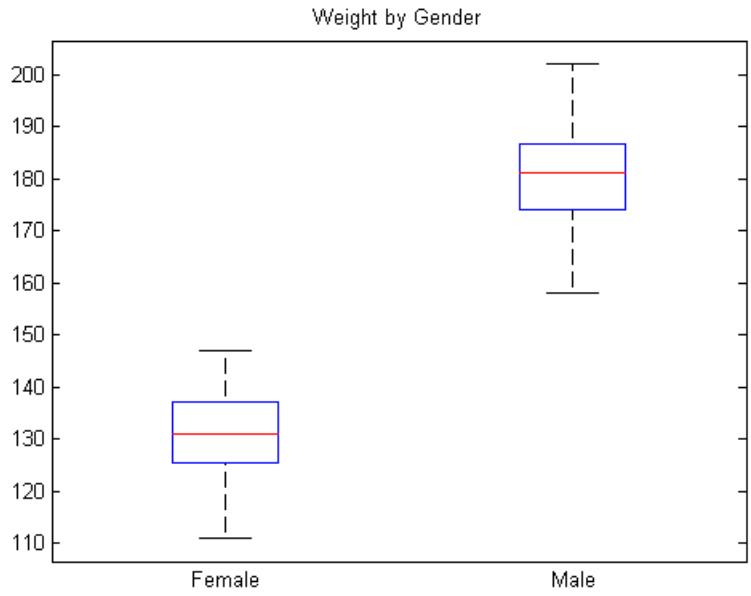
```
    Female      Male
```

By default, the order of the nominal categories is in ascending alphabetical order of the labels.

Plot data grouped by category level.

Draw box plots of weight, grouped by gender.

```
figure()
boxplot(hospital.Weight,hospital.Sex)
title('Weight by Gender')
```



The box plots appear in the same alphabetical order returned by `getlevels`.

Change the category order.

Change the order of the category levels.

```
hospital.Sex = reorderlevels(hospital.Sex,{'Male','Female'});
```

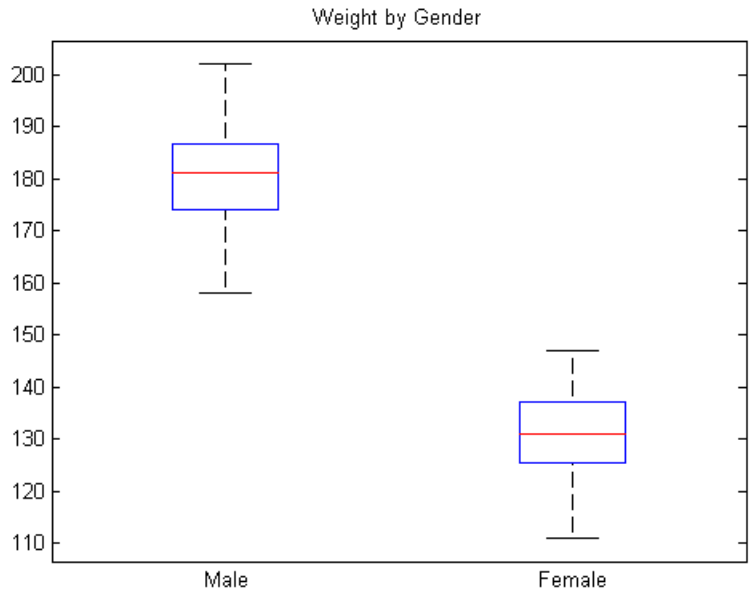
```
getlevels(hospital.Sex)

ans =

     Male       Female
```

The levels are in the newly specified order.

Plot data in new order.

Draw box plots of weight by gender.

```
figure()
boxplot(hospital.Weight,hospital.Sex)
title('Weight by Gender')
```



The order of the box plots corresponds to the new level order.

See Also

`fitlm` | `getlevels` | `nominal` | `ordinal` | `reorderlevels`

Related Examples

- “Change Category Labels” on page 2-9
- “Merge Category Levels” on page 2-19
- “Add and Drop Category Levels” on page 2-21
- “Index and Search Using Categorical Arrays” on page 2-47

More About

- “Categorical Arrays” on page 2-42
- “Advantages of Using Categorical Arrays” on page 2-44

Categorize Numeric Data

This example shows how to categorize numeric data into a categorical ordinal array using `ordinal`. This is useful for discretizing continuous data.

Load sample data.

The dataset array, `hospital`, contains variables measured on a sample of patients. Compute the minimum, median, and maximum of the variable `Age`.

```
load('hospital')
quantile(hospital.Age,[0,.5,1])
```

```
ans =

    25    39    50
```

The patient ages range from 25 to 50.

Convert a numeric array to an ordinal array.

Group patients into the age categories `Under 30`, `30-39`, `Over 40`.

```
hospital.AgeCat = ordinal(hospital.Age,{'Under 30','30-39','Over 40'},...
                          [],[25,30,40,50]);
getlevels(hospital.AgeCat)
```

```
ans =

    Under 30      30-39      Over 40
```

The last input argument to `ordinal` has the endpoints for the categories. The first category begins at age 25, the second at age 30, and so on. The last category contains ages 40 and above, so begins at 40 and ends at 50 (the maximum age in the data set). To specify three categories, you must specify four endpoints (the last endpoint is the upper bound of the last category).

Explore categories.

Display the age and age category for the second patient.

```
dataset({hospital.Age(2),'Age'},...
        {hospital.AgeCat(2),'AgeCategory'})
```

```
ans =
```

```
    Age    AgeCategory
    43     Over 40
```

When you discretize a numeric array into categories, the categorical array loses all information about the actual numeric values. In this example, `AgeCat` is not numeric, and you cannot recover the raw data values from it.

Categorize a numeric array into quartiles.

The variable `Weight` has weight measurements for the sample patients. Categorize the patient weights into four categories, by quartile.

```
p = 0:.25:1;
breaks = quantile(hospital.Weight,p);
hospital.WeightQ = ordinal(hospital.Weight,{'Q1','Q2','Q3','Q4'},...
                   [],breaks);
getlevels(hospital.WeightQ)

ans =

     Q1      Q2      Q3      Q4
```

Explore categories.

Display the weight and weight quartile for the second patient.

```
dataset({hospital.Weight(2),'Weight'},...
        {hospital.WeightQ(2),'WeightQuartile'})

ans =

    Weight    WeightQuartile
    163       Q3
```

Summary statistics grouped by category levels.

Compute the mean systolic and diastolic blood pressure for each age and weight category.

```
grpstats(hospital,{'AgeCat','WeightQ'},'mean','DataVars','BloodPressure')

ans =

                   AgeCat      WeightQ    GroupCount    mean_BloodPressure
    Under 30_Q1    Under 30    Q1          6            123.17      79.667
```

```
Under 30_Q2    Under 30    Q2          3          120.33      79.667
Under 30_Q3    Under 30    Q3          2           127.5        86.5
Under 30_Q4    Under 30    Q4          4             122          78
30-39_Q1       30-39       Q1         12          121.75       81.75
30-39_Q2       30-39       Q2          9          119.56      82.556
30-39_Q3       30-39       Q3          9             121      83.222
30-39_Q4       30-39       Q4         11          125.55      87.273
Over 40_Q1     Over 40     Q1          7          122.14      84.714
Over 40_Q2     Over 40     Q2         13          123.38      79.385
Over 40_Q3     Over 40     Q3         14          123.07      84.643
Over 40_Q4     Over 40     Q4         10           124.6        85.1
```

The variable `BloodPressure` is a matrix with two columns. The first column is systolic blood pressure, and the second column is diastolic blood pressure. The group in the sample with the highest mean diastolic blood pressure, `87.273`, is aged 30–39 and in the highest weight quartile, `30-39_Q4`.

See Also

`grpstats` | `ordinal`

Related Examples

- "Create Nominal and Ordinal Arrays" on page 2-4
- "Merge Category Levels" on page 2-19
- "Plot Data Grouped by Category" on page 2-25
- "Index and Search Using Categorical Arrays" on page 2-47

More About

- "Categorical Arrays" on page 2-42
- "Advantages of Using Categorical Arrays" on page 2-44

Merge Category Levels

This example shows how to merge categories in a categorical array using `mergelevels`. This is useful for collapsing categories with few observations.

Load sample data.

```
load('carsmall')
```

Create a nominal array.

The variable `Origin` is a character array containing the country of origin for 100 sample cars. Convert `Origin` to a nominal array.

```
Origin = nominal(Origin);
getlevels(Origin)
```

```
ans =

    France      Germany      Italy      Japan      Sweden      USA
```

There are six unique countries of origin in the data.

Tabulate category counts.

Explore the elements of the categorical array.

```
tabulate(Origin)
```

```
    Value    Count   Percent
   France        4      4.00%
  Germany        9      9.00%
    Italy        1      1.00%
    Japan       15     15.00%
   Sweden        2      2.00%
      USA       69     69.00%
```

There are relatively few observations in each European country.

Merge categories.

Merge the categories `France`, `Germany`, `Italy`, and `Sweden` into one category called `Europe`.

```
Origin = mergelevels(Origin,{'France','Germany','Italy','Sweden'},...
```

```
                    'Europe');
getlevels(Origin)

ans =

     Japan      USA      Europe
```

The variable `Origin` now has only three category levels.

Tabulate category counts.

Explore the elements of the merged categories.

```
tabulate(Origin)
```

```
   Value    Count   Percent
   Japan       15     15.00%
     USA       69     69.00%
  Europe       16     16.00%
```

The category `Europe` has the 16% of observations that were previously distributed across four countries.

See Also

`mergelevels` | `nominal`

Related Examples

- “Create Nominal and Ordinal Arrays” on page 2-4
- “Add and Drop Category Levels” on page 2-21
- “Index and Search Using Categorical Arrays” on page 2-47

More About

- “Categorical Arrays” on page 2-42
- “Advantages of Using Categorical Arrays” on page 2-44

Add and Drop Category Levels

This example shows how to add and drop levels from a categorical array.

Load sample data.

```
load('examgrades')
```

The array `grades` contains exam scores from 0 to 100 on five exams for a sample of 120 students.

Create an ordinal array.

Assign letter grades to each student for each test using these categories.

Grade Range	Letter Grade
100	A+
90–99	A
80–89	B
70–79	C
60–69	D

```
letter = ordinal(grades,{'D','C','B','A','A+'},[],...
                 [60,70,80,90,100,100]);
getlevels(letter)
```

```
ans =

     D       C       B       A       A+
```

There are five grade categories, in the specified order D < C < B < A < A+.

Check for undefined categories.

Check whether or not there are any exam scores that do not fall into the five letter categories.

```
any(isundefined(letter))
```

```
ans =
```

```
     1     0     1     1     0
```

Recall that there are five exam scores for each student. The previous command returns a logical value for each of the five exams, indicating whether there are any scores that are <undefined>. There are scores for the first, third, and fourth exams that are <undefined>, that is, missing a category level.

Identify elements in undefined categories.

You can find the exam scores that do not have a letter grade using the `isundefined` logical condition.

```
grades(isundefined(letter))
```

```
ans =

    55
    59
    58
    59
    54
    57
    56
    59
    59
    50
    59
    52
```

The exam scores that are in the 50s do not have a letter grade.

Add a new category.

Put all scores that are <undefined> into a new category labeled `D-`.

```
letter(isundefined(letter)) = 'D-';
getlevels(letter)
```

```
Warning: Categorical level 'D-' being added.
> In categorical.subsasgn at 55

ans =

     D      C      B      A      A+      D-
```

The ordinal variable, `letter`, has a new category added to the end.

Reorder category levels.

Reorder the categories so that D- < D.

```
letter = reorderlevels(letter,{'D-','D','C','B','A','A+'});
getlevels(letter)
```

```
ans =

     D-      D      C      B      A      A+
```

Compare elements.

Now that all exam scores have a letter grade, count how many students received a higher letter grade on the second test than on the first test.

```
sum(letter(:,2) > letter(:,1))
```

```
ans =

    32
```

Thirty-two students improved their letter grade between the first two exams.

Explore categories.

Count the number of A+ scores in each of the five exams.

```
sum(letter=='A+')
```

```
ans =

     0     0     0     0     0
```

There are no A+ scores on any of the five exams.

Drop a category.

Drop the category A+ from the ordinal variable, `letter`.

```
letter = droplevels(letter,'A+');
getlevels(letter)
```

```
ans =

     D-      D      C      B      A
```

Category A+ is no longer in the ordinal variable, `letter`.

See Also

`droplevels` | `ordinal` | `reorderlevels`

Related Examples

- "Create Nominal and Ordinal Arrays" on page 2-4
- "Reorder Category Levels" on page 2-11
- "Merge Category Levels" on page 2-19
- "Index and Search Using Categorical Arrays" on page 2-47

More About

- "Categorical Arrays" on page 2-42
- "Advantages of Using Categorical Arrays" on page 2-44

Plot Data Grouped by Category

This example shows how to plot data grouped by the levels of a categorical variable.

Load sample data.

```
load('carsmall')
```

The variable `Acceleration` contains acceleration measurements on 100 sample cars. The variable `Origin` is a character array containing the country of origin for each car.

Create a nominal array.

Convert `Origin` to a nominal array.

```
Origin = nominal(Origin);
getlevels(Origin)
```

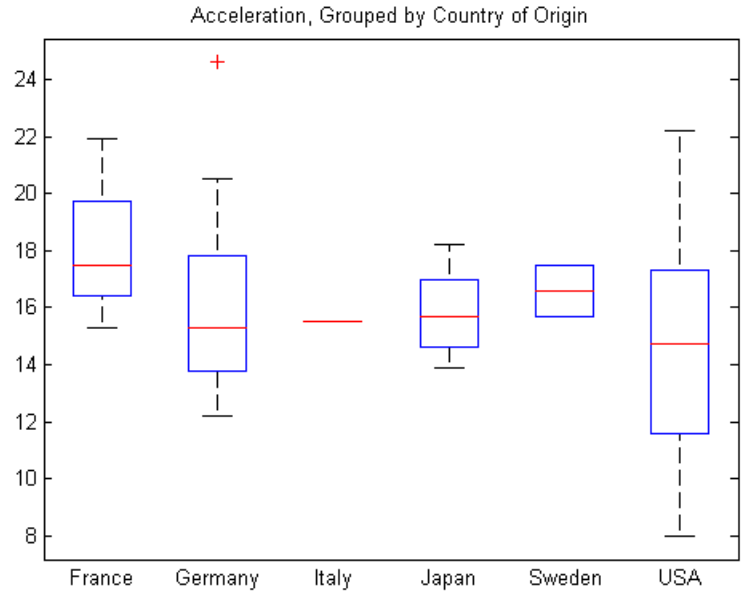
```
ans =

     France       Germany       Italy       Japan       Sweden       USA
```

There are six unique countries of origin in the sample. By default, `nominal` orders the countries in ascending alphabetical order.

Plot data grouped by category.

Draw box plots for `Acceleration`, grouped by `Origin`.

```
figure()
boxplot(Acceleration,Origin)
title('Acceleration, Grouped by Country of Origin')
```



The box plots appear in the same order as the categorical levels (use `reorderlevels` to change the order of the categories).

Few observations have Italy as the country of origin.

Tabulate category counts.

Tabulate the number of sample cars from each country.

```
tabulate(Origin)
```

```
    Value    Count   Percent
   France        4      4.00%
  Germany        9      9.00%
    Italy        1      1.00%
    Japan       15     15.00%
   Sweden        2      2.00%
      USA       69     69.00%
```

Only one car is made in Italy.

Drop a category.

Delete the Italian car from the sample.

```
Acceleration2 = Acceleration(Origin~='Italy');
Origin2 = Origin(Origin~='Italy');
getlevels(Origin2)

ans =

     France       Germany       Italy       Japan       Sweden       USA
```

Even though the car from Italy is no longer in the sample, the nominal variable, `Origin2`, still has the category `Italy`. Note that this is intentional—the levels of a categorical array do not necessarily coincide with the values.

Drop a category level.

Use `droplevels` to remove the `Italy` category.

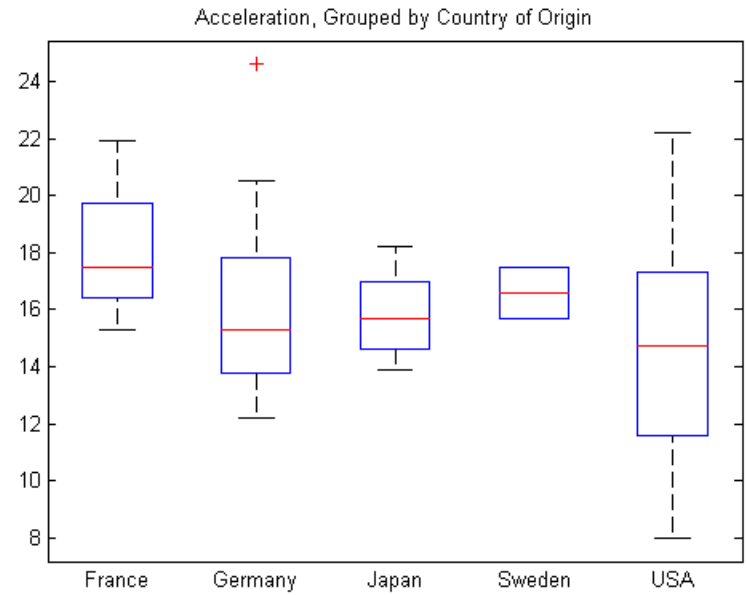
```
Origin2 = droplevels(Origin2,'Italy');
tabulate(Origin2)

tabulate(Origin2)
    Value    Count   Percent
   France        4      4.04%
  Germany        9      9.09%
    Japan       15     15.15%
   Sweden        2      2.02%
      USA       69     69.70%
```

The `Italy` category is no longer in the nominal array, `Origin2`.

Plot data grouped by category.

Draw box plots of `Acceleration2`, grouped by `Origin2`.

```
figure()
boxplot(Acceleration2,Origin2)
title('Acceleration, Grouped by Country of Origin')
```



The plot no longer includes the car from Italy.

See Also

`boxplot` | `droplevels` | `nominal` | `reorderlevels`

Related Examples

- “Test Differences Between Category Means” on page 2-29
- “Summary Statistics Grouped by Category” on page 2-38
- “Regression with Categorical Covariates” on page 2-58

More About

- “Categorical Arrays” on page 2-42
- “Advantages of Using Categorical Arrays” on page 2-44
- “Grouping Variables” on page 2-52

Test Differences Between Category Means

This example shows how to test for significant differences between category (group) means using a *t*-test, two-way ANOVA (analysis of variance), and ANOCOVA (analysis of covariance) analysis.

The goal is determining if the expected miles per gallon for a car depends on the decade in which it was manufactured, or the location where it was manufactured.

Load sample data.

```
load('carsmall')
unique(Model_Year)
```

```
ans =

    70
    76
    82
```

The variable `MPG` has miles per gallon measurements on a sample of 100 cars. The variables `Model_Year` and `Origin` contain the model year and country of origin for each car.

The first factor of interest is the decade of manufacture. There are three manufacturing years in the data.

Create a factor for the decade of manufacture.

Create an ordinal array named `Decade` by merging the observations from years `70` and `76` into a category labeled `1970s`, and putting the observations from `82` into a category labeled `1980s`.

```
Decade = ordinal(Model_Year,{'1970s','1980s'},[],[70 77 82]);
getlevels(Decade)
```

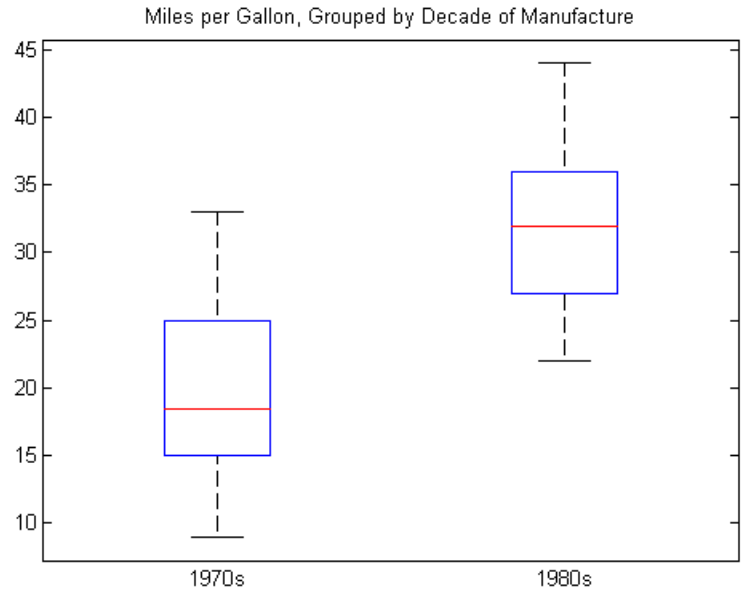
```
ans =

     1970s       1980s
```

Plot data grouped by category.

Draw a box plot of miles per gallon, grouped by the decade of manufacture.

```
figure()
```

```
boxplot(MPG,Decade)
title('Miles per Gallon, Grouped by Decade of Manufacture')
```



The box plot suggests that miles per gallon is higher in cars manufactured during the 1980s compared to the 1970s.

Compute summary statistics.

Compute the mean and variance of miles per gallon for each decade.

```
[xbar,s2,grp] = grpstats(MPG,Decade,{'mean','var','gname'})
```

```
xbar =

   19.7857
   31.7097


s2 =
```

```
   35.1429
   29.0796


grp =

    '1970s'
    '1980s'
```

This output shows that the mean miles per gallon in the 1980s was `31.71`, compared to `19.79` in the 1970s. The variances in the two groups are similar.

Conduct a two-sample t-test for equal group means.

Conduct a two-sample *t*-test, assuming equal variances, to test for a significant difference between the group means. The hypothesis is

$$H_0 : \mu_{70} = \mu_{80}$$
$$H_A : \mu_{70} \neq \mu_{80}.$$

```
MPG70 = MPG(Decade=='1970s');
MPG80 = MPG(Decade=='1980s');
[h,p] = ttest2(MPG70,MPG80)
```

```
h =

     1


p =

   3.4809e-15
```

The logical value `1` indicates the null hypothesis is rejected at the default 0.05 significance level. The p-value for the test is very small. There is sufficient evidence that the mean miles per gallon in the 1980s differs from the mean miles per gallon in the 1970s.

Create a factor for the location of manufacture.

The second factor of interest is the location of manufacture. First, convert `Origin` to a nominal array.

```
Location = nominal(Origin);
tabulate(Location)
```

```
tabulate(Location)
    Value    Count   Percent
   France        4      4.00%
  Germany        9      9.00%
    Italy        1      1.00%
    Japan       15     15.00%
   Sweden        2      2.00%
      USA       69     69.00%
```

There are six different countries of manufacture. The European countries have relatively few observations.

Merge categories.

Combine the categories `France`, `Germany`, `Italy`, and `Sweden` into a new category named `Europe`.

```
Location = mergelevels(Location,{'France','Germany','Italy','Sweden'},...
                       'Europe');
tabulate(Location)
```

```
   Value    Count   Percent
   Japan       15     15.00%
     USA       69     69.00%
  Europe       16     16.00%
```

Compute summary statistics.

Compute the mean miles per gallon, grouped by the location of manufacture.

```
[xbar,grp] = grpstats(MPG,Location,{'mean','gname'})
```

```
xbar =

   31.8000
   21.1328
   26.6667


grp =

    'Japan'
    'USA'
    'Europe'
```

This result shows that average miles per gallon is lowest for the sample of cars manufactured in the U.S.

Conduct two-way ANOVA.

Conduct a two-way ANOVA to test for differences in expected miles per gallon between factor levels for `Decade` and `Location`.

The statistical model is

$$MPG_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}, \quad i = 1,2; j = 1,2,3,$$

where MPG_{ij} is the response, miles per gallon, for cars made in decade i at location j. The treatment effects for the first factor, decade of manufacture, are the α_i terms (constrained to sum to zero). The treatment effects for the second factor, location of manufacture, are the β_j terms (constrained to sum to zero). The ε_{ij} are uncorrelated, normally distributed noise terms.

The hypotheses to test are equality of decade effects,

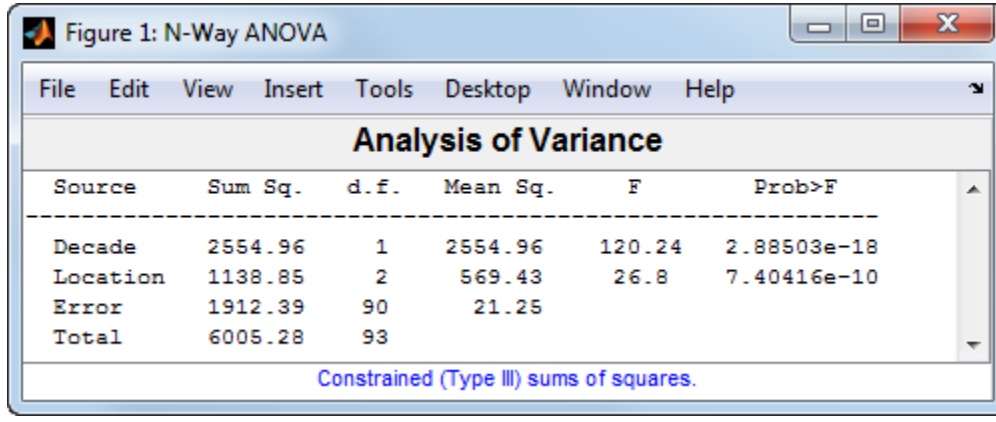
$$H_0 : \alpha_1 = \alpha_2 = 0$$
$$H_A : at\ least\ one\ \alpha_i \neq 0,$$

and equality of location effects,

$$H_0 : \beta_1 = \beta_2 = \beta_3 = 0$$
$$H_A : at\ least\ one\ \beta_j \neq 0.$$

You can conduct a multiple-factor ANOVA using `anovan`.

```
anovan(MPG,{Decade,Location},'varnames',{'Decade','Location'});
```



This output shows the results of the two-way ANOVA. The p-value for testing the equality of decade effects is `2.88503e-18`, so the null hypothesis is rejected at the 0.05 significance level. The p-value for testing the equality of location effects is `7.40416e-10`, so this null hypothesis is also rejected.

Conduct ANOCOVA analysis.

A potential confounder in this analysis is car weight. Cars with greater weight are expected to have lower gas mileage. Include the variable `Weight` as a continuous covariate in the ANOVA; that is, conduct an ANOCOVA analysis.

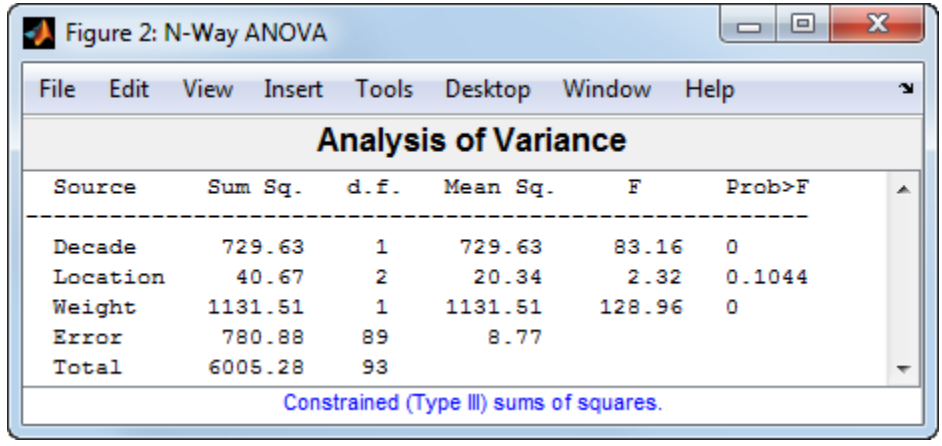
Assuming parallel lines, the statistical model is

$$MPG_{ijk} = \mu + \alpha_i + \beta_j + \gamma Weight_{ijk} + \varepsilon_{ijk},\ i = 1,2;\ j = 1,2,3;\ k = 1,\ldots,100.$$

The difference between this model and the two-way ANOVA model is the inclusion of the continuous predictor, $Weight_{ijk}$, the weight for the kth car, which was made in the ith decade and in the jth location. The slope parameter is γ.

Add the continuous covariate as a third group in the second `anovan` input argument. Use the name-value pair argument `Continuous` to specify that `Weight` (the third group) is continuous.

```
anovan(MPG,{Decade,Location,Weight},'Continuous',3,...
       'varnames',{'Decade','Location','Weight'});
```



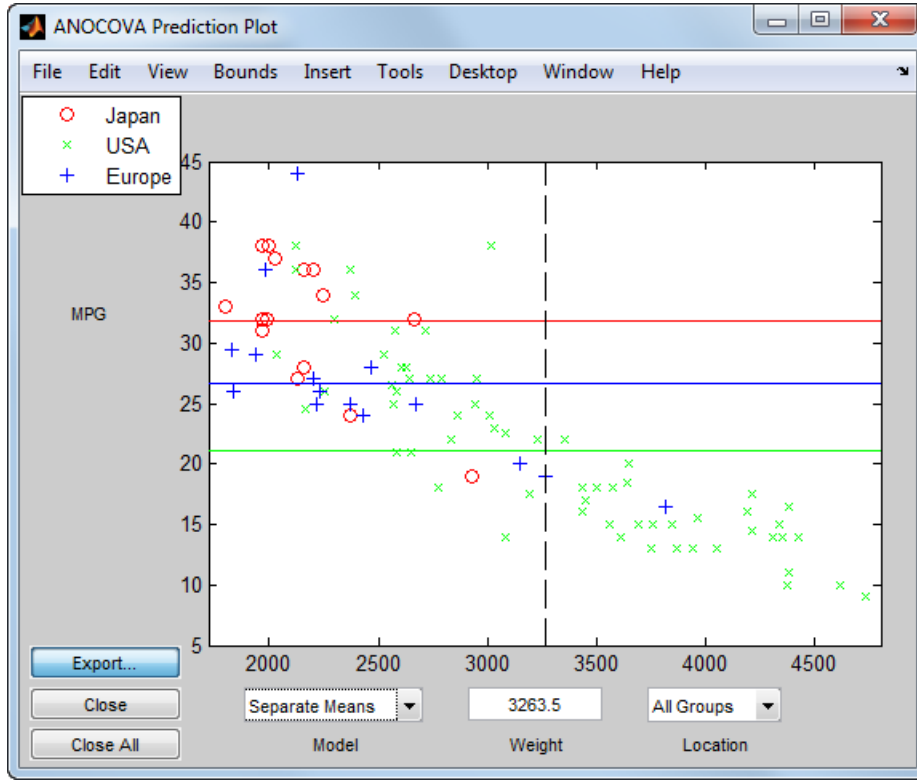
This output shows that when car weight is considered, there is insufficient evidence of a manufacturing location effect (p-value = `0.1044`).

Use interactive tool.

You can use the interactive `aoctool` to explore this result.

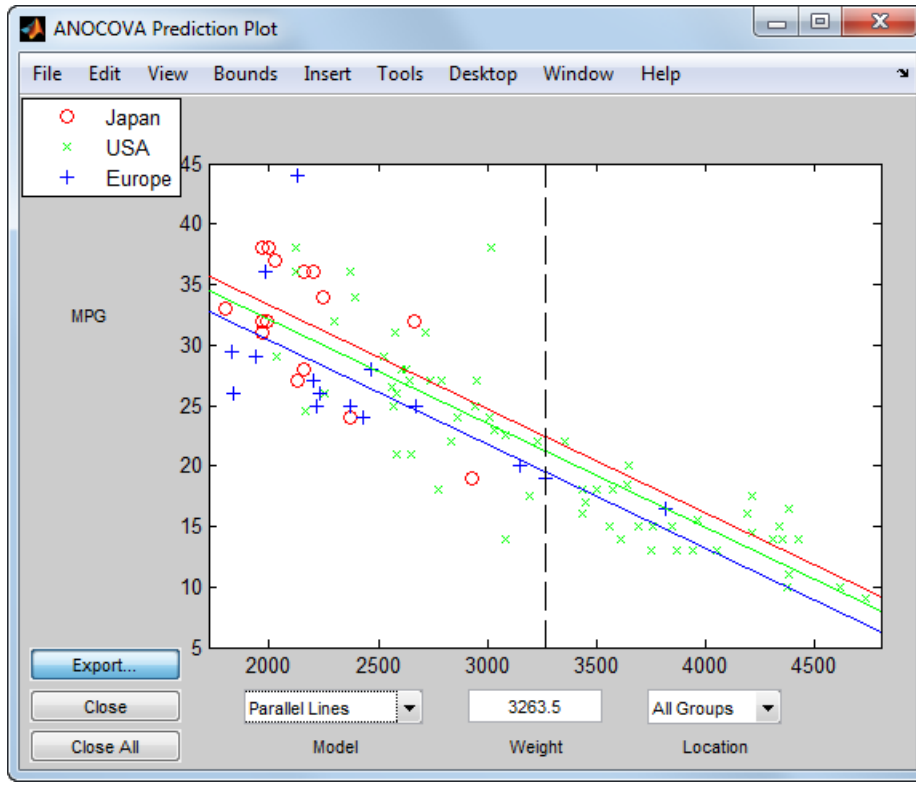
```
aoctool(Weight,MPG,Location);
```

This command opens three dialog boxes. In the ANOCOVA Prediction Plot dialog box, select the **Separate Means** model.



This output shows that when you do not include `Weight` in the model, there are fairly large differences in the expected miles per gallon among the three manufacturing locations. Note that here the model does not adjust for the decade of manufacturing.

Now, select the **Parallel Lines** model.



When you include `Weight` in the model, the difference in expected miles per gallon among the three manufacturing locations is much smaller.

See Also

`anovan` | `aoctool` | `boxplot` | `grpstats` | `nominal` | `ordinal` | `ttest2`

Related Examples

- “Plot Data Grouped by Category” on page 2-25
- “Summary Statistics Grouped by Category” on page 2-38
- “Regression with Categorical Covariates” on page 2-58

More About

- "Categorical Arrays" on page 2-42
- "Advantages of Using Categorical Arrays" on page 2-44
- "Grouping Variables" on page 2-52

Summary Statistics Grouped by Category

This example shows how to compute summary statistics grouped by levels of a categorical variable. You can compute group summary statistics for a numeric array or a dataset array using `grpstats`.

Load sample data.

```
load('hospital')
```

The dataset array, `hospital`, has 7 variables (columns) and 100 observations (rows).

Compute summary statistics by category.

The variable `Sex` is a nominal array with two levels, `Male` and `Female`. Compute the minimum and maximum weights for each gender.

```
stats = grpstats(hospital,'Sex',{'min','max'},'DataVars','Weight')
```

```
stats =

              Sex       GroupCount    min_Weight    max_Weight
    Female    Female    53            111           147
    Male      Male      47            158           202
```

The dataset array, `stats`, has observations corresponding to the levels of the variable `Sex`. The variable `min_Weight` contains the minimum weight for each group, and the variable `max_Weight` contains the maximum weight for each group.

Compute summary statistics by multiple categories.

The variable `Smoker` is a logical array with value `1` for smokers and value `0` for nonsmokers. Compute the minimum and maximum weights for each gender and smoking combination.

```
stats = grpstats(hospital,{'Sex','Smoker'},{'min','max'},...
                 'DataVars','Weight')
```

```
stats =

                Sex       Smoker    GroupCount    min_Weight    max_Weight
    Female_0    Female    false     40            111           147
    Female_1    Female    true      13            115           146
    Male_0      Male      false     26            158           194
    Male_1      Male      true      21            164           202
```

The dataset array, `stats`, has an observation row for each combination of levels of `Sex` and `Smoker` in the original data.

See Also

`dataset` | `grpstats` | `nominal`

Related Examples

- "Plot Data Grouped by Category" on page 2-25
- "Test Differences Between Category Means" on page 2-29
- "Calculations on Dataset Arrays" on page 2-108

More About

- "Grouping Variables" on page 2-52
- "Categorical Arrays" on page 2-42
- "Dataset Arrays" on page 2-132

Sort Ordinal Arrays

This example shows how to determine sorting order for ordinal arrays.

Load sample data.

```
AllSizes = {'medium','large','small','small','medium',...
            'large','medium','small'};
```

The created variable, `AllSizes`, is a cell array of strings containing size measurements on eight objects.

Create an ordinal array.

Convert `AllSizes` to an ordinal array with levels `small` < `medium` < `large`.

```
AllSizes = ordinal(AllSizes,{},{'small','medium','large'});
getlevels(AllSizes)
```

```
ans =

     small      medium      large
```

Sort the ordinal array.

When you sort ordinal arrays, the sorted observations are in the same order as the category levels.

```
sizeSort = sort(AllSizes);
sizeSort(:)
```

```
ans =

     small
     small
     small
     medium
     medium
     medium
     large
     large
```

The sorted ordinal array, `sizeSort`, contains the observations ordered from small to large.

See Also

`ordinal`

Related Examples

- "Reorder Category Levels" on page 2-11
- "Add and Drop Category Levels" on page 2-21

More About

- "Categorical Arrays" on page 2-42
- "Advantages of Using Categorical Arrays" on page 2-44

Categorical Arrays

Note: The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

In this section...

What Are Categorical Arrays?

Categorical arrays are Statistics and Machine Learning Toolbox data types for storing categorical values. Categorical arrays store data that have a finite set of discrete levels, which might or might not have a natural order. There are two types of categorical arrays:

- `ordinal` arrays store categorical values with ordered levels. For example, an ordinal variable might have levels {small, medium, large}.
- `nominal` arrays store categorical values with unordered levels. For example, a nominal variable might have levels {red, blue, green}.

In experimental design, these variables are often called *factors*, with ordered or unordered *factor levels*.

Categorical arrays are convenient and memory efficient containers for storing categorical variables. In addition to storing information about which category each observation belongs to, categorical arrays store descriptive metadata including category labels and order.

Categorical arrays have associated methods that streamline common tasks such as merging categories, adding or dropping levels, and changing level labels.

Categorical Array Conversion

You can easily convert to and from categorical arrays. To create a nominal or ordinal array, use `nominal` or `ordinal`, respectively. You can convert these data types to categorical arrays:

- Numeric array
- Logical array
- Character array
- Cell array of strings

See Also

`nominal` | `ordinal`

Related Examples

- “Create Nominal and Ordinal Arrays” on page 2-4
- “Summary Statistics Grouped by Category” on page 2-38
- “Plot Data Grouped by Category” on page 2-25
- “Index and Search Using Categorical Arrays” on page 2-47

More About

- “Advantages of Using Categorical Arrays” on page 2-44
- “Grouping Variables” on page 2-52

Advantages of Using Categorical Arrays

Note: The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

In this section...

Manipulate Category Levels

When working with categorical variables and their levels, you'll encounter some typical challenges. This table summarizes the functions you can use with categorical arrays to manipulate category levels. For additional functions, type `methods nominal` or `methods ordinal` at the command line, or see the `nominal` and `ordinal` reference pages.

Task	Function
Add new category levels	`addlevels`
Drop category levels	`droplevels`
Combine category levels	`mergelevels`
Reorder category levels	`reorderlevels`
Count the number of observations in each category	`levelcounts`
Change the label or name of category levels	`setlabels`
Create an interaction factor	`times`
Find observations that are not in a defined category	`isundefined`

Analysis Using Categorical Arrays

You can use categorical arrays in a variety of statistical analyses. For example, you might want to compute descriptive statistics for data grouped by the category levels,

conduct statistical tests on differences between category means, or perform regression analysis using categorical predictors.

Statistics and Machine Learning Toolbox functions that accept a grouping variable as an input argument accept categorical arrays. This includes descriptive functions such as:

- `grpstats`
- `gscatter`
- `boxplot`
- `gplotmatrix`

You can also use categorical arrays as input arguments to analysis functions and methods based on models, such as:

- `anovan`
- `fitlm`
- `fitglm`
- `fitnlm`

When you use a categorical array as a predictor in these functions, the fitting function automatically recognizes the categorical predictor, and constructs appropriate dummy indicator variables for analysis. Alternatively, you can construct your own dummy indicator variables using `dummyvar`.

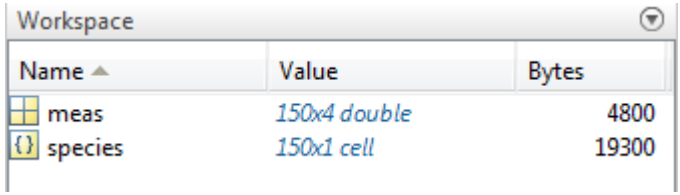
Reduce Memory Requirements

The levels of categorical variables are often defined as text strings, which can be costly to store and manipulate in a cell array of strings or `char` array. Categorical arrays separately store category membership and category labels, greatly reducing the amount of memory required to store the variable.

For example, load some sample data:

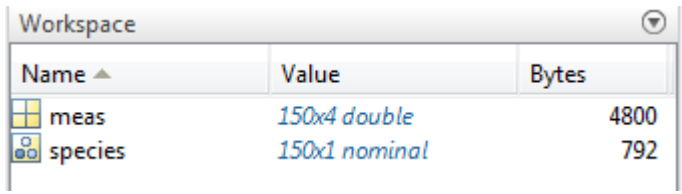
```
load('fisheriris')
```

The variable `species` is a cell array of strings requiring 19,300 bytes of memory.



Convert `species` to a nominal array:

```
species = nominal(species);
```



There is a 95% reduction in memory required to store the variable.

See Also

`nominal` | `ordinal`

Related Examples

- "Create Nominal and Ordinal Arrays" on page 2-4
- "Test Differences Between Category Means" on page 2-29
- "Regression with Categorical Covariates" on page 2-58
- "Index and Search Using Categorical Arrays" on page 2-47

More About

- "Categorical Arrays" on page 2-42
- "Grouping Variables" on page 2-52
- "Dummy Indicator Variables" on page 2-55

Index and Search Using Categorical Arrays

Note: The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Index By Category

It is often useful to index and search data by its category, or group. If you store categories as string labels inside a cell array of strings or `char` array, it can be difficult to index and search the categories. When using categorical arrays, you can easily:

- **Index elements from particular categories.** For both nominal and ordinal arrays, you can use the logical operators `==` and `~=` to index the observations that are in, or not in, a particular category. For ordinal arrays, which have an encoded order, you can also use inequalities, `>`, `>=`, `<`, and `<=`, to find observations in categories above or below a particular category.
- **Search for members of a category.** In addition to the logical operator `==`, you can use `ismember` to find observations in a particular group.
- **Find elements that are not in a defined category.** Categorical arrays indicate which elements do not belong to a defined category by `<undefined>`. You can use `isundefined` to find observations missing a category.
- **Delete observations that are in a particular category.** You can use logical operators to include or exclude observations from particular categories. Even if you remove all observations from a category, the category level remains defined unless you remove it using `droplevels`.

Common Indexing and Searching Methods

This example shows several common indexing and searching methods.

Load the sample data.

```
load carsmall;
```

Convert the `char` array, `Origin`, to a nominal array. This variable contains the country of origin, or manufacture, for each sample car.

```
Origin = nominal(Origin);
```

Search for observations in a category. Determine if there are any cars in the sample that were manufactured in Canada.

```
any(Origin=='Canada')
```

```
ans =

     0
```

There are no sample cars manufactured in Canada.

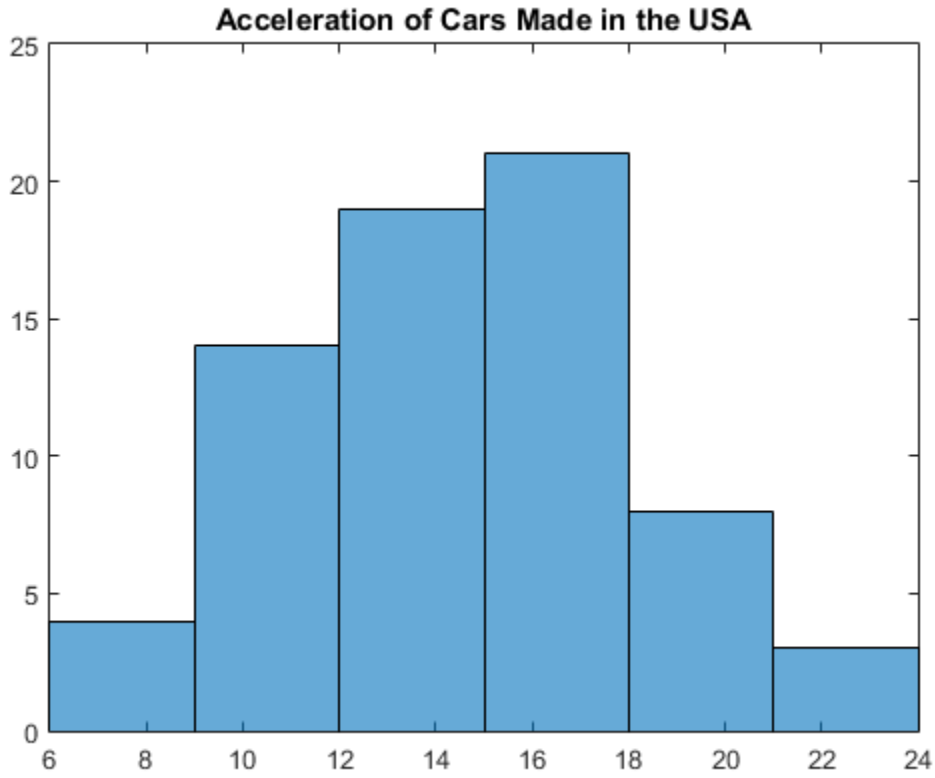
List the countries that are levels of `Origin`.

```
getlevels(Origin)
```

```
ans =

     France       Germany       Italy       Japan       Sweden       USA
```

Index elements that are in a particular category. Plot a histogram of the acceleration measurements for cars made in the U.S.

```
figure();
histogram(Acceleration(Origin=='USA'))
title('Acceleration of Cars Made in the USA')
```



Delete observations that are in a particular category. Delete all cars made in Sweden from `Origin`.

```
Origin = Origin(Origin~='Sweden');
any(ismember(Origin,'Sweden'))
```

```
ans =

     0
```

The cars made in Sweden are deleted from `Origin`, but `Sweden` is still a level of `Origin`.

```
getlevels(Origin)
```

```
ans =

     France       Germany       Italy       Japan       Sweden       USA
```

Remove `Sweden` from the levels of `Origin`.

```
Origin = droplevels(Origin,'Sweden');
getlevels(Origin)
```

```
ans =

     France       Germany       Italy       Japan       USA
```

Check for observations not in a defined category. Get the indices for the cars made in France.

```
ix = find(Origin=='France')
```

```
ix =

    11
    27
    39
    61
```

There are four cars from France. Remove `France` from the levels of `Origin`.

```
Origin = droplevels(Origin,'France');
```

This returns a warning indicating that you are dropping a category level that has elements in it. These observations are no longer in a defined category, indicated by `undefined`.

```
Origin(ix)
```

```
ans =

     <undefined>
```

```
     <undefined>
     <undefined>
     <undefined>
```

You can use `isundefined` to search for observations with an undefined category.

```
find(isundefined(Origin))
```

```
ans =

    11
    27
    39
    61
```

These indices correspond to the observations that were in category `France`, before that category was dropped from `Origin`.

See Also

`droplevels` | `nominal` | `ordinal`

Related Examples

- "Create Nominal and Ordinal Arrays" on page 2-4
- "Reorder Category Levels" on page 2-11
- "Merge Category Levels" on page 2-19
- "Add and Drop Category Levels" on page 2-21

More About

- "Categorical Arrays" on page 2-42
- "Advantages of Using Categorical Arrays" on page 2-44

Grouping Variables

In this section...

What Are Grouping Variables?

Grouping variables are utility variables used to group, or categorize, observations. Grouping variables are useful for summarizing or visualizing data by group. A grouping variable can be any of these data types:

- Numeric vector
- Logical vector
- String array (also called character arrays)
- Cell array of strings
- Categorical vector

A grouping variable must have the same number of observations (rows) as the table, dataset array, or numeric array you are grouping. Observations that have the same grouping variable value belong to the same group.

For example, the following variables comprise the same groups. Each grouping variable divides five observations into two groups. The first group contains the first and fourth observations. The other three observations are in the second group.

Data Type	Grouping Variable
Numeric vector	`[1 2 2 1 2]`
Logical vector	`[0 1 1 0 1]`
Cell array of strings	`{'Male','Female','Female','Male','Female'}`
Categorical vector	`Male Female Female Male Female`

Grouping variables with string labels give each group a meaningful name. A categorical array is an efficient and flexible choice of grouping variable.

Group Definition

Typically, there are as many groups as unique values in the grouping variable. However, categorical arrays can have levels that are not represented in the data. The groups and the order of the groups depend on the data type of the grouping variable. Suppose `G` is a grouping variable.

- If `G` is a numeric or logical vector, then the groups correspond to the distinct values in `G`, in the sorted order of the unique values.
- If `G` is a string array or cell array of strings, then the groups correspond to the distinct strings in `G`, in the order of their first appearance.
- If `G` is a categorical vector, then the groups correspond to the unique category levels in `G`, in the order returned by `getlevels`.

Some functions, such as `grpstats`, accept multiple grouping variables specified as a cell array of grouping variables, for example, `{G1,G2,G3}`. In this case, the groups are defined by the unique combinations of values in the grouping variables. The order is decided first by the order of the first grouping variable, then by the order of the second grouping variable, and so on.

Analysis Using Grouping Variables

This table lists common tasks you might want to perform using grouping variables.

Grouping Task	Function Accepting Grouping Variable
Draw side-by-side boxplots for data in different groups.	`boxplot`
Draw a scatter plot with markers colored by group.	`gscatter`
Draw a scatter plot matrix with markers colored by group.	`gplotmatrix`
Compute summary statistics by group.	`grpstats`
Test for differences between group means.	`anovan`

Grouping Task	Function Accepting Grouping Variable
Create an index vector from a grouping variable.	`grp2idx`

Missing Group Values

Grouping variables can have missing values provided you include a valid indicator.

Grouping Variable Data Type	Missing Value Indicator
Numeric vector	`NaN`
Logical vector	(Cannot be missing)
String array	Row of spaces
Cell array of strings	`''`
Categorical vector	`<undefined>`

See Also

`nominal` | `ordinal`

Related Examples

- “Plot Data Grouped by Category” on page 2-25
- “Summary Statistics Grouped by Category” on page 2-38

More About

- “Categorical Arrays” on page 2-42
- “Advantages of Using Categorical Arrays” on page 2-44
- Using nominal Objects
- Using ordinal Objects

Dummy Indicator Variables

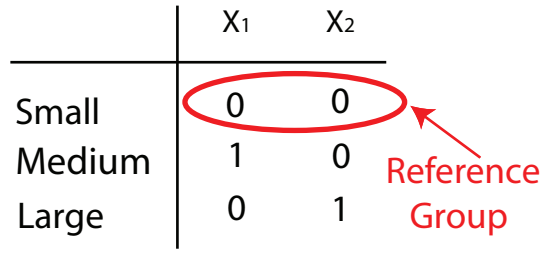
In this section...

What Are Dummy Variables?

When performing regression analysis, it is common to include both continuous and categorical (quantitative and qualitative) predictor variables. When including a categorical independent variable, it is important not to input the variable as a numeric array. Numeric arrays have both order and magnitude. A categorical variable might have order (for example, an ordinal variable), but it does not have magnitude. Using a numeric array implies a known "distance" between the categories.

The appropriate way to include categorical predictors is as dummy indicator variables. An indicator variable has values 0 and 1. A categorical variable with c categories can be represented by $c - 1$ indicator variables.

For example, suppose you have a categorical variable with levels `{Small,Medium,Large}`. You can represent this variable using two dummy variables, as shown in this figure.



In this example, X_1 is a dummy variable that has value 1 for the `Medium` group, and 0 otherwise. X_2 is a dummy variable that has value 1 for the `Large` group, and 0 otherwise. Together, these two variables represent the three categories. Observations in the `Small` group have 0s for both dummy variables.

The category represented by all 0s is the *reference group*. When you include the dummy variables in a regression model, the coefficients of the dummy variables are interpreted with respect to the reference group.

Creating Dummy Variables

Automatic Creation of Dummy Variables

The regression fitting functions, `fitlm`, `fitglm`, and `fitnlm`, recognize categorical array inputs as categorical predictors. That is, if you input your categorical predictor as a `nominal` or `ordinal` array, the fitting function automatically creates the required dummy variables. The first level returned by `getlevels` is the reference group. To use a different reference group, use `reorderlevels` to change the level order.

If there are c unique levels in the categorical array, then the fitting function estimates $c - 1$ regression coefficients for the categorical predictor.

Note: The fitting functions use every level of the categorical array returned by `getlevels`, even if there are levels with no observations. To remove levels from the categorical array, use `droplevels`.

Manual Creation of Dummy Variables

If you prefer to create your own dummy variable design matrix, use `dummyvar`. This function accepts a numeric or categorical column vector, and returns a matrix of indicator variables. The dummy variable design matrix has a column for every group, and a row for every observation.

For example,

```
gender = nominal({'Male';'Female';'Female';'Male';'Female'});
dv = dummyvar(gender)
```

```
dv =
```

```
     0     1
     1     0
     1     0
     0     1
     1     0
```

There are five rows corresponding to the number of rows in `gender`, and two columns for the unique groups, `Female` and `Male`. Column order corresponds to the order of the levels in `gender`. For nominal arrays, the default order is ascending alphabetical.

To use these dummy variables in a regression model, you must either delete a column (to create a reference group), or fit a regression model with no intercept term. For the gender example, only one dummy variable is needed to represent two genders. Notice what happens if you add an intercept term to the complete design matrix, `dv`.

```
X = [ones(5,1) dv]

X =

     1     0     1
     1     1     0
     1     1     0
     1     0     1
     1     1     0

rank(X)

ans =

     2
```

The design matrix with an intercept term is not of full rank, and is not invertible. Because of this linear dependence, use only $c - 1$ indicator variables to represent a categorical variable with c categories in a regression model with an intercept term.

See Also

`dummyvar` | `fitglm` | `fitlm` | `fitnlm` | `nominal` | `ordinal`

Related Examples

- “Regression with Categorical Covariates” on page 2-58
- “Test Differences Between Category Means” on page 2-29

Regression with Categorical Covariates

This example shows how to perform a regression with categorical covariates using categorical arrays and `fitlm`.

Load sample data.

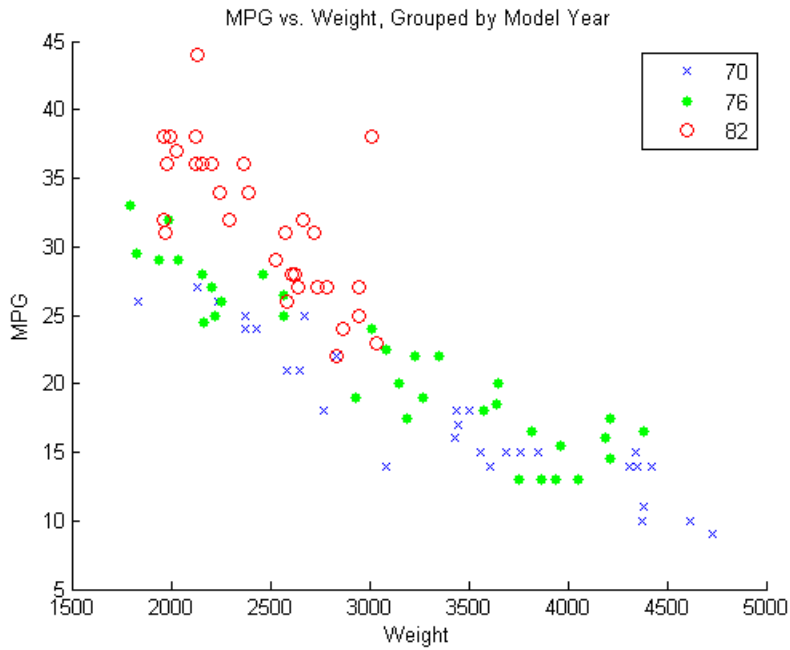
```
load('carsmall')
```

The variable `MPG` contains measurements on the miles per gallon of 100 sample cars. The model year of each car is in the variable `Model_Year`, and `Weight` contains the weight of each car.

Plot grouped data.

Draw a scatter plot of `MPG` against `Weight`, grouped by model year.

```
figure()
gscatter(Weight,MPG,Model_Year,'bgr','x.o')
title('MPG vs. Weight, Grouped by Model Year')
```



The grouping variable, `Model_Year`, has three unique values, `70`, `76`, and `82`, corresponding to model years 1970, 1976, and 1982.

Create table and nominal arrays.

Create a table that contains the variables `MPG`, `Weight`, and `Model_Year`. Convert the variable `Model_Year` to a nominal array.

```
cars = table(MPG,Weight,Model_Year);
cars.Model_Year = nominal(cars.Model_Year);
```

Fit a regression model.

Fit a regression model using `fitlm` with `MPG` as the dependent variable, and `Weight` and `Model_Year` as the independent variables. Because `Model_Year` is a categorical covariate with three levels, it should enter the model as two indicator variables.

The scatter plot suggests that the slope of `MPG` against `Weight` might differ for each model year. To assess this, include weight-year interaction terms.

The proposed model is

$$E(MPG) = \beta_0 + \beta_1 Weight + \beta_2 I[1976] + \beta_3 I[1982] + \beta_4 Weight \times I[1976] + \beta_5 Weight \times I[1982],$$

where $I[1976]$ and $I[1982]$ are dummy variables indicating the model years 1976 and 1982, respectively. $I[1976]$ takes the value 1 if model year is 1976 and takes the value 0 if it is not. $I[1982]$ takes the value 1 if model year is 1982 and takes the value 0 if it is not. In this model, 1970 is the reference year.

```
fit = fitlm(cars,'MPG~Weight*Model_Year')
```

```
fit =


Linear regression model:
    MPG ~ 1 + Weight*Model_Year

Estimated Coefficients:
                            Estimate          SE
                           __________    __________

    (Intercept)                37.399        2.1466
    Weight                -0.0058437    0.00061765
    Model_Year_76              4.6903        2.8538
    Model_Year_82              21.051         4.157
```

```
    Weight:Model_Year_76    -0.00082009    0.00085468
    Weight:Model_Year_82     -0.0050551     0.0015636


                             tStat        pValue
                            ________    __________

    (Intercept)               17.423    2.8607e-30
    Weight                   -9.4612    4.6077e-15
    Model_Year_76             1.6435       0.10384
    Model_Year_82             5.0641    2.2364e-06
    Weight:Model_Year_76    -0.95953       0.33992
    Weight:Model_Year_82     -3.2329     0.0017256


Number of observations: 94, Error degrees of freedom: 88
Root Mean Squared Error: 2.79
R-squared: 0.886,  Adjusted R-Squared 0.88
F-statistic vs. constant model: 137, p-value = 5.79e-40
```

The regression output shows:

- `fitlm`recognizes `Model_Year` as a nominal variable, and constructs the required indicator (dummy) variables. By default, the first level, `70`, is the reference group (use `reorderlevels` to change the reference group).
- The model specification, `MPG~Weight*Model_Year`, specifies the first-order terms for `Weight` and `Model_Year`, and all interactions.
- The model $R^2 = 0.886$, meaning the variation in miles per gallon is reduced by 88.6% when you consider weight, model year, and their interactions.
- The fitted model is

$$\hat{MPG} = 37.4 - 0.006Weight + 4.7I[1976] + 21.1I[1982] - 0.0008Weight \times I[1976] - 0.005Weight \times I[19$$

Thus, the estimated regression equations for the model years are as follows.

Model Year	Predicted MPG Against Weight
1970	$\hat{MPG} = 37.4 - 0.006Weight$
1976	$\hat{MPG} = (37.4 + 4.7) - (0.006 + 0.0008)Weight$

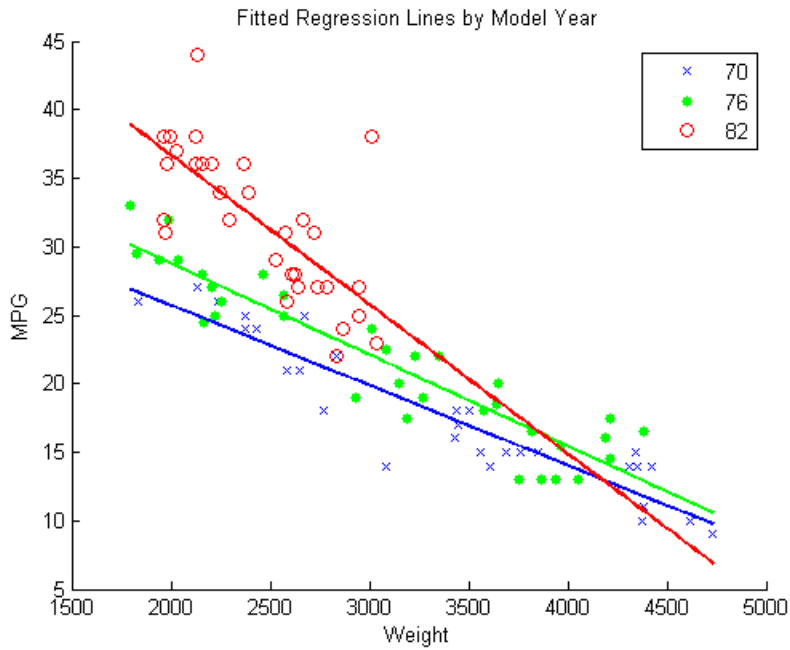
Model Year	Predicted MPG Against Weight
1982	$\hat{MPG} = (37.4 + 21.1) - (0.006 + 0.005)Weight$

The relationship between `MPG` and `Weight` has an increasingly negative slope as the model year increases.

Plot fitted regression lines.

Plot the data and fitted regression lines.

```
w = linspace(min(Weight),max(Weight));

figure()
gscatter(Weight,MPG,Model_Year,'bgr','x.o')
line(w,feval(fit,w,'70'),'Color','b','LineWidth',2)
line(w,feval(fit,w,'76'),'Color','g','LineWidth',2)
line(w,feval(fit,w,'82'),'Color','r','LineWidth',2)
title('Fitted Regression Lines by Model Year')
```



Test for different slopes.

Test for significant differences between the slopes. This is equivalent to testing the hypothesis

$$H_0 : \beta_4 = \beta_5 = 0$$
$$H_A : \beta_i \neq 0 \text{ for at least one } i.$$

```
anova(fit)
```

```
ans =

                       SumSq     DF    MeanSq    F         pValue
    Weight             2050.2     1    2050.2    263.87    3.2055e-28
    Model_Year         807.69     2    403.84    51.976    1.2494e-15
    Weight:Model_Year  81.219     2    40.609    5.2266     0.0071637
    Error              683.74    88    7.7698
```

This output shows that the p-value for the test is `0.0072` (from the interaction row, `Weight:Model_Year`), so the null hypothesis is rejected at the 0.05 significance level. The value of the test statistic is `5.2266`. The numerator degrees of freedom for the test is `2`, which is the number of coefficients in the null hypothesis.

There is sufficient evidence that the slopes are not equal for all three model years.

See Also

`dataset` | `fitlm` | `nominal` | `reorderlevels`

Related Examples

- “Plot Data Grouped by Category” on page 2-25
- “Test Differences Between Category Means” on page 2-29
- “Summary Statistics Grouped by Category” on page 2-38

More About

- “Advantages of Using Categorical Arrays” on page 2-44
- “Grouping Variables” on page 2-52
- “Dummy Indicator Variables” on page 2-55

Create a Dataset Array from Workspace Variables

Note: The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

In this section...

Create a Dataset Array from a Numeric Array

This example shows how to create a dataset array from a numeric array existing in the MATLAB workspace.

Load sample data.

```
load('fisheriris')
```

Two variables load into the workspace: `meas`, a 150-by-4 numeric array, and `species`, a 150-by-1 cell array of strings containing species labels.

Create a dataset array.

Use `mat2dataset` to convert the numeric array, `meas`, into a dataset array.

```
ds = mat2dataset(meas);
ds(1:10,:)
```

```
ans =

    meas1    meas2    meas3    meas4
    5.1      3.5      1.4      0.2
    4.9        3      1.4      0.2
    4.7      3.2      1.3      0.2
    4.6      3.1      1.5      0.2
      5      3.6      1.4      0.2
    5.4      3.9      1.7      0.4
    4.6      3.4      1.4      0.3
```

```
    5      3.4      1.5      0.2
  4.4      2.9      1.4      0.2
  4.9      3.1      1.5      0.1
```

The array, `meas`, has four columns, so the dataset array, `ds`, has four variables. The default variable names are the array name, `meas`, with column numbers appended.

You can specify your own variable or observation names using the name-value pair arguments `VarNames` and `ObsNames`, respectively.

If you use `dataset` to convert a numeric array to a dataset array, by default, the resulting dataset array has one variable that is an array instead of separate variables for each column.

Examine the dataset array.

Return the size of the dataset array, `ds`.

```
size(ds)
```

```
ans =

   150     4
```

The dataset array, `ds`, is the same size as the numeric array, `meas`. Variable names and observation names do not factor into the size of a dataset array.

Explore dataset array metadata.

Return the metadata properties of the dataset array, `ds`.

```
ds.Properties
```

```
ans =

       Description: ''
    VarDescription: {}
             Units: {}
        DimNames: {'Observations'  'Variables'}
        UserData: []
        ObsNames: {}
        VarNames: {'meas1'  'meas2'  'meas3'  'meas4'}
```

You can also access the properties individually. For example, you can retrieve the variable names using `ds.Properties.VarNames`.

Access data in a dataset array variable.

You can use variable names with dot indexing to access the data in a dataset array. For example, find the minimum value in the first variable, `meas1`.

```
min(ds.meas1)
```

```
ans =

    4.3000
```

Change variable names.

The four variables in `ds` are actually measurements of sepal length, sepal width, petal length, and petal width. Modify the variable names to be more descriptive.

```
ds.Properties.VarNames = {'SLength','SWidth','PLength','PWidth'};
```

Add description.

you can add a description for the dataset array.

```
ds.Properties.Description = 'Fisher iris data';
ds.Properties
```

```
ans =

       Description: 'Fisher iris data'
    VarDescription: {}
             Units: {}
          DimNames: {'Observations'  'Variables'}
          UserData: []
          ObsNames: {}
          VarNames: {'SLength'  'SWidth'  'PLength'  'PWidth'}
```

The dataset array properties are updated with the new variable names and description.

Add a variable to the dataset array.

The variable `species` is a cell array of strings containing species labels. Add `species` to the dataset array, `ds`, as a nominal array named `Species`. Display the first five observations in the dataset array.

```
ds.Species = nominal(species);
ds(1:5,:)
```

```
ans =

    SLength    SWidth    PLength    PWidth    Species
    5.1        3.5       1.4        0.2       setosa
    4.9          3       1.4        0.2       setosa
    4.7        3.2       1.3        0.2       setosa
    4.6        3.1       1.5        0.2       setosa
      5        3.6       1.4        0.2       setosa
```

The dataset array, `ds`, now has the fifth variable, `Species`.

Create Dataset Array from Heterogeneous Workspace Variables

This example shows how to create a dataset array from heterogeneous variables existing in the MATLAB workspace.

Load sample data.

```
load('carsmall')
```

Create a dataset array.

Create a dataset array from a subset of the workspace variables.

```
ds = dataset(Origin,Acceleration,Cylinders,MPG);
ds.Properties.VarNames(:)
```

```
ans =

    'Origin'
    'Acceleration'
    'Cylinders'
    'MPG'
```

When creating the dataset array, you do not need to enter variable names. `dataset` automatically uses the name of each workspace variable.

Notice that the dataset array, `ds`, contains a collection of variables with heterogeneous data types. `Origin` is a character array, and the other variables are numeric.

Examine a dataset array.

Display the first five observations in the dataset array.

```
ds(1:5,:)

ans =

    Origin     Acceleration    Cylinders    MPG
    USA          12            8            18
    USA        11.5            8            15
    USA          11            8            18
    USA          12            8            16
    USA        10.5            8            17
```

Apply a function to a dataset array.

Use `datasetfun` to return the data type of each variable in `ds`.

```
varclass = datasetfun(@class,ds,'UniformOutput',false);
varclass(:)

ans =

    'char'
    'double'
    'double'
    'double'
```

You can get additional information about the variables using `summary(ds)`.

Modify a dataset array.

`Cylinders` is a numeric variable that has values `4`, `6`, and `8` for the number of cylinders. Convert `Cylinders` to a nominal array with levels `four`, `six`, and `eight`.

Display the country of origin and number of cylinders for the first 15 cars.

```
ds.Cylinders = nominal(ds.Cylinders,{'four','six','eight'});
ds(1:15,{'Origin','Cylinders'})

ans =

    Origin     Cylinders
    USA        eight
    USA        eight
    USA        eight
    USA        eight
    USA        eight
```

```
USA         eight
USA         eight
USA         eight
USA         eight
USA         eight
France      four
USA         eight
USA         eight
USA         eight
USA         eight
```

The variable `Cylinders` has a new data type.

See Also

`dataset` | `datasetfun` | `mat2dataset` | `nominal`

Related Examples

- “Create a Dataset Array from a File” on page 2-69
- “Export Dataset Arrays” on page 2-111
- “Dataset Arrays in the Variables Editor” on page 2-118
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132

Create a Dataset Array from a File

Note: The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

In this section...

Create a Dataset Array from a Tab-Delimited Text File

This example shows how to create a dataset array from the contents of a tab-delimited text file.

Create a dataset array using default settings.

Navigate to the folder containing sample data. Import the text file `hospitalSmall.txt` as a dataset array using the default settings.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
ds = dataset('File','hospitalSmall.txt')
```

```
ds =

    name              sex        age    wgt    smoke
    'SMITH'           'm'        38     176    1
    'JOHNSON'         'm'        43     163    0
    'WILLIAMS'        'f'        38     131    0
    'JONES'           'f'        40     133    0
    'BROWN'           'f'        49     119    0
    'DAVIS'           'f'        46     142    0
    'MILLER'          'f'        33     142    1
    'WILSON'          'm'        40     180    0
    'MOORE'           'm'        28     183    0
    'TAYLOR'          'f'        31     132    0
```

```
    'ANDERSON'        'f'        45     128    0
    'THOMAS'          'f'        42     137    0
    'JACKSON'         'm'        25     174    0
    'WHITE'           'm'        39     202    1
```

By default, `dataset` uses the first row of the text file for variable names. If the first row does not contain variable names, you can specify the optional name-value pair argument `'ReadVarNames',false` to change the default behavior.

The dataset array contains heterogeneous variables. The variables `id`, `name`, and `sex` are cell arrays of strings, and the other variables are numeric.

Summarize the dataset array.

You can see the data type and other descriptive statistics for each variable by using `summary` to summarize the dataset array.

```
summary(ds)
```

```
name: [14x1 cell string]

sex: [14x1 cell string]

age: [14x1 double]

    min    1st quartile    median    3rd quartile    max
    25     33              39.5      43              49

wgt: [14x1 double]

    min    1st quartile    median    3rd quartile    max
    119    132             142       176             202

smoke: [14x1 double]

    min    1st quartile    median    3rd quartile    max
    0      0               0         0               1
```

Import observation names.

Import the text file again, this time specifying that the first column contains observation names.

```
ds = dataset('File','hospitalSmall.txt','ReadObsNames',true)
```

```
ds =

               sex        age    wgt    smoke
    SMITH      'm'        38     176    1
    JOHNSON    'm'        43     163    0
    WILLIAMS   'f'        38     131    0
    JONES      'f'        40     133    0
    BROWN      'f'        49     119    0
    DAVIS      'f'        46     142    0
    MILLER     'f'        33     142    1
    WILSON     'm'        40     180    0
    MOORE      'm'        28     183    0
    TAYLOR     'f'        31     132    0
    ANDERSON   'f'        45     128    0
    THOMAS     'f'        42     137    0
    JACKSON    'm'        25     174    0
    WHITE      'm'        39     202    1
```

The elements of the first column in the text file, last names, are now observation names. Observation names and row names are dataset array properties. You can always add or change the observation names of an existing dataset array by modifying the property `ObsNames`.

Change dataset array properties.

By default, the `DimNames` property of the dataset array has `name` as the descriptor of the observation (row) dimension. `dataset` got this name from the first row of the first column in the text file.

Change the first element of `DimNames` to `LastName`.

```
ds.Properties.DimNames{1} = 'LastName';
ds.Properties
```

```
ans =

       Description: ''
    VarDescription: {}
             Units: {}
          DimNames: {'LastName'  'Variables'}
          UserData: []
          ObsNames: {14x1 cell}
          VarNames: {'sex'  'age'  'wgt'  'smoke'}
```

Index into dataset array.

You can use observation names to index into a dataset array. For example, return the data for the patient with last name BROWN.

```
ds('BROWN',:)
```

```
ans =

            sex         age     wgt     smoke
    BROWN   'f'         49      119     0
```

Note that observation names must be unique.

Create a Dataset Array from a Comma-Separated Text File

This example shows how to create a dataset array from the contents of a comma-separated text file.

Create a dataset array.

Navigate to the folder containing sample data. Import the file `hospitalSmall.csv` as a dataset array, specifying the comma-delimited format.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
ds = dataset('File','hospitalSmall.csv','Delimiter',',')
```

```
ds =

    id              name              sex         age     wgt     smoke
    'YPL-320'       'SMITH'           'm'         38      176     1
    'GLI-532'       'JOHNSON'         'm'         43      163     0
    'PNI-258'       'WILLIAMS'        'f'         38      131     0
    'MIJ-579'       'JONES'           'f'         40      133     0
    'XLK-030'       'BROWN'           'f'         49      119     0
    'TFP-518'       'DAVIS'           'f'         46      142     0
    'LPD-746'       'MILLER'          'f'         33      142     1
    'ATA-945'       'WILSON'          'm'         40      180     0
    'VNL-702'       'MOORE'           'm'         28      183     0
    'LQW-768'       'TAYLOR'          'f'         31      132     0
    'QFY-472'       'ANDERSON'        'f'         45      128     0
    'UJG-627'       'THOMAS'          'f'         42      137     0
    'XUE-826'       'JACKSON'         'm'         25      174     0
```

```
    'TRW-072'        'WHITE'           'm'        39     202    1
```

By default, `dataset` uses the first row in the text file as variable names.

Add observation names.

Use the unique identifiers in the variable `id` as observation names. Then, delete the variable `id` from the dataset array.

```
ds.Properties.ObsNames = ds.id;
ds.id = []
```

```
ds =

              name              sex        age    wgt    smoke
    YPL-320   'SMITH'           'm'        38     176    1
    GLI-532   'JOHNSON'         'm'        43     163    0
    PNI-258   'WILLIAMS'        'f'        38     131    0
    MIJ-579   'JONES'           'f'        40     133    0
    XLK-030   'BROWN'           'f'        49     119    0
    TFP-518   'DAVIS'           'f'        46     142    0
    LPD-746   'MILLER'          'f'        33     142    1
    ATA-945   'WILSON'          'm'        40     180    0
    VNL-702   'MOORE'           'm'        28     183    0
    LQW-768   'TAYLOR'          'f'        31     132    0
    QFY-472   'ANDERSON'        'f'        45     128    0
    UJG-627   'THOMAS'          'f'        42     137    0
    XUE-826   'JACKSON'         'm'        25     174    0
    TRW-072   'WHITE'           'm'        39     202    1
```

Delete observations.

Delete any patients with the last name `BROWN`. You can use `strcmp` to match the string `'BROWN'` with the elements of the variable containing last names, `name`.

```
toDelete = strcmp(ds.name,'BROWN');
ds(toDelete,:) = []
```

```
ds =

              name              sex        age    wgt    smoke
    YPL-320   'SMITH'           'm'        38     176    1
    GLI-532   'JOHNSON'         'm'        43     163    0
    PNI-258   'WILLIAMS'        'f'        38     131    0
    MIJ-579   'JONES'           'f'        40     133    0
```

```
    TFP-518    'DAVIS'           'f'        46     142    0
    LPD-746    'MILLER'          'f'        33     142    1
    ATA-945    'WILSON'          'm'        40     180    0
    VNL-702    'MOORE'           'm'        28     183    0
    LQW-768    'TAYLOR'          'f'        31     132    0
    QFY-472    'ANDERSON'        'f'        45     128    0
    UJG-627    'THOMAS'          'f'        42     137    0
    XUE-826    'JACKSON'         'm'        25     174    0
    TRW-072    'WHITE'           'm'        39     202    1
```

One patient having last name `BROWN` is deleted from the dataset array.

Return size of dataset array.

The array now has 13 observations.

```
size(ds)
```

```
ans =

    13     5
```

Note that the row and column corresponding to variable and observation names, respectively, are not included in the size of a `dataset` array.

Create a Dataset Array from an Excel File

This example shows how to create a dataset array from the contents of an Excel® spreadsheet file.

Create a dataset array.

Navigate to the folder containing sample data. Import the data from the first worksheet in the file `hospitalSmall.xlsx`, specifying that the data file is an Excel spreadsheet.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
ds = dataset('XLSFile','hospitalSmall.xlsx')
```

```
ds =

    id              name              sex        age    wgt    smoke
    'YPL-320'       'SMITH'           'm'        38     176    1
    'GLI-532'       'JOHNSON'         'm'        43     163    0
```

```
    'PNI-258'        'WILLIAMS'        'f'        38     131    0
    'MIJ-579'        'JONES'           'f'        40     133    0
    'XLK-030'        'BROWN'           'f'        49     119    0
    'TFP-518'        'DAVIS'           'f'        46     142    0
    'LPD-746'        'MILLER'          'f'        33     142    1
    'ATA-945'        'WILSON'          'm'        40     180    0
    'VNL-702'        'MOORE'           'm'        28     183    0
    'LQW-768'        'TAYLOR'          'f'        31     132    0
    'QFY-472'        'ANDERSON'        'f'        45     128    0
    'UJG-627'        'THOMAS'          'f'        42     137    0
    'XUE-826'        'JACKSON'         'm'        25     174    0
    'TRW-072'        'WHITE'           'm'        39     202    1
```

By default, `dataset` creates variable names using the contents of the first row in the spreadsheet.

Specify which worksheet to import.

Import the data from the second worksheet into a new dataset array.

```
ds2 = dataset('XLSFile','hospitalSmall.xlsx','Sheet',2)
```

```
ds2 =

    id               name              sex        age    wgt    smoke
    'TRW-072'        'WHITE'           'm'        39     202    1
    'ELG-976'        'HARRIS'          'f'        36     129    0
    'KOQ-996'        'MARTIN'          'm'        48     181    1
    'YUZ-646'        'THOMPSON'        'm'        32     191    1
    'XBR-291'        'GARCIA'          'f'        27     131    1
    'KPW-846'        'MARTINEZ'        'm'        37     179    0
    'XBA-581'        'ROBINSON'        'm'        50     172    0
    'BKD-785'        'CLARK'           'f'        48     133    0
```

See Also

`dataset` | `summary`

Related Examples

- “Create a Dataset Array from Workspace Variables” on page 2-63
- “Clean Messy and Missing Data” on page 2-113
- “Export Dataset Arrays” on page 2-111

- "Dataset Arrays in the Variables Editor" on page 2-118
- "Index and Search Dataset Arrays" on page 2-135

More About

- "Dataset Arrays" on page 2-132

Add and Delete Observations

This example shows how to add and delete observations in a dataset array. You can also edit dataset arrays using the Variables editor.

Load sample data.

Navigate to the folder containing sample data. Import the data from the first worksheet in `hospitalSmall.xlsx` into a dataset array.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
ds = dataset('XLSFile','hospitalSmall.xlsx');
size(ds)
```

```
ans =

    14     6
```

The dataset array, `ds`, has 14 observations (rows) and 6 variables (columns).

Add observations by concatenation.

The second worksheet in `hospitalSmall.xlsx` has additional patient data. Append the observations in this spreadsheet to the end of `ds`.

```
ds2 = dataset('XLSFile','hospitalSmall.xlsx','Sheet',2);
dsNew = [ds;ds2];
size(dsNew)
```

```
ans =

    22     6
```

The dataset array `dsNew` has 22 observations. In order to vertically concatenate two dataset arrays, both arrays must have the same number of variables, with the same variable names.

Add observations from a cell array.

If you want to append new observations stored in a cell array, first convert the cell array to a dataset array, and then concatenate the dataset arrays.

```
cellObs = {'id','name','sex','age','wgt','smoke';
```

```
                'YQR-965','BAKER','M',36,160,0;
                'LFG-497','WALL' ,'F',28,125,1;
                'KSD-003','REED' ,'M',32,187,0};
dsNew = [dsNew;cell2dataset(cellObs)];
size(dsNew)

ans =

    25     6
```

Add observations from a structure.

You can also append new observations stored in a structure. Convert the structure to a dataset array, and then concatenate the dataset arrays.

```
structObs(1,1).id = 'GHK-842';
structObs(1,1).name = 'GEORGE';
structObs(1,1).sex = 'M';
structObs(1,1).age = 45;
structObs(1,1).wgt = 182;
structObs(1,1).smoke = 1;

structObs(2,1).id = 'QRH-308';
structObs(2,1).name = 'BAILEY';
structObs(2,1).sex = 'F';
structObs(2,1).age = 29;
structObs(2,1).wgt = 120;
structObs(2,1).smoke = 0;

dsNew = [dsNew;struct2dataset(structObs)];
size(dsNew)

ans =

    27     6
```

Delete duplicate observations.

Use `unique` to delete any observations in a dataset array that are duplicated.

```
dsNew = unique(dsNew);
size(dsNew)

ans =
```

```
    21     6
```

One duplicated observation is deleted.

Delete observations by observation number.

Delete observations 18, 20, and 21 from the dataset array.

```
dsNew([18,20,21],:) = [];
size(dsNew)
```

```
ans =

    18     6
```

The dataset array has only 18 observations now.

Delete observations by observation name.

First, specify the variable of identifiers, `id`, as observation names. Then, delete the variable `id` from `dsNew`. You can use the observation name to index observations.

```
dsNew.Properties.ObsNames = dsNew.id;
dsNew.id = [];
dsNew('KOQ-996',:) = [];
size(dsNew)
```

```
ans =

    17     5
```

The dataset array now has one less observation and one less variable.

Search for observations to delete.

You can also search for observations in the dataset array. For example, delete observations for any patients with the last name `WILLIAMS`.

```
toDelete = strcmp(dsNew.name,'WILLIAMS');
dsNew(toDelete,:) = [];
size(dsNew)
```

```
ans =

    16     5
```

The dataset array now has one less observation.

See Also

`cell2dataset` | `dataset` | `struct2dataset`

Related Examples

- “Add and Delete Variables” on page 2-81
- “Select Subsets of Observations” on page 2-91
- “Dataset Arrays in the Variables Editor” on page 2-118
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132

Add and Delete Variables

This example shows how to add and delete variables in a dataset array. You can also edit dataset arrays using the Variables editor.

Load sample data.

Navigate to the folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Import the data from the first worksheet in `hospitalSmall.xlsx` into a dataset array.

```
ds = dataset('XLSFile','hospitalSmall.xlsx');
size(ds)
```

```
ans =

    14     6
```

The dataset array, `ds`, has 14 observations (rows) and 6 variables (columns).

Add variables by concatenating dataset arrays.

The worksheet `Heights` in `hospitalSmall.xlsx` has heights for the patients on the first worksheet. Concatenate the data in this spreadsheet with `ds`.

```
ds2 = dataset('XLSFile','hospitalSmall.xlsx','Sheet','Heights');
ds = [ds ds2];
size(ds)
```

```
ans =

    14     7
```

The dataset array now has seven variables. You can only horizontally concatenate dataset arrays with observations in the same position, or with the same observation names.

```
ds.Properties.VarNames{end}
```

```
ans =
```

```
hgt
```

The name of the last variable in `ds` is `hgt`, which `dataset` read from the first row of the imported spreadsheet.

Delete variables by variable name.

First, specify the unique identifiers in the variable `id` as observation names. Then, delete the variable `id` from the dataset array.

```
ds.Properties.ObsNames = ds.id;
ds.id = [];
size(ds)
```

```
ans =

    14     6
```

The dataset array now has six variables. List the variable names.

```
ds.Properties.VarNames(:)
```

```
ans =

    'name'
    'sex'
    'age'
    'wgt'
    'smoke'
    'hgt'
```

There is no longer a variable called `id`.

Add a new variable by name.

Add a new variable, `bmi`—which contains the body mass index (BMI) for each patient—to the dataset array. BMI is a function of height and weight. Display the last name, gender, and BMI for each patient.

```
ds.bmi = ds.wgt*703./ds.hgt.^2;
ds(:,{'name','sex','bmi'})
```

```
ans =

                name              sex        bmi
```

```
    YPL-320    'SMITH'           'm'        24.544
    GLI-532    'JOHNSON'         'm'        24.068
    PNI-258    'WILLIAMS'        'f'        23.958
    MIJ-579    'JONES'           'f'        25.127
    XLK-030    'BROWN'           'f'        21.078
    TFP-518    'DAVIS'           'f'        27.729
    LPD-746    'MILLER'          'f'        26.828
    ATA-945    'WILSON'          'm'         24.41
    VNL-702    'MOORE'           'm'        27.822
    LQW-768    'TAYLOR'          'f'        22.655
    QFY-472    'ANDERSON'        'f'        23.409
    UJG-627    'THOMAS'          'f'        25.883
    XUE-826    'JACKSON'         'm'        24.265
    TRW-072    'WHITE'           'm'        29.827
```

The operators `./` and `.^` in the calculation of BMI indicate element-wise division and exponentiation, respectively.

Delete variables by variable number.

Delete the variable `wgt`, the fourth variable in the dataset array.

```
ds(:,4) = [];
ds.Properties.VarNames(:)

ans =

    'name'
    'sex'
    'age'
    'smoke'
    'hgt'
    'bmi'
```

The variable `wgt` is deleted from the dataset array.

See Also

`dataset`

Related Examples

- “Add and Delete Observations” on page 2-77
- “Merge Dataset Arrays” on page 2-99

- "Calculations on Dataset Arrays" on page 2-108
- "Dataset Arrays in the Variables Editor" on page 2-118
- "Index and Search Dataset Arrays" on page 2-135

More About

- "Dataset Arrays" on page 2-132

Access Data in Dataset Array Variables

This example shows how to work with dataset array variables and their data.

Access variables by name.

You can access variable data, or select a subset of variables, by using variable (column) names and dot indexing. Load a sample dataset array. Display the names of the variables in `hospital`.

```
load hospital
hospital.Properties.VarNames(:)
```

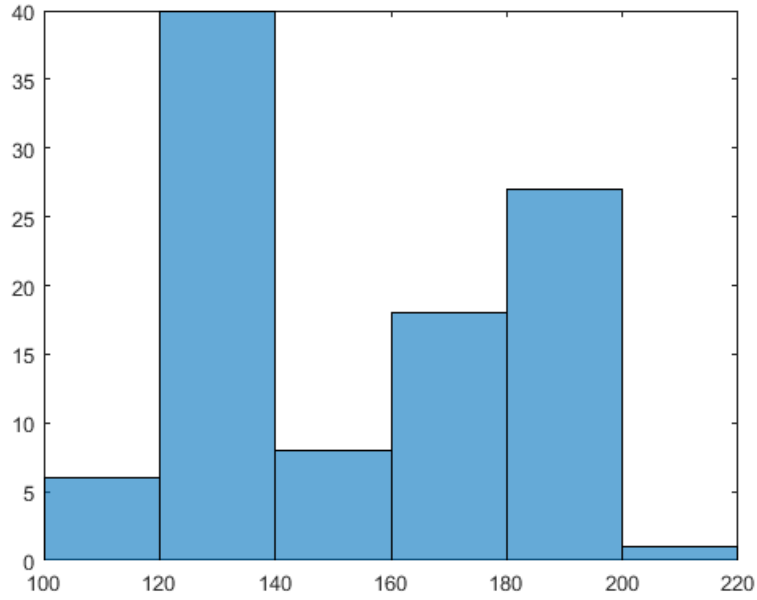
```
ans =

    'LastName'
    'Sex'
    'Age'
    'Weight'
    'Smoker'
    'BloodPressure'
    'Trials'
```

The dataset array has 7 variables (columns) and 100 observations (rows). You can double-click `hospital` in the Workspace window to view the dataset array in the Variables editor.

Plot histogram.

Plot a histogram of the data in the variable `Weight`.

```
figure
histogram(hospital.Weight)
```

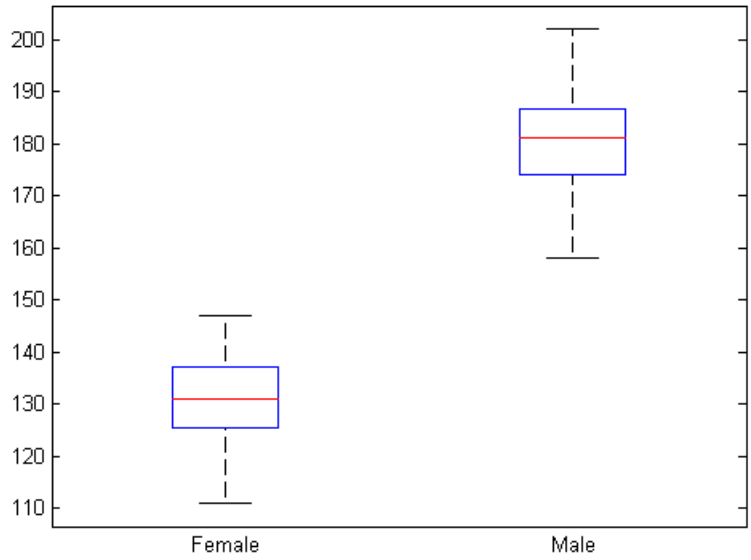


The histogram shows that the weight distribution is bimodal.

Plot data grouped by category.

Draw box plots of `Weight` grouped by the values in `Sex` (Male and Female). That is, use the variable `Sex` as a grouping variable.

```
figure()
boxplot(hospital.Weight,hospital.Sex)
```



The box plot suggests that gender accounts for the bimodality in weight.

Select a subset of variables.

Create a new dataset array with only the variables `LastName`, `Sex`, and `Weight`. You can access the variables by name or column number.

```
ds1 = hospital(:,{'LastName','Sex','Weight'});
ds2 = hospital(:,[1,2,4]);
```

The dataset arrays `ds1` and `ds2` are equivalent. Use parentheses `( )` when indexing dataset arrays to preserve the data type; that is, to create a dataset array from a subset of a dataset array. You can also use the Variables editor to create a new dataset array from a subset of variables and observations.

Convert the variable data type.

Convert the data type of the variable `Smoker` from logical to nominal with labels `No` and `Yes`.

```
hospital.Smoker = nominal(hospital.Smoker,{'No','Yes'});
class(hospital.Smoker)
```

```
ans =

nominal
```

Explore data.

Display the first 10 elements of `Smoker`.

```
hospital.Smoker(1:10)
```

```
ans =

     Yes
     No
     No
     No
     No
     No
     Yes
     No
     No
     No
```

If you want to change the level labels in a nominal array, use `setlabels`.

Add variables.

The variable `BloodPressure` is a 100-by-2 array. The first column corresponds to systolic blood pressure, and the second column to diastolic blood pressure. Separate this array into two new variables, `SysPressure` and `DiaPressure`.

```
hospital.SysPressure = hospital.BloodPressure(:,1);
hospital.DiaPressure = hospital.BloodPressure(:,2);
hospital.Properties.VarNames(:)
```

```
ans =

    'LastName'
    'Sex'
    'Age'
    'Weight'
    'Smoker'
    'BloodPressure'
```

```
    'Trials'
    'SysPressure'
    'DiaPressure'
```

The dataset array, `hospital`, has two new variables.

Search for variables by name.

Use `regexp` to find variables in `hospital` with the string `'Pressure'` in their name. Create a new dataset array containing only these variables.

```
bp = regexp(hospital.Properties.VarNames,'Pressure');
bpIdx = cellfun(@isempty,bp);
bpData = hospital(:,~bpIdx);
bpData.Properties.VarNames(:)
```

```
ans =

    'BloodPressure'
    'SysPressure'
    'DiaPressure'
```

The new dataset array, `bpData`, contains only the blood pressure variables.

Delete variables.

Delete the variable `BloodPressure` from the dataset array, `hospital`.

```
hospital.BloodPressure = [];
hospital.Properties.VarNames(:)
```

```
ans =

    'LastName'
    'Sex'
    'Age'
    'Weight'
    'Smoker'
    'Trials'
    'SysPressure'
    'DiaPressure'
```

The variable `BloodPressure` is no longer in the dataset array.

See Also

`dataset`

Related Examples

- “Add and Delete Variables” on page 2-81
- “Calculations on Dataset Arrays” on page 2-108
- “Dataset Arrays in the Variables Editor” on page 2-118
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132
- “Grouping Variables” on page 2-52

Select Subsets of Observations

This example shows how to select an observation or subset of observations from a dataset array.

Load sample data.

Load the sample dataset array, `hospital`. Dataset arrays can have observation (row) names. This array has observation names corresponding to unique patient identifiers.

```
load('hospital')
hospital.Properties.ObsNames(1:10)
```

```
ans =

    'YPL-320'
    'GLI-532'
    'PNI-258'
    'MIJ-579'
    'XLK-030'
    'TFP-518'
    'LPD-746'
    'ATA-945'
    'VNL-702'
    'LQW-768'
```

These are the first 10 observation names.

Index an observation by name.

You can use the observation names to index into the dataset array. For example, extract the last name, sex, and age for the patient with identifier `XLK-030`.

```
hospital('XLK-030',{'LastName','Sex','Age'})
```

```
ans =

                LastName        Sex       Age
    XLK-030     'BROWN'         Female    49
```

Index a subset of observations by number.

Create a new dataset array containing the first 50 patients.

```
ds50 = hospital(1:50,:);
```

```
size(ds50)

ans =

    50     7
```

Search observations using a logical condition.

Create a new dataset array containing only male patients. To find the male patients, use a logical condition to search the variable containing gender information.

```
dsMale = hospital(hospital.Sex=='Male',:);
dsMale(1:10,{'LastName','Sex'})

ans =

                LastName          Sex
    YPL-320     'SMITH'           Male
    GLI-532     'JOHNSON'         Male
    ATA-945     'WILSON'          Male
    VNL-702     'MOORE'           Male
    XUE-826     'JACKSON'         Male
    TRW-072     'WHITE'           Male
    KOQ-996     'MARTIN'          Male
    YUZ-646     'THOMPSON'        Male
    KPW-846     'MARTINEZ'        Male
    XBA-581     'ROBINSON'        Male
```

Search observations using multiple conditions.

You can use multiple conditions to search the dataset array. For example, create a new dataset array containing only female patients older than 40.

```
dsFemale = hospital(hospital.Sex=='Female' & hospital.Age > 40,:);
dsFemale(1:10,{'LastName','Sex','Age'})

ans =

                LastName          Sex       Age
    XLK-030     'BROWN'           Female    49
    TFP-518     'DAVIS'           Female    46
    QFY-472     'ANDERSON'        Female    45
    UJG-627     'THOMAS'          Female    42
    BKD-785     'CLARK'           Female    48
    VWL-936     'LEWIS'           Female    41
```

```
    AAX-056    'LEE'              Female    44
    AFK-336    'WRIGHT'           Female    45
    KKL-155    'ADAMS'            Female    48
    RBA-579    'SANCHEZ'          Female    44
```

Select a random subset of observations.

Create a new dataset array containing a random subset of 20 patients from the dataset array `hospital`.

```
rng('default') % For reproducibility
dsRandom = hospital(randsample(length(hospital),20),:);
dsRandom.Properties.ObsNames
```

```
ans =

    'DAU-529'
    'AGR-528'
    'RBO-332'
    'QOO-305'
    'RVS-253'
    'QEQ-082'
    'EHE-616'
    'HVR-372'
    'KOQ-996'
    'REV-997'
    'PUE-347'
    'LQW-768'
    'YLN-495'
    'HJQ-495'
    'ELG-976'
    'XUE-826'
    'MEZ-469'
    'UDS-151'
    'MIJ-579'
    'DGC-290'
```

Delete observations by name.

Delete the data for the patient with observation name `HVR-372`.

```
hospital('HVR-372',:) = [];
size(hospital)
```

```
ans =
```

```
    99     7
```

The dataset array has one less observation.

See Also

`dataset`

Related Examples

- “Add and Delete Observations” on page 2-77
- “Clean Messy and Missing Data” on page 2-113
- “Dataset Arrays in the Variables Editor” on page 2-118
- “Sort Observations in Dataset Arrays” on page 2-95
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132

Sort Observations in Dataset Arrays

This example shows how to sort observations (rows) in a dataset array using the command line. You can also sort rows using the Variables editor.

Sort observations in ascending order.

Load the sample dataset array, `hospital`. Sort the observations by the values in `Age`, in ascending order.

```
load('hospital')
dsAgeUp = sortrows(hospital,'Age');
dsAgeUp(1:10,{'LastName','Age'})
```

```
ans =

            LastName           Age
    XUE-826    'JACKSON'          25
    FZR-250    'HALL'             25
    PUE-347    'YOUNG'            25
    LIM-480    'HILL'             25
    SCQ-914    'JAMES'            25
    REV-997    'ALEXANDER'        25
    XBR-291    'GARCIA'           27
    VNL-702    'MOORE'            28
    DTT-578    'WALKER'           28
    XAX-646    'COOPER'           28
```

The youngest patients are age 25.

Sort observations in descending order.

Sort the observations by `Age` in descending order.

```
dsAgeDown = sortrows(hospital,'Age','descend');
dsAgeDown(1:10,{'LastName','Age'})
```

```
ans =

            LastName           Age
    XBA-581    'ROBINSON'         50
    DAU-529    'REED'             50
    XLK-030    'BROWN'            49
    FLJ-908    'STEWART'          49
```

```
    GGU-691    'HUGHES'          49
    MEZ-469    'GRIFFIN'         49
    KOQ-996    'MARTIN'          48
    BKD-785    'CLARK'           48
    KKL-155    'ADAMS'           48
    NSK-403    'RAMIREZ'         48
```

The oldest patients are age 50.

Sort observations by the values of two variables.

Sort the observations in `hospital` by `Age`, and then by `LastName`.

```
dsName = sortrows(hospital,{'Age','LastName'});
dsName(1:10,{'LastName','Age'})
```

```
ans =

               LastName           Age
    REV-997    'ALEXANDER'        25
    FZR-250    'HALL'             25
    LIM-480    'HILL'             25
    XUE-826    'JACKSON'          25
    SCQ-914    'JAMES'            25
    PUE-347    'YOUNG'            25
    XBR-291    'GARCIA'           27
    XAX-646    'COOPER'           28
    QEQ-082    'COX'              28
    NSU-424    'JENKINS'          28
```

Now the names are sorted alphabetically within increasing age groups.

Sort observations in mixed order.

Sort the observations in `hospital` by `Age` in an increasing order, and then by `Weight` in a decreasing order.

```
dsWeight = sortrows(hospital,{'Age','Weight'},{'ascend','descend'});
dsWeight(1:10,{'LastName','Age','Weight'})
```

```
ans =

               LastName           Age    Weight
    FZR-250    'HALL'             25     189
    SCQ-914    'JAMES'            25     186
```

```
    XUE-826    'JACKSON'          25     174
    REV-997    'ALEXANDER'        25     171
    LIM-480    'HILL'             25     138
    PUE-347    'YOUNG'            25     114
    XBR-291    'GARCIA'           27     131
    NSU-424    'JENKINS'          28     189
    VNL-702    'MOORE'            28     183
    XAX-646    'COOPER'           28     127
```

This shows that the maximum weight among patients that are age 25 is 189 lbs.

Sort observations by observation name.

Sort the observations in `hospital` by the observation names.

```
dsObs = sortrows(hospital,'obsnames');
dsObs(1:10,{'LastName','Age'})
```

```
ans =

               LastName          Age
    AAX-056    'LEE'             44
    AFB-271    'PEREZ'           44
    AFK-336    'WRIGHT'          45
    AGR-528    'SIMMONS'         45
    ATA-945    'WILSON'          40
    BEZ-311    'DIAZ'            45
    BKD-785    'CLARK'           48
    DAU-529    'REED'            50
    DGC-290    'BUTLER'          38
    DTT-578    'WALKER'          28
```

The observations are sorted by observation name in ascending alphabetical order.

See Also

`dataset` | `sortrows`

Related Examples

- “Select Subsets of Observations” on page 2-91
- “Stack or Unstack Dataset Arrays” on page 2-103
- “Dataset Arrays in the Variables Editor” on page 2-118
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132

Merge Dataset Arrays

This example shows how to merge dataset arrays using `join`.

Load sample data.

Navigate to a folder containing sample data. Import the data from the first worksheet in `hospitalSmall.xlsx` into a dataset array, then keep only a few of the variables.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
ds1 = dataset('XLSFile','hospitalSmall.xlsx');
ds1 = ds1(:,{'id','name','sex','age'})
```

```
ds1 =

    id              name              sex        age
    'YPL-320'       'SMITH'           'm'        38
    'GLI-532'       'JOHNSON'         'm'        43
    'PNI-258'       'WILLIAMS'        'f'        38
    'MIJ-579'       'JONES'           'f'        40
    'XLK-030'       'BROWN'           'f'        49
    'TFP-518'       'DAVIS'           'f'        46
    'LPD-746'       'MILLER'          'f'        33
    'ATA-945'       'WILSON'          'm'        40
    'VNL-702'       'MOORE'           'm'        28
    'LQW-768'       'TAYLOR'          'f'        31
    'QFY-472'       'ANDERSON'        'f'        45
    'UJG-627'       'THOMAS'          'f'        42
    'XUE-826'       'JACKSON'         'm'        25
    'TRW-072'       'WHITE'           'm'        39
```

The dataset array, `ds1`, has 14 observations (rows) and 4 variables (columns).

Import the data from the worksheet `Heights2` in `hospitalSmall.xlsx`.

```
ds2 = dataset('XLSFile','hospitalSmall.xlsx','Sheet','Heights2')
```

```
ds2 =

    id              hgt
    'LPD-746'       61
    'PNI-258'       62
    'XUE-826'       71
```

```
    'ATA-945'        72
    'XLK-030'        63
```

`ds2` has height measurements for a subset of five individuals from the first dataset array, `ds1`.

Merge only the matching subset of observations.

Use `join` to merge the two dataset arrays, `ds1` and `ds2`, keeping only the subset of observations that are in `ds2`.

```
JoinSmall = join(ds2,ds1)
```

```
JoinSmall =

    id              hgt    name              sex        age
    'LPD-746'       61     'MILLER'          'f'        33
    'PNI-258'       62     'WILLIAMS'        'f'        38
    'XUE-826'       71     'JACKSON'         'm'        25
    'ATA-945'       72     'WILSON'          'm'        40
    'XLK-030'       63     'BROWN'           'f'        49
```

In `JoinSmall`, the variable `id` only appears once. This is because it is the key variable—the variable that links observations between the two dataset arrays—and has the same variable name in both `ds1` and `ds2`.

Include incomplete observations in the merge.

Merge `ds1` and `ds2` keeping all observations in the larger `ds1`.

```
joinAll = join(ds2,ds1,'type','rightouter','mergekeys',true)
```

```
joinAll =

    id              hgt    name              sex        age
    'ATA-945'        72    'WILSON'          'm'        40
    'GLI-532'       NaN    'JOHNSON'         'm'        43
    'LPD-746'        61    'MILLER'          'f'        33
    'LQW-768'       NaN    'TAYLOR'          'f'        31
    'MIJ-579'       NaN    'JONES'           'f'        40
    'PNI-258'        62    'WILLIAMS'        'f'        38
    'QFY-472'       NaN    'ANDERSON'        'f'        45
    'TFP-518'       NaN    'DAVIS'           'f'        46
    'TRW-072'       NaN    'WHITE'           'm'        39
```

```
    'UJG-627'        NaN    'THOMAS'          'f'        42
    'VNL-702'        NaN    'MOORE'           'm'        28
    'XLK-030'         63    'BROWN'           'f'        49
    'XUE-826'         71    'JACKSON'         'm'        25
    'YPL-320'        NaN    'SMITH'           'm'        38
```

Each observation in `ds1` without corresponding height measurements in `ds2` has height value `NaN`. Also, because there is no `id` value in `ds2` for each observation in `ds1`, you need to merge the keys using the option `'MergeKeys',true`. This merges the key variable, `id`.

Merge dataset arrays with different key variable names.

When using `join`, it is not necessary for the key variable to have the same name in the dataset arrays to be merged. Import the data from the worksheet named `Heights3` in `hospitalSmall.xlsx`.

```
ds3 = dataset('XLSFile','hospitalSmall.xlsx','Sheet','Heights3')
```

```
ds3 =

    identifier       hgt
    'GLI-532'        69
    'QFY-472'        62
    'MIJ-579'        61
    'VNL-702'        68
    'XLK-030'        63
    'LPD-746'        61
    'TFP-518'        60
    'YPL-320'        71
    'ATA-945'        72
    'LQW-768'        64
    'PNI-258'        62
    'UJG-627'        61
    'XUE-826'        71
    'TRW-072'        69
```

`ds3` has height measurements for each observation in `ds1`. This dataset array has the same patient identifiers as `ds1`, but they are under the variable name `identifier`, instead of `id` (and in a different order).

Specify key variable.

You can easily change the variable name of the key variable in `ds3` by setting `d3.Properties.VarNames` or using the Variables editor, but it is not required to

perform a merge. Instead, you can specify the name of the key variable in each dataset array using `LeftKeys` and `RightKeys`.

```
joinDiff = join(ds3,ds1,'LeftKeys','identifier','RightKeys','id')
```

```
joinDiff =

    identifier       hgt    name              sex        age
    'GLI-532'        69     'JOHNSON'         'm'        43
    'QFY-472'        62     'ANDERSON'        'f'        45
    'MIJ-579'        61     'JONES'           'f'        40
    'VNL-702'        68     'MOORE'           'm'        28
    'XLK-030'        63     'BROWN'           'f'        49
    'LPD-746'        61     'MILLER'          'f'        33
    'TFP-518'        60     'DAVIS'           'f'        46
    'YPL-320'        71     'SMITH'           'm'        38
    'ATA-945'        72     'WILSON'          'm'        40
    'LQW-768'        64     'TAYLOR'          'f'        31
    'PNI-258'        62     'WILLIAMS'        'f'        38
    'UJG-627'        61     'THOMAS'          'f'        42
    'XUE-826'        71     'JACKSON'         'm'        25
    'TRW-072'        69     'WHITE'           'm'        39
```

The merged dataset array, `joinDiff`, has the same key variable order and name as the first dataset array input to `join`, `ds3`.

See Also

`dataset` | `join`

Related Examples

- “Add and Delete Variables” on page 2-81
- “Stack or Unstack Dataset Arrays” on page 2-103
- “Dataset Arrays in the Variables Editor” on page 2-118
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132

Stack or Unstack Dataset Arrays

This example shows how to reformat dataset arrays between wide and tall (or long) format using `stack` and `unstack`.

Load sample data.

Navigate to the folder containing sample data. Import the data from the comma-separated text file `testScores.csv`.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
ds = dataset('File','testScores.csv','Delimiter',',')
```

```
ds =

    LastName          Sex             Test1    Test2    Test3    Test4
    'HOWARD'          'male'          90       87       93       92
    'WARD'            'male'          87       85       83       90
    'TORRES'          'male'          86       85       88       86
    'PETERSON'        'female'        75       80       72       77
    'GRAY'            'female'        89       86       87       90
    'RAMIREZ'         'female'        96       92       98       95
    'JAMES'           'male'          78       75       77       77
    'WATSON'          'female'        91       94       92       90
    'BROOKS'          'female'        86       83       85       89
    'KELLY'           'male'          79       76       82       80
```

Each of the 10 students has 4 test scores, displayed here in wide format.

Perform calculations on dataset array.

With the data in this format, you can, for example, calculate the average test score for each student. The test scores are in columns 3 to 6.

```
ds.TestAve = mean(double(ds(:,3:6)),2);
ds(:,{'LastName','Sex','TestAve'})
```

```
ans =

    LastName          Sex             TestAve
    'HOWARD'          'male'           90.5
    'WARD'            'male'          86.25
```

```
    'TORRES'          'male'          86.25
    'PETERSON'        'female'           76
    'GRAY'            'female'           88
    'RAMIREZ'         'female'        95.25
    'JAMES'           'male'          76.75
    'WATSON'          'female'        91.75
    'BROOKS'          'female'        85.75
    'KELLY'           'male'          79.25
```

A new variable with average test scores is added to the dataset array, `ds`.

Reformat the dataset array into tall format.

Stack the test score variables into a new variable, `Scores`.

```
dsTall = stack(ds,{'Test1','Test2','Test3','Test4'},...
           'newDataVarName','Scores')
```

```
dsTall =

    LastName          Sex             TestAve    Scores_Indicator    Scores
    'HOWARD'          'male'           90.5      Test1               90
    'HOWARD'          'male'           90.5      Test2               87
    'HOWARD'          'male'           90.5      Test3               93
    'HOWARD'          'male'           90.5      Test4               92
    'WARD'            'male'          86.25      Test1               87
    'WARD'            'male'          86.25      Test2               85
    'WARD'            'male'          86.25      Test3               83
    'WARD'            'male'          86.25      Test4               90
    'TORRES'          'male'          86.25      Test1               86
    'TORRES'          'male'          86.25      Test2               85
    'TORRES'          'male'          86.25      Test3               88
    'TORRES'          'male'          86.25      Test4               86
    'PETERSON'        'female'           76      Test1               75
    'PETERSON'        'female'           76      Test2               80
    'PETERSON'        'female'           76      Test3               72
    'PETERSON'        'female'           76      Test4               77
    'GRAY'            'female'           88      Test1               89
    'GRAY'            'female'           88      Test2               86
    'GRAY'            'female'           88      Test3               87
    'GRAY'            'female'           88      Test4               90
    'RAMIREZ'         'female'        95.25      Test1               96
    'RAMIREZ'         'female'        95.25      Test2               92
    'RAMIREZ'         'female'        95.25      Test3               98
    'RAMIREZ'         'female'        95.25      Test4               95
```

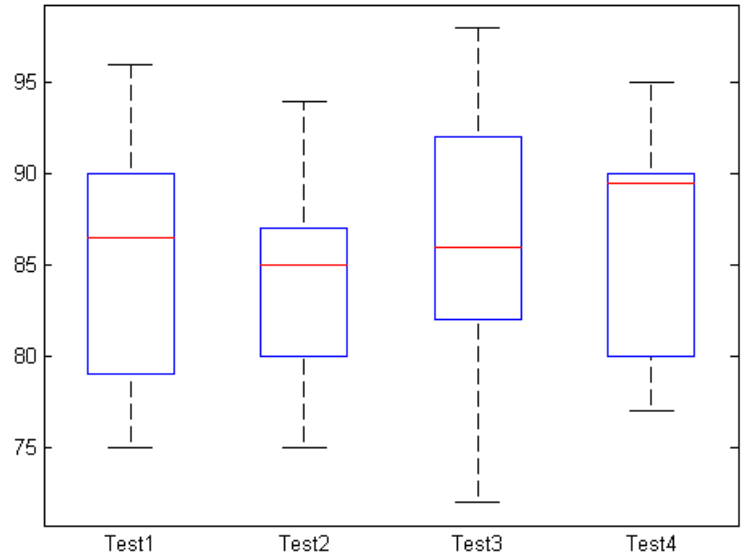
```
'JAMES'          'male'          76.75      Test1              78
'JAMES'          'male'          76.75      Test2              75
'JAMES'          'male'          76.75      Test3              77
'JAMES'          'male'          76.75      Test4              77
'WATSON'         'female'        91.75      Test1              91
'WATSON'         'female'        91.75      Test2              94
'WATSON'         'female'        91.75      Test3              92
'WATSON'         'female'        91.75      Test4              90
'BROOKS'         'female'        85.75      Test1              86
'BROOKS'         'female'        85.75      Test2              83
'BROOKS'         'female'        85.75      Test3              85
'BROOKS'         'female'        85.75      Test4              89
'KELLY'          'male'          79.25      Test1              79
'KELLY'          'male'          79.25      Test2              76
'KELLY'          'male'          79.25      Test3              82
'KELLY'          'male'          79.25      Test4              80
```

The original test variable names, `Test1`, `Test2`, `Test3`, and `Test4`, appear as levels in the combined test scores indicator variable, `Scores_Indicator`.

Plot data grouped by category.

With the data in this format, you can use `Scores_Indicator` as a grouping variable, and draw box plots of test scores grouped by test.

```
figure()
boxplot(dsTall.Scores,dsTall.Scores_Indicator)
```



Reformat the dataset array into wide format.

Reformat `dsTall` back into its original wide format.

```
dsWide = unstack(dsTall,'Scores','Scores_Indicator');
dsWide(:,{'LastName','Test1','Test2','Test3','Test4'})
```

```
ans =

    LastName          Test1    Test2    Test3    Test4
    'HOWARD'          90       87       93       92
    'WARD'            87       85       83       90
    'TORRES'          86       85       88       86
    'PETERSON'        75       80       72       77
    'GRAY'            89       86       87       90
    'RAMIREZ'         96       92       98       95
    'JAMES'           78       75       77       77
    'WATSON'          91       94       92       90
    'BROOKS'          86       83       85       89
    'KELLY'           79       76       82       80
```

The dataset array is back in wide format. `unstack` reassigns the levels of the indicator variable, `Scores_Indicator`, as variable names in the unstacked dataset array.

See Also

`dataset` | `double` | `stack` | `unstack`

Related Examples

- "Access Data in Dataset Array Variables" on page 2-85
- "Calculations on Dataset Arrays" on page 2-108
- "Index and Search Dataset Arrays" on page 2-135

More About

- "Dataset Arrays" on page 2-132
- "Grouping Variables" on page 2-52

Calculations on Dataset Arrays

This example shows how to perform calculations on dataset arrays.

Load sample data.

Navigate to the folder containing sample data. Import the data from the comma-separated text file `testScores.csv`.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
ds = dataset('File','testScores.csv','Delimiter',',')
```

```
ds =

    LastName          Sex             Test1    Test2    Test3    Test4
    'HOWARD'          'male'          90       87       93       92
    'WARD'            'male'          87       85       83       90
    'TORRES'          'male'          86       85       88       86
    'PETERSON'        'female'        75       80       72       77
    'GRAY'            'female'        89       86       87       90
    'RAMIREZ'         'female'        96       92       98       95
    'JAMES'           'male'          78       75       77       77
    'WATSON'          'female'        91       94       92       90
    'BROOKS'          'female'        86       83       85       89
    'KELLY'           'male'          79       76       82       80
```

There are 4 test scores for each of 10 students, in wide format.

Average dataset array variables.

Compute the average (mean) test score for each student in the dataset array, and store it in a new variable, `TestAvg`. Test scores are in columns 3 to 6.

Use `double` to convert the specified dataset array variables into a numeric array. Then, calculate the mean across the second dimension (across columns) to get the test average for each student.

```
ds.TestAvg = mean(double(ds(:,3:6)),2);
ds(:,{'LastName','TestAvg'})
```

```
ans =

    LastName          TestAvg
```

```
    'HOWARD'          90.5
    'WARD'           86.25
    'TORRES'         86.25
    'PETERSON'          76
    'GRAY'              88
    'RAMIREZ'        95.25
    'JAMES'          76.75
    'WATSON'         91.75
    'BROOKS'         85.75
    'KELLY'          79.25
```

Summarize the dataset array using a grouping variable.

Compute the mean and maximum average test scores for each gender.

```
stats = grpstats(ds,'Sex',{'mean','max'},'DataVars','TestAvg')
```

```
stats =

              Sex             GroupCount    mean_TestAvg    max_TestAvg
    male      'male'          5              83.8            90.5
    female    'female'        5             87.35           95.25
```

This returns a new dataset array containing the specified summary statistics for each level of the grouping variable, `Sex`.

Replace data values.

The denominator for each test score is 100. Convert the test score denominator to 25.

```
scores = double(ds(:,3:6));
newScores = scores*25/100;
ds = replacedata(ds,newScores,3:6)
```

```
ds =

    LastName          Sex             Test1    Test2    Test3    Test4    TestAvg
    'HOWARD'          'male'           22.5    21.75    23.25       23     90.5
    'WARD'            'male'          21.75    21.25    20.75     22.5    86.25
    'TORRES'          'male'           21.5    21.25       22     21.5    86.25
    'PETERSON'        'female'        18.75       20       18    19.25       76
    'GRAY'            'female'        22.25     21.5    21.75     22.5       88
    'RAMIREZ'         'female'           24       23     24.5    23.75    95.25
    'JAMES'           'male'           19.5    18.75    19.25    19.25    76.75
    'WATSON'          'female'        22.75     23.5       23     22.5    91.75
```

```
    'BROOKS'          'female'         21.5    20.75    21.25    22.25    85.75
    'KELLY'           'male'          19.75       19     20.5       20    79.25
```

The first two lines of code extract the test data and perform the desired calculation. Then, `replacedata` inserts the new test scores back into the dataset array.

The variable of test score averages, `TestAvg`, is now the final score for each student.

Change variable name.

Change the variable name to `Final`.

```
ds.Properties.VarNames{end} = 'Final';
ds
```

```
ds =

    LastName          Sex              Test1    Test2    Test3    Test4    Final
    'HOWARD'          'male'            22.5    21.75    23.25       23     90.5
    'WARD'            'male'           21.75    21.25    20.75     22.5    86.25
    'TORRES'          'male'            21.5    21.25       22     21.5    86.25
    'PETERSON'        'female'         18.75       20       18    19.25       76
    'GRAY'            'female'         22.25     21.5    21.75     22.5       88
    'RAMIREZ'         'female'            24       23     24.5    23.75    95.25
    'JAMES'           'male'            19.5    18.75    19.25    19.25    76.75
    'WATSON'          'female'         22.75     23.5       23     22.5    91.75
    'BROOKS'          'female'          21.5    20.75    21.25    22.25    85.75
    'KELLY'           'male'           19.75       19     20.5       20    79.25
```

See Also

`dataset` | `double` | `grpstats` | `replacedata`

Related Examples

- “Stack or Unstack Dataset Arrays” on page 2-103
- “Access Data in Dataset Array Variables” on page 2-85
- “Select Subsets of Observations” on page 2-91
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132

Export Dataset Arrays

This example shows how to export a dataset array from the MATLAB workspace to a text or spreadsheet file.

Load sample data.

```
load('hospital')
```

The dataset array has 100 observations and 7 variables.

Export to a text file.

Export the dataset array, `hospital`, to a text file named `hospital.txt`. By default, `export` writes to a tab-delimited text file with the same name as the dataset array, appended by `.txt`.

```
export(hospital)
```

This creates the file `hospital.txt` in the current working folder, if it does not previously exist. If the file already exists in the current working folder, `export` overwrites the existing file.

By default, variable names are in the first line of the text file. Observation names, if present, are in the first column.

Export without variable names.

Export `hospital` with variable names suppressed to a text file named `NoLabels.txt`.

```
export(hospital,'File','NoLabels.txt','WriteVarNames',false)
```

There are no variable names in the first line of the created text file, `NoLabels.txt`.

Export to a comma-delimited format.

Export `hospital` to a comma-delimited text file, `hospital.csv`.

```
export(hospital,'File','hospital.csv','Delimiter',',')
```

Export to an Excel spreadsheet.

Export `hospital` to an Excel spreadsheet named `hospital.xlsx`.

```
export(hospital,'XLSFile','hospital.xlsx')
```

By default, the first row of `hospital.xlsx` has variable names, and the first column has observation names.

See Also

`dataset` | `export`

Related Examples

- “Create a Dataset Array from Workspace Variables” on page 2-63
- “Create a Dataset Array from a File” on page 2-69

More About

- “Dataset Arrays” on page 2-132

Clean Messy and Missing Data

This example shows how to find, clean, and delete observations with missing data in a dataset array.

Load sample data.

Navigate to the folder containing sample data. Import the data from the spreadsheet `messy.xlsx`.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
messyData = dataset('XLSFile','messy.xlsx')
```

```
messyData =

    var1          var2          var3          var4          var5
    'afe1'        '3'           'yes'         '3'             3
    'egh3'        '.'           'no'          '7'             7
    'wth4'        '3'           'yes'         '3'             3
    'atn2'        '23'          'no'          '23'           23
    'arg1'        '5'           'yes'         '5'             5
    'jre3'        '34.6'        'yes'         '34.6'       34.6
    'wen9'        '234'         'yes'         '234'         234
    'ple2'        '2'           'no'          '2'             2
    'dbo8'        '5'           'no'          '5'             5
    'oii4'        '5'           'yes'         '5'             5
    'wnk3'        '245'         'yes'         '245'         245
    'abk6'        '563'         ''            '563'         563
    'pnj5'        '463'         'no'          '463'         463
    'wnn3'        '6'           'no'          '6'             6
    'oks9'        '23'          'yes'         '23'           23
    'wba3'        ''            'yes'         'NaN'          14
    'pkn4'        '2'           'no'          '2'             2
    'adw3'        '22'          'no'          '22'           22
    'poj2'        '-99'         'yes'         '-99'         -99
    'bas8'        '23'          'no'          '23'           23
    'gry5'        'NA'          'yes'         'NaN'          21
```

When you import data from a spreadsheet, `dataset` reads any variables with nonnumeric elements as a cell array of strings. This is why the variable `var2` is a cell array of strings. When importing data from a text file, you have more flexibility to specify which nonnumeric expressions to treat as missing using the option `TreatAsEmpty`.

There are many different missing data indicators in `messy.xlsx`, such as:

- Empty cells
- A period (`.`)
- `NA`
- `NaN`
- `-99`

Find observations with missing values.

Display the subset of observations that have at least one missing value using `ismissing`.

```
ix = ismissing(messyData,'NumericTreatAsMissing',-99,...
                 'StringTreatAsMissing',{'NaN','.','NA'});
messyData(any(ix,2),:)
```

```
ans =

    var1          var2          var3          var4          var5
    'egh3'        '.'           'no'          '7'             7
    'abk6'        '563'         ''            '563'         563
    'wba3'        ''            'yes'         'NaN'          14
    'poj2'        '-99'         'yes'         '-99'         -99
    'gry5'        'NA'          'yes'         'NaN'          21
```

By default, `ismissing` recognizes the following missing value indicators:

- `NaN` for numeric arrays
- `''` for string arrays
- `<undefined>` for categorical arrays

Use the `NumericTreatAsMissing` and `StringTreatAsMissing` options to specify other values to treat as missing.

Convert string arrays to double arrays.

You can convert the string variables that should be numeric using `str2double`.

```
messyData.var2 = str2double(messyData.var2);
messyData.var4 = str2double(messyData.var4)
```

```
messyData =

    var1          var2    var3          var4    var5
    'afe1'          3     'yes'          3       3
    'egh3'        NaN     'no'           7       7
    'wth4'          3     'yes'          3       3
    'atn2'         23     'no'          23      23
    'arg1'          5     'yes'          5       5
    'jre3'       34.6     'yes'       34.6    34.6
    'wen9'        234     'yes'        234     234
    'ple2'          2     'no'           2       2
    'dbo8'          5     'no'           5       5
    'oii4'          5     'yes'          5       5
    'wnk3'        245     'yes'        245     245
    'abk6'        563     ''           563     563
    'pnj5'        463     'no'         463     463
    'wnn3'          6     'no'           6       6
    'oks9'         23     'yes'         23      23
    'wba3'        NaN     'yes'        NaN      14
    'pkn4'          2     'no'           2       2
    'adw3'         22     'no'          22      22
    'poj2'        -99     'yes'        -99     -99
    'bas8'         23     'no'          23      23
    'gry5'        NaN     'yes'        NaN      21
```

Now, `var2` and `var4` are numeric arrays. During the conversion, `str2double` replaces the nonnumeric elements of the variables `var2` and `var4` with the value `NaN`. However, there are no changes to the numeric missing value indicator, `-99`.

When applying the same function to many dataset array variables, it can sometimes be more convenient to use `datasetfun`. For example, to convert both `var2` and `var4` to numeric arrays simultaneously, you can use:

```
messyData(:,[2,4]) = datasetfun(@str2double,messyData,'DataVars',[2,4],...
                     'DatasetOutput',true);
```

Replace missing value indicators.

Clean the data so that the missing values indicated by the code `-99` have the standard MATLAB numeric missing value indicator, `NaN`.

```
messyData = replaceWithMissing(messyData,'NumericValues',-99)

messyData =
```

```
    var1          var2    var3          var4    var5
    'afe1'           3    'yes'            3       3
    'egh3'         NaN    'no'             7       7
    'wth4'           3    'yes'            3       3
    'atn2'          23    'no'            23      23
    'arg1'           5    'yes'            5       5
    'jre3'        34.6    'yes'         34.6    34.6
    'wen9'         234    'yes'          234     234
    'ple2'           2    'no'             2       2
    'dbo8'           5    'no'             5       5
    'oii4'           5    'yes'            5       5
    'wnk3'         245    'yes'          245     245
    'abk6'         563    ''             563     563
    'pnj5'         463    'no'           463     463
    'wnn3'           6    'no'             6       6
    'oks9'          23    'yes'           23      23
    'wba3'         NaN    'yes'          NaN      14
    'pkn4'           2    'no'             2       2
    'adw3'          22    'no'            22      22
    'poj2'         NaN    'yes'          NaN     NaN
    'bas8'          23    'no'            23      23
    'gry5'         NaN    'yes'          NaN      21
```

Create a dataset array with complete observations.

Create a new dataset array that contains only the complete observations—those without missing data.

```
ix = ismissing(messyData);
completeData = messyData(~any(ix,2),:)
```

```
completeData =

    var1          var2    var3          var4    var5
    'afe1'           3    'yes'            3       3
    'wth4'           3    'yes'            3       3
    'atn2'          23    'no'            23      23
    'arg1'           5    'yes'            5       5
    'jre3'        34.6    'yes'         34.6    34.6
    'wen9'         234    'yes'          234     234
    'ple2'           2    'no'             2       2
    'dbo8'           5    'no'             5       5
    'oii4'           5    'yes'            5       5
    'wnk3'         245    'yes'          245     245
    'pnj5'         463    'no'           463     463
```

```
    'wnn3'          6    'no'           6       6
    'oks9'         23    'yes'         23      23
    'pkn4'          2    'no'           2       2
    'adw3'         22    'no'          22      22
    'bas8'         23    'no'          23      23
```

See Also

`dataset` | `ismissing` | `replaceWithMissing`

Related Examples

- “Select Subsets of Observations” on page 2-91
- “Calculations on Dataset Arrays” on page 2-108
- “Index and Search Dataset Arrays” on page 2-135

More About

- “Dataset Arrays” on page 2-132

Dataset Arrays in the Variables Editor

Note: The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

In this section...

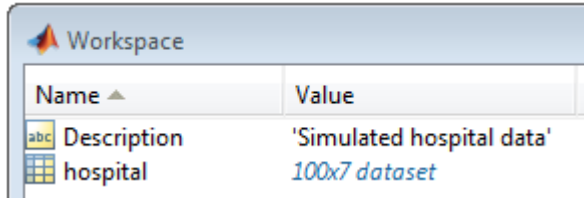
Open Dataset Arrays in the Variables Editor

The MATLAB Variables editor provides a convenient interface for viewing, modifying, and plotting dataset arrays.

First, load the sample data set, `hospital`.

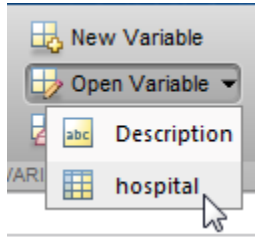
```
load hospital
```

The dataset array, `hospital`, is created in the MATLAB workspace.



The dataset array has 100 observations and 7 variables.

To open `hospital` in the Variables editor, click **Open Variable**, and select `hospital`.



The Variables editor opens, displaying the contents of the dataset array (only the first 10 observations are shown here).

hospital

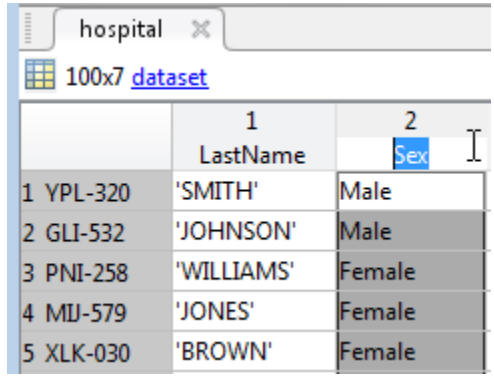
100x7 dataset

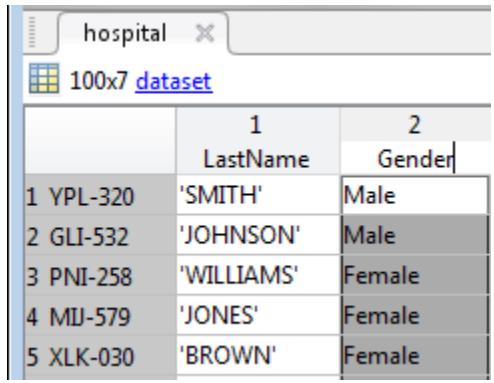
	1 LastName	2 Sex	3 Age	4 Weight	5 Smoker	6 BloodPressure		7 Trials
1	YPL-320	'SMITH'	Male	38	176	1	124	93	18
2	GLI-532	'JOHNSON'	Male	43	163	0	109	77	[11,13,22]
3	PNI-258	'WILLIAMS'	Female	38	131	0	125	83	[]
4	MIJ-579	'JONES'	Female	40	133	0	117	75	[6,12]
5	XLK-030	'BROWN'	Female	49	119	0	122	80	[14,23]
6	TFP-518	'DAVIS'	Female	46	142	0	121	70	19
7	LPD-746	'MILLER'	Female	33	142	1	130	88	13
8	ATA-945	'WILSON'	Male	40	180	0	115	82	[]
9	VNL-702	'MOORE'	Male	28	183	0	115	78	2
10	LQW-768	'TAYLOR'	Female	31	132	0	118	86	11

In the Variables editor, you can see the names of the seven variables along the top row, and the observations names down the first column.

Modify Variable and Observation Names

You can modify variable and observation names by double-clicking a name, and then typing new text.

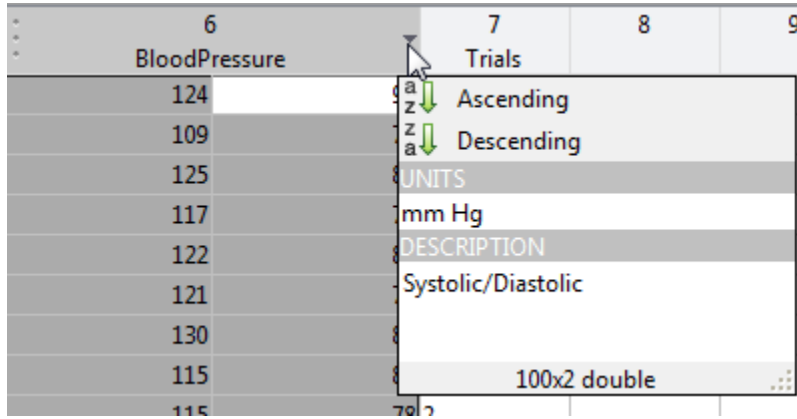




All changes made in the Variables editor are also sent to the command line.

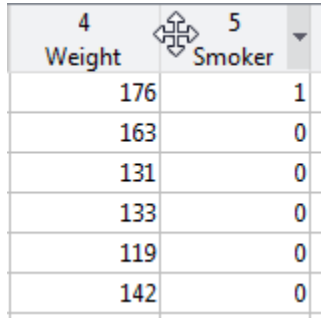
```
Command Window
>> hospital.Properties.VarNames{2} = 'Gender';
>>
```

The sixth variable in the data set, `BloodPressure`, is a numeric array with two columns. The first column shows systolic blood pressure, and the second column shows diastolic blood pressure. Click the arrow that appears on the right side of the variable name cell to see the units and description of the variable. You can type directly in the units and description fields to modify the text. The variable data type and size are shown under the variable description.



Reorder or Delete Variables

You can reorder variables in a dataset array using the Variables editor. Hover over the left side of a variable name cell until a four-headed arrow appears.



After the arrow appears, click and drag the variable column to a new location.

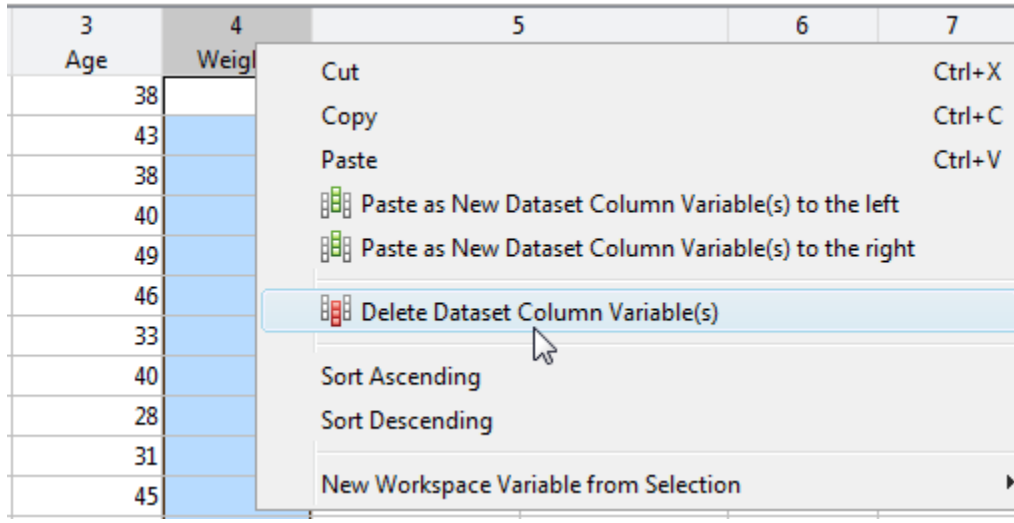
4 Weight	5 Smoke	5 Smoker	6 BloodPressure
176	1	1	124
163	0	0	109
131	0	0	125
133	0	0	117
119	0	0	122
142	0	0	121
142	1	1	130
180	0	0	115
183	0	0	115
132	0	0	118
128	0	0	114
137	0	0	115
174	0	0	127

5 BloodPressure		6 Smoker	7 Trials
124	93	1	18
109	77	0	[11,13,22]
125	83	0	[]
117	75	0	[6,12]
122	80	0	[14,23]
121	70	0	19

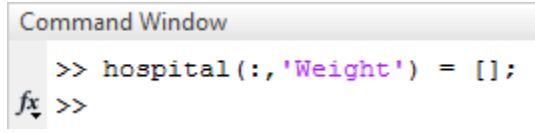
The command for the variable reordering appears in the command line.

```
Command Window
>> hospital = hospital(:,[1:4 6 5 end]);
>>
```

You can delete a variable in the Variables editor by selecting the variable column, right-clicking, and selecting **Delete Column Variable(s)**.

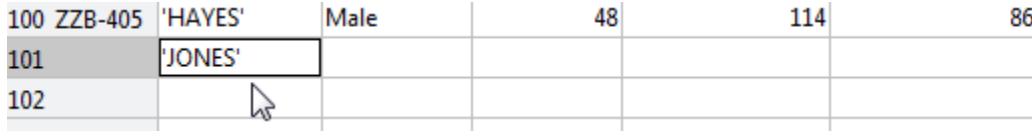


The command for the variable deletion appears in the command line.

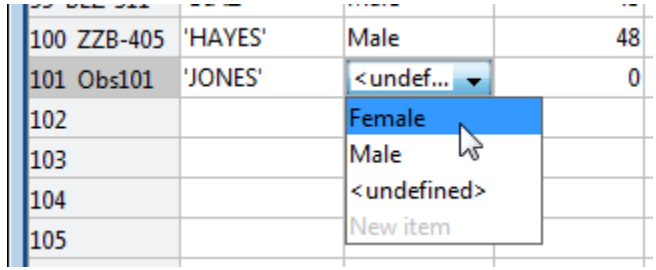


Add New Data

You can enter new data values directly into the Variables editor. For example, you can add a new patient observation to the `hospital` data set. To enter a new last name, add a string to the end of the variable `LastName`.

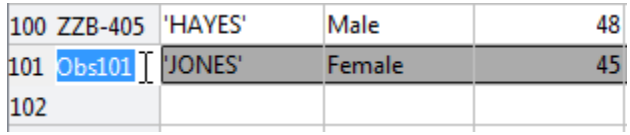


The variable `Gender` is a `nominal` array. The levels of the categorical variable appear in a drop-down list when you double-click a cell in the `Gender` column. You can choose one of the levels previously used, or create a new level by selecting **New Item**.



You can continue to add data for the remaining variables.

To change the observation name, click the observation name and type the new name.



The commands for entering the new data appear at the command line.

```
Command Window
>> hospital.LastName{101} = 'JONES';
Warning: Observations with default values added to dataset
variables.
> In dataset.subsasgn at 584
>> hospital.Sex(101) = 'Female';
>> hospital.Age(101) = 45;
>> hospital.BloodPressure(101,2) = 85;
>> hospital.BloodPressure(101,1) = 120;
>> hospital.Properties.ObsNames{101} = 'QPO-187';
fx >>
```

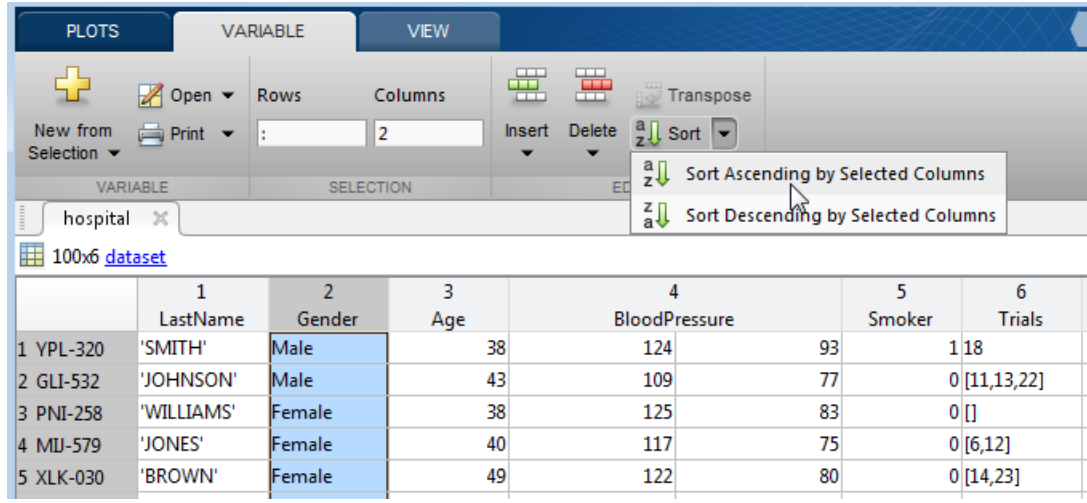
Notice the warning that appears after the first assignment. When you enter the first piece of data in the new observation row—here, the last name—default values are assigned to all other variables. Default assignments are:

- `0` for numeric variables
- `<undefined>` for categorical variables
- `[]` for cell arrays

You can also copy and paste data from one dataset array to another using the Variables editor.

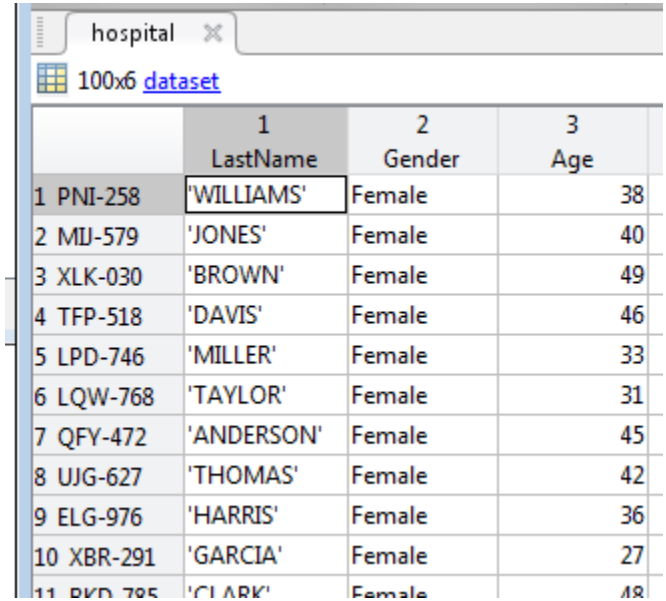
Sort Observations

You can use the Variables editor to sort dataset array observations by the values of one or more variables. To sort by gender, for example, select the variable `Gender`. Then click **Sort**, and choose to sort rows by ascending or descending values of the selected variable.



	1 LastName	2 Gender	3 Age	4 BloodPressure		5 Smoker	6 Trials
1 YPL-320	'SMITH'	Male	38	124	93	1	18
2 GLI-532	'JOHNSON'	Male	43	109	77	0	[11,13,22]
3 PNI-258	'WILLIAMS'	Female	38	125	83	0	[]
4 MIJ-579	'JONES'	Female	40	117	75	0	[6,12]
5 XLK-030	'BROWN'	Female	49	122	80	0	[14,23]

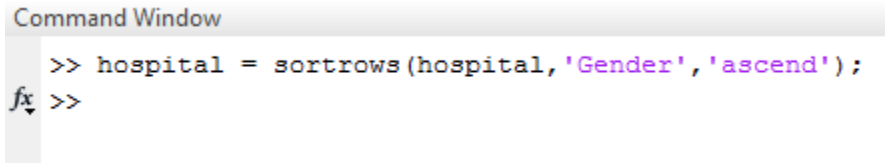
When sorting by variables that are cell arrays of strings or of nominal data type, observations are sorted alphabetically. For ordinal variables, rows are sorted by the ordering of the levels. For example, when the observations of `hospital` are sorted by the values in `Gender`, the females are grouped together, followed by the males.



	1 LastName	2 Gender	3 Age
1 PNI-258	'WILLIAMS'	Female	38
2 MIJ-579	'JONES'	Female	40
3 XLK-030	'BROWN'	Female	49
4 TFP-518	'DAVIS'	Female	46
5 LPD-746	'MILLER'	Female	33
6 LQW-768	'TAYLOR'	Female	31
7 QFY-472	'ANDERSON'	Female	45
8 UJG-627	'THOMAS'	Female	42
9 ELG-976	'HARRIS'	Female	36
10 XBR-291	'GARCIA'	Female	27
11 RKD-785	'CLARK'	Female	48

To sort by the values of multiple variables, press **Ctrl** while you select multiple variables.

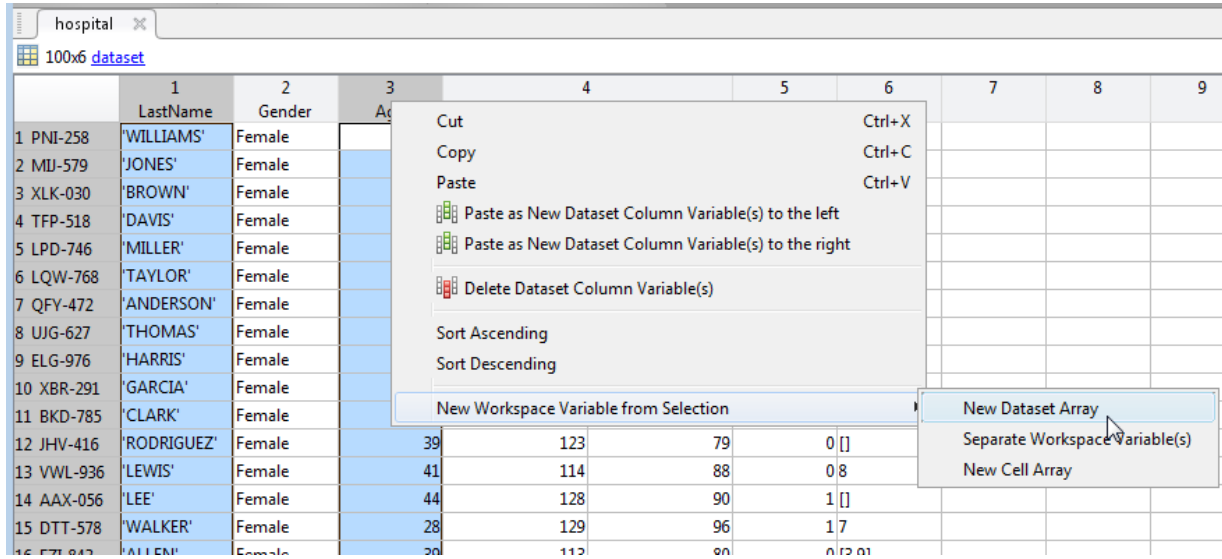
When you use the Variables editor to sort rows, it is the same as calling `sortrows`. You can see this at the command line after executing the sorting.



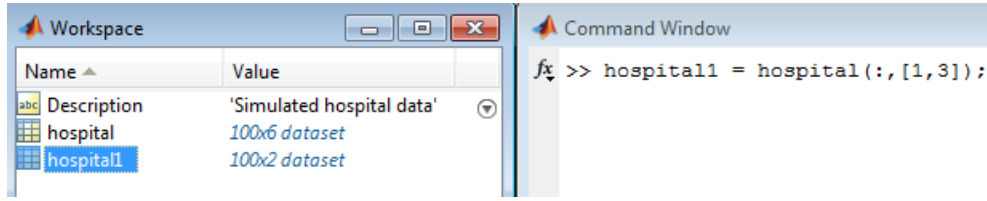
Select a Subset of Data

You can select a subset of data from a dataset array in the Variables editor, and create a new dataset array from the selection. For example, to create a dataset array containing only the variables `LastName` and `Age`:

1. Hold **Ctrl** while you click the variables `LastName` and `Age`.
2. Right-click, and select **New Workspace Variable from Selection > New Dataset Array**.

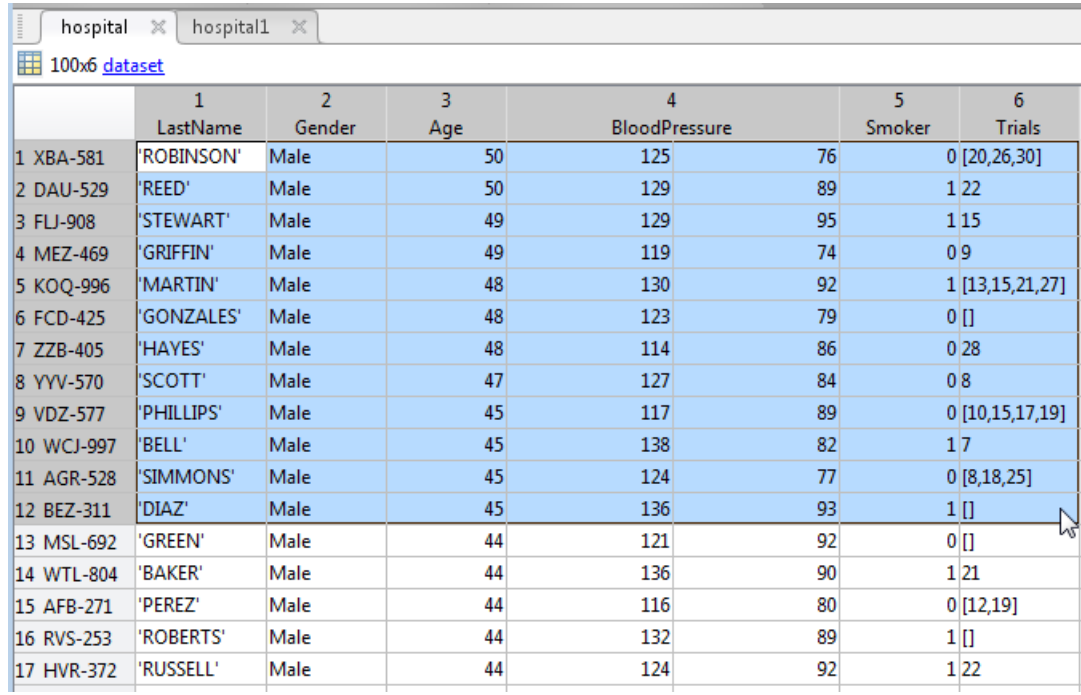


The new dataset array appears in the Workspace window with the name `hospital1`. The Command Window shows the commands that execute the selection.



You can use the same steps to select any subset of data. To select observations according to some logical condition, you can use a combination of sorting and selecting. For example, to create a new dataset array containing only males aged 45 and older:

1. Sort the observations of `hospital` by the values in `Gender` and `Age`, descending.
2. Select the male observations with age 45 and older.

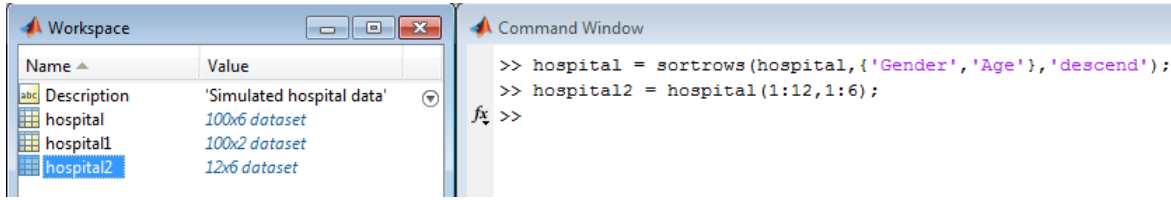


hospital | hospital1

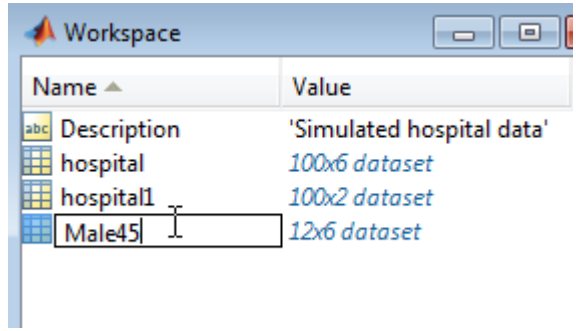
100x6 dataset

	1 LastName	2 Gender	3 Age	4 BloodPressure		5 Smoker	6 Trials
1	XBA-581	'ROBINSON'	Male	50	125	76	0 [20,26,30]
2	DAU-529	'REED'	Male	50	129	89	1 22
3	FLJ-908	'STEWART'	Male	49	129	95	1 15
4	MEZ-469	'GRIFFIN'	Male	49	119	74	0 9
5	KOQ-996	'MARTIN'	Male	48	130	92	1 [13,15,21,27]
6	FCD-425	'GONZALES'	Male	48	123	79	0 []
7	ZZB-405	'HAYES'	Male	48	114	86	0 28
8	YYV-570	'SCOTT'	Male	47	127	84	0 8
9	VDZ-577	'PHILLIPS'	Male	45	117	89	0 [10,15,17,19]
10	WCJ-997	'BELL'	Male	45	138	82	1 7
11	AGR-528	'SIMMONS'	Male	45	124	77	0 [8,18,25]
12	BEZ-311	'DIAZ'	Male	45	136	93	1 []
13	MSL-692	'GREEN'	Male	44	121	92	0 []
14	WTL-804	'BAKER'	Male	44	136	90	1 21
15	AFB-271	'PEREZ'	Male	44	116	80	0 [12,19]
16	RVS-253	'ROBERTS'	Male	44	132	89	1 []
17	HVR-372	'RUSSELL'	Male	44	124	92	1 22

3 Right-click, and select **New Workspace Variables from Selection > New Dataset Array**. The new dataset array, `hospital2`, is created in the Workspace window.



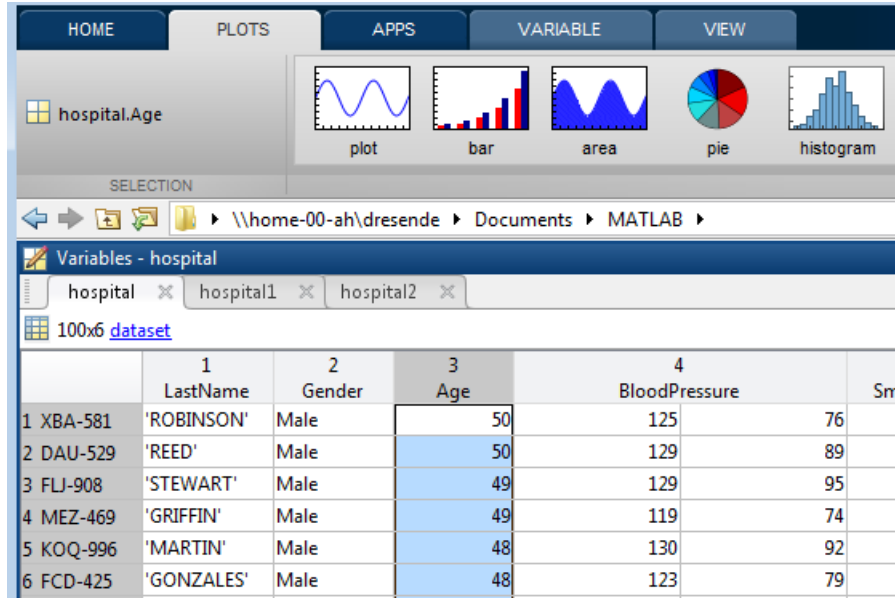
4 You can rename the dataset array in the Workspace window.



Create Plots

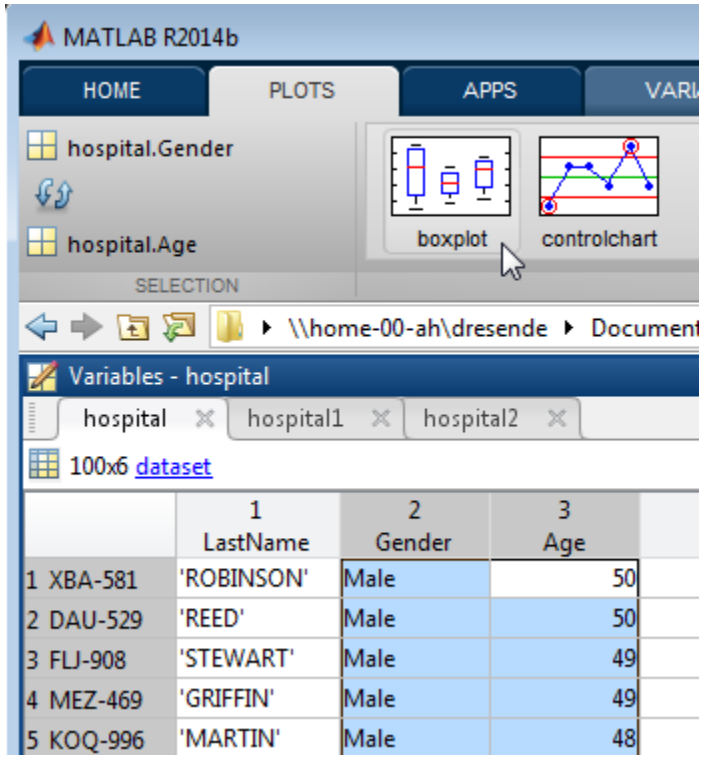
You can plot data from a dataset array using plotting options in the Variables editor. Available plot choices depend on the data types of variables to be plotted.

For example, if you select the variable `Age`, you can see in the **Plots** tab some plotting options that are appropriate for a univariate, numeric variable.



	1 LastName	2 Gender	3 Age	4 BloodPressure	
1	XBA-581	'ROBINSON'	Male	50	125	76
2	DAU-529	'REED'	Male	50	129	89
3	FLJ-908	'STEWART'	Male	49	129	95
4	MEZ-469	'GRIFFIN'	Male	49	119	74
5	KOQ-996	'MARTIN'	Male	48	130	92
6	FCD-425	'GONZALES'	Male	48	123	79

Sometimes, there are plot options for multiple variables, depending on their data types. For example, if you select both `Age` and `Gender`, you can draw box plots of age, grouped by gender.



See Also

`dataset` | `sortrows`

Related Examples

- “Add and Delete Observations” on page 2-77
- “Add and Delete Variables” on page 2-81
- “Access Data in Dataset Array Variables” on page 2-85
- “Select Subsets of Observations” on page 2-91
- “Sort Observations in Dataset Arrays” on page 2-95

More About

- "Dataset Arrays" on page 2-132

Dataset Arrays

Note: The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

In this section...

What Are Dataset Arrays?

Statistics and Machine Learning Toolbox has *dataset arrays* for storing variables with heterogeneous data types. For example, you can combine numeric data, logical data, cell arrays of strings, and categorical arrays in one dataset array variable.

Within a dataset array, each variable (column) must be one homogeneous data type, but the different variables can be of heterogeneous data types. A dataset array is usually interpreted as a set of variables measured on many units of observation. That is, each row in a dataset array corresponds to an observation, and each column to a variable. In this sense, a dataset array organizes data like a typical spreadsheet.

Dataset arrays are a unique data type, with a corresponding set of valid operations. Even if a dataset array contains only numeric variables, you cannot operate on the dataset array like a numeric variable. The valid operations for dataset arrays are the methods of the `dataset` class.

Dataset Array Conversion

You can create a dataset array by combining variables that exist in the MATLAB workspace, or directly importing data from a file, such as a text file or spreadsheet. This table summarizes the functions you can use to create dataset arrays.

Data Source	Conversion to Dataset Array
Data from a file	`dataset`

Data Source	Conversion to Dataset Array
Heterogeneous collection of workspace variables	`dataset`
Numeric array	`mat2dataset`
Cell array	`cell2dataset`
Structure array	`struct2dataset`
Table	`table2dataset`

You can export dataset arrays to text or spreadsheet files using `export`. To convert a dataset array to a cell array or structure array, use `dataset2cell` or `dataset2struct`. To convert a dataset array to a table, use `dataset2table`.

Dataset Array Properties

In addition to storing data in a dataset array, you can store metadata such as:

- Variable and observation names
- Data descriptions
- Units of measurement
- Variable descriptions

This information is stored as dataset array properties. For a dataset array named `ds`, you can view the dataset array metadata by entering `ds.Properties` at the command line. You can access a specific property, such as variable names—property `VarNames`—using `ds.Properties.VarNames`. You can both retrieve and modify property values using this syntax.

Variable and observation names are included in the display of a dataset array. Variable names display across the top row, and observation names, if present, appear in the first column. Note that variable and observation names do not affect the size of a dataset array.

See Also

`cell2dataset` | `dataset` | `dataset2cell` | `dataset2struct` | `dataset2table` | `export` | `mat2dataset` | `struct2dataset` | `table2dataset`

Related Examples

- “Create a Dataset Array from Workspace Variables” on page 2-63
- “Create a Dataset Array from a File” on page 2-69
- “Export Dataset Arrays” on page 2-111
- “Dataset Arrays in the Variables Editor” on page 2-118
- “Index and Search Dataset Arrays” on page 2-135

Index and Search Dataset Arrays

Note: The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Ways To Index and Search

There are many ways to index into dataset arrays. For example, for a dataset array, `ds`, you can:

- Use `()` to create a new dataset array from a subset of `ds`. For example, `ds1 = ds(1:5,:)` creates a new dataset array, `ds1`, consisting of the first five rows of `ds`. Metadata, including variable and observation names, transfers to the new dataset array.
- Use variable names with dot notation to index individual variables in a dataset array. For example, `ds.Height` indexes the variable named `Height`.
- Use observation names to index individual observations in a dataset array. For example, `ds('Obs1',:)` gives data for the observation named `Obs1`.
- Use observation or variable numbers. For example, `ds(:,[1,3,5])` gives the data in the first, third, and fifth variables (columns) of `ds`.
- Use logical indexing to search for observations in `ds` that satisfy a logical condition. For example, `ds(ds.Gender=='Male',:)` gives the observations in `ds` where the variable named `Gender`, a nominal array, has the value `Male`.
- Use `ismissing` to find missing data in the dataset array.

Examples

Common Indexing and Searching Methods

This example shows several indexing and searching methods for categorical arrays.

Load the sample data.

```
load hospital;
size(hospital)
```

```
ans =

   100     7
```

The dataset array has 100 observations and 7 variables.

Index a variable by name. Return the minimum age in the dataset array.

```
min(hospital.Age)
```

```
ans =

    25
```

Delete the variable `Trials`.

```
hospital.Trials = [];
size(hospital)
```

```
ans =

   100     6
```

Index an observation by name. Display measurements on the first five variables for the observation named `PUE-347`.

```
hospital('PUE-347',1:5)
```

```
ans =

              LastName       Sex       Age    Weight    Smoker
    PUE-347    'YOUNG'        Female    25     114       false
```

Index variables by number. Create a new dataset array containing the first four variables of `hospital`.

```
dsNew = hospital(:,1:4);
```

```
dsNew.Properties.VarNames(:)
```

```
ans =

    'LastName'
    'Sex'
    'Age'
    'Weight'
```

Index observations by number. Delete the last 10 observations.

```
hospital(end-9:end,:) = [];
size(hospital)
```

```
ans =

    90     6
```

Search for observations by logical condition. Create a new dataset array containing only females who smoke.

```
dsFS = hospital(hospital.Sex=='Female' & hospital.Smoker==true,:);
dsFS(:,{'LastName','Sex','Smoker'})
```

```
ans =

              LastName           Sex       Smoker
    LPD-746    'MILLER'          Female    true
    XBR-291    'GARCIA'          Female    true
    AAX-056    'LEE'             Female    true
    DTT-578    'WALKER'          Female    true
    AFK-336    'WRIGHT'          Female    true
    RBA-579    'SANCHEZ'         Female    true
    HAK-381    'MORRIS'          Female    true
    NSK-403    'RAMIREZ'         Female    true
    ILS-109    'WATSON'          Female    true
    JDR-456    'SANDERS'         Female    true
    HWZ-321    'PATTERSON'       Female    true
    GGU-691    'HUGHES'          Female    true
    WUS-105    'FLORES'          Female    true
```

See Also

`dataset`

Related Examples

- “Access Data in Dataset Array Variables” on page 2-85
- “Select Subsets of Observations” on page 2-91

More About

- “Dataset Arrays” on page 2-132

3

Descriptive Statistics

Introduction to Descriptive Statistics

You may need to summarize large, complex data sets—both numerically and visually—to convey their essence to the data analyst and to allow for further processing.

Measures of Central Tendency

Measures of central tendency locate a distribution of data along an appropriate scale.

The following table lists the functions that calculate the measures of central tendency.

Function Name	Description
`geomean`	Geometric mean
`harmmean`	Harmonic mean
`mean`	Arithmetic average
`median`	50th percentile
`mode`	Most frequent value
`trimmean`	Trimmed mean

The average is a simple and popular estimate of location. If the data sample comes from a normal distribution, then the sample mean is also optimal (minimum variance unbiased estimator (MVUE) of μ).

Unfortunately, outliers, data entry errors, or glitches exist in almost all real data. The sample mean is sensitive to these problems. One bad data value can move the average away from the center of the rest of the data by an arbitrarily large distance.

The median and trimmed mean are two measures that are resistant (robust) to outliers. The median is the 50th percentile of the sample, which will only change slightly if you add a large perturbation to any value. The idea behind the trimmed mean is to ignore a small percentage of the highest and lowest values of a sample when determining the center of the sample.

The geometric mean and harmonic mean, like the average, are not robust to outliers. They are useful when the sample is distributed lognormal or heavily skewed. This example shows the behavior of the measures of location for a sample with one outlier:

```
x = [ones(1,6) 100];
locate = [geomean(x) harmmean(x) mean(x) median(x)...
          trimmean(x,25)]


locate =
```

```
    1.9307    1.1647   15.1429    1.0000    1.0000
```

You can see that the mean is far from any data value because of the influence of the outlier. The median and trimmed mean ignore the outlying value and describe the location of the rest of the data values.

Measures of Dispersion

The purpose of measures of dispersion is to find out how spread out the data values are on the number line. Another term for these statistics is measures of spread.

The table gives the function names and descriptions.

Function Name	Description
`iqr`	Interquartile range
`mad`	Mean absolute deviation
`moment`	Central moment of all orders
`range`	Range
`std`	Standard deviation
`var`	Variance

The range (the difference between the maximum and minimum values) is the simplest measure of spread. But if there is an outlier in the data, it will be the minimum or maximum value. Thus, the range is not robust to outliers.

The standard deviation and the variance are popular measures of spread that are optimal for normally distributed samples. The sample variance is the minimum variance unbiased estimator (MVUE) of the normal parameter σ^2. The standard deviation is the square root of the variance and has the desirable property of being in the same units as the data. That is, if the data is in meters, the standard deviation is in meters as well. The variance is in meters^2, which is more difficult to interpret.

Neither the standard deviation nor the variance is robust to outliers. A data value that is separate from the body of the data can increase the value of the statistics by an arbitrarily large amount.

The mean absolute deviation (MAD) is also sensitive to outliers. But the MAD does not move quite as much as the standard deviation or variance in response to bad data.

The interquartile range (IQR) is the difference between the 75th and 25th percentile of the data. Since only the middle 50% of the data affects this measure, it is robust to outliers.

This example shows the behavior of the measures of dispersion for a sample with one outlier:

```
x = [ones(1,6) 100]
stats = [iqr(x) mad(x) range(x) std(x)]


x =

     1     1     1     1     1     1   100


stats =

         0   24.2449   99.0000   37.4185
```

Quantiles and Percentiles

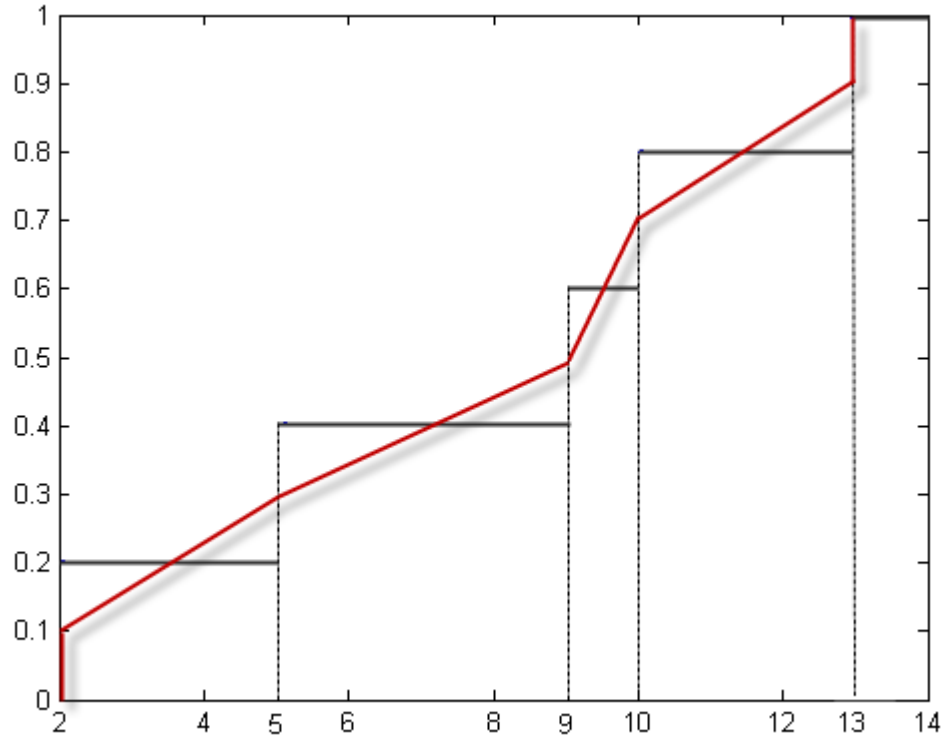
This section explains how the Statistics and Machine Learning Toolbox functions `quantile` and `prctile` compute quantiles and percentiles.

The `prctile` function calculates the percentiles in a similar way as `quantile` calculates quantiles. The following steps in the computation of quantiles are also true for percentiles, given the fact that, for the same data sample, the quantile at the value Q is the same as the percentile at the value P = 100*Q.

1. `quantile` initially assigns the sorted values in `X` to the (0.5/n), (1.5/n), ..., ([n – 0.5]/n) quantiles. For example:

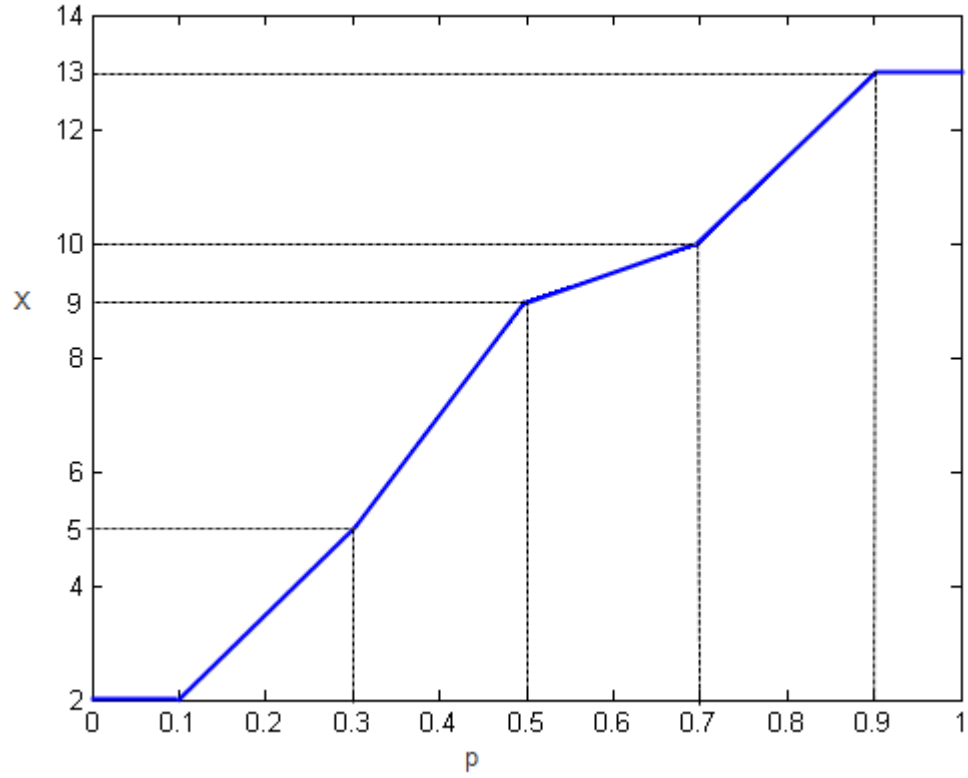
   - For a data vector of six elements such as {6, 3, 2, 10, 8, 1}, the sorted elements {1, 2, 3, 6, 8, 10} respectively correspond to the (0.5/6), (1.5/6), (2.5/6), (3.5/6), (4.5/6), and (5.5/6) quantiles.
   - For a data vector of five elements such as {2, 10, 5, 9, 13}, the sorted elements {2, 5, 9, 10, 13} respectively correspond to the 0.1, 0.3, 0.5, 0.7, and 0.9 quantiles.

   The following figure illustrates this approach for data vector X = {2, 10, 5, 9, 13}. The first observation corresponds to the cumulative probability 1/5 = 0.2, the second observation corresponds to the cumulative probability 2/5 = 0.4, and so on. The step function in this figure shows these cumulative probabilities. `quantile` instead places the observations in midpoints, such that the first corresponds to 0.5/5 = 0.1, the second corresponds to 1.5/5 = 0.3, and so on, and then connects these midpoints. The red lines in the following figure connect the midpoints.



Assigning Observations to Quantiles

By switching the axes, as the next figure, you can see the values of the variable X that correspond to the p quantiles.



Quantiles of *X*

2 `quantile` finds any quantiles between the data values using linear interpolation.

Linear interpolation uses linear polynomials to approximate a function f(x) and construct new data points within the range of a known set of data points. Algebraically, given the data points (x_1, y_1) and (x_2, y_2), where $y_1 = f(x_1)$ and $y_2 = f(x_2)$, linear interpolation finds $y = f(x)$ for a given x between x_1 and x_2 as follows:

$$y = f(x) = y_1 + \frac{(x - x_1)}{(x_2 - x_1)}(y_2 - y_1).$$

Similarly, if the $1.5/n$ quantile is $y_{1.5/n}$ and the $2.5/n$ quantile is $y_{2.5/n}$, then linear interpolation finds the $2.3/n$ quantile $y_{2.3/n}$ as

$$y_{\frac{2.3}{n}} = y_{\frac{1.5}{n}} + \frac{\left(\frac{2.3}{n} - \frac{1.5}{n}\right)}{\left(\frac{2.5}{n} - \frac{1.5}{n}\right)}\left(y_{\frac{2.5}{n}} - y_{\frac{1.5}{n}}\right).$$

3 `quantile` assigns the first and last values of X to the quantiles for probabilities less than $(0.5/n)$ and greater than $([n–0.5]/n)$, respectively.

References

[1] Langford, E. "Quartiles in Elementary Statistics", *Journal of Statistics Education*. Vol. 14, No. 3, 2006.

See Also

`median` | `prctile` | `quantile`

Exploratory Analysis of Data

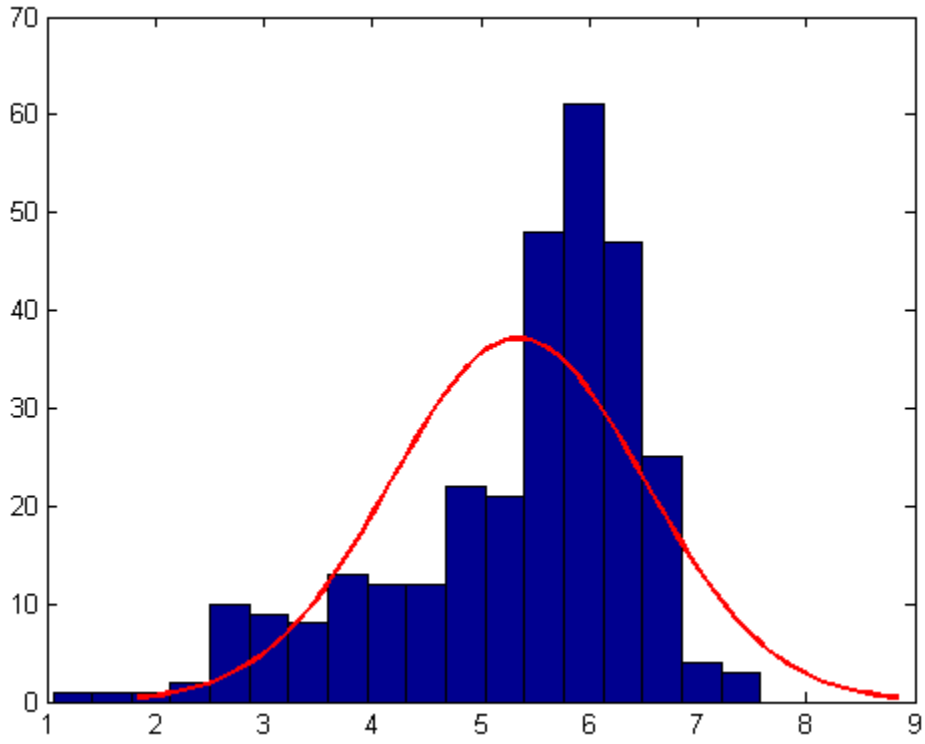
This example shows how to explore the distribution of data using descriptive statistics.

Generate sample data.

```
rng('default') % for reproducibility
x = [normrnd(4,1,1,100) normrnd(6,0.5,1,200)];
```

Create a histogram of data with normal density fit.

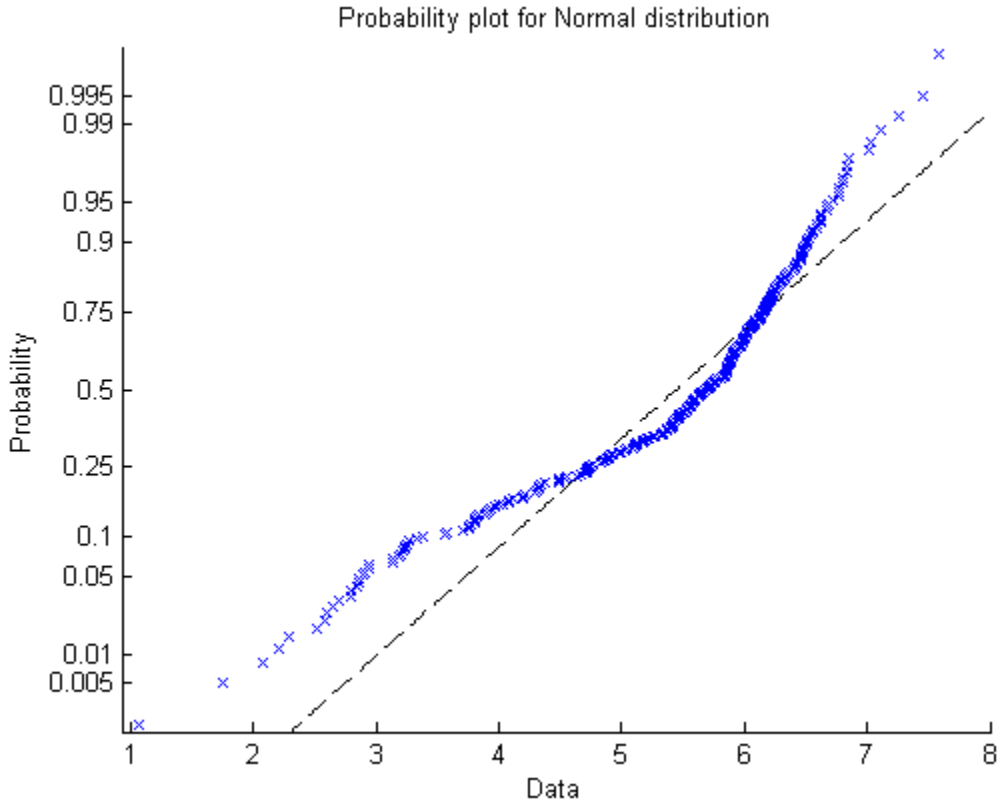
```
histfit(x)
```



The distribution of the data seems left skewed and normal distribution does not look like a good fit to this distribution.

Obtain a normal probability plot.

```
probplot('normal',x)
```



This probability plot also clearly shows the deviation of data from normality.

Compute quantiles of data.

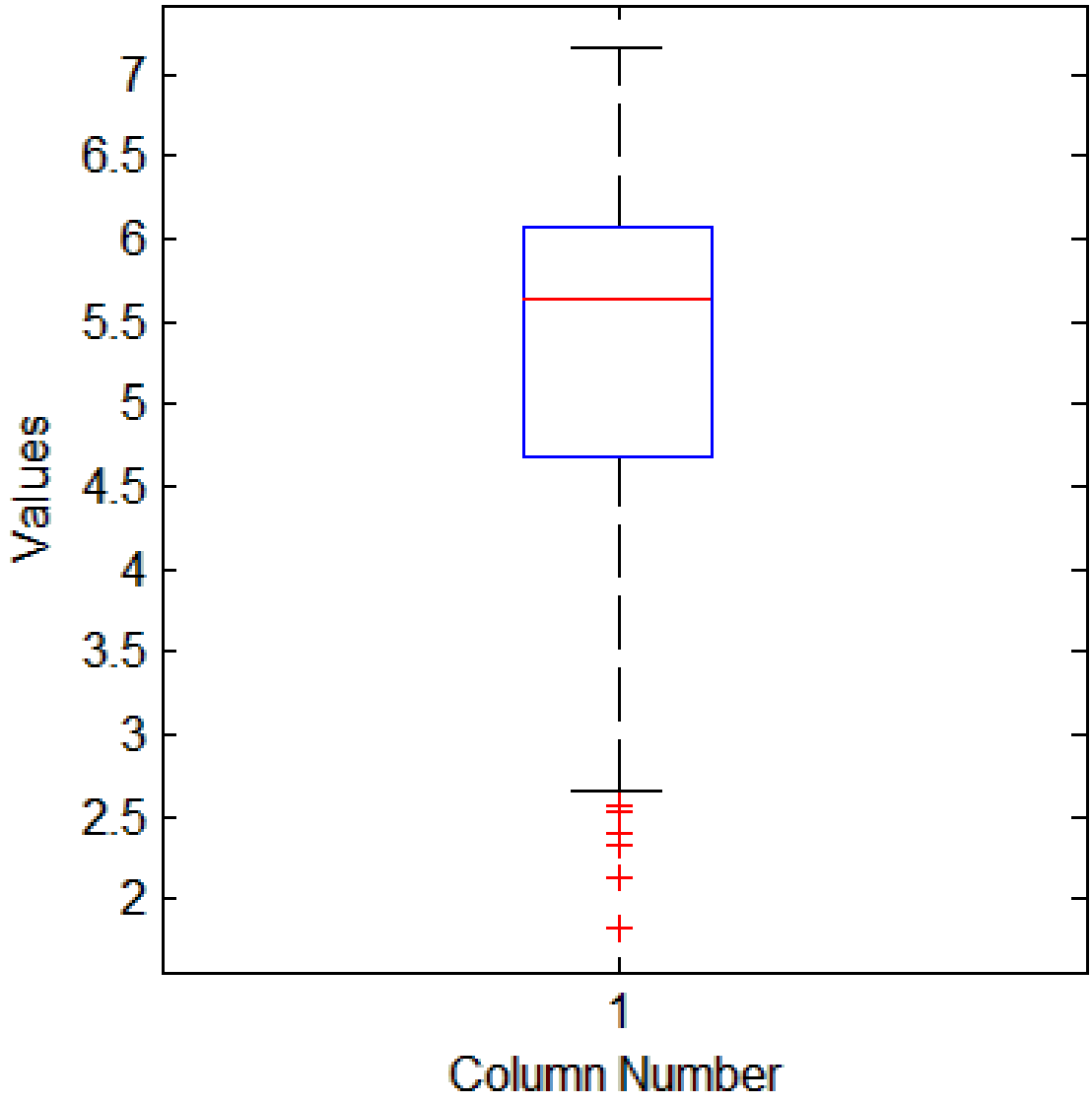
```
p = 0:0.25:1;
y = quantile(x,p);
z = [p;y]
```

```
z =

         0    0.2500    0.5000    0.7500    1.0000
    1.0557    4.7375    5.6872    6.1526    7.5784
```

Plot a box plot.

A box plot helps to visualize the statistics.

```
boxplot(x)
```



You can also see the 0.25, 0.5, and 0.75 quantiles in the box plot. The long lower tail and plus signs also show the lack of symmetry in the sample values.

Compute the mean and median of data.

```
 y = [mean(x) median(x)]

y =

    5.3438    5.6872
```

The mean and median values seem close to each other, but a mean smaller than the median usually flags left skewness of the data.

Compute the skewness and kurtosis of data.

```
y = [skewness(x) kurtosis(x)]

y =

   -1.0417    3.5895
```

A negative skewness value means the data is left skewed. The data has a larger peakedness than a normal distribution because the kurtosis value is greater than 3.

Identify possible outliers.

Compute z-scores. Find the z-scores that are greater than 3 or less than –3.

```
Z = zscore(x);
find(abs(Z)>3);

ans =

     3    35
```

The 3rd and 35th observations might be outliers.

See Also

`boxplot` | `histfit` | `kurtosis` | `mean` | `median` | `prctile` | `quantile` | `skewness`

More About

- “Box Plots” on page 4-6
- “Measures of Central Tendency” on page 3-3
- “Measures of Dispersion” on page 3-5

- “Quantiles and Percentiles” on page 3-7

Resampling Statistics

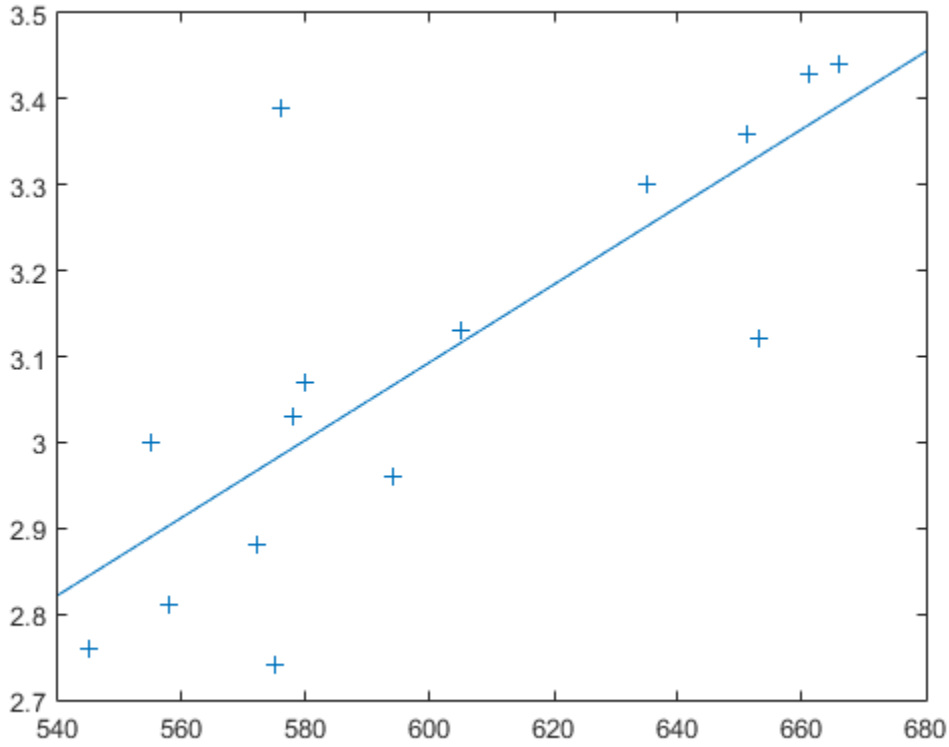
In this section...

Bootstrap Resampling

The bootstrap procedure involves choosing random samples with replacement from a data set and analyzing each sample the same way. Sampling with replacement means that each observation is selected separately at random from the original dataset. So a particular data point from the original data set could appear multiple times in a given bootstrap sample. The number of elements in each bootstrap sample equals the number of elements in the original data set. The range of sample estimates you obtain enables you to establish the uncertainty of the quantity you are estimating.

This example from Efron and Tibshirani compares Law School Admission Test (LSAT) scores and subsequent law school grade point average (GPA) for a sample of 15 law schools.

```
load lawdata
plot(lsat,gpa,'+')
lsline
```



The least-squares fit line indicates that higher LSAT scores go with higher law school GPAs. But how certain is this conclusion? The plot provides some intuition, but nothing quantitative.

You can calculate the correlation coefficient of the variables using the `corr` function.

```
rhohat = corr(lsat,gpa)
```

```
rhohat =

    0.7764
```

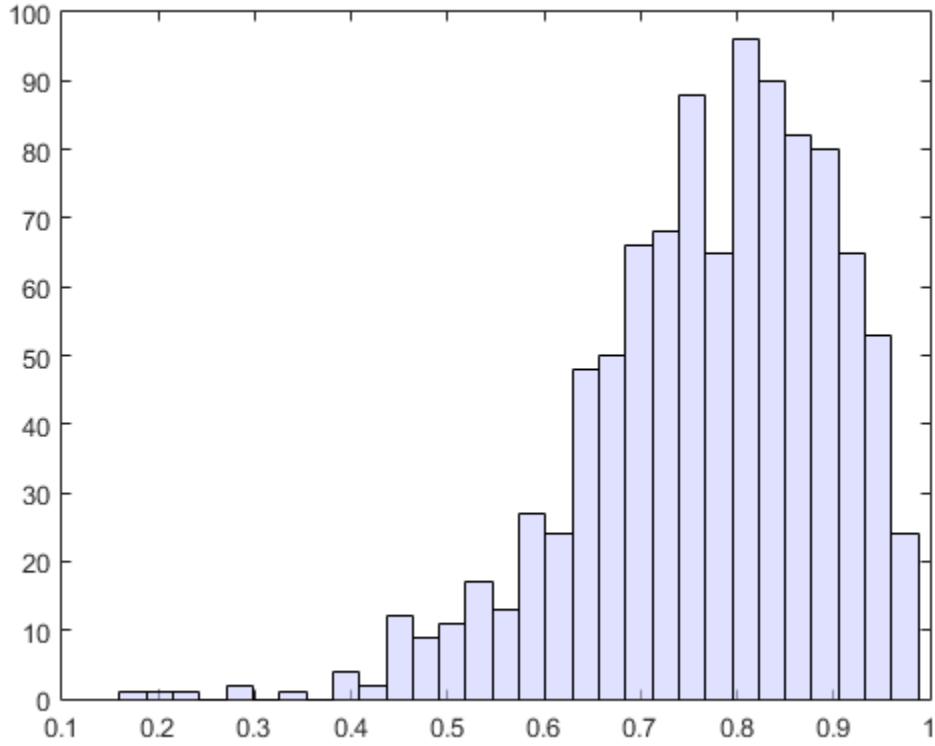
Now you have a number describing the positive connection between LSAT and GPA; though it may seem large, you still do not know if it is statistically significant.

Using the `bootstrp` function you can resample the `lsat` and `gpa` vectors as many times as you like and consider the variation in the resulting correlation coefficients.

```
rng default  % For reproducibility
rhos1000 = bootstrp(1000,'corr',lsat,gpa);
```

This resamples the `lsat` and `gpa` vectors 1000 times and computes the `corr` function on each sample. You can then plot the result in a histogram.

```
histogram(rhos1000,30,'FaceColor',[.8 .8 1])
```



Nearly all the estimates lie on the interval [0.4 1.0].

It is often desirable to construct a confidence interval for a parameter estimate in statistical inferences. Using the `bootci` function, you can use bootstrapping to obtain a confidence interval for the `lsat` and `gpa` data.

```
ci = bootci(5000,@corr,lsat,gpa)
```

```
ci =

    0.3319
    0.9427
```

Therefore, a 95% confidence interval for the correlation coefficient between LSAT and GPA is [0.33 0.94]. This is strong quantitative evidence that LSAT and subsequent GPA are positively correlated. Moreover, this evidence does not require any strong assumptions about the probability distribution of the correlation coefficient.

Although the `bootci` function computes the Bias Corrected and accelerated (BCa) interval as the default type, it is also able to compute various other types of bootstrap confidence intervals, such as the studentized bootstrap confidence interval.

Jackknife Resampling

Similar to the bootstrap is the jackknife, which uses resampling to estimate the bias of a sample statistic. Sometimes it is also used to estimate standard error of the sample statistic. The jackknife is implemented by the Statistics and Machine Learning Toolbox™ function `jackknife`.

The jackknife resamples systematically, rather than at random as the bootstrap does. For a sample with `n` points, the jackknife computes sample statistics on `n` separate samples of size `n`-1. Each sample is the original data with a single observation omitted.

In the bootstrap example, you measured the uncertainty in estimating the correlation coefficient. You can use the jackknife to estimate the bias, which is the tendency of the sample correlation to over-estimate or under-estimate the true, unknown correlation. First compute the sample correlation on the data.

```
load lawdata
rhohat = corr(lsat,gpa)
```

```
rhohat =

    0.7764
```

Next compute the correlations for jackknife samples, and compute their mean.

```
rng default;  % For reproducibility
jackrho = jackknife(@corr,lsat,gpa);
meanrho = mean(jackrho)
```

```
meanrho =

    0.7759
```

Now compute an estimate of the bias.

```
n = length(lsat);
biasrho = (n-1) * (meanrho-rhohat)
```

```
biasrho =

   -0.0065
```

The sample correlation probably underestimates the true correlation by about this amount.

Parallel Computing Support for Resampling Methods

For information on computing resampling statistics in parallel, see Parallel Computing Toolbox™.

Data with Missing Values

Many data sets have one or more missing values. It is convenient to code missing values as `NaN` (Not a Number) to preserve the structure of data sets across multiple variables and observations.

For example:

```
X = magic(3);
X([1 5]) = [NaN NaN]
```

```
X =

   NaN     1     6
     3   NaN     7
     4     9     2
```

Normal MATLAB arithmetic operations yield `NaN` values when operands are `NaN`:

```
s1 = sum(X)
```

```
s1 =

   NaN   NaN    15
```

Removing the `NaN` values would destroy the matrix structure. Removing the rows containing the `NaN` values would discard data. Statistics and Machine Learning Toolbox functions in the following table remove `NaN` values only for the purposes of computation.

Function	Description
`nancov`	Covariance matrix, ignoring `NaN` values
`nanmax`	Maximum, ignoring `NaN` values
`nanmean`	Mean, ignoring `NaN` values
`nanmedian`	Median, ignoring `NaN` values
`nanmin`	Minimum, ignoring `NaN` values
`nanstd`	Standard deviation, ignoring `NaN` values

Function	Description
`nansum`	Sum, ignoring `NaN` values
`nanvar`	Variance, ignoring `NaN` values

For example:

```
s2 = nansum(X)
```

```
s2 =

     7     10     15
```

Other Statistics and Machine Learning Toolbox functions also ignore `NaN` values. These include `iqr`, `kurtosis`, `mad`, `prctile`, `range`, `skewness`, and `trimmean`.

4

Statistical Visualization

Introduction to Statistical Visualization

Statistics and Machine Learning Toolbox data visualization functions add to the extensive graphics capabilities already in MATLAB.

- Scatter plots are a basic visualization tool for multivariate data. They are used to identify relationships among variables. Grouped versions of these plots use different plotting symbols to indicate group membership. The `gname` function is used to label points on these plots with a text label or an observation number.
- Box plots display a five-number summary of a set of data: the median, the two ends of the interquartile range (the box), and two extreme values (the whiskers) above and below the box. Because they show less detail than histograms, box plots are most useful for side-by-side comparisons of two distributions.
- Distribution plots help you identify an appropriate distribution family for your data. They include normal and Weibull probability plots, quantile-quantile plots, and empirical cumulative distribution plots.

Advanced Statistics and Machine Learning Toolbox visualization functions are available for specialized statistical analyses.

Create Scatter Plots Using Grouped Data

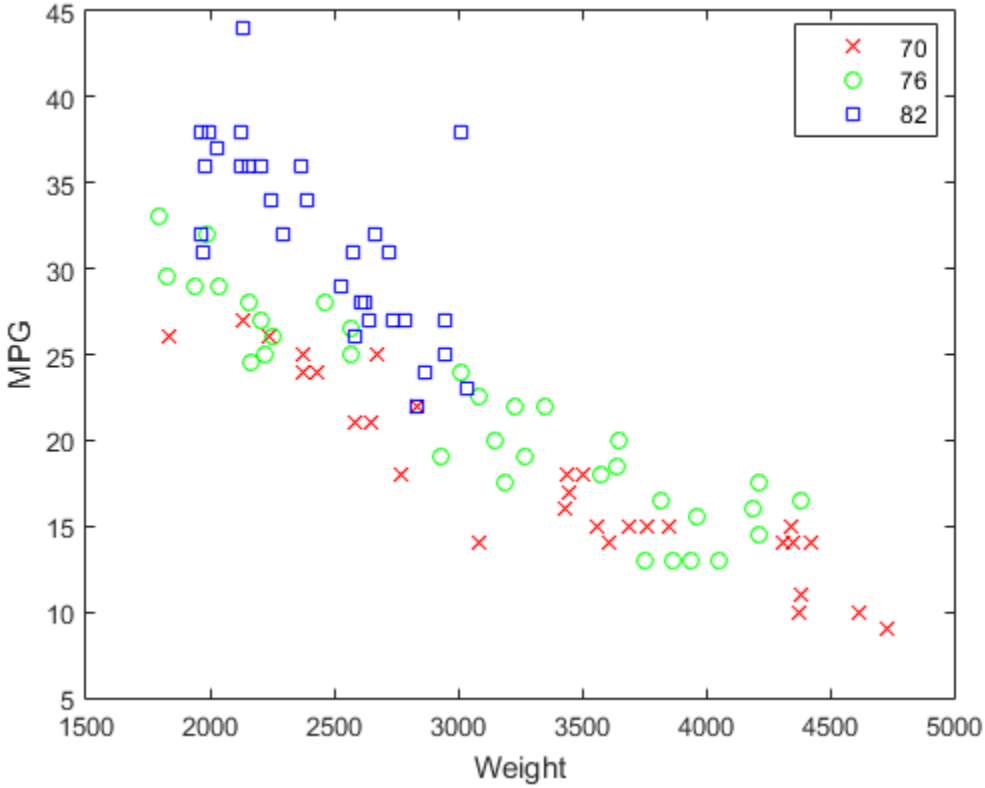
This example shows how to create scatter plots using grouped sample data.

A scatter plot is a simple plot of one variable against another. The MATLAB® functions `plot` and `scatter` produce scatter plots. The MATLAB function `plotmatrix` can produce a matrix of such plots showing the relationship between several pairs of variables.

Statistics and Machine Learning Toolbox™ functions `gscatter` and `gplotmatrix` produce grouped versions of these plots. These are useful for determining whether the values of two variables or the relationship between those variables is the same in each group.

Suppose you want to examine the weight and mileage of cars from three different model years.

```
load carsmall
gscatter(Weight,MPG,Model_Year,'','xos')
```

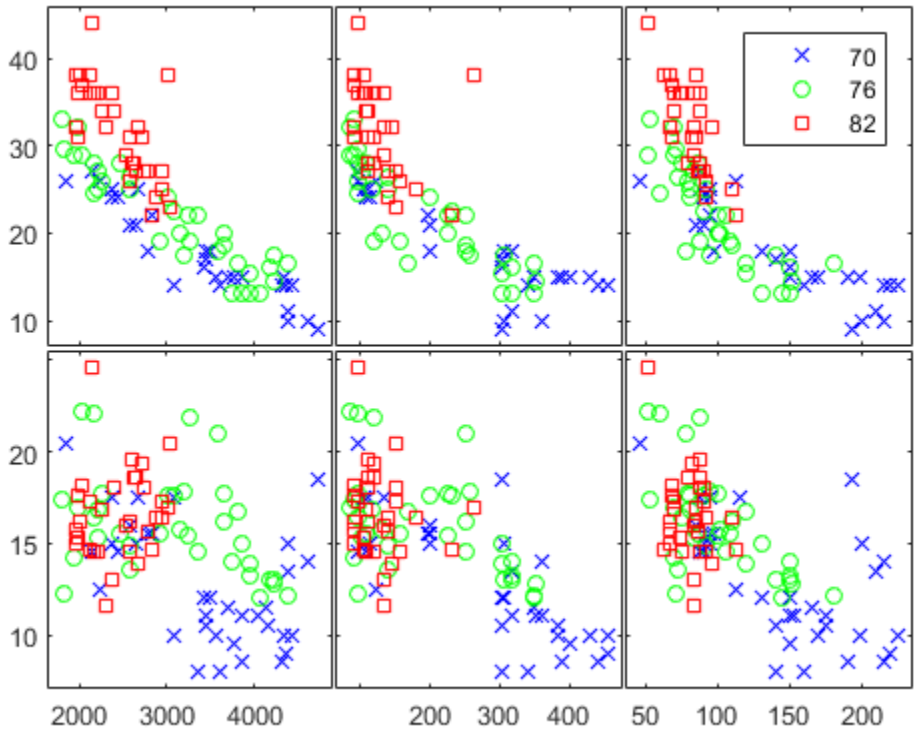


This shows that not only is there a strong relationship between the weight of a car and its mileage, but also that newer cars tend to be lighter and have better gas mileage than older cars.

The default arguments for `gscatter` produce a scatter plot with the different groups shown with the same symbol but different colors. The last two arguments above request that all groups be shown in default colors and with different symbols.

The `carsmall` data set contains other variables that describe different aspects of cars. You can examine several of them in a single display by creating a grouped plot matrix.

```
xvars = [Weight Displacement Horsepower];
yvars = [MPG Acceleration];
gplotmatrix(xvars,yvars,Model_Year,'','xos')
```



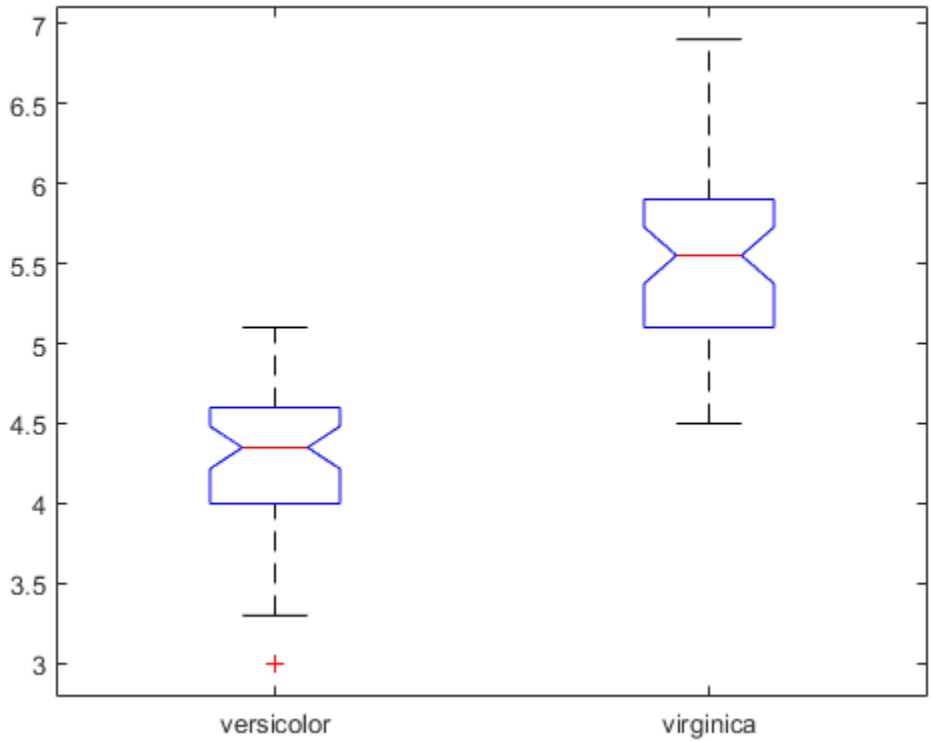
The upper right subplot displays `MPG` against `Horsepower`, and shows that over the years the horsepower of the cars has decreased but the gas mileage has improved.

The `gplotmatrix` function can also graph all pairs from a single list of variables, along with histograms for each variable. See MANOVA.

Box Plots

The graph below, created with the `boxplot` command, compares petal lengths in samples from two species of iris.

```
load fisheriris
s1 = meas(51:100,3);
s2 = meas(101:150,3);
figure;
boxplot([s1 s2],'notch','on',...
        'labels',{'versicolor','virginica'})
```



This plot has the following features:

- The tops and bottoms of each “box” are the 25th and 75th percentiles of the samples, respectively. The distances between the tops and bottoms are the interquartile ranges.
- The line in the middle of each box is the sample median. If the median is not centered in the box, it shows sample skewness.
- The whiskers are lines extending above and below each box. Whiskers are drawn from the ends of the interquartile ranges to the furthest observations within the whisker length (the *adjacent values*).
- Observations beyond the whisker length are marked as outliers. By default, an outlier is a value that is more than 1.5 times the interquartile range away from the top or bottom of the box, but this value can be adjusted with additional input arguments. Outliers are displayed with a red + sign.
- Notches display the variability of the median between samples. The width of a notch is computed so that box plots whose notches do not overlap (as above) have different medians at the 5% significance level. The significance level is based on a normal distribution assumption, but comparisons of medians are reasonably robust for other distributions. Comparing box-plot medians is like a visual hypothesis test, analogous to the *t* test used for means.

Distribution Plots

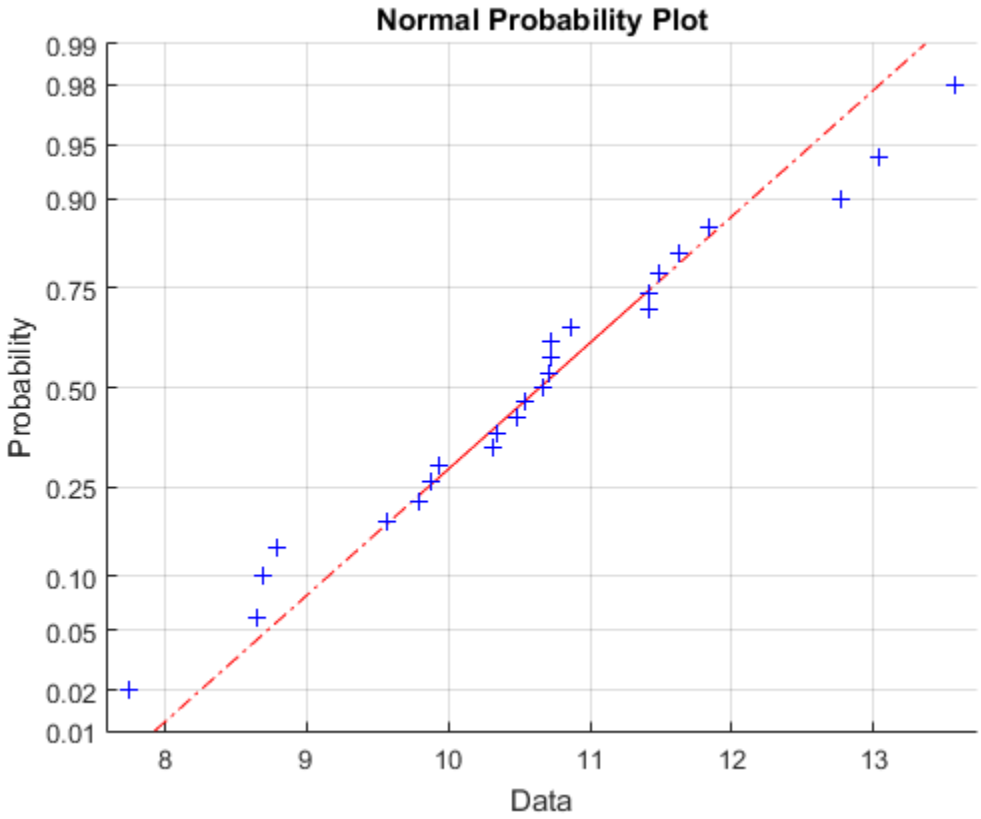
In this section...

Normal Probability Plots

Normal probability plots are used to assess whether data comes from a normal distribution. Many statistical procedures make the assumption that an underlying distribution is normal, so normal probability plots can provide some assurance that the assumption is justified, or else provide a warning of problems with the assumption. An analysis of normality typically combines normal probability plots with hypothesis tests for normality.

This example generates a data sample of 25 random numbers from a normal distribution with `mu = 10` and `sigma = 1`, and creates a normal probability plot of the data.

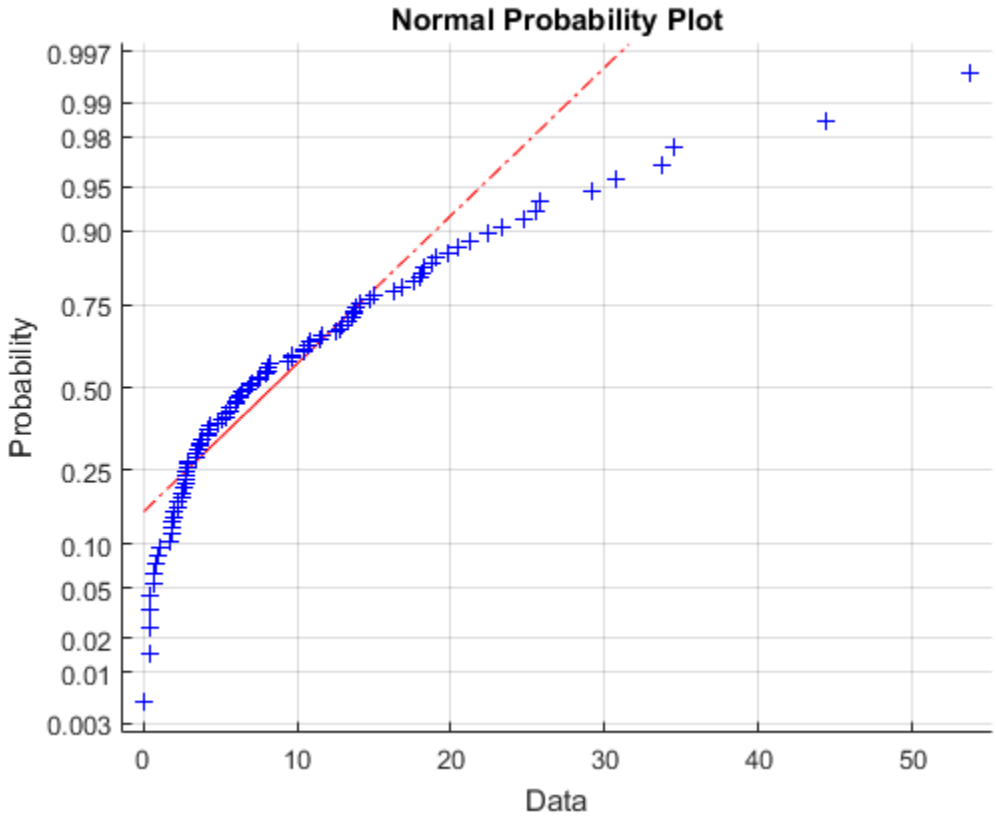
```
rng default;  % For reproducibility
x = normrnd(10,1,25,1);
normplot(x)
```



The plus signs plot the empirical probability versus the data value for each point in the data. A solid line connects the 25th and 75th percentiles in the data, and a dashed line extends it to the ends of the data. The *y*-axis values are probabilities from zero to one, but the scale is not linear. The distance between tick marks on the *y*-axis matches the distance between the quantiles of a normal distribution. The quantiles are close together near the median (probability = 0.5) and stretch out symmetrically as you move away from the median.

In a normal probability plot, if all the data points fall near the line, an assumption of normality is reasonable. Otherwise, the points will curve away from the line, and an assumption of normality is not justified. For example, the following generates a data sample of 100 random numbers from an exponential distribution with `mu = 10`, and creates a normal probability plot of the data.

```
x = exprnd(10,100,1);
normplot(x)
```



The plot is strong evidence that the underlying distribution is not normal.

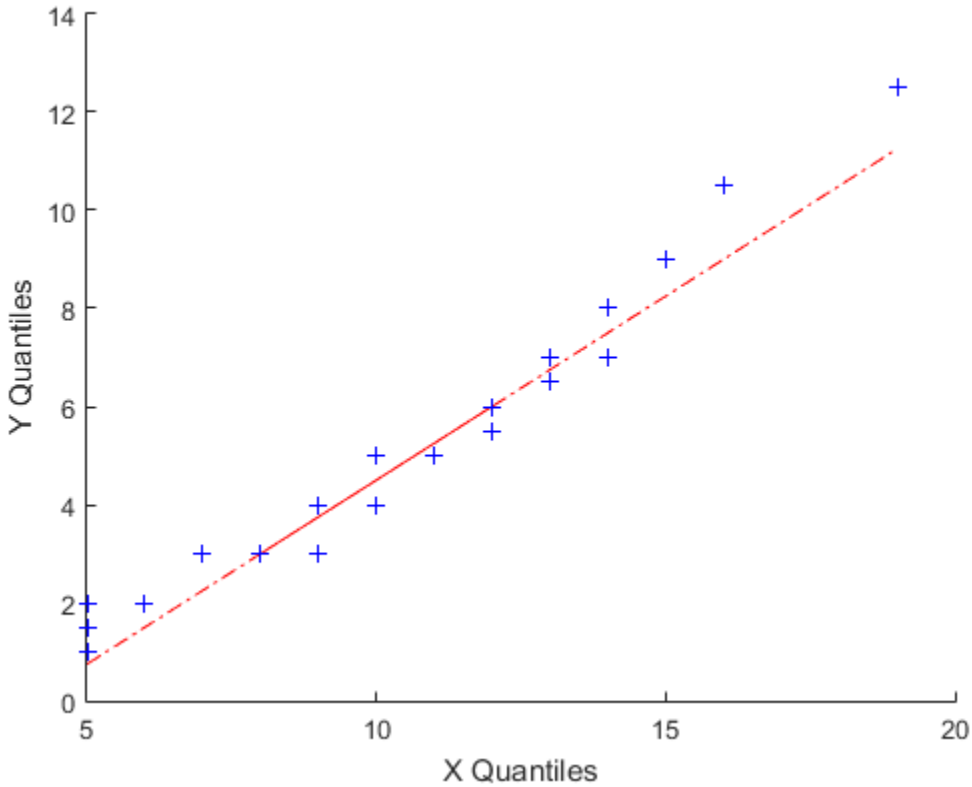
Quantile-Quantile Plots

Quantile-quantile plots are used to determine whether two samples come from the same distribution family. They are scatter plots of quantiles computed from each sample, with a line drawn between the first and third quartiles. If the data falls near the line, it is reasonable to assume that the two samples come from the same distribution. The method is robust with respect to changes in the location and scale of either distribution.

To create a quantile-quantile plot, use the `qqplot` function.

The following example generates two data samples containing random numbers from Poisson distributions with different parameter values, and creates a quantile-quantile plot. The data in `x` is from a Poisson distribution with `lambda = 10`, and the data in `y` is from a Poisson distribution with `lambda = 5`.

```
x = poissrnd(10,50,1);
y = poissrnd(5,100,1);
qqplot(x,y);
```

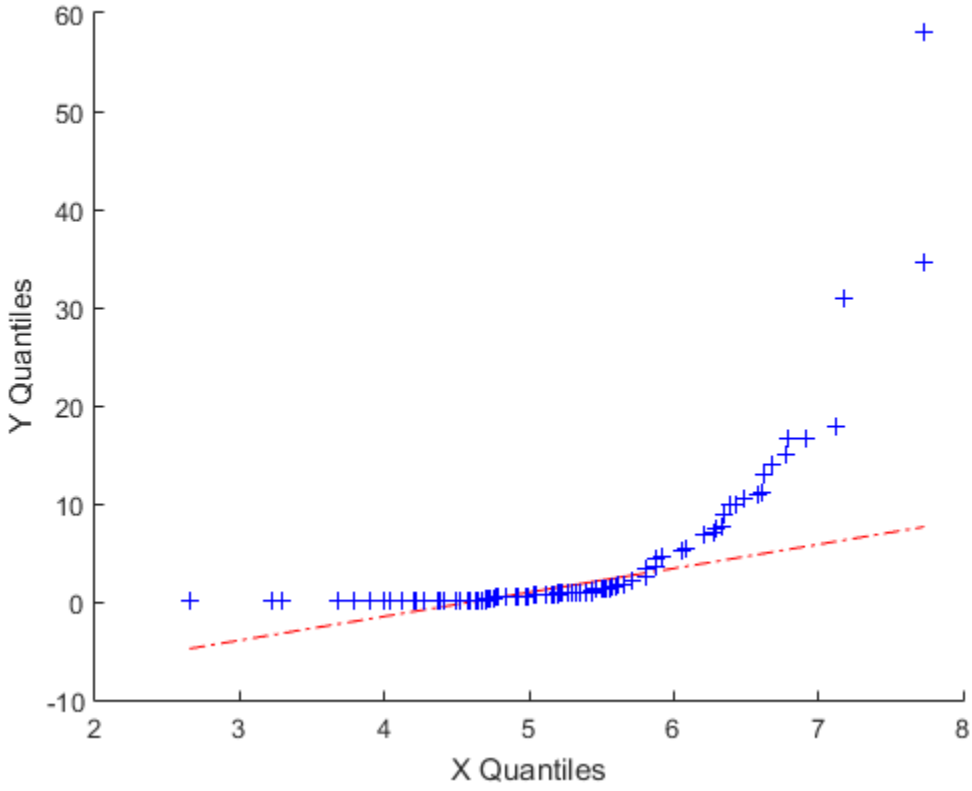


Even though the parameters and sample sizes are different, the approximate linear relationship suggests that the two samples may come from the same distribution family.

As with normal probability plots, hypothesis tests can provide additional justification for such an assumption. For statistical procedures that depend on the two samples coming from the same distribution, however, a linear quantile-quantile plot is often sufficient.

The following example shows what happens when the underlying distributions are not the same. Here, `x` contains 100 random numbers generated from a normal distribution with `mu = 5` and `sigma = 1`, while `y` contains 100 random numbers generated from a Weibull distribution with `A = 2` and `B = 0.5`.

```
x = normrnd(5,1,100,1);
y = wblrnd(2,0.5,100,1);
qqplot(x,y);
```



These samples clearly are not from the same distribution family.

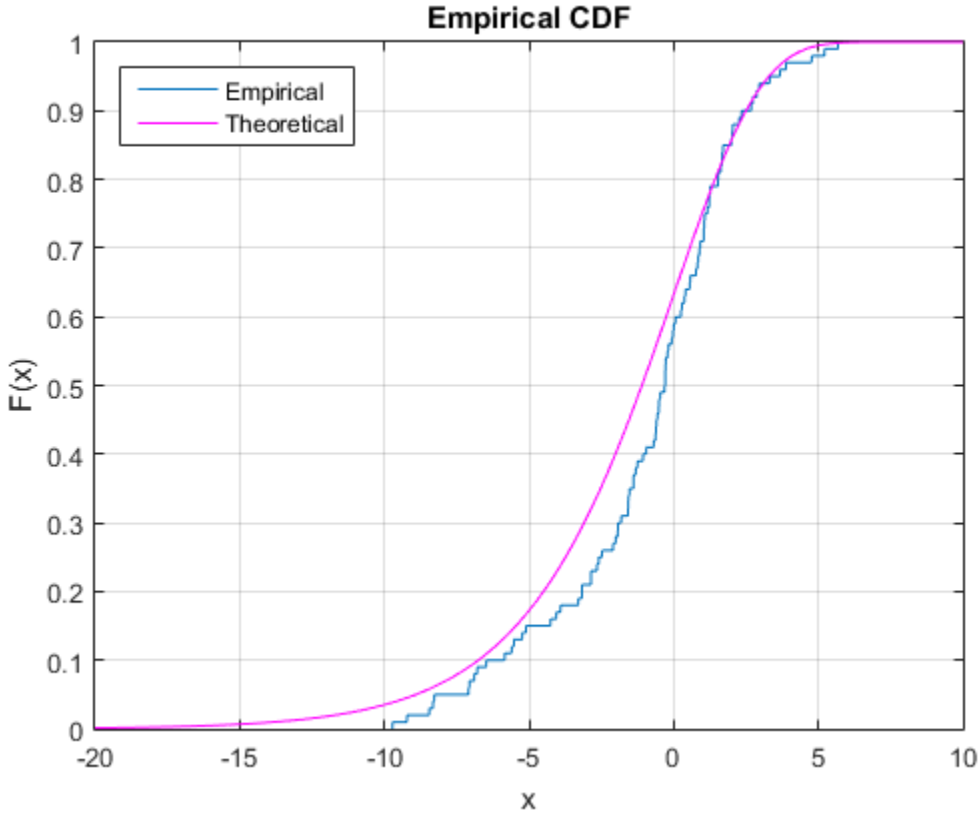
Cumulative Distribution Plots

An empirical cumulative distribution function (cdf) plot shows the proportion of data less than each x value, as a function of x. The scale on the y-axis is linear; in particular, it is not scaled to any particular distribution. Empirical cdf plots are used to compare data cdfs to cdfs for particular distributions.

To create an empirical cdf plot, use the `cdfplot` function (or `ecdf` and `stairs`).

The following example compares the empirical cdf for a sample from an extreme value distribution with a plot of the cdf for the sampling distribution. In practice, the sampling distribution would be unknown, and would be chosen to match the empirical cdf.

```
y = evrnd(0,3,100,1);
cdfplot(y)
hold on
x = -20:0.1:10;
f = evcdf(x,0,3);
plot(x,f,'m')
legend('Empirical','Theoretical','Location','NW')
```



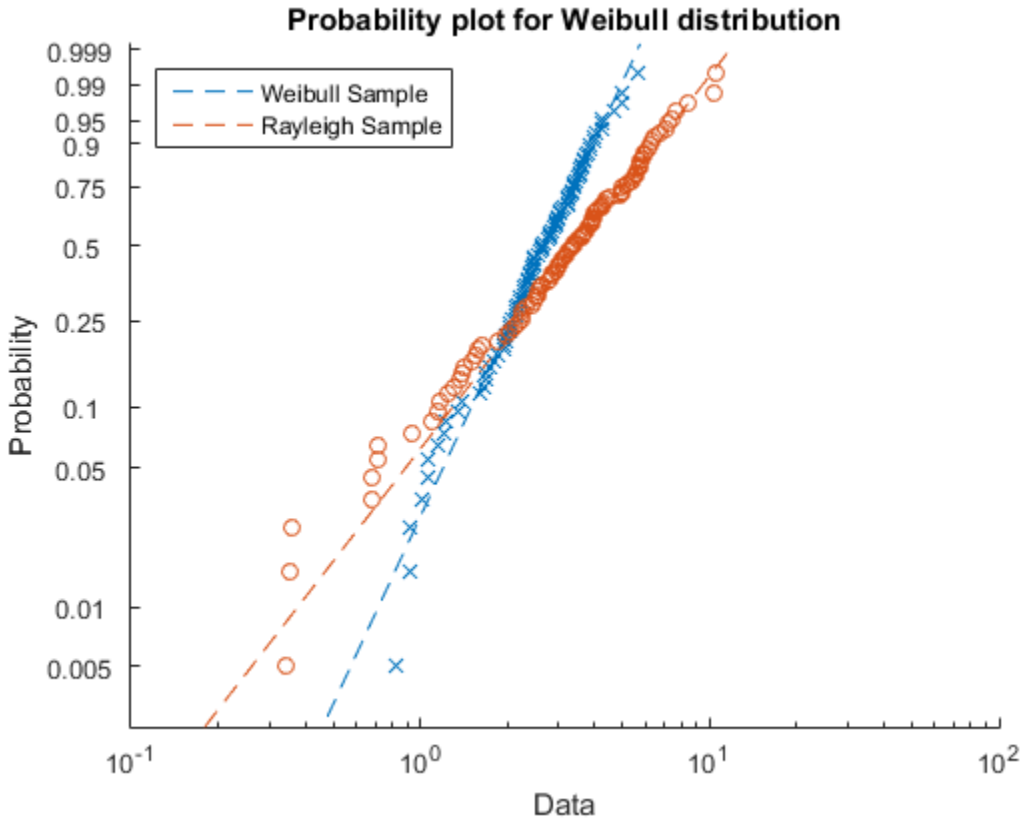
Other Probability Plots

A probability plot, like the normal probability plot, is just an empirical cdf plot scaled to a particular distribution. The *y*-axis values are probabilities from zero to one, but the scale is not linear. The distance between tick marks is the distance between quantiles of the distribution. In the plot, a line is drawn between the first and third quartiles in the data. If the data falls near the line, it is reasonable to choose the distribution as a model for the data.

To create probability plots for different distributions, use the `probplot` function.

The following example assesses two samples, one from a Weibull distribution with `A = 3` and `B = 3`, and one from a Rayleigh distribution with `B = 3`, to see if either distribution may have come from a Weibull population.

```
x1 = wblrnd(3,3,100,1);
x2 = raylrnd(3,100,1);
probplot('weibull',[x1 x2])
legend('Weibull Sample','Rayleigh Sample','Location','NW')
```



The plot gives justification for modeling the first sample with a Weibull distribution; much less so for the second sample.

A distribution analysis typically combines probability plots with hypothesis tests for a particular distribution.

Probability Distributions

Working with Probability Distributions

In this section...

Types of Probability Distributions

Probability distributions are theoretical distributions based on assumptions about a source population. The distributions assign probability to the event that a random variable has a specific, discrete value, or falls within a specified range of continuous values.

Statistics and Machine Learning Toolbox offers several ways to work with probability distributions.

- Use "Probability Distribution Objects" on page 5-4 to fit a probability distribution object to sample data, or to create a probability distribution object with specified parameter values.
- Use "Probability Distribution Functions" on page 5-8 to work with data input from matrices, tables, and dataset arrays.
- Use "Probability Distribution Apps and User Interfaces" on page 5-10 to interactively fit, explore, and generate random numbers from probability distributions. Available apps and user interfaces include:
  - The Distribution Fitting app (`dfittool`)
  - The Probability Distribution Function user interface (`disttool`)
  - The Random Number Generation user interface (`randtool`)

For a list of distributions supported by Statistics and Machine Learning Toolbox, see "Supported Distributions" on page 5-17.

Probability Distribution Objects

Probability distribution objects allow you to fit a probability distribution to sample data, or define a distribution by specifying parameter values. You can then perform a variety of analyses on the distribution object.

Create Probability Distribution Objects

Estimate probability distribution parameters from sample data by fitting a probability distribution object to the data using `fitdist`. You can fit a single specified parametric or nonparametric distribution to the sample data. You can also fit multiple distributions of the same type to the sample data based on grouping variables. For most distributions, `fitdist` uses maximum likelihood estimation (MLE) to estimate the distribution parameters from the sample data. For more information and additional syntax options, see `fitdist`.

Alternatively, you can create a probability distribution object with specified parameter values using `makedist`.

Work with Probability Distribution Objects

Once you create a probability distribution object, you can use object functions to:

- Compute confidence intervals for the distribution parameters (`paramci`).
- Compute summary statistics, including mean (`mean`), median (`median`), interquartile range (`iqr`), variance (`var`), and standard deviation (`std`).
- Evaluate the probability density function (`pdf`).
- Evaluate the cumulative distribution function (`cdf`) or the inverse cumulative distribution function (`icdf`).
- Compute the negative log likelihood (`negloglik`) and profile likelihood function (`proflik`) for the distribution.
- Generate random numbers from the distribution (`random`).
- Truncate the distribution to specified lower and upper limits (`truncate`).

Save a Probability Distribution Object

To save your probability distribution object to a .MAT file:

- In the toolbar, click **Save Workspace**. This option saves all of the variables in your workspace, including any probability distribution objects.

- In the workspace browser, right-click the probability distribution object and select **Save as**. This option saves only the selected probability distribution object, not the other variables in your workspace.

Alternatively, you can save a probability distribution object directly from the command line by using the `save` function. `save` enables you to choose a file name and specify the probability distribution object you want to save. If you do not specify an object (or other variable), MATLAB saves all of the variables in your workspace, including any probability distribution objects, to the specified file name. For more information and additional syntax options, see `save`.

Example

This example shows how to use probability distribution objects to perform a multistep analysis on a fitted distribution.

The following analysis illustrates how to:

- Fit a probability distribution object to sample data that contains 120 students' exam grades, using `fitdist`.
- Compute the mean of the exam grades, using `mean`.
- Plot a histogram of the exam grade data, overlaid with a plot of the pdf of the fitted distribution, using `plot` and `pdf`.
- Compute the boundary for the top 10 percent of student grades, using `icdf`.
- Save the fitted probability distribution object, using `save`.

Load the sample data.

```
load examgrades
```

The sample data contains a 120-by-5 matrix of students' exam grades. The exams are scored on a scale of 0 to 100.

Create a vector containing the first column of students' exam grade data.

```
x = grades(:,1);
```

Fit a normal distribution to the sample data by using `fitdist` to create a probability distribution object.

```
pd = fitdist(x,'Normal')

pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

`fitdist` returns a probability distribution object, `pd`, of the type `NormalDistribution`. This object contains the estimated parameter values, `mu` and `sigma`, for the fitted normal distribution.

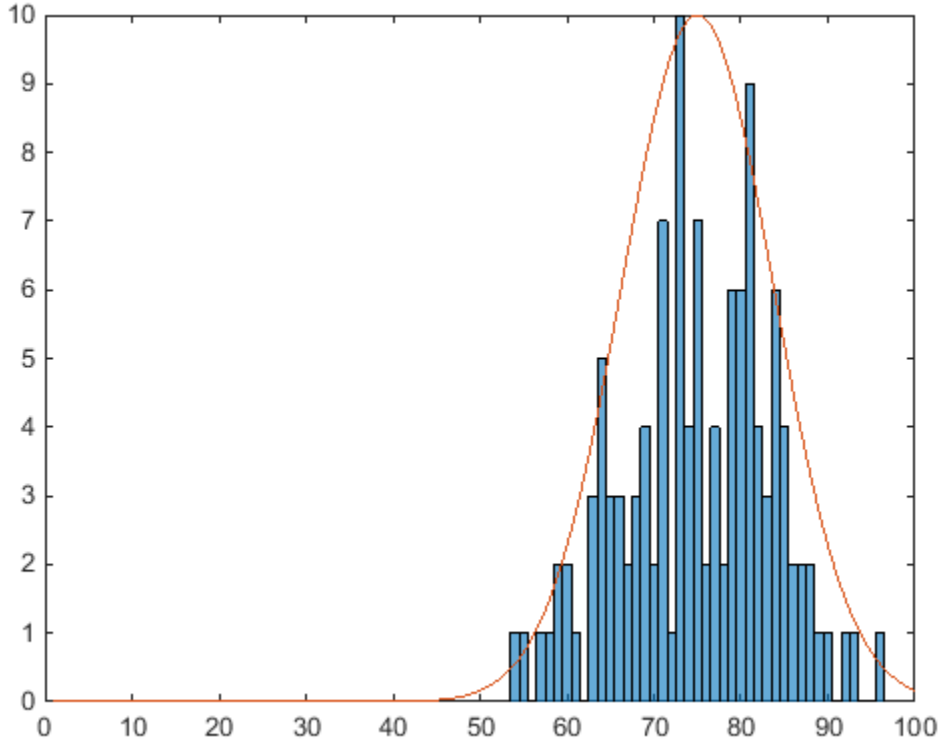
Compute the mean of the students' exam grades using the fitted distribution object, `pd`.

```
m = mean(pd)

m =

   75.0083
```

The mean of the exam grades is equal to the `mu` parameter estimated by `fitdist`.

Plot a histogram of the exam grades. Overlay a scaled plot of the fitted pdf to visually compare the fitted normal distribution with the actual exam grades.

```
x_pdf = [1:0.1:100];
y = pdf(pd,x_pdf);

figure
histogram(x)
hold on
scale = 10/max(y);
plot((x_pdf),(y.*scale))
hold off
```



The pdf of the fitted distribution follows the same shape as the histogram of the exam grades.

Use the inverse cumulative distribution function (icdf) to determine the boundary for the upper 10 percent of student exam grades. This boundary is equivalent to the value at which the cdf of the probability distribution is equal to 0.9. In other words, 90 percent of the exam grades are less than or equal to this boundary value.

```
A = icdf(pd,0.9)
```

```
A =

   86.1837
```

Based on the fitted distribution, 10 percent of students received an exam grade greater than 86.1837. Equivalently, 90 percent of students received an exam grade less than or equal to 86.1837.

Save the fitted probability distribution, `pd`, as a file named `myobject.mat`.

```
save myobject.mat pd
```

Probability Distribution Functions

You can also work with probability distributions using command-line functions. Command-line functions let you further explore parametric and nonparametric distributions, fit relevant models to your data, and generate random data from a specified distribution. For a list of supported probability distributions, see "Supported Distributions" on page 5-17.

Probability distribution functions are useful for generating random numbers and computing summary statistics inside a loop or script, or passing a cdf or pdf as a function handle (using the `function_handle` operator, `@`) to another function. You can also use functions if your desired distribution is not available as a probability distribution object.

Examples

This example shows how to use the probability distribution function `normcdf` as a function handle in the chi-square goodness of fit test (`chi2gof`).

This example tests the null hypothesis that the sample data contained in the input vector, `x`, comes from a normal distribution with parameters μ and σ equal to the mean (`mean`) and standard deviation (`std`) of the sample data, respectively.

```
rng default
x = normrnd(50,5,100,1);
h = chi2gof(x,'cdf',{@normcdf,mean(x),std(x)})
```

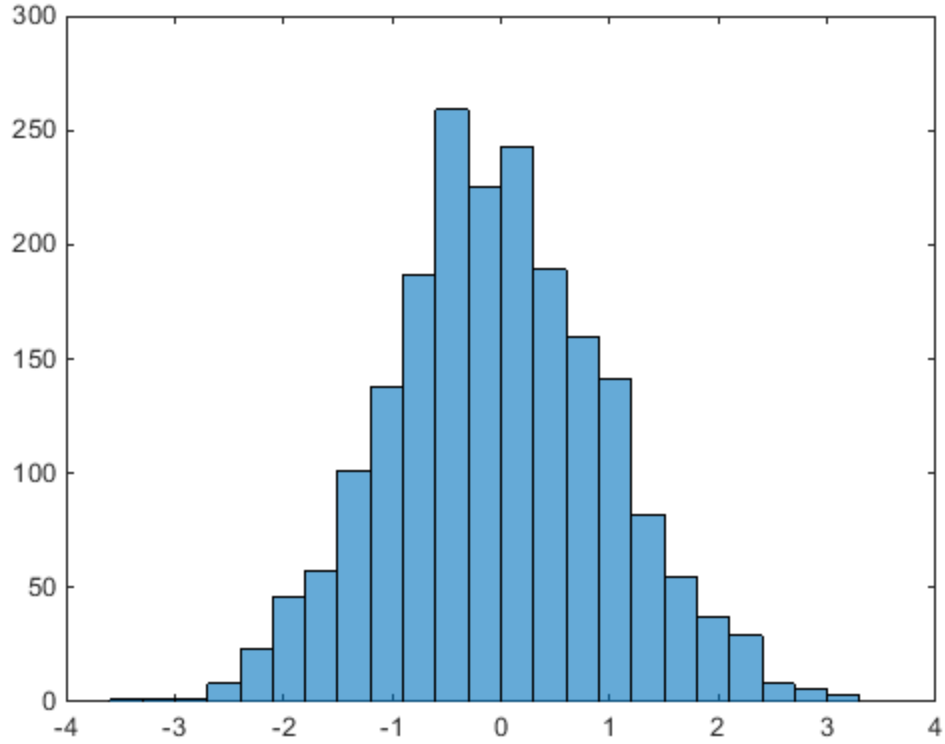
```
h =

     0
```

The returned result `h = 0` indicates that `chi2gof` does not reject the null hypothesis at the default 5% significance level.

This next example illustrates how to use probability distribution functions as a function handle in the slice sampler (`slicesample`). The example uses `normpdf` to generate

a random sample of 2,000 values from a standard normal distribution, and plots a histogram of the resulting values.

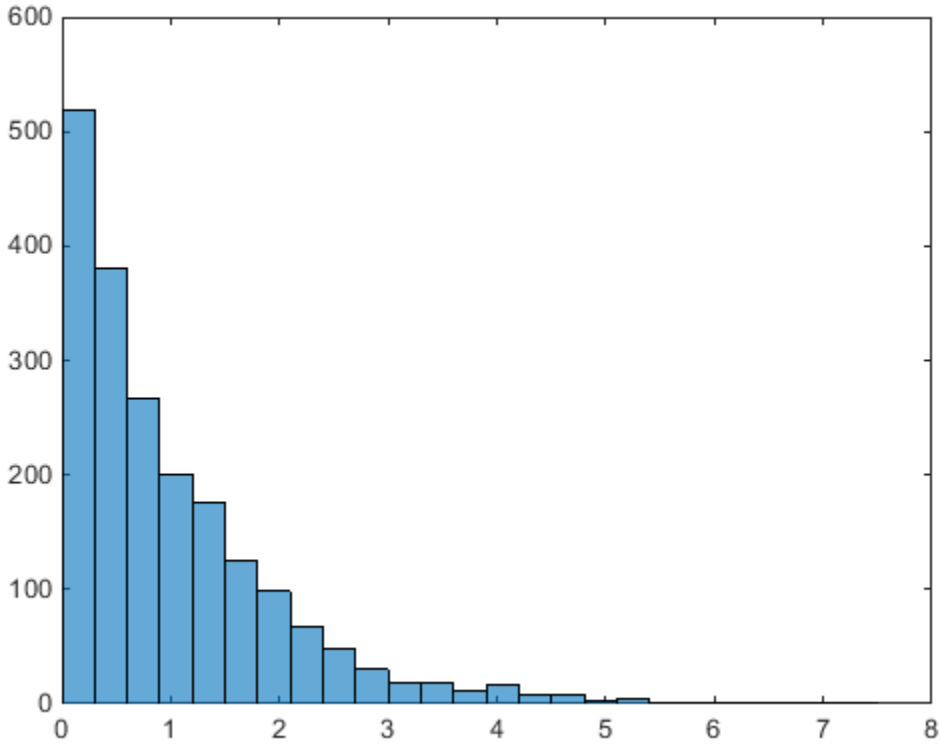
```
rng default
x = slicesample(1,2000,'pdf',@normpdf,'thin',5,'burnin',1000);
h = histogram(x)
```



The histogram shows that, when using `normpdf`, the resulting random sample has a standard normal distribution.

If you pass the probability distribution function for the exponential distribution pdf (`exppdf`) as a function handle instead of `normpdf`, then `slicesample` generates the 2,000 random samples from an exponential distribution with a default parameter value of μ equal to 1.

```
rng default
x = slicesample(1,2000,'pdf',@exppdf,'thin',5,'burnin',1000);
h = histogram(x)
```



The histogram shows that the resulting random sample when using `exppdf` has an exponential distribution.

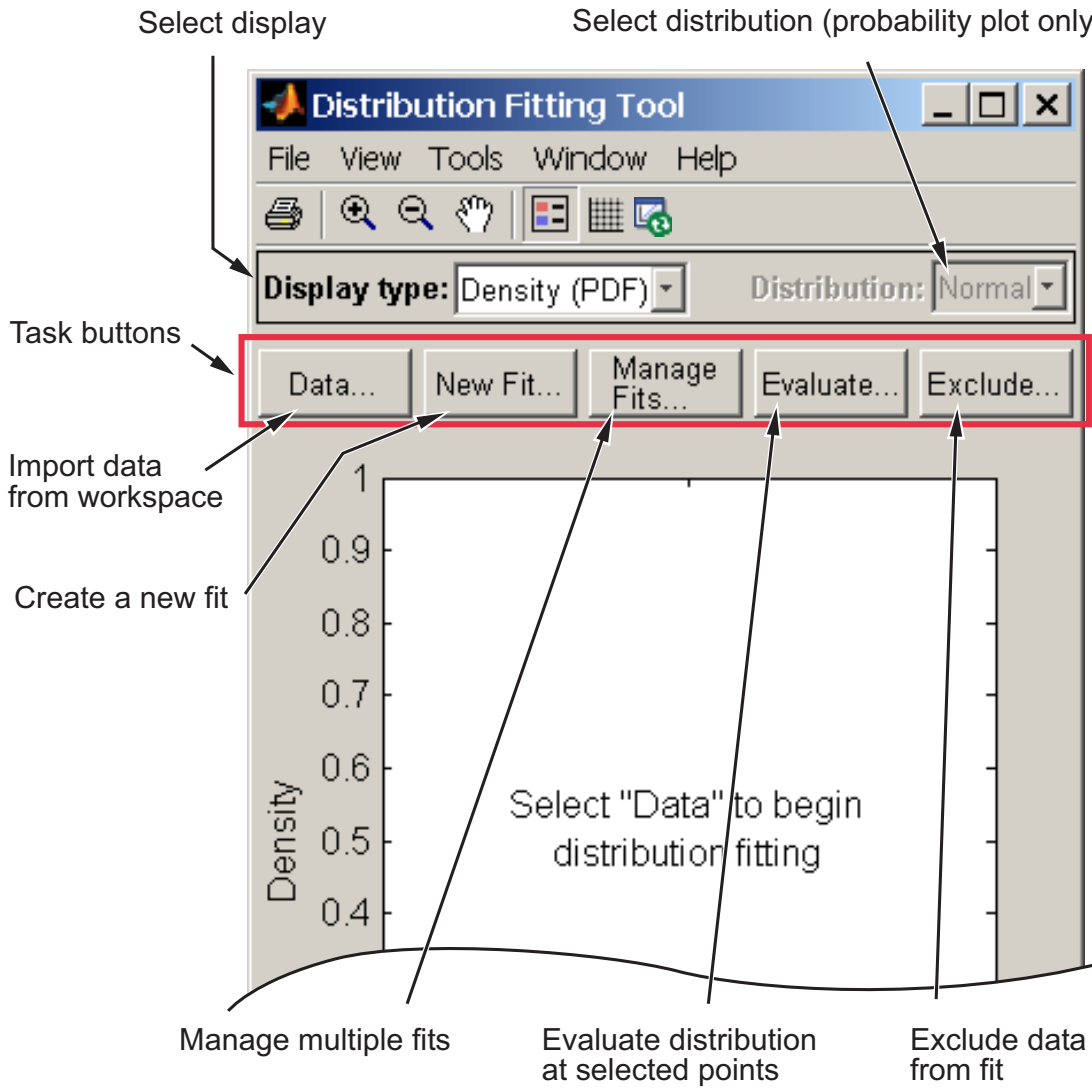
Probability Distribution Apps and User Interfaces

Apps and user interfaces provide an interactive approach to working with parametric and nonparametric probability distributions.

Distribution Fitting App

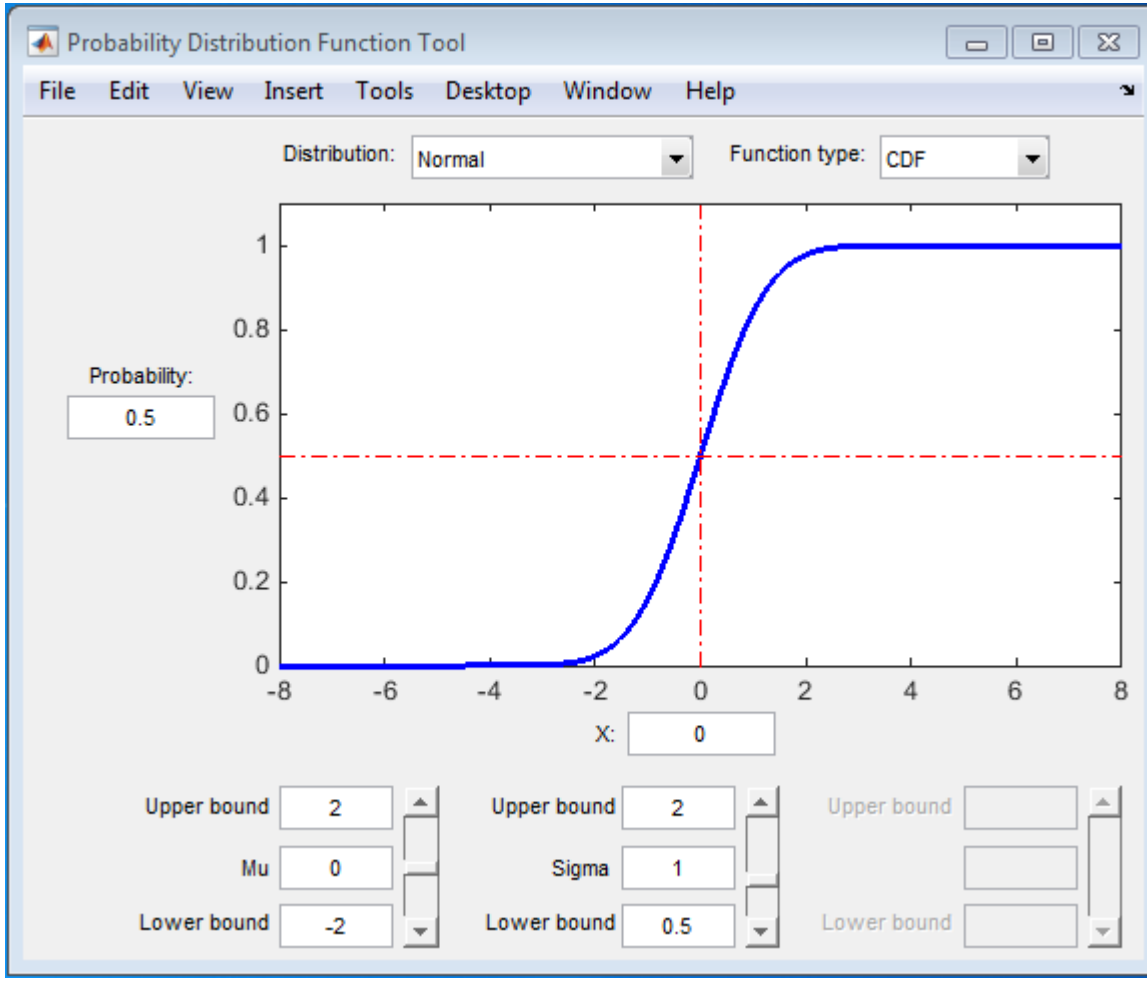
The Distribution Fitting app allows you to interactively fit a probability distribution to your data. You can display different types of plots, compute confidence bounds, and evaluate the fit of the data. You can also exclude data from the fit. You can save the data, and export the fit to your workspace as a probability distribution object to perform further analysis.

Load the Distribution Fitting app from the Apps tab, or by entering `dfittool` in the command window. For more information, see "Model Data Using the Distribution Fitting App" on page 5-74.



Probability Distribution Function Tool

The Probability Distribution Function user interface visually explores probability distributions. You can load the Probability Distribution Function user interface by entering `disttool` in the command window.

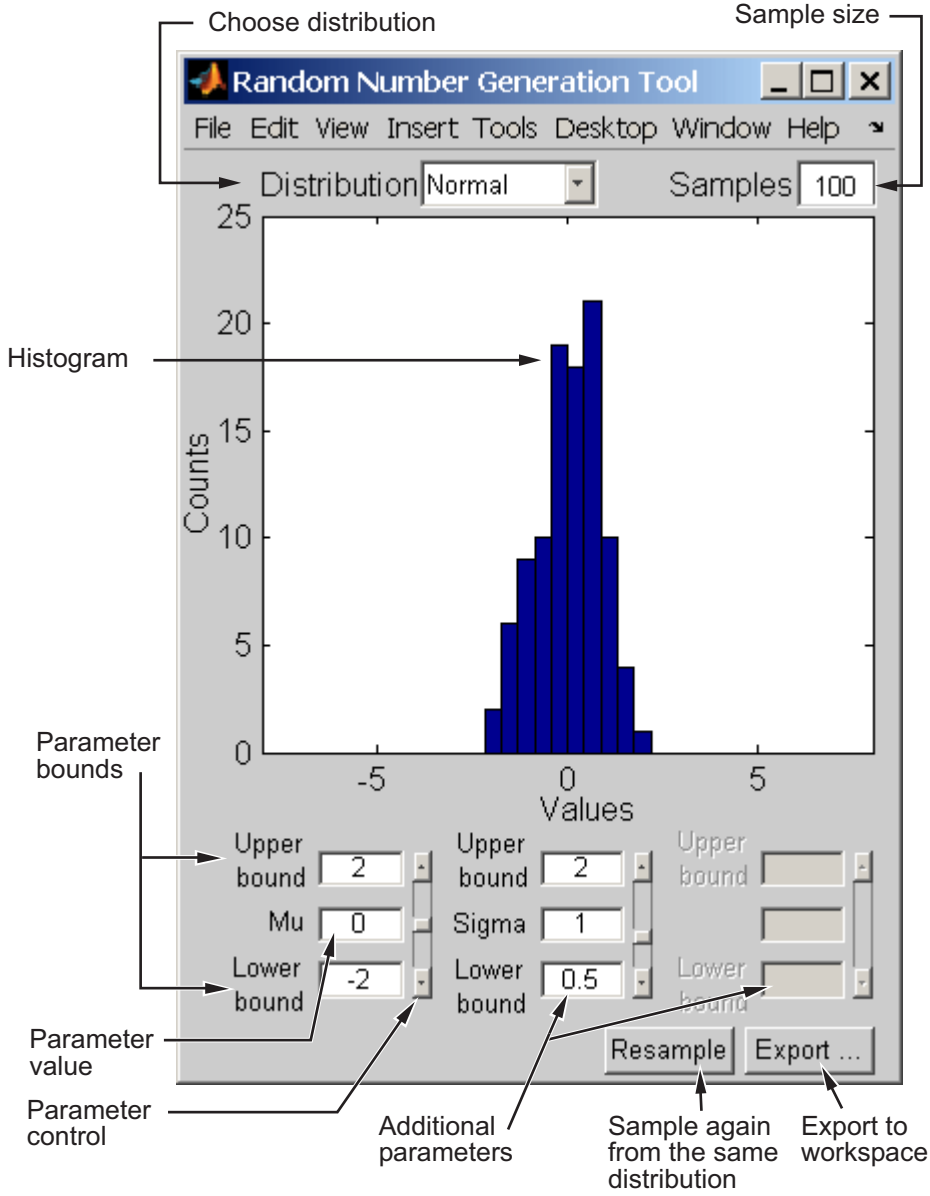


Random Number Generation Tool

The Random Number Generation user interface generates random data from a specified distribution and exports the results to your workspace. You can use this tool to explore the effects of changing parameters and sample size on the distributions.

The Random Number Generation user interface allows you to set parameter values for the distribution and change their lower and upper bounds; draw another sample from the same distribution, using the same size and parameters; and export the current random

sample to your workspace for use in further analysis. A dialog box enables you to provide a name for the sample.


Choose distribution
Sample size
Random Number Generation Tool
File Edit View Insert Tools Desktop Window Help
Distribution
Normal
Samples
100
Histogram
Counts
Values
Parameter bounds
Upper bound
Mu
Lower bound
Sigma
Resample
Export ...
Parameter value
Parameter control
Additional parameters
Sample again from the same distribution
Export to workspace

See Also

`dfittool` | `disttool` | `fitdist` | `makedist` | `randtool`

More About

- "Supported Distributions" on page 5-17

Supported Distributions

In this section...

Statistics and Machine Learning Toolbox supports more than 30 probability distributions, including parametric, nonparametric, continuous, and discrete distributions.

The toolbox provides several ways to work with probability distributions.

- Use *probability distribution objects* to fit a probability distribution object to sample data, or to create a probability distribution object with specified parameter values. The Using Objects page for each distribution provides information about the object's properties and the functions you can use to work with the object.
- Use *probability distribution functions* to work with data input from matrices, tables, and dataset arrays. Some of the supported distributions have distribution-specific functions. These functions use the following abbreviations:

  - pdf — Probability density functions
  - cdf — Cumulative distribution functions
  - inv — Inverse cumulative distribution functions
  - stat — Distribution statistics functions
  - fit — Distribution fitting functions
  - like — Negative log-likelihood functions
  - rnd — Random number generators

  You can also use the following generic functions to work with most of the distributions:

  - `pdf` — Probability density function

  - `cdf` — Cumulative distribution function
  - `icdf` — Inverse cumulative distribution function
  - `mle` — Distribution fitting function
  - `random` — Random number generating function
- Use *probability distribution apps and user interfaces* to interactively fit, explore, and generate random numbers from probability distributions. Available apps and user interfaces include:
  - The **Distribution Fitting** app (`dfittool`), to interactively fit a distribution to sample data, and export a probability distribution object to the workspace.
  - The Probability Distribution Function user interface (`disttool`), to visually explore the effect on the pdf and cdf of changing the distribution parameter values.
  - The Random Number Generation user interface (`randtool`), to interactively generate random numbers from a probability distribution with specified parameter values and export them to the workspace.

For more information on the different ways to work with probability distributions, see "Working with Probability Distributions" on page 5-3.

Continuous Distributions (Data)

Distribution	Using Objects	Legacy Functions	Apps and UIs

Beta	`BetaDistribution`	`betapdf`
		`betacdf`
		`betainv`
		`betastat`
		`betafit`
		`betalike`
		`betarnd`
			`dfittool`
			`disttool`
			`randtool`

Birnbaum-Saunders	`BirnbaumSaundersDi`	`pdf`
		`cdf`
		`icdf`
		`mle`
		`random`
			`dfittool`

Burr Type XII	`BurrDistribution`	`pdf`
		`cdf`
		`icdf`
		`mle`
		`random`
			`dfittool`
			`disttool`
			`randtool`

Exponential	`ExponentialDistrib`	`exppdf`
		`expcdf`
		`expinv`
		`expstat`
		`expfit`
		`explike`
			`dfittool`
			`disttool`
			`randtool`

Extreme value	`ExtremeValueDistri`	`evpdf`
		`evcdf`
		`evinv`
		`evstat`
		`evfit`
		`evlike`
		`evrnd`
			`dfittool`
			`disttool`
			`randtool`

Gamma	`GammaDistribution`	`gampdf`
		`gamcdf`
		`gaminv`
		`gamstat`
			`dfittool`
			`disttool`
			`randtool`

Distribution	Using Objects	Legacy Functions	Apps and UIs

		`gamfit`
		`gamlike`
		`gamrnd`	

Generalized extreme value	`GeneralizedExtreme`	`gevpdf`
		`gevcdf`
		`gevinv`
		`gevstat`
		`gevfit`
		`gevlike`
		`gevrnd`
			`dfittool`
			`disttool`
			`randtool`

Generalized Pareto	`GeneralizedParetoD`	`gppdf`
		`gpcdf`
		`gpinv`
		`gpstat`
		`gpfit`
		`gplike`
		`gprnd`
			`dfittool`
			`disttool`
			`randtool`

Inverse Gaussian	`InverseGaussianDis`	`pdf`
		`cdf`
		`icdf`
		`mle`
		`random`
			`dfittool`

Logistic	`LogisticDistributi`	`pdf`
		`cdf`
		`icdf`
		`mle`
		`random`
			`dfittool`

Loglogistic	`LoglogisticDistrib`	`pdf`
		`cdf`
		`icdf`
		`mle`
		`random`
			`dfittool`

Distribution	Using Objects	Legacy Functions	Apps and UIs

Lognormal	`LognormalDistribut`	`lognpdf`
		`logncdf`
		`logninv`
		`lognstat`
		`lognfit`
		`lognlike`
		`lognrnd`
			`dfittool`
			`disttool`
			`randtool`

Nakagami	`NakagamiDistributi`	`pdf`
		`cdf`
		`icdf`
		`mle`
		`random`
			`dfittool`

Normal (Gaussian)	`NormalDistributior`	`normpdf`
		`normcdf`
		`norminv`
		`normstat`
		`normfit`
		`normlike`
		`normrnd`
			`dfittool`
			`disttool`
			`randtool`

Piecewise linear	`PiecewiseLinearDis`	`pdf`
		`cdf`
		`icdf`
		`random`	

Rayleigh	`RayleighDistributi`	`raylpdf`
		`raylcdf`
		`raylinv`
		`raylstat`
		`raylfit`
		`raylrnd`
			`dfittool`
			`disttool`
			`randtool`

Rician	`RicianDistributior`	`pdf`
		`cdf`
		`icdf`
		`mle`
		`random`
			`dfittool`

Triangular	`TriangularDistribu`		

Distribution	Using Objects	Legacy Functions	Apps and UIs

Uniform (continuous)	`UniformDistributio`	`unifpdf`
		`unifcdf`
		`unifinv`
		`unifstat`
		`unifit`
		`unifrnd`
			`disttool`
			`randtool`

Weibull	`WeibullDistributio`	`wblpdf`
		`wblcdf`
		`wblinv`
		`wblstat`
		`wblfit`
		`wbllike`
		`wblrnd`
			`dfittool`
			`disttool`
			`randtool`

Continuous Distributions (Statistics)

Distribution	Using Objects	Legacy Functions	Apps and UIs

Chi-square		`chi2pdf`
		`chi2cdf`
		`chi2inv`
		`chi2stat`
		`chi2rnd`
			`disttool`
			`randtool`

F		`fpdf`
		`fcdf`
		`finv`
		`fstat`
		`frnd`
			`disttool`
			`randtool`

Noncentral chi-square		`ncx2pdf`
		`ncx2cdf`
		`ncx2inv`
		`ncx2stat`
		`ncx2rnd`
			`disttool`
			`randtool`

Noncentral *F*		`ncfpdf`
		`ncfcdf`
		`ncfinv`
		`ncfstat`
		`ncfrnd`
			`disttool`
			`randtool`

Noncentral *t*		`nctpdf`
		`nctcdf`
		`nctinv`
		`nctstat`
		`nctrnd`
			`disttool`
			`randtool`

Student's *t*		`tpdf`
		`tcdf`
		`tinv`
		`tstat`
		`trnd`
			`disttool`
			`randtool`

t location- scale	`tLocationScaleDistr`	`pdf`
		`cdf`
		`icdf`
		`mle`
			`dfittool`

Distribution	Using Objects	Legacy Functions	Apps and UIs
		`random`	

Discrete Distributions

Distribution	Using Objects	Legacy Functions	Apps/UIs

Binomial	`BinomialDistributio`	`binopdf`
		`binocdf`
		`binoinv`
		`binostat`
		`binofit`
		`binornd`
			`disttool`
			`randtool`

Bernoulli		`mle`	

Geometric		`geopdf`
		`geocdf`
		`geoinv`
		`geostat`
		`mle`
		`geornd`
			`disttool`
			`randtool`

Hypergeometric		`hygepdf`
		`hygecdf`
		`hygeinv`
		`hygestat`
		`hygernd`
			`disttool`
			`randtool`

Multinomial	`MultinomialDistribu`	`mnpdf` `mnrnd`	

Negative binomial	`NegativeBinomialDis`	`nbinpdf`
		`nbincdf`
		`nbininv`
		`nbinstat`
		`nbinfit`
		`nbinrnd`
			`dfittool`
			`disttool`
			`randtool`

Poisson	`PoissonDistribution`	`poisspdf`
		`poisscdf`
		`poissinv`
		`poisstat`
		`poissfit`
		`poissrnd`
			`dfittool`
			`disttool`
			`randtool`

Uniform (discrete)		`unidpdf`	`disttool`

Distribution	Using Objects	Legacy Functions	Apps/UIs

		`unidcdf`
		`unidinv`
		`unidstat`
		`mle`
		`unidrnd`
			`randtool`

Multivariate Distributions

Distribution	Object	Legacy Functions	Apps/UI

Gaussian copula		`copulapdf`
		`copulacdf`
		`copulastat`
		`copulafit`
		`copularnd`	

Gaussian mixture	`gmdistribution`	`pdf`
		`cdf`
		`fit`
		`random`	

t copula		`copulapdf`
		`copulacdf`
		`copulastat`
		`copulafit`
		`copularnd`	

Clayton copula		`copulapdf`
		`copulacdf`
		`copulastat`
		`copulafit`
		`copularnd`	

Frank copula		`copulapdf`
		`copulacdf`
		`copulastat`
		`copulafit`
		`copularnd`	

Gumbel copula		`copulapdf`
		`copulacdf`
		`copulastat`
		`copulafit`
		`copularnd`	

Inverse Wishart		`iwishrnd`	

Multivariate normal		`mvnpdf`
		`mvncdf`
		`mvnrnd`	

Distribution	Object	Legacy Functions	Apps/UI

Multivariate t		`mvtpdf`
		`mvtcdf`
		`mvtrnd`	

Wishart		`wishrnd`	

Nonparametric Distributions

Distribution	Using Objects	Legacy Functions	Apps/UIs
Nonparametric (kernel)	`KernelDistribution`	`ksdensity`	`dfittool`
Pareto	`paretotails`		

Flexible Distribution Families

Distribution	Using Objects	Legacy Functions	Apps/UIs
Pearson system		`pearsrnd`	
Johnson system		`johnsrnd`	

More About

- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40

Maximum Likelihood Estimation

The Statistics and Machine Learning Toolbox function `mle` is a convenient front end to the individual distribution fitting functions, and more. The function computes maximum likelihood estimates (MLEs) for distributions beyond those for which Statistics and Machine Learning Toolbox software provides specific pdf functions.

For some pdfs, MLEs can be given in closed form and computed directly. For other pdfs, a search for the maximum likelihood must be employed. The search can be controlled with an `options` input argument, created using the `statset` function. For efficient searches, it is important to choose a reasonable distribution model and set appropriate convergence tolerances.

MLEs can be heavily biased, especially for small samples. As sample size increases, however, MLEs become unbiased minimum variance estimators with approximate normal distributions. This is used to compute confidence bounds for the estimates.

For example, consider the following distribution of means from repeated random samples of an exponential distribution:

```
mu = 1; % Population parameter
n = 1e3; % Sample size
ns = 1e4; % Number of samples

rng default  % For reproducibility
samples = exprnd(mu,n,ns); % Population samples
means = mean(samples); % Sample means
```

The Central Limit Theorem says that the means will be approximately normally distributed, regardless of the distribution of the data in the samples. The `normfit` function can be used to find the normal distribution that best fits the means:

```
[muhat,sigmahat,muci,sigmaci] = normfit(means)
```

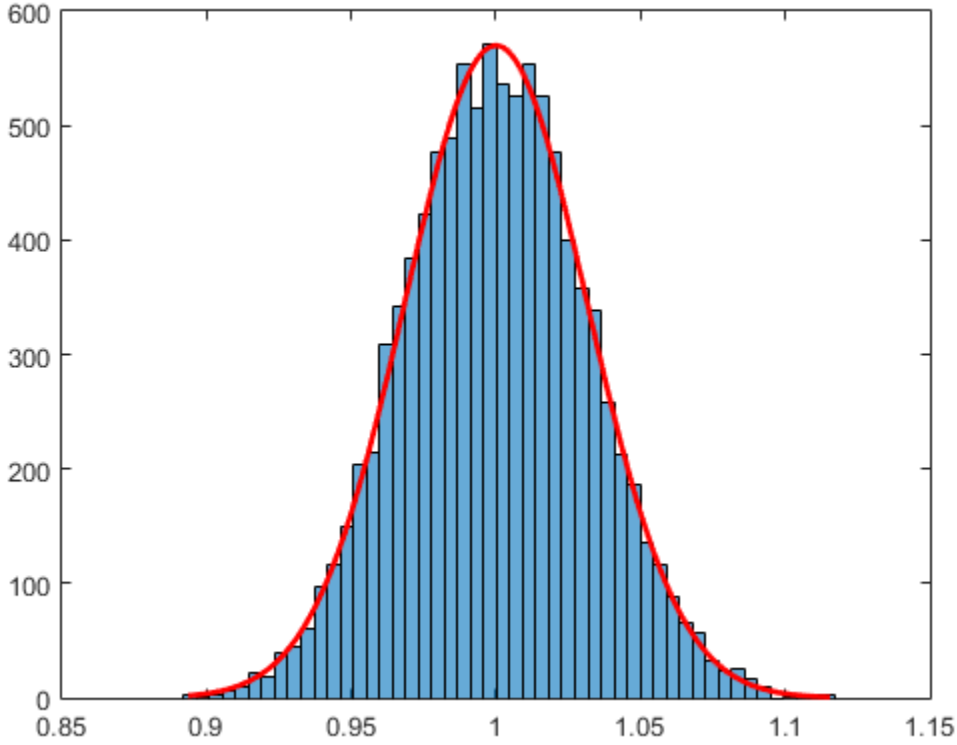
```
muhat =

    1.0000

sigmahat =
```

```
    0.0315


muci =

    0.9994
    1.0006


sigmaci =

    0.0311
    0.0319
```

The function returns MLEs for the mean and standard deviation and their 95% confidence intervals.

To visualize the distribution of sample means together with the fitted normal distribution, you must scale the fitted pdf, with area = 1, to the area of the histogram being used to display the means:

```
numbins = 50;
histogram(means,numbins)
hold on
[bincounts,binpositions] = hist(means,numbins);
binwidth = binpositions(2) - binpositions(1);
histarea = binwidth*sum(bincounts);
x = binpositions(1):0.001:binpositions(end);
y = normpdf(x,muhat,sigmahat);
plot(x,histarea*y,'r','LineWidth',2)
```


600
500
400
300
200
100
0
0.85
0.9
0.95
1
1.05
1.1
1.15

Negative Loglikelihood Functions

Negative loglikelihood functions for supported Statistics and Machine Learning Toolbox distributions all end with `like`, as in `explike`. Each function represents a parametric family of distributions. Input arguments are lists of parameter values specifying a particular member of the distribution family followed by an array of data. Functions return the negative log-likelihood of the parameters, given the data.

Negative log-likelihood functions are used as objective functions in search algorithms such as the one implemented by the MATLAB function `fminsearch`. Additional search algorithms are implemented by Optimization Toolbox™ functions and Global Optimization Toolbox functions.

When used to compute maximum likelihood estimates (MLEs), negative log-likelihood functions allow you to choose a search algorithm and exercise low-level control over algorithm execution. By contrast, the functions discussed in "Maximum Likelihood Estimation" on page 5-30 use preset algorithms with options limited to those set by the `statset` function.

Likelihoods are conditional probability densities. A parametric family of distributions is specified by its pdf $f(x,a)$, where x and a represent the variables and parameters, respectively. When a is fixed, the pdf is used to compute the density at x, $f(x \mid a)$. When x is fixed, the pdf is used to compute the *likelihood* of the parameters a, $f(a \mid x)$. The joint likelihood of the parameters over an independent random sample X is

$$L(a) = \prod_{x \in X} f(a \mid x)$$

Given X, MLEs maximize $L(a)$ over all possible a.

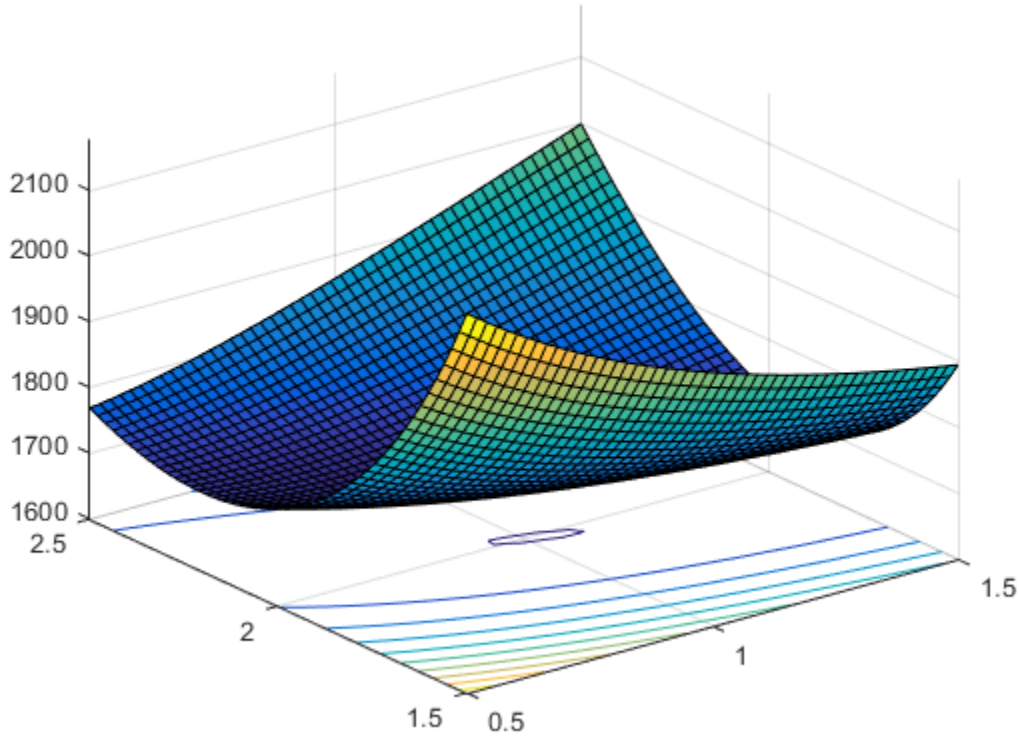
In numerical algorithms, the log-likelihood function, $\log(L(a))$, is (equivalently) optimized. The logarithm transforms the product of potentially small likelihoods into a sum of logs, which is easier to distinguish from 0 in computation. For convenience, Statistics and Machine Learning Toolbox negative log-likelihood functions return the *negative* of this sum, since the optimization algorithms to which the values are passed typically search for minima rather than maxima.

For example, use `gamrnd` to generate a random sample from a specific gamma distribution:

```
rng default;  % for reproducibility
a = [1,2];
X = gamrnd(a(1),a(2),1e3,1);
```

Given `X`, the `gamlike` function can be used to visualize the likelihood surface in the neighborhood of `a`:

```
mesh = 50;
delta = 0.5;
a1 = linspace(a(1)-delta,a(1)+delta,mesh);
a2 = linspace(a(2)-delta,a(2)+delta,mesh);
logL = zeros(mesh); % Preallocate memory
for i = 1:mesh
    for j = 1:mesh
        logL(i,j) = gamlike([a1(i),a2(j)],X);
    end
end

[A1,A2] = meshgrid(a1,a2);
surfc(A1,A2,logL)
```



The MATLAB function `fminsearch` is used to search for the minimum of the likelihood surface:

```
LL = @(u)gamlike([u(1),u(2)],X); % Likelihood given X
MLES = fminsearch(LL,[1,2])
```

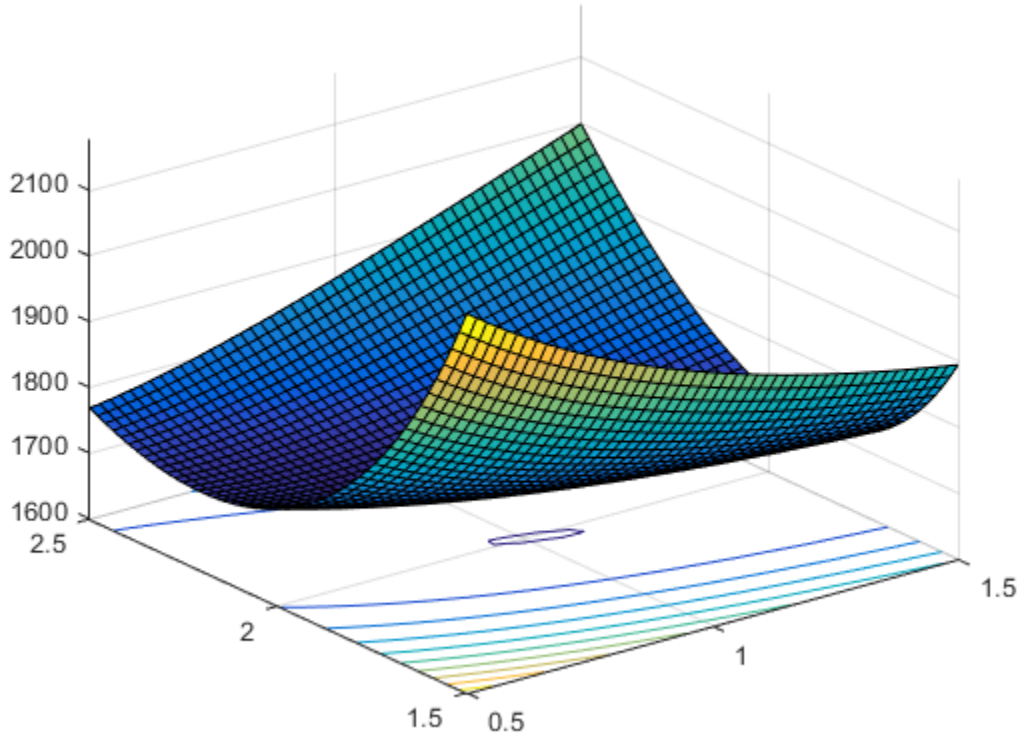
```
MLES =

    0.9980    2.0172
```

These can be compared to the MLEs returned by the `gamfit` function, which uses a combination search and solve algorithm:

```
ahat = gamfit(X)

ahat =

    0.9980    2.0172
```

The MLEs can be added to the surface plot (rotated to show the minimum):

```
hold on
plot3(MLES(1),MLES(2),LL(MLES),...
      'ro','MarkerSize',5,...
      'MarkerFaceColor','r')
```



Random Number Generation

Statistics and Machine Learning Toolbox supports the generation of random numbers from various distributions. Each RNG represents a parametric family of distributions. RNGs return random numbers from the specified distribution in an array of the specified dimensions.

Other random number generation functions which do not support specific distributions include:

- `cvpartition`
- `datasample`
- `hmmgenerate`
- `lhsdesign`
- `lhsnorm`
- `mhsample`
- `random`
- `randsample`
- `slicesample`

RNGs in Statistics and Machine Learning Toolbox software depend on MATLAB's default random number stream via the `rand` and `randn` functions, each RNG uses one of the techniques discussed in “Common Generation Methods” on page 6-5 to generate random numbers from a given distribution.

By controlling the default random number stream and its state, you can control how the RNGs in Statistics and Machine Learning Toolbox software generate random values. For example, to reproduce the same sequence of values from an RNG, you can save and restore the default stream's state, or reset the default stream. For details on managing the default random number stream, see “Managing the Global Stream”.

MATLAB initializes the default random number stream to the same state each time it starts up. Thus, RNGs in Statistics and Machine Learning Toolbox software will generate the same sequence of values for each MATLAB session unless you modify that state at startup. One simple way to do that is to add commands to `startup.m` such as

```
rng shuffle
```

that initialize MATLAB's default random number stream to a different state for each session.

The following table lists the dependencies of Statistics and Machine Learning Toolbox RNGs on the MATLAB base RNGs `rand`, `randi`, and/or `randn`.

RNG	MATLAB Base RNG
`betarnd`	`rand, randn`
`binornd`	`rand`
`chi2rnd`	`rand, randn`
`evrnd`	`rand`
`exprnd`	`rand`
`datasample`	`rand, randi, randperm`
`frnd`	`rand, randn`
`gamrnd`	`rand, randn`
`geornd`	`rand`
`gevrnd`	`rand`
`gprnd`	`rand`
`hygernd`	`rand`
`iwishrnd`	`rand, randn`
`johnsrnd`	`randn`
`lhsdesign`	`rand`
`lhsnorm`	`rand`
`lognrnd`	`randn`
`mhsample`	`rand` or `randn`, depending on the RNG given for the proposal distribution
`mvnrnd`	`randn`
`mvtrnd`	`rand, randn`
`nbinrnd`	`rand, randn`
`ncfrnd`	`rand, randn`
`nctrnd`	`rand, randn`

RNG	MATLAB Base RNG
ncx2rnd	randn
normrnd	randn
pearsrnd	rand or randn, depending on the distribution type
poissrnd	rand, randn
random	rand or randn, depending on the specified distribution
randsample	rand
raylrnd	randn
slicesample	rand
trnd	rand, randn
unidrnd	rand
unifrnd	rand
wblrnd	rand
wishrnd	rand, randn

Nonparametric and Empirical Probability Distributions

In this section...

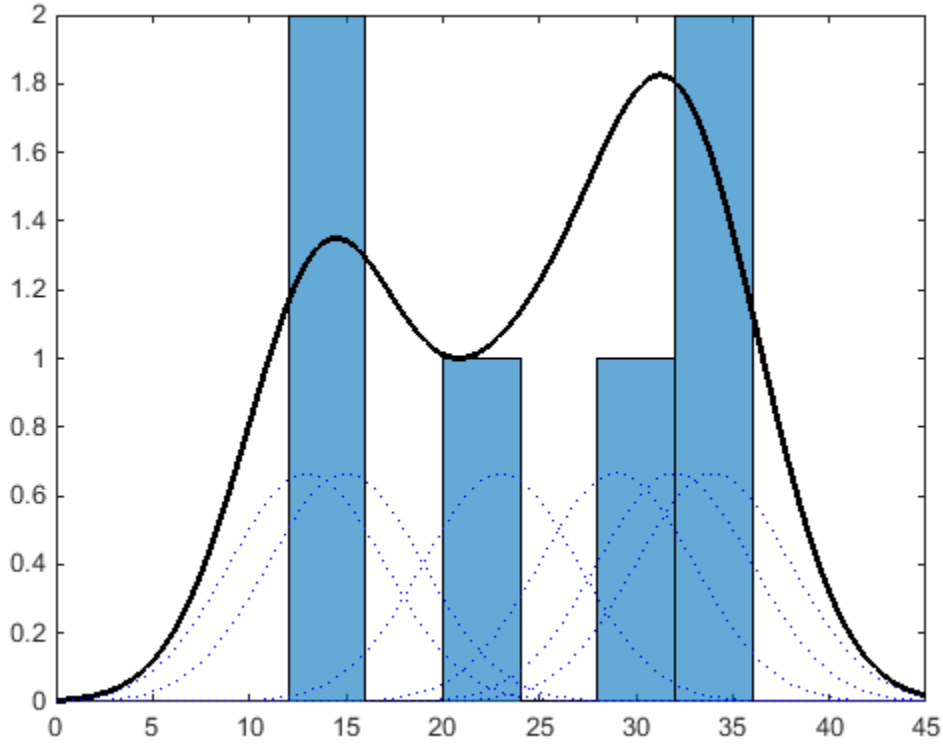
Overview

In some situations, you cannot accurately describe a data sample using a parametric distribution. Instead, the probability density function (pdf) or cumulative distribution function (cdf) must be estimated from the data. Statistics and Machine Learning Toolbox provides several options for estimating the pdf or cdf from sample data.

Kernel Distribution

A kernel distribution produces a nonparametric probability density estimate that adapts itself to the data, rather than selecting a density with a particular parametric form and estimating the parameters. This distribution is defined by a kernel density estimator, a smoothing function that determines the shape of the curve used to generate the pdf, and a bandwidth value that controls the smoothness of the resulting density curve.

Similar to a histogram, the kernel distribution builds a function to represent the probability distribution using the sample data. But unlike a histogram, which places the values into discrete bins, a kernel distribution sums the component smoothing functions for each data value to produce a smooth, continuous probability curve. The following plot shows a visual comparison of a histogram and a kernel distribution generated from the same sample data.



A histogram represents the probability distribution by establishing bins and placing each data value in the appropriate bin. Because of this bin count approach, the histogram produces a discrete probability density function. This might be unsuitable for certain applications, such as generating random numbers from a fitted distribution.

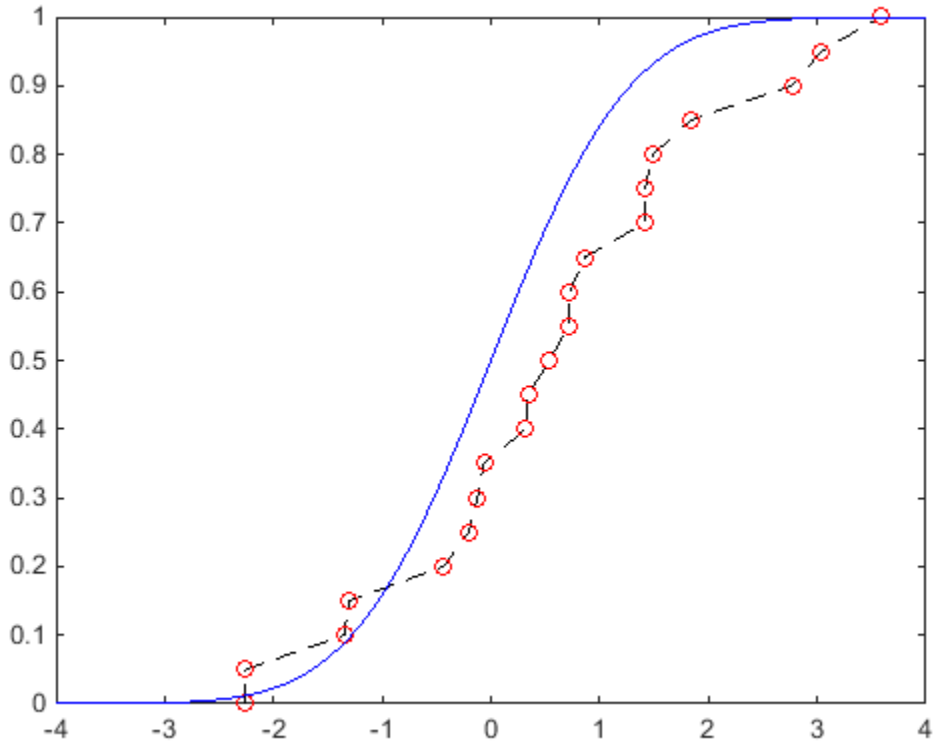
Alternatively, the kernel distribution builds the probability density function (pdf) by creating an individual probability density curve for each data value, then summing the smooth curves. This approach creates one smooth, continuous probability density function for the data set.

For more general information about kernel distributions, see “Kernel Distribution” on page B-81. For information on how to work with a kernel distribution, see `Using KernelDistribution Objects` and `ksdensity`.

Empirical Cumulative Distribution Function

An empirical cumulative distribution function (`ecdf`) estimates the cdf of a random variable by assigning equal probability to each observation in a sample. Because of this approach, the ecdf is a discrete cumulative distribution function that creates an exact match between the ecdf and the distribution of the sample data.

The following plot shows a visual comparison of the ecdf of 20 random numbers generated from a standard normal distribution, and the theoretical cdf of a standard normal distribution. The circles indicate the value of the ecdf calculated at each sample data point. The dashed line that passes through each circle visually represents the ecdf, although the ecdf is not a continuous function. The solid line shows the theoretical cdf of the standard normal distribution from which the random numbers in the sample data were drawn.



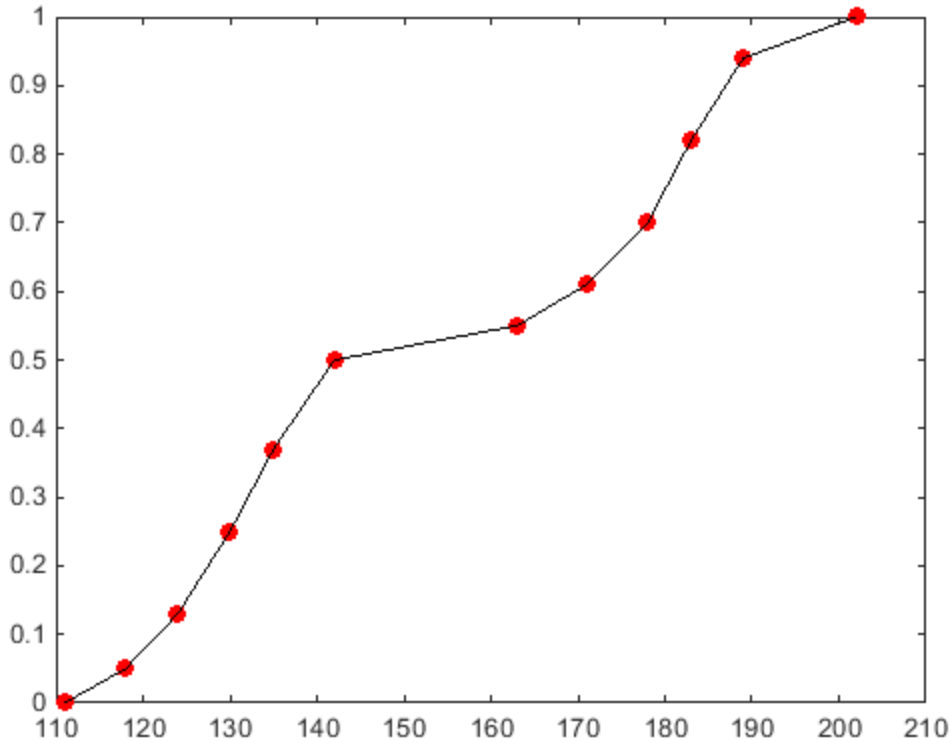
The ecdf is similar in shape to the theoretical cdf, although it is not an exact match. Instead, the ecdf is an exact match to the sample data. The ecdf is a discrete function, and is not smooth, especially in the tails where data might be sparse. You can smooth the distribution with Pareto tails, using the `paretotails` function.

For more information and additional syntax options, see `ecdf`. To construct a continuous function based on cdf values computed from sample data, see “Piecewise Linear Distribution” on page 5-44.

Piecewise Linear Distribution

A piecewise linear distribution estimates an overall cdf for the sample data by computing the cdf value at each individual point, and then linearly connecting these values to form a continuous curve.

The following plot shows the cdf for a piecewise linear distribution based on a sample of hospital patients' weight measurements. The circles represent each individual data point (weight measurement). The black line that passes through each data point represents the piecewise linear distribution cdf for the sample data.



A piecewise linear distribution linearly connects the cdf values calculated at each sample data point to form a continuous curve. By contrast, an empirical cumulative distribution

function constructed using the `ecdf` function produces a discrete cdf. For example, random numbers generated from the ecdf can only include x values contained in the original sample data. Random numbers generated from a piecewise linear distribution can include any x value between the lower and upper boundaries of the sample data.

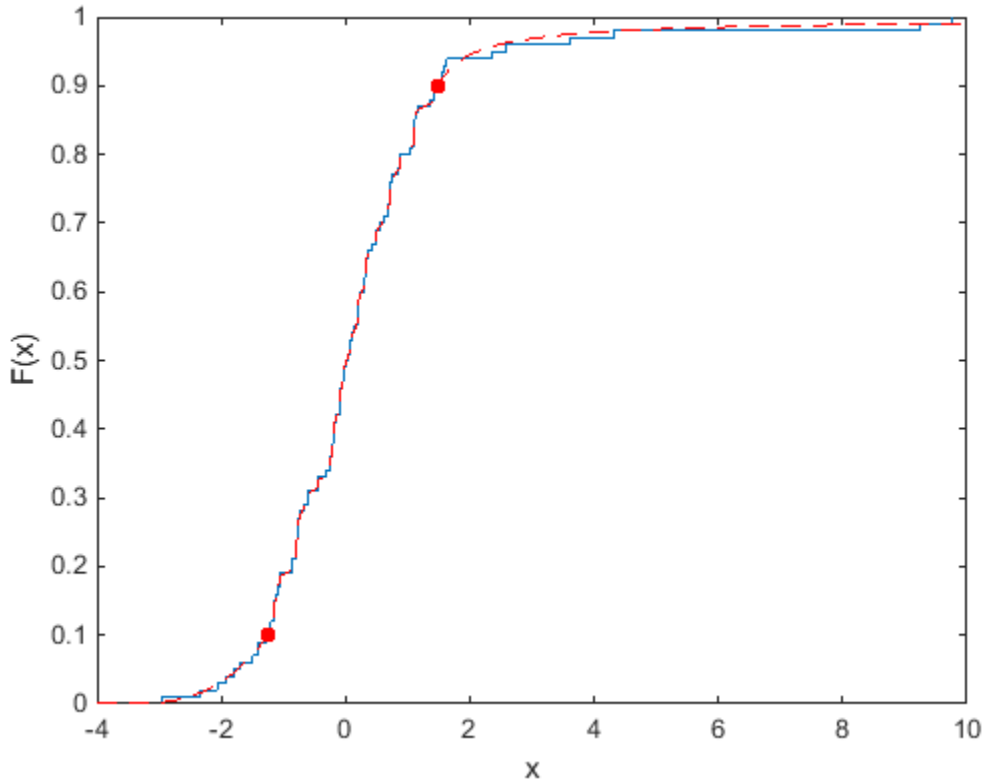
Because the piecewise linear distribution cdf is constructed from the values contained in the sample data, the resulting curve is often not smooth, especially in the tails where data might be sparse. You can smooth the distribution with Pareto tails, using the `paretotails` function.

For information on how to work with a piecewise linear distribution, see Using `PiecewiseLinearDistribution` Objects.

Pareto Tails

Pareto tails use a piecewise approach to improve the fit of a nonparametric cdf or pdf by smoothing the tails of the distribution. You can fit a kernel distribution, empirical cdf, or piecewise linear distribution to the middle data values, then fit generalized Pareto distribution curves to the tails. This technique is especially useful when the sample data is sparse in the tails.

The following plot shows the empirical cdf (ecdf) of a data sample containing 20 random numbers. The solid line represents the ecdf, and the dashed line represents the empirical cdf with Pareto tails fit to the lower and upper 10 percent of the data. The circles denote the boundaries for the lower and upper 10 percent of the data.

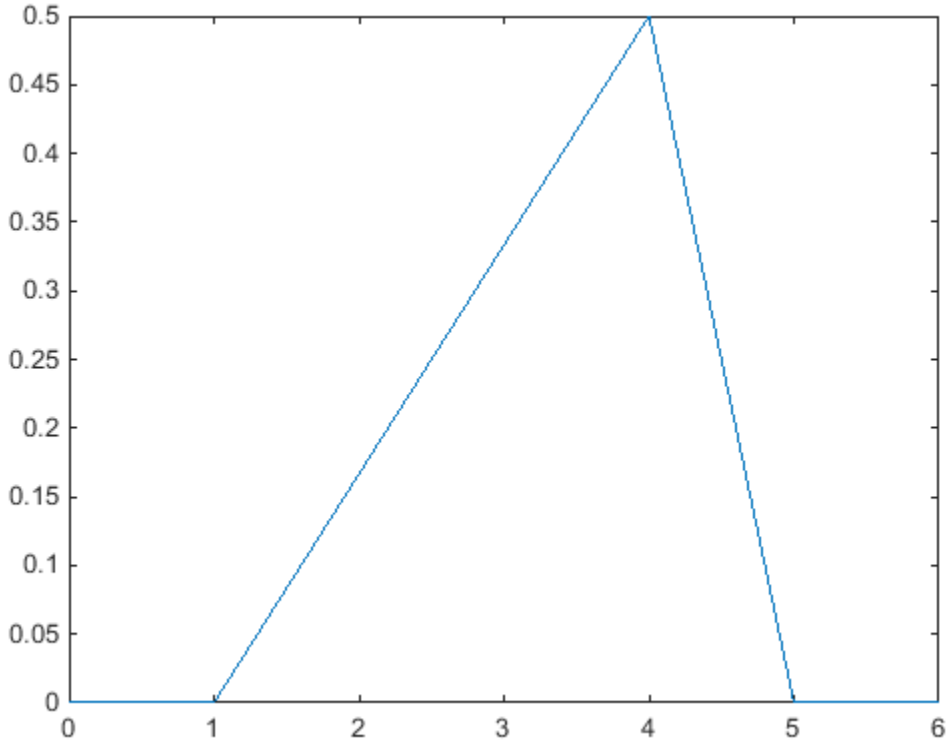


Fitting Pareto tails to the lower and upper 10 percent of the sample data makes the cdf smoother in the tails, where the data is sparse. For more information on working with Pareto tails, see `paretotails`.

Triangular Distribution

A "Triangular Distribution" on page B-157 provides a simplistic representation of the probability distribution when limited sample data is available. This continuous distribution is parameterized by a lower limit, peak location, and upper limit. These points are linearly connected to estimate the pdf of the sample data. You can use the mean, median, or mode of the data as the peak location.

The following plot shows the triangular distribution pdf of a random sample of 10 integers from 0 to 5. The lower limit is the smallest integer in the sample data, and the upper limit is the largest integer. The peak for this plot is at the mode, or most frequently-occurring value, in the sample data.



Business applications such as simulation and project management sometimes use a triangular distribution to create models when limited sample data exists. For more information, see “Triangular Distribution” on page B-157.

See Also

`ecdf` | `ksdensity` | `paretotails`

Related Examples

- “Fit a Nonparametric Distribution with Pareto Tails” on page 5-61

More About

- “Kernel Distribution” on page B-81
- “Piecewise Linear Distribution” on page B-136
- “Triangular Distribution” on page B-157

Fit Kernel Distribution Object to Data

This example shows how to fit a kernel probability distribution object to sample data.

Step 1. Load sample data.

Load the sample data.

```
load carsmall;
```

This data contains miles per gallon (`MPG`) measurements for different makes and models of cars, grouped by country of origin (`Origin`), model year (`Year`), and other vehicle characteristics.

Step 2. Fit a kernel distribution object.

Use `fitdist` to fit a kernel probability distribution object to the miles per gallon (`MPG`) data for all makes of cars.

```
pd = fitdist(MPG,'Kernel')
```

```
pd =

  KernelDistribution

    Kernel = normal
    Bandwidth = 4.11428
    Support = unbounded
```

This creates a `prob.KernelDistribution` object. By default, `fitdist` uses a normal kernel smoothing function and chooses an optimal bandwidth for estimating normal densities, unless you specify otherwise. You can access information about the fit and perform further calculations using the related object functions.

Step 3. Compute descriptive statistics.

Compute the mean, median, and standard deviation of the fitted kernel distribution.

```
m = mean(pd)
med = median(pd)
s = std(pd)
```

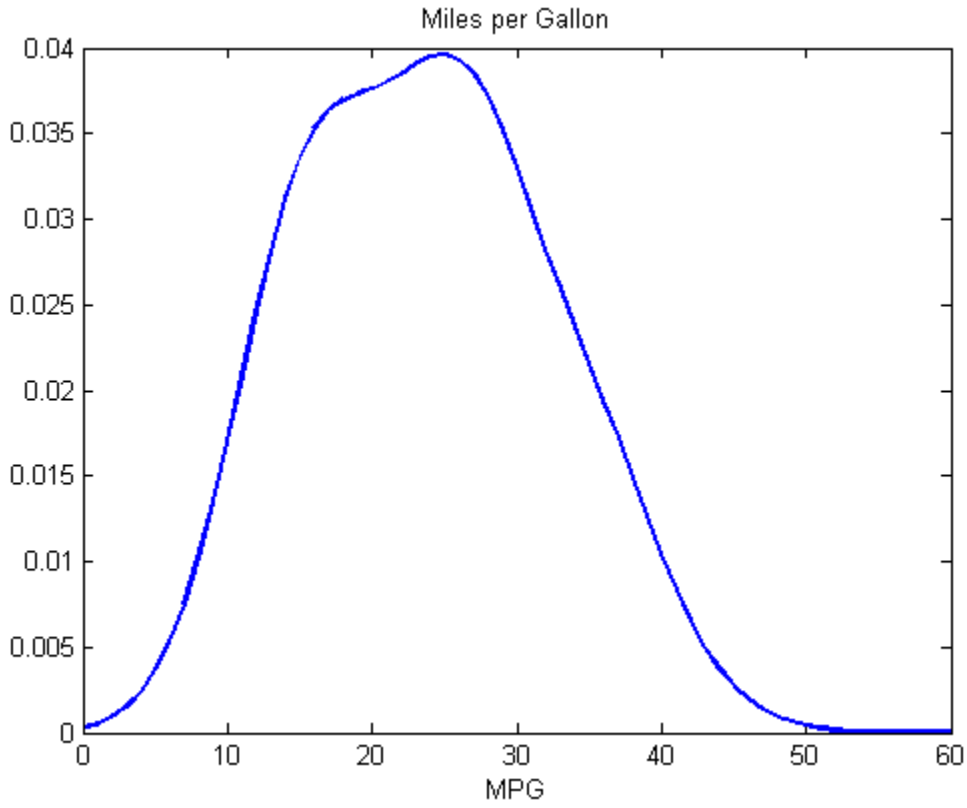
```
m =
```

```
   23.7181

med =

   23.4841

s =

    8.9896
```

Step 4. Compute and plot the pdf.

Compute and plot the pdf of the fitted kernel distribution.

```
figure;
x = 0:1:60;
y = pdf(pd,x);
plot(x,y,'LineWidth',2);
title('Miles per Gallon');
xlabel('MPG');
```



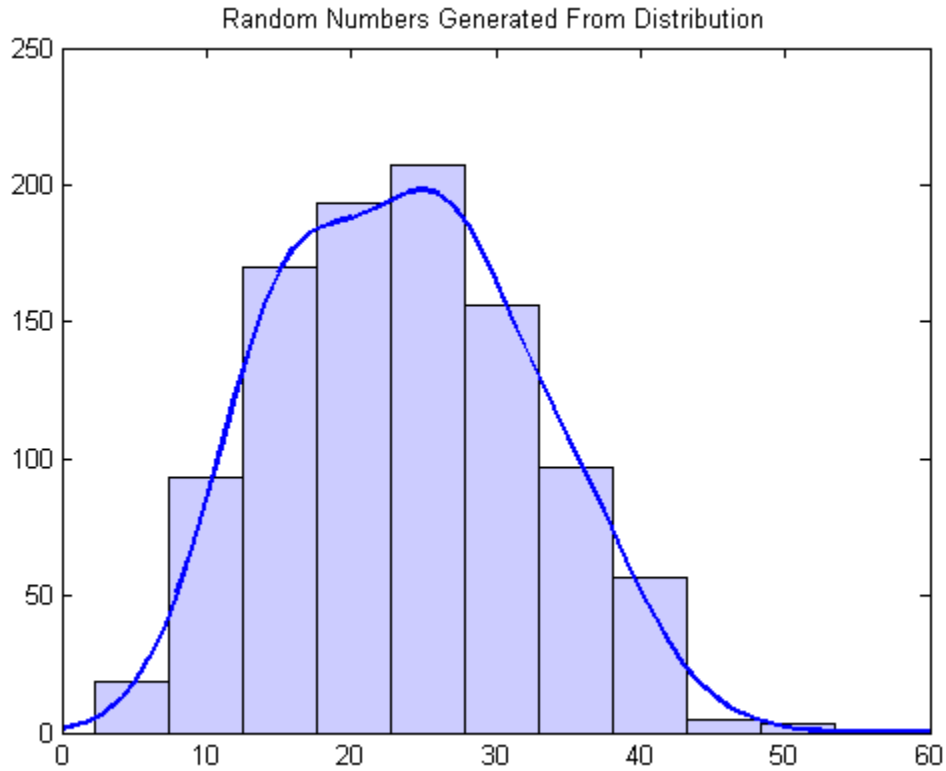
The plot shows the pdf of the kernel distribution fit to the MPG data across all makes of cars. The distribution is smooth and fairly symmetrical, although it is slightly skewed with a heavier right tail.

Step 5. Generate random numbers.

Generate a vector of random numbers from the fitted kernel distribution.

```
rng('default')  % For reproducibility
r = random(pd,1000,1);
figure;
hist(r);
set(get(gca,'Children'),'FaceColor',[.8 .8 1]);
hold on;
```

```
y = y*5000;  % Scale pdf to overlay on histogram
plot(x,y,'LineWidth',2);
title('Random Numbers Generated From Distribution');
hold off;
```



The histogram has a similar shape to the pdf plot because the random numbers generate from the nonparametric kernel distribution fit to the sample data.

See Also

`fitdist`

Related Examples

- “Fit Kernel Distribution Using ksdensity” on page 5-54

More About

- “Kernel Distribution” on page B-81

Fit Kernel Distribution Using ksdensity

This example shows how to generate a kernel probability density estimate from sample data using the `ksdensity` function.

Step 1. Load sample data.

Load the sample data.

```
load carsmall;
```

This data contains miles per gallon (`MPG`) measurements for different makes and models of cars, grouped by country of origin (`Origin`), model year (`Year`), and other vehicle characteristics.

Step 2. Generate a kernel probability density estimate.

Use `ksdensity` to generate a kernel probability density estimate for the miles per gallon (`MPG`) data.

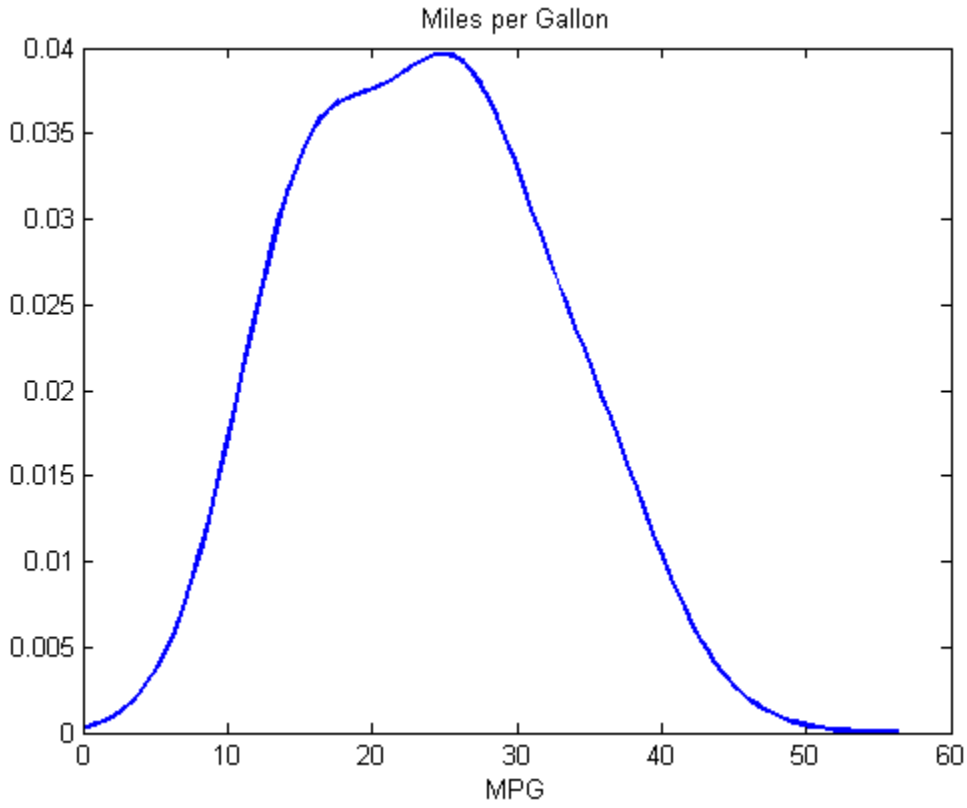
```
[f,xi] = ksdensity(MPG);
```

By default, `ksdensity` uses a normal kernel smoothing function and chooses an optimal bandwidth for estimating normal densities, unless you specify otherwise.

Step 3. Plot the kernel probability density estimate.

Plot the kernel probability density estimate to visualize the |MPG| distribution.

```
figure;
plot(xi,f,'LineWidth',2);
title('Miles per Gallon');
xlabel('MPG');
```



The plot shows the pdf of the kernel distribution fit to the `MPG` data across all makes of cars. The distribution is smooth and fairly symmetrical, although it is slightly skewed with a heavier right tail.

See Also

`ksdensity`

Related Examples

- “Fit Kernel Distribution Object to Data” on page 5-49

More About

- “Kernel Distribution” on page B-81

Fit Distributions to Grouped Data Using ksdensity

This example shows how to fit kernel distributions to grouped sample data using the `ksdensity` function.

Step 1. Load sample data.

Load the sample data.

```
load carsmall;
```

The data contains miles per gallon (`MPG`) measurements for different makes and models of cars, grouped by country of origin (`Origin`), model year (`Model_Year`), and other vehicle characteristics.

Step 2. Group sample data by origin.

Group the `MPG` data by origin (`Origin`) for cars made in the USA, Japan, and Germany.

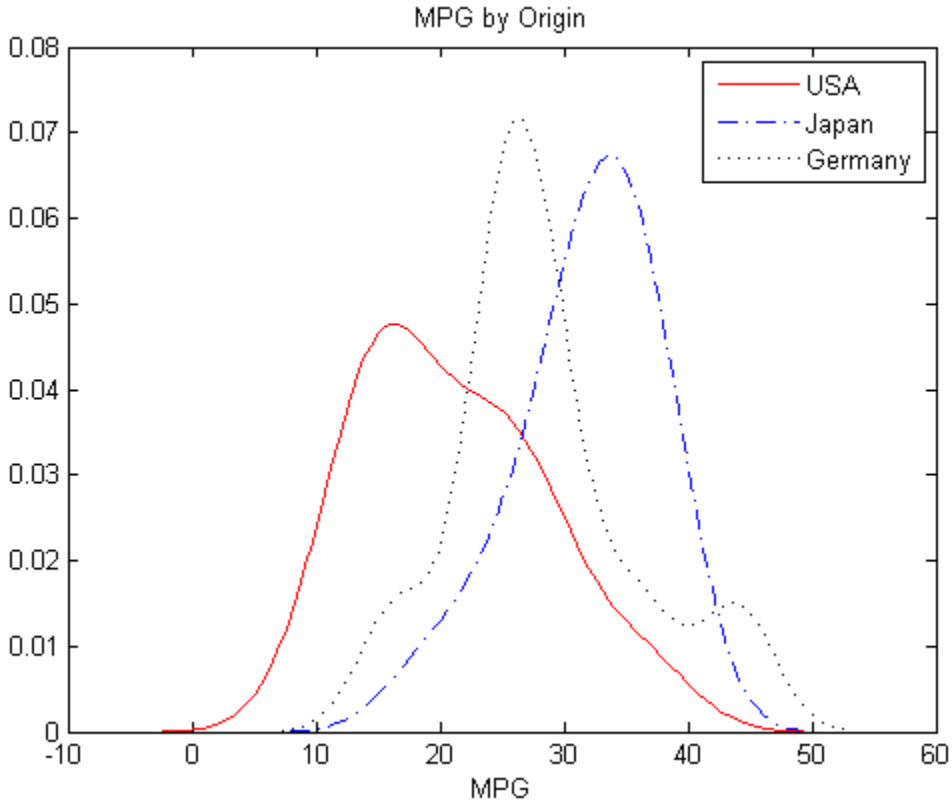
```
Origin = nominal(Origin);
MPG_USA = MPG(Origin=='USA');
MPG_Japan = MPG(Origin=='Japan');
MPG_Germany = MPG(Origin=='Germany');
```

Step 3. Compute and plot the pdf.

Compute and plot the pdf for each group.

```
figure;

[fi,xi] = ksdensity(MPG_USA);
plot(xi,fi,'r-');
hold on;

[fj,xj] = ksdensity(MPG_Japan);
plot(xj,fj,'b-.')

[fk,xk] = ksdensity(MPG_Germany);
plot(xk,fk,'k:')

legend('USA','Japan','Germany')
title('MPG by Origin');
xlabel('MPG');
```

```
hold off;
```



The plot shows how miles per gallon (`MPG`) performance differs by country of origin (`Origin`). Using this data, the USA has the widest distribution, and its peak is at the lowest `MPG` value of the three origins. Japan has the most regular distribution with a slightly heavier left tail, and its peak is at the highest `MPG` value of the three origins. The peak for Germany is between the USA and Japan, and the second bump near 44 miles per gallon suggests that there might be multiple modes in the data.

See Also

`makedist`

Related Examples

- "Fit Kernel Distribution Using ksdensity" on page 5-54
- "Fit Probability Distribution Objects to Grouped Data" on page 5-124

More About

- "Kernel Distribution" on page B-81
- "Grouping Variables" on page 2-52

Create and Plot Empirical Cumulative Distribution Functions

This example shows how to create and plot an empirical cumulative distribution function based on sample data.

Step 1. Load sample data.

Load the sample data.

Step 2. Compute the empirical cumulative distribution.

The empirical cdf assigns the probability $1/n$ to each of n observations in a data sample. It returns the values of a function F such that $F(x)$ represents the proportion of observations in a sample less than or equal to x. The empirical distributions computed by `ecdf` assign equal probability to each observation in a sample, providing an exact match of the sample distribution. However, the distributions are not smooth, especially in the tails where data may be sparse. In this situation, you can use Pareto tails to smooth the cdf in the tails.

Step 3. Plot the ecdf.

The graph of an empirical cdf has a stair-step appearance. If a sample comes from a distribution in a parametric family (such as a normal distribution), its empirical cdf is likely to resemble the parametric distribution. If not, its empirical distribution still gives an estimate of the cdf for the distribution that generated the data.

Fit a Nonparametric Distribution with Pareto Tails

This example shows how to fit a nonparametric probability distribution to sample data using Pareto tails to smooth the distribution in the tails.

Step 1. Generate sample data.

Generate sample data that contains more outliers than expected from a standard normal distribution.

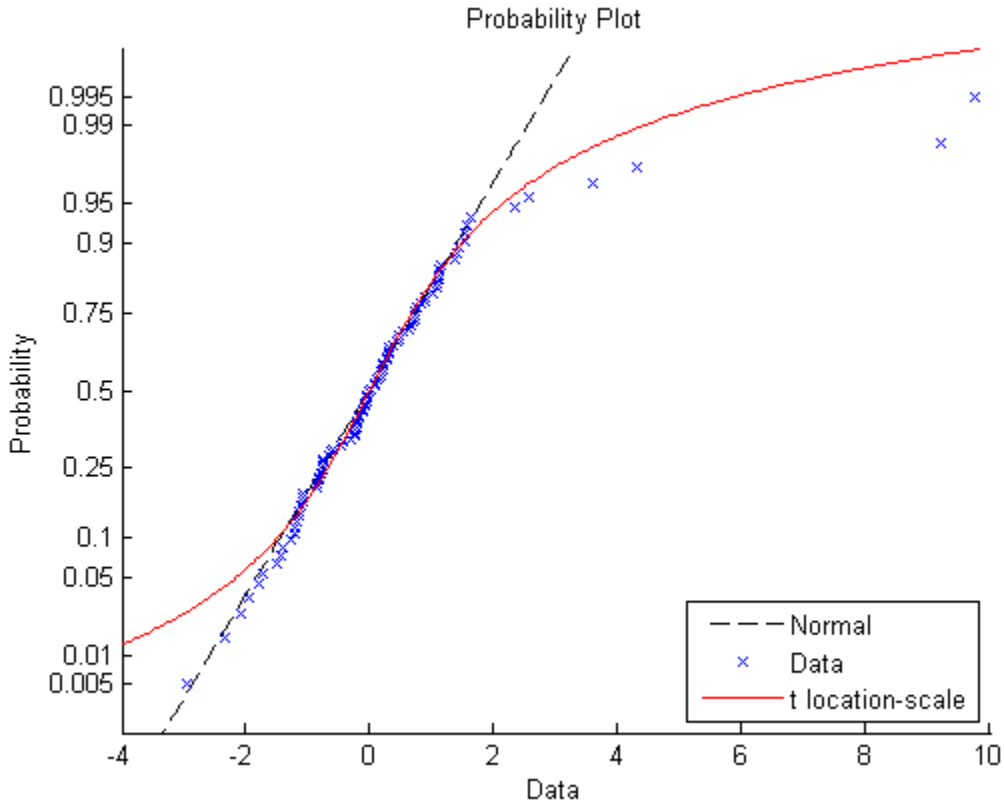
```
rng('default')  % For reproducibility
left_tail = -exprnd(1,10,1);
right_tail = exprnd(5,10,1);
center = randn(80,1);
data = [left_tail;center;right_tail];
```

The data contains 80% values from a standard normal distribution, 10% from an exponential distribution with a mean of 5, and 10% from an exponential distribution with mean of –1. the data contains random numbers from an exponential distribution. Compared to a standard normal distribution, the exponential values are more likely to be outliers, especially in the upper tail.

Step 2. Fit probability distributions to the data.

Fit a normal distribution and a *t* location-scale distribution to the data, and plot for a visual comparison.

```
figure;
probplot(data);
p = fitdist(data,'tlocationscale');
h = probplot(gca,p);
set(h,'color','r','linestyle','-');
title('Probability Plot');
legend('Normal','Data','t location-scale','Location','SE');
```

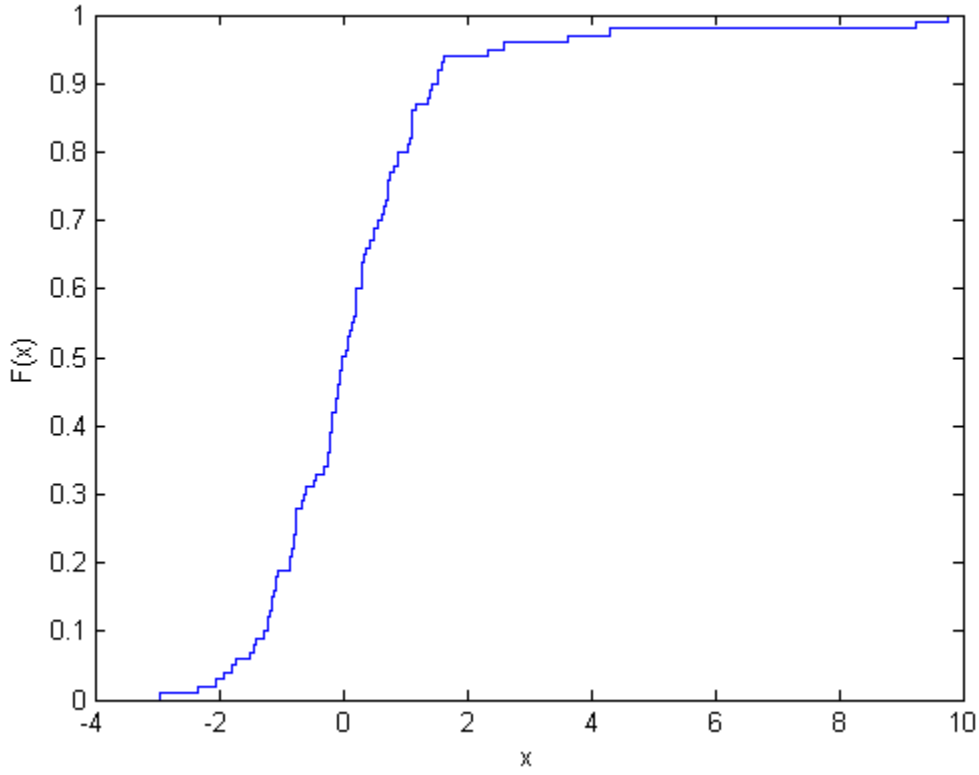


Both distributions appear to fit reasonably well in the center, but neither the normal distribution nor the *t* location-scale distribution fit the tails very well.

Step 3. Generate an empirical distribution.

To obtain a better fit, use `ecdf` to generate an empirical cdf based on the sample data.

```
figure;
ecdf(data)
```



The empirical distribution provides a perfect fit, but the outliers make the tails very discrete. Random samples generated from this distribution using the inversion method might include, for example, values near 4.33 and 9.25, but no values in between.

Step 4. Fit a distribution using Pareto tails.

Use `paretotails` to generate an empirical cdf for the middle 80% of the data and fit generalized Pareto distributions to the lower and upper 10%.

```
pfit = paretotails(data,0.1,0.9)
```

```
pfit =

Piecewise distribution with 3 segments
```

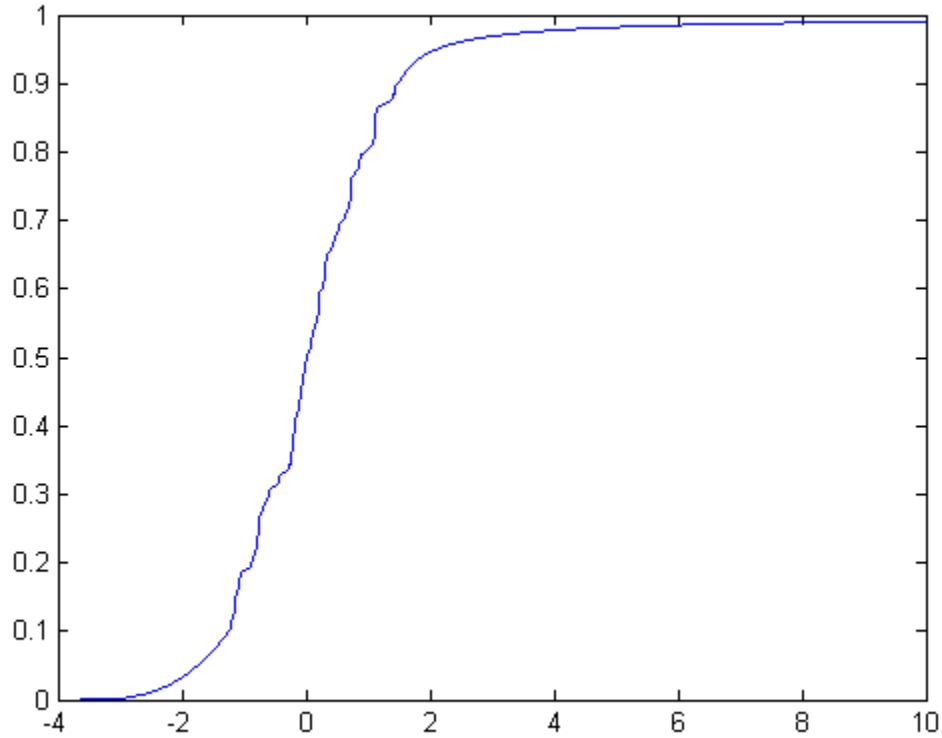
```
    -Inf < x < -1.24623    (0 < p < 0.1): lower tail, GPD(-0.334156,0.798745)
-1.24623 < x < 1.48551  (0.1 < p < 0.9): interpolated empirical cdf
     1.48551 < x < Inf    (0.9 < p < 1): upper tail, GPD(1.23681,0.581868)
```

To obtain a better fit, `paretotails` fits a distribution by piecing together an ecdf or kernel distribution in the center of the sample, and smooth generalized Pareto distributions (GPDs) in the tails. The `paretotails` function creates a `paretotails` probability distribution object. You can access information about the fit and perform further calculations on the object using the methods of the `paretotails` class. For example, you can evaluate the cdf or generate random numbers from the distribution.

Step 5. Compute and plot the cdf.

Compute and plot the cdf of the fitted `paretotails` distribution.

```
x = -4:0.01:10;
plot(x,cdf(pfit,x));
```



The `paretotails` cdf closely fits the data but is smoother in the tails than the ecdf generated in Step 3.

Generate Random Numbers Using the Triangular Distribution

This example shows how to create a triangular probability distribution object based on sample data, and generate random numbers for use in a simulation.

Step 1. Input sample data.

Input the data vector `time`, which contains the observed length of time (in seconds) that 10 different cars stopped at a highway tollbooth.

```
time = [6 14 8 7 16 8 23 6 7 15];
```

The data shows that, while most cars stopped for 6 to 16 seconds, one outlier stopped for 23 seconds.

Step 2. Estimate distribution parameters.

Estimate the triangular distribution parameters from the sample data.

```
lower = min(time);
peak = median(time);
upper = max(time);
```

A triangular distribution provides a simplistic representation of the probability distribution when sample data is limited. Estimate the lower and upper boundaries of the distribution by finding the minimum and maximum values of the sample data. For the peak parameter, the median might provide a better estimate of the mode than the mean, since the data includes an outlier.

Step 3. Create a probability distribution object.

Create a triangular probability distribution object using the estimated parameter values.

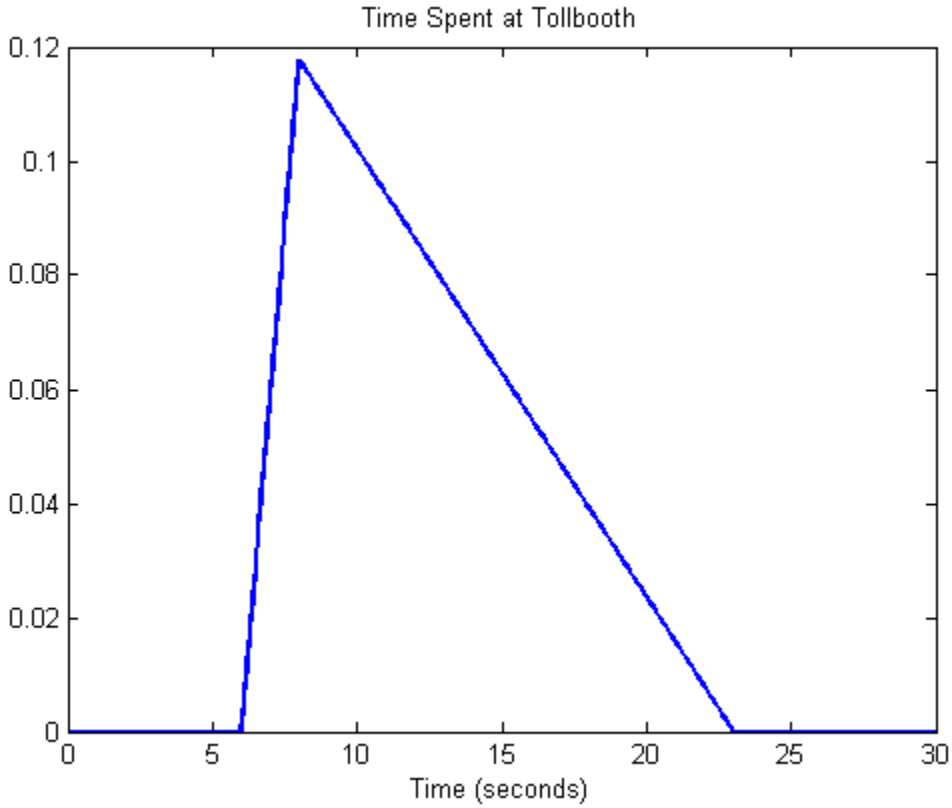
```
pd = makedist('Triangular','a',lower,'b',peak,'c',upper)
```

```
pd =

  TriangularDistribution

A = 6, B = 8, C = 23
```

Compute and plot the pdf of the triangular distribution.

```
figure;
x = 0:.1:230;
```

```
y = pdf(pd,x);
plot(x,y);
title('Time Spent at Tollbooth');
xlabel('Time (seconds)');
```



The plot shows that this triangular distribution is skewed to the right. However, since the estimated peak value is the sample median, the distribution should be symmetrical about the peak. Because of its skew, this model might, for example, generate random numbers that seem unusually high when compared to the initial sample data.

Step 4. Generate random numbers.

Generate random numbers from this distribution to simulate future traffic flow through the tollbooth.

```
rng('default');  % For reproducibility
r = random(pd,10,1)

r =

   16.1265
   18.0987
    8.0796
   18.3001
   13.3176
    7.8211
    9.4360
   12.2508
   19.7082
   20.0078
```

The returned values in `r` are the time in seconds that the next 10 simulated cars spend at the tollbooth. These values seem high compared to the values in the original data vector `time` because the outlier skewed the distribution to the right. Using the second-highest value as the upper limit parameter might mitigate the effects of the outlier and generate a set of random numbers more similar to the initial sample data.

Step 5. Revise estimated parameters.

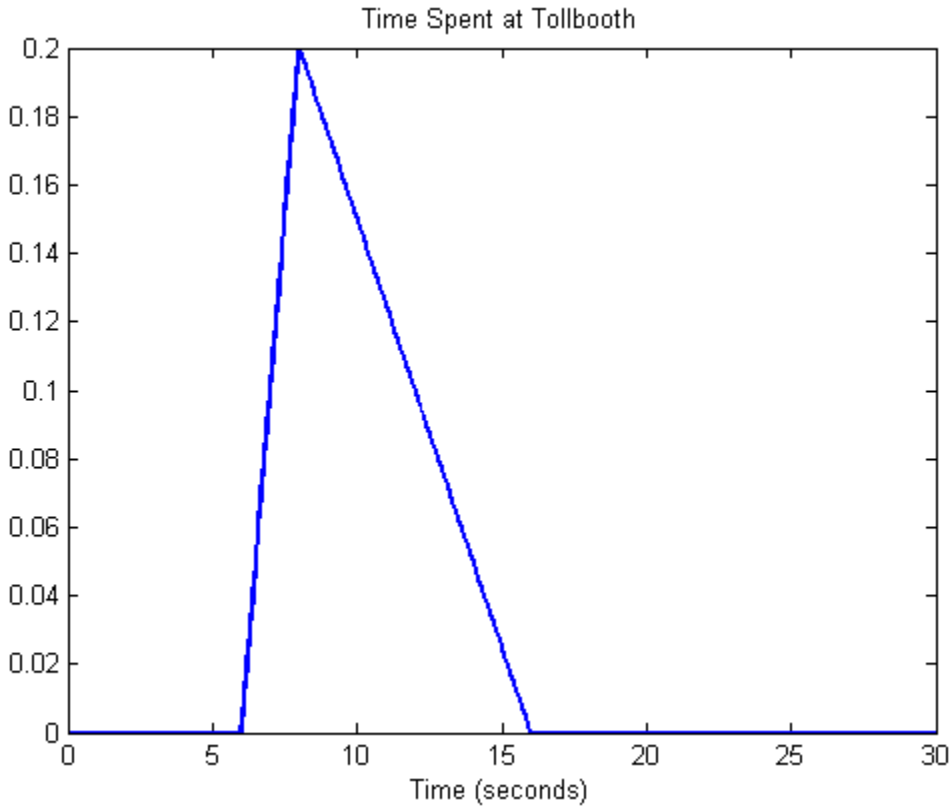
Estimate the upper boundary of the distribution using the second largest value in the sample data.

```
sort_time = sort(time,'descend');
secondLargest = sort_time(2);
```

Step 6. Create a new distribution object and plot the pdf.

Create a new triangular probability distribution object using the revised estimated parameters, and plot its pdf.

```
figure;
pd2 = makedist('Triangular','a',lower,'b',peak,'c',secondLargest);
y2 = pdf(pd2,x);
plot(x,y2,'LineWidth',2);
title('Time Spent at Tollbooth');
xlabel('Time (seconds)');
```



The plot shows that this triangular distribution is still slightly skewed to the right. However, it is much more symmetrical about the peak than the distribution that used the maximum sample data value to estimate the upper limit.

Step 7. Generate new random numbers.

Generate new random numbers from the revised distribution.

```
rng('default'); % For reproducibility
r2 = random(pd2,10,1)
```

```
r2 =

   12.1501
```

```
   13.2547
    7.5937
   13.3675
   10.5768
    7.3967
    8.4026
    9.9792
   14.1562
   14.3240
```

These new values more closely resemble those in the original data vector `time`. They are also closer to the sample median than the random numbers generated by the distribution that used the outlier to estimate its upper limit. This example does not remove the outlier from the sample data when computing the median. Other options for parameter estimation include removing outliers from the sample data altogether, or using the mean or mode of the sample data as the peak value.

See Also

`makedist` | `pdf` | `random`

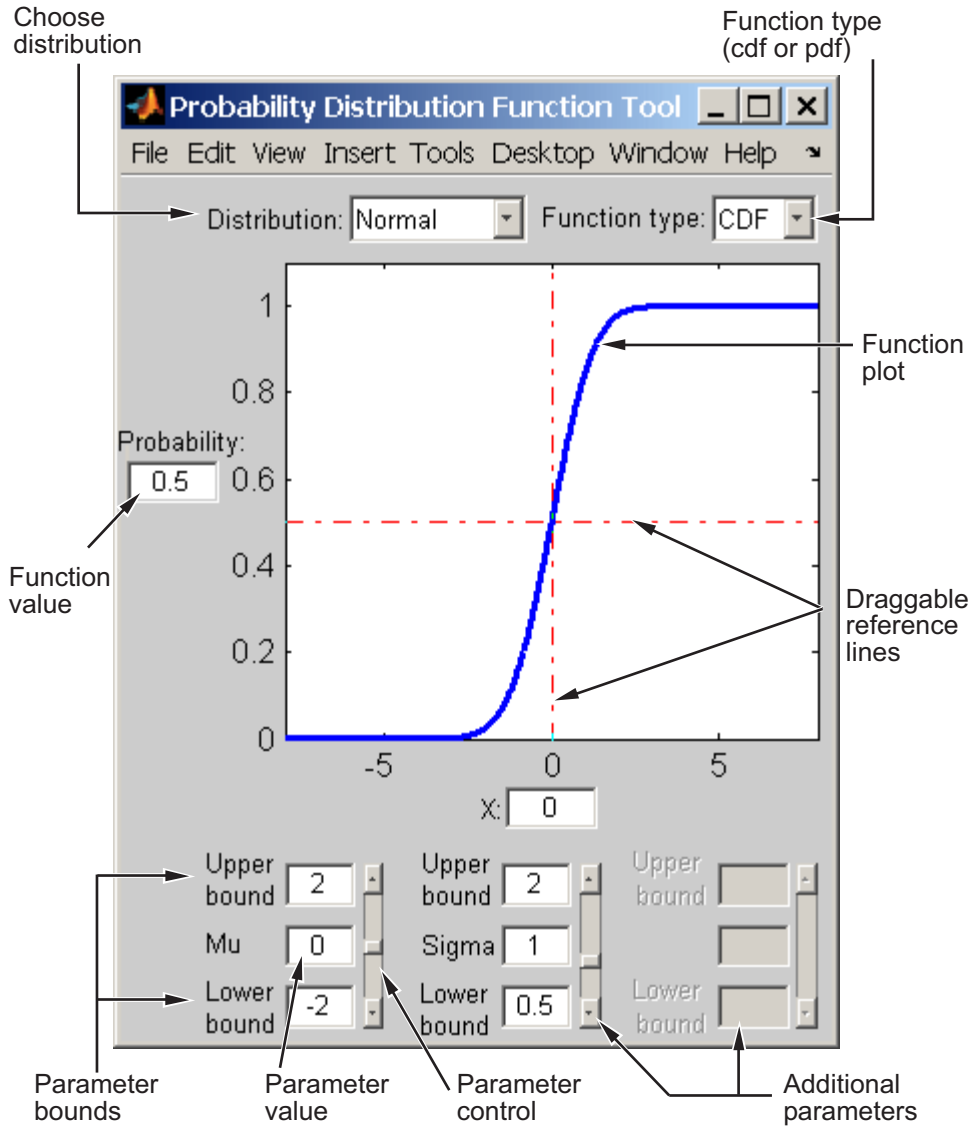
More About

- "Triangular Distribution" on page B-157

Explore the Probability Distribution Function UI

The Probability Distribution Function user interface (UI) interactively displays the influence of parameter changes on the shapes of the pdfs and cdfs of supported Statistics and Machine Learning Toolbox distributions.

Run the user interface by typing `disttool` at the command line.



Start by selecting a distribution. Then choose the function type: probability density function (pdf) or cumulative distribution function (cdf).

After the plot appears, you can

- Calculate a new function value by
  - Typing a new `x` value in the text box on the *x*-axis
  - Dragging the vertical reference line.
  - Clicking in the figure where you want the line to be.

  The new function value appears in the text box to the left of the plot.
- For cdf plots, find critical values corresponding to a specific probability by typing the desired probability in the text box on the *y*-axis or by dragging the horizontal reference line.
- Use the controls at the bottom of the window to set parameter values for the distribution and to change their upper and lower bounds.

Model Data Using the Distribution Fitting App

The Distribution Fitting app provides a visual, interactive approach to fitting univariate distributions to data.

In this section...

Explore Probability Distributions Interactively

You can use the Distribution Fitting app to interactively fit probability distributions to data imported from the MATLAB workspace. You can choose from 22 built-in probability distributions, or create your own custom distribution. The app displays the fitted distribution over plots of the empirical distributions, including pdf, cdf, probability plots, and survivor functions. You can export the fit data, including fitted parameter values, to the workspace for further analysis.

Distribution Fitting App Workflow

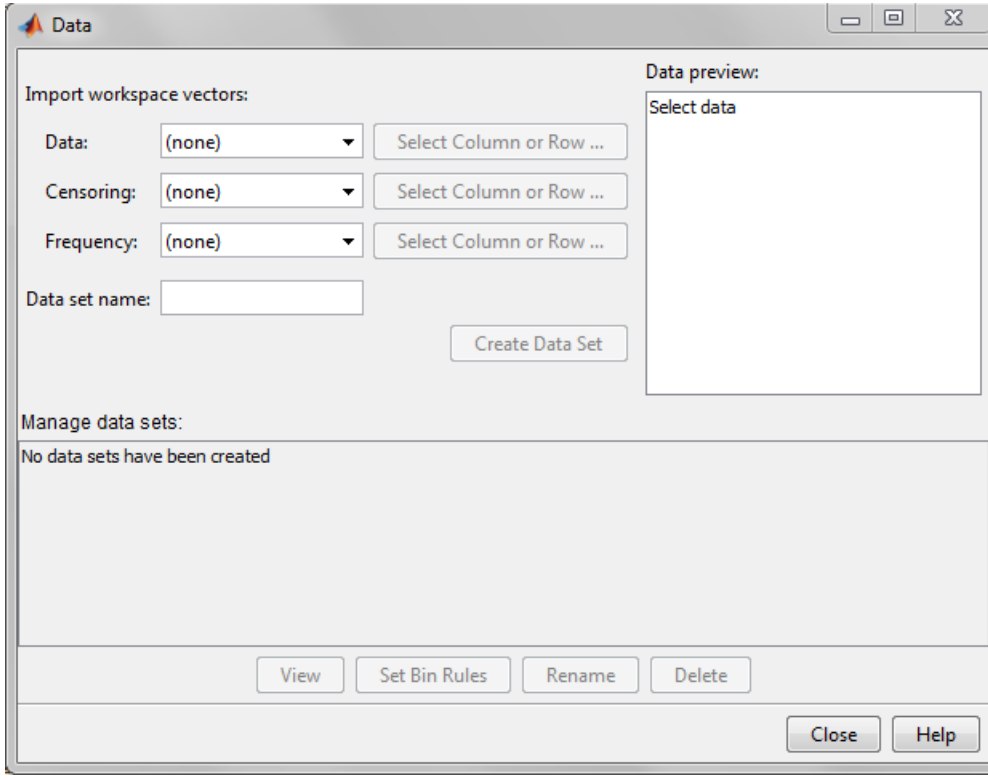
To fit a probability distribution to your sample data:

1. On the MATLAB Toolstrip, click the Apps tab. In the Math, Statistics and Optimization group, open the Distribution Fitting app. Alternatively, at the command prompt, enter `dfittool`.
2. Import your sample data, or create a data vector directly in the app. You can also manage your data sets and choose which one to fit. See "Create and Manage Data Sets" on page 5-75.

3. Create a new fit for your data. See “Create a New Fit” on page 5-80.
4. Display the results of the fit. You can choose to display the density (pdf), cumulative probability (cdf), quantile (inverse cdf), probability plot (choose one of several distributions), survivor function, and cumulative hazard. See “Display Results” on page 5-85.
5. You can create additional fits, and manage multiple fits from within the app. See “Manage Fits” on page 5-87.
6. Evaluate probability functions for the fit. You can choose to evaluate the density (pdf), cumulative probability (cdf), quantile (inverse cdf), survivor function, and cumulative hazard. See “Evaluate Fits” on page 5-88.
7. Improve the fit by excluding certain data. You can specify bounds for the data to exclude, or you can exclude data graphically using a plot of the values in the sample data. See “Exclude Data” on page 5-92.
8. Save your current Distribution Fitting app session so you can open it later. See “Save and Load Sessions” on page 5-98.

Create and Manage Data Sets

To open the Data dialog box, click the **Data** button in the Distribution Fitting app.



Import Data

Create a data set by importing a vector from the MATLAB workspace using the **Import workspace vectors** pane.

- **Data** — In the **Data** field, the drop-down list contains the names of all matrices and vectors, other than 1-by-1 matrices (scalars) in the MATLAB workspace. Select the array containing the data that you want to fit. The actual data you import must be a vector. If you select a matrix in the **Data** field, the first column of the matrix is imported by default. To select a different column or row of the matrix, click **Select Column or Row**. The matrix displays in the Variables editor. You can select a row or column by highlighting it.

  Alternatively, you can enter any valid MATLAB expression in the **Data** field.

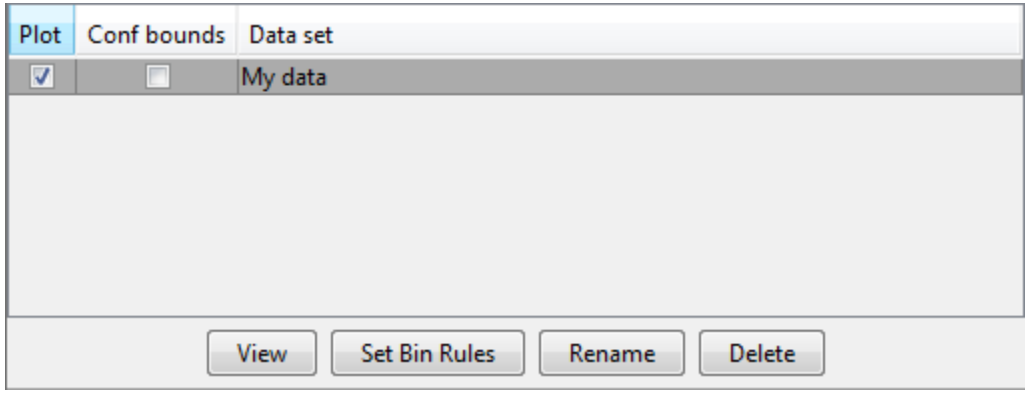
When you select a vector in the **Data** field, a histogram of the data appears in the **Data preview** pane.

- **Censoring** — If some of the points in the data set are censored, enter a Boolean vector of the same size as the data vector, specifying the censored entries of the data. A `1` in the censoring vector specifies that the corresponding entry of the data vector is censored. A `0` specifies that the entry is not censored. If you enter a matrix, you can select a column or row by clicking **Select Column or Row**. If you do not have censored data, leave the **Censoring** field blank.
- **Frequency** — Enter a vector of positive integers of the same size as the data vector to specify the frequency of the corresponding entries of the data vector. For example, a value of `7` in the 15th entry of frequency vector specifies that there are 7 data points corresponding to the value in the 15th entry of the data vector. If all entries of the data vector have frequency 1, leave the **Frequency** field blank.
- **Data set name** — Enter a name for the data set that you import from the workspace, such as `My data`.

After you have entered the information in the preceding fields, click **Create Data Set** to create the data set `My data`.

Manage Data Sets

View and manage the data sets that you create using the **Manage data sets** pane. When you create a data set, its name appears in the **Data sets** list. The following figure shows the **Manage data sets** pane after creating the data set `My data`.



For each data set in the **Data sets** list, you can:

- Select the **Plot** check box to display a plot of the data in the main Distribution Fitting app window. When you create a new data set, **Plot** is selected by default. Clearing the **Plot** check box removes the data from the plot in the main window. You can specify the type of plot displayed in the **Display type** field in the main window.
- If **Plot** is selected, you can also select **Bounds** to display confidence interval bounds for the plot in the main window. These bounds are pointwise confidence bounds around the empirical estimates of these functions. The bounds are displayed only when you set **Display Type** in the main window to one of the following:
  - `Cumulative probability (CDF)`
  - `Survivor function`
  - `Cumulative hazard`

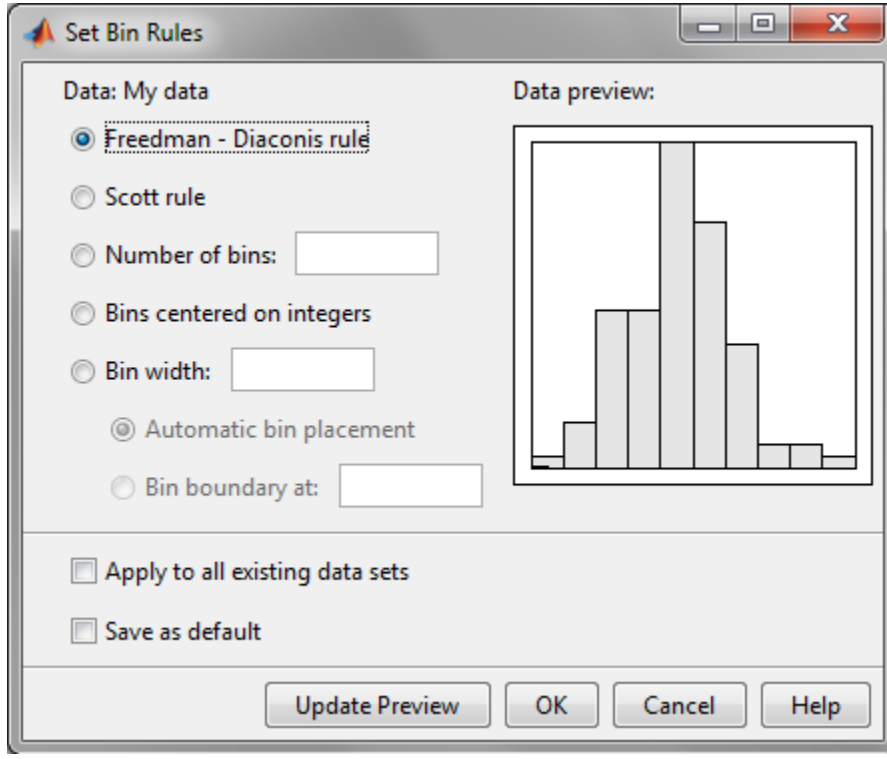
The Distribution Fitting app cannot display confidence bounds on density (`PDF`), quantile (`inverse CDF`), or probability plots. Clearing the **Bounds** check box removes the confidence bounds from the plot in the main window.

When you select a data set from the list, you can access the following buttons:

- **View** — Display the data in a table in a new window.
- **Set Bin Rules** — Defines the histogram bins used in a density (PDF) plot.
- **Rename** — Rename the data set.
- **Delete** — Delete the data set.

Set Bin Rules

To set bin rules for the histogram of a data set, click **Set Bin Rules** to open the **Set Bin Width Rules** dialog box.



You can select from the following rules:

- **Freedman-Diaconis rule** — Algorithm that chooses bin widths and locations automatically, based on the sample size and the spread of the data. This rule, which is the default, is suitable for many kinds of data.
- **Scott rule** — Algorithm intended for data that are approximately normal. The algorithm chooses bin widths and locations automatically.
- **Number of bins** — Enter the number of bins. All bins have equal widths.
- **Bins centered on integers** — Specifies bins centered on integers.
- **Bin width** — Enter the width of each bin. If you select this option, you can also select:
  - **Automatic bin placement** — Place the edges of the bins at integer multiples of the **Bin width**.

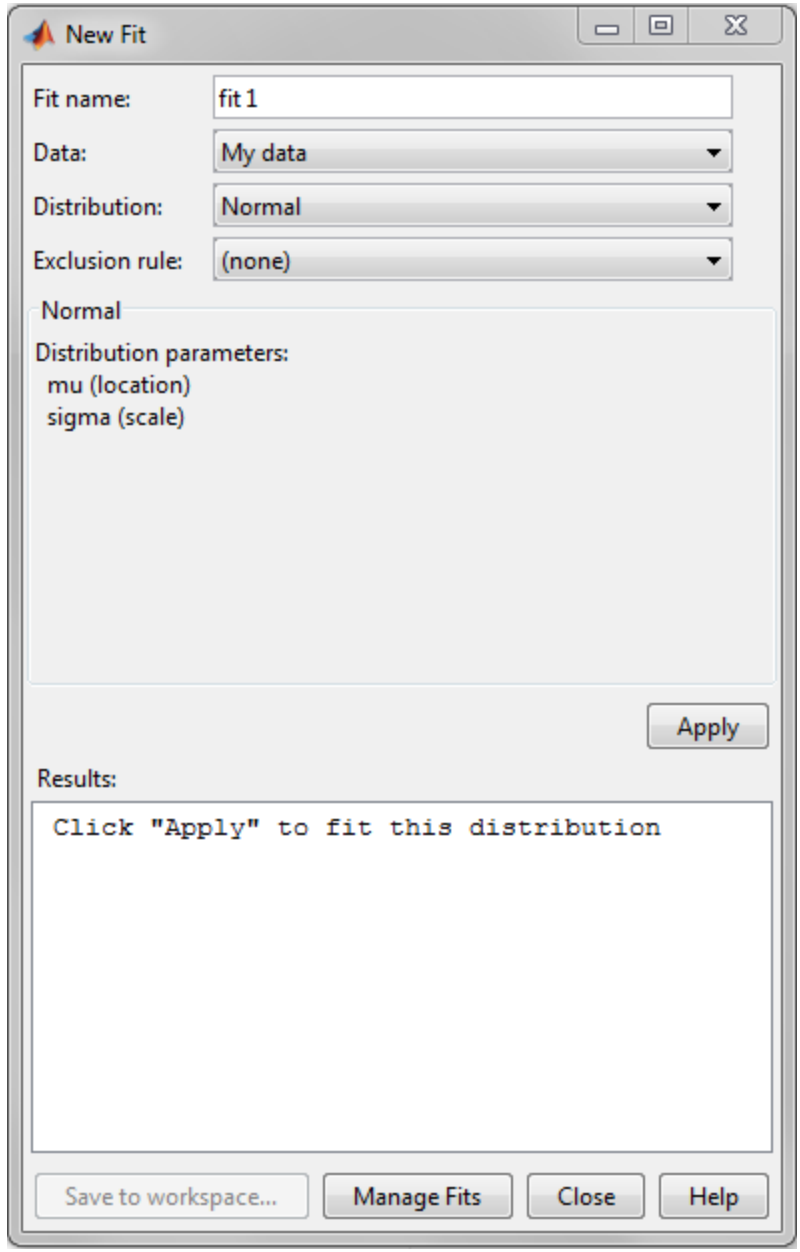
- **Bin boundary at** — Enter a scalar to specify the boundaries of the bins. The boundary of each bin is equal to this scalar plus an integer multiple of the **Bin width**.

You can also:

- **Apply to all existing data sets** — Apply the rule to all data sets. Otherwise, the rule is applied only to the data set currently selected in the Data dialog box.
- **Save as default** — Apply the current rule to any new data sets that you create. You can set default bin width rules by selecting **Set Default Bin Rules** from the **Tools** menu in the main window.

Create a New Fit

Click the **New Fit** button at the top of the main window to open the New Fit dialog box. If you created the data set `My data`, it appears in the **Data** field.


New Fit
Fit name:
fit 1
Data:
My data
Distribution:
Normal
Exclusion rule:
(none)
Normal
Distribution parameters:
mu (location)
sigma (scale)
Apply
Results:
Click "Apply" to fit this distribution
Save to workspace...
Manage Fits
Close
Help

Field Name	Description
Fit Name	Enter a name for the fit.
Data	Select the data set to which you want to fit a distribution from the drop-down list.
Distribution	Select the type of distribution to fit from the **Distribution** drop-down list. Only the distributions that apply to the values of the selected data set appear in the **Distribution** field. For example, when the data include values that are zero or negative, positive distributions are not displayed . You can specify either a parametric or a nonparametric distribution. When you select a parametric distribution from the drop-down list, a description of its parameters appears. The Distribution Fitting Tool estimates these parameters to fit the distribution to the data set. If you select the binomial distribution or the generalized extreme value distribution, you must specify a fixed value for one of the parameters. The pane contains a text field into which you can specify that parameter. When you select `Nonparametric fit`, options for the fit appear in the pane, as described in "Further Options for Nonparametric Fits" on page 5-84.
Exclusion rule	Specify a rule to exclude some data. Create an exclusion rule by clicking **Exclude** in the Distribution Fitting app. For more information, see "Exclude Data" on page 5-92.

Apply the New Fit

Click **Apply** to fit the distribution. For a parametric fit, the **Results** pane displays the values of the estimated parameters. For a nonparametric fit, the **Results** pane displays information about the fit.

When you click **Apply**, the Distribution Fitting app displays a plot of the distribution and the corresponding data.

Note When you click **Apply**, the title of the dialog box changes to Edit Fit. You can now make changes to the fit you just created and click **Apply** again to save them. After closing the Edit Fit dialog box, you can reopen it from the Fit Manager dialog box at any time to edit the fit.

After applying the fit, you can save the information to the workspace using probability distribution objects by clicking **Save to workspace**.

Available Distributions

All of the distributions available in the Distribution Fitting app are supported elsewhere in Statistics and Machine Learning Toolbox software. You can use the `fitdist` function to fit any of the distributions supported by the app. Many distributions also have dedicated fitting functions. These functions compute the majority of the fits in the Distribution Fitting app, and are referenced in the following list. Other fits are computed using functions internal to the Distribution Fitting app.

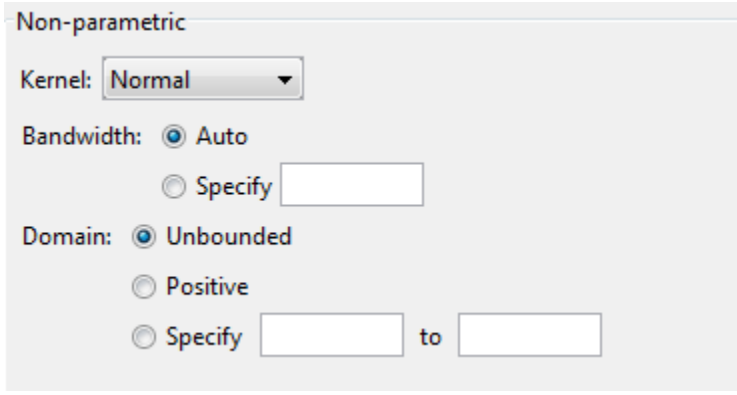
Not all of the distributions listed are available for all data sets. The Distribution Fitting app determines the extent of the data (nonnegative, unit interval, etc.) and displays appropriate distributions in the **Distribution** drop-down list. Distribution data ranges are given parenthetically in the following list.

- Beta (unit interval values) distribution, fit using the function `betafit`.
- Binomial (nonnegative integer values) distribution, fit using the function `binopdf`.
- Birnbaum-Saunders (positive values) distribution.
- Burr Type XII (positive values) distribution.
- Exponential (nonnegative values) distribution, fit using the function `expfit`.
- Extreme value (all values) distribution, fit using the function `evfit`.
- Gamma (positive values) distribution, fit using the function `gamfit`.
- Generalized extreme value (all values) distribution, fit using the function `gevfit`.
- Generalized Pareto (all values) distribution, fit using the function `gpfit`.
- Inverse Gaussian (positive values) distribution.
- Logistic (all values) distribution.
- Loglogistic (positive values) distribution.
- Lognormal (positive values) distribution, fit using the function `lognfit`.
- Nakagami (positive values) distribution.

- Negative binomial (nonnegative integer values) distribution, fit using the function `nbinpdf`.
- Nonparametric (all values) distribution, fit using the function `ksdensity`.
- Normal (all values) distribution, fit using the function `normfit`.
- Poisson (nonnegative integer values) distribution, fit using the function `poisspdf`.
- Rayleigh (positive values) distribution using the function `raylfit`.
- Rician (positive values) distribution.
- *t* location-scale (all values) distribution.
- Weibull (positive values) distribution using the function `wblfit`.

Further Options for Nonparametric Fits

When you select `Non-parametric` in the **Distribution** field, a set of options appears in the **Non-parametric** pane, as shown in the following figure.



The options for nonparametric distributions are:

- **Kernel** — Type of kernel function to use.
  - `Normal`
  - `Box`
  - `Triangle`
  - `Epanechnikov`
- **Bandwidth** — The bandwidth of the kernel smoothing window. Select **Auto** for a default value that is optimal for estimating normal densities. After you click **Apply**,

this value appears in the **Fit results** pane. Select **Specify** and enter a smaller value to reveal features such as multiple modes or a larger value to make the fit smoother.

- **Domain** — The allowed *x*-values for the density.
  - **Unbounded** — The density extends over the whole real line.
  - **Positive** — The density is restricted to positive values.
  - **Specify** — Enter lower and upper bounds for the domain of the density.

  When you select **Positive** or **Specify**, the nonparametric fit has zero probability outside the specified domain.

Display Results

The Distribution Fitting app window displays plots of:

- The data sets for which you select **Plot** in the Data dialog box.
- The fits for which you select **Plot** in the Fit Manager dialog box.
- Confidence bounds for:
  - The data sets for which you select **Bounds** in the Data dialog box.
  - The fits for which you select **Bounds** in the Fit Manager dialog box.

Adjust the plot display using the buttons at the top of the tool:

-  — Toggle the legend on (default) or off.
-  — Toggle grid lines on or off (default).
-  — Restore default axes limits.

The following fields are available.

Display Type

Specify the type of plot to display using the **Display Type** field in the main app window. Each type corresponds to a probability function, for example, a probability density function. You can choose from the following display types:

- `Density (PDF)` — Display a probability density function (PDF) plot for the fitted distribution. The main window displays data sets using a probability histogram, in

which the height of each rectangle is the fraction of data points that lie in the bin divided by the width of the bin. This makes the sum of the areas of the rectangles equal to 1.

- `Cumulative probability (CDF)` — Display a cumulative probability plot of the data. The main window displays data sets using a cumulative probability step function. The height of each step is the cumulative sum of the heights of the rectangles in the probability histogram.
- `Quantile (inverse CDF)` — Display a quantile (inverse CDF) plot.
- `Probability plot` — Display a probability plot of the data. Specify the type of distribution used to construct the probability plot in the **Distribution** field. This field is only available when you select `Probability plot`. The choices for the distribution are:

  - `Exponential`
  - `Extreme value`
  - `Logistic`
  - `Log-Logistic`
  - `Lognormal`
  - `Normal`
  - `Rayleigh`
  - `Weibull`

  You can also create a probability plot against a parametric fit that you create in the **New Fit** pane. When you create these fits, they are added at the bottom of the **Distribution** drop-down list.
- `Survivor function` — Display survivor function plot of the data.
- `Cumulative hazard` — Display cumulative hazard plot of the data.

Note If the plotted data includes `0` or negative values, some distributions are unavailable.

Confidence Bounds

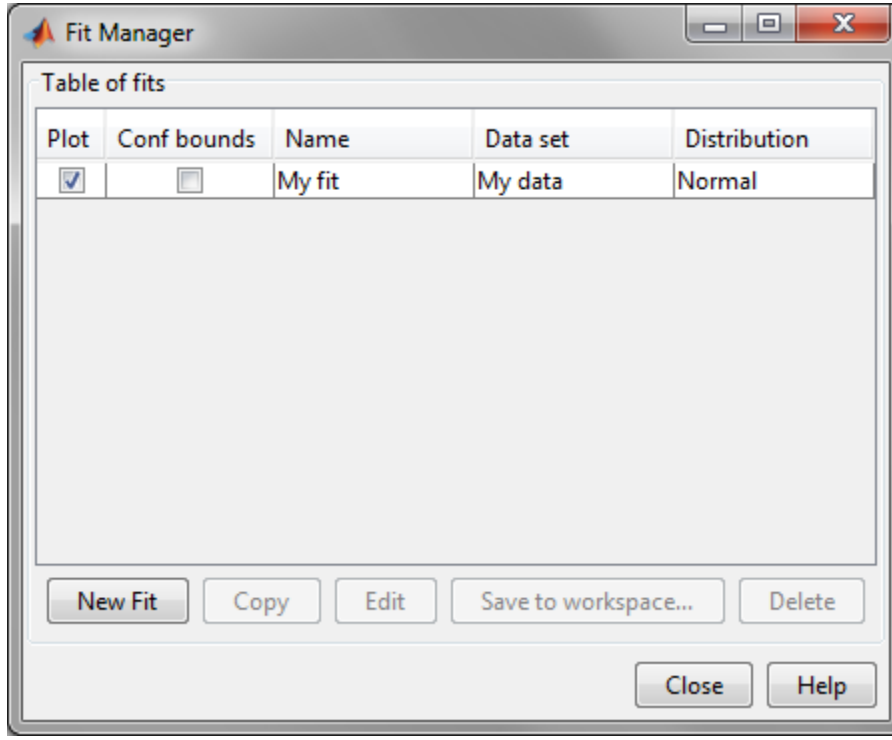
You can display confidence bounds for data sets and fits when you set **Display Type** to `Cumulative probability (CDF)`, `Survivor function`, `Cumulative hazard`, or, for fits only, `Quantile (inverse CDF)`.

- To display bounds for a data set, select **Bounds** next to the data set in the **Data sets** pane of the Data dialog box.
- To display bounds for a fit, select **Bounds** next to the fit in the Fit Manager dialog box. Confidence bounds are not available for all fit types.

To set the confidence level for the bounds, select `Confidence Level` from the **View** menu in the main window and choose from the options.

Manage Fits

Click the **Manage Fits** button to open the **Fit Manager** dialog box.



The **Table of fits** displays a list of the fits that you create, with the following options:

- **Plot** — Displays a plot of the fit in the main window of the Distribution Fitting app. When you create a new fit, **Plot** is selected by default. Clearing the **Plot** check box removes the fit from the plot in the main window.

- **Bounds** — If you select **Plot**, you can also select **Bounds** to display confidence bounds in the plot. The bounds are displayed when you set **Display Type** in the main window to one of the following:

  - `Cumulative probability (CDF)`
  - `Quantile (inverse CDF)`
  - `Survivor function`
  - `Cumulative hazard`

  The Distribution Fitting app cannot display confidence bounds on density (`PDF`) or probability plots. Bounds are not supported for nonparametric fits and some parametric fits.

  Clearing the **Bounds** check box removes the confidence intervals from the plot in the main window.

  When you select a fit in the **Table of fits**, the following buttons are enabled below the table:

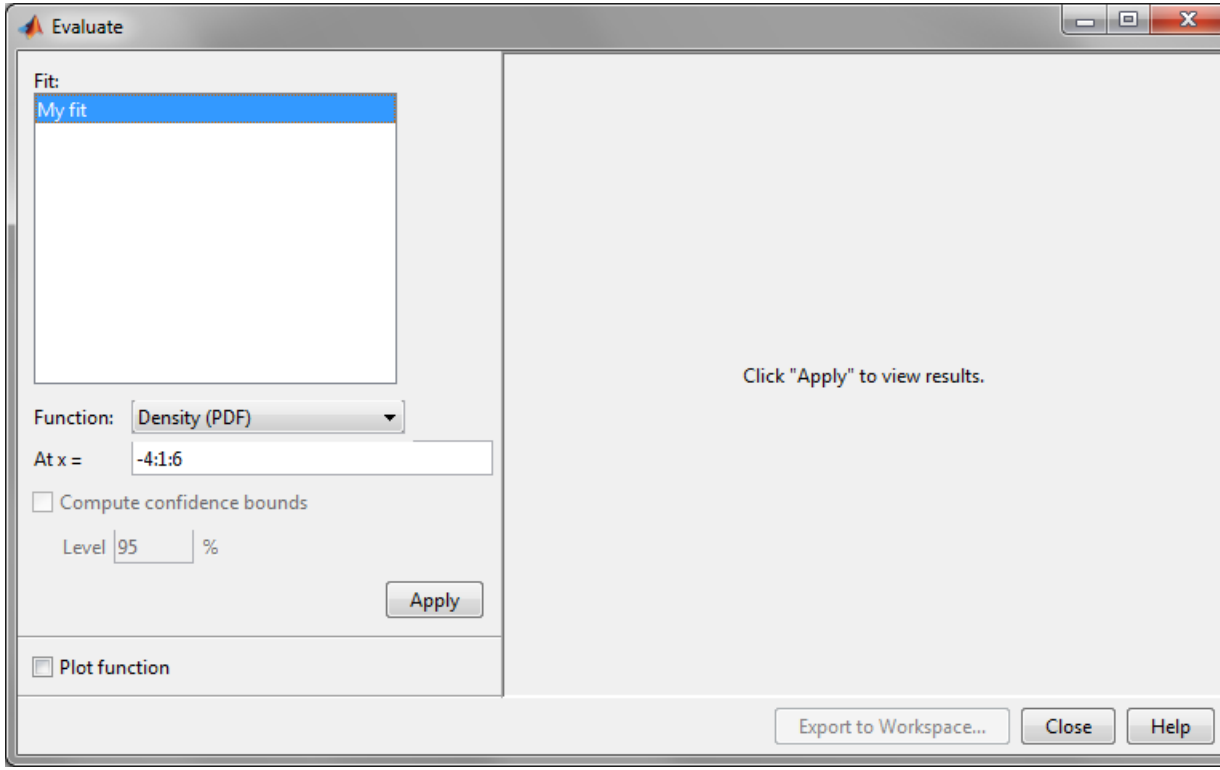
  - **New Fit** — Open a New Fit window.
  - **Copy** — Create a copy of the selected fit.
  - **Edit** — Open an Edit Fit dialog box, to edit the fit.

    Note You can edit only the currently selected fit in the Edit Fit dialog box. To edit a different fit, select it in the **Table of fits** and click **Edit** to open another Edit Fit dialog box.

  - **Save to workspace** — Save the selected fit as a distribution object.
  - **Delete** — Delete the selected fit.

Evaluate Fits

Use the **Evaluate** dialog box to evaluate your fitted distribution at any data points you choose. To open the dialog box, click the **Evaluate** button.



In the **Evaluate** dialog box, choose from the following items:

- **Fit** pane — Display the names of existing fits. Select one or more fits that you want to evaluate. Using your platform specific functionality, you can select multiple fits.
- **Function** — Select the type of probability function that you want to evaluate for the fit. The available functions are:
  - `Density (PDF)` — Computes a probability density function.
  - `Cumulative probability (CDF)` — Computes a cumulative probability function.
  - `Quantile (inverse CDF)` — Computes a quantile (inverse CDF) function.
  - `Survivor function` — Computes a survivor function.
  - `Cumulative hazard` — Computes a cumulative hazard function.

  - `Hazard rate` — Computes the hazard rate.

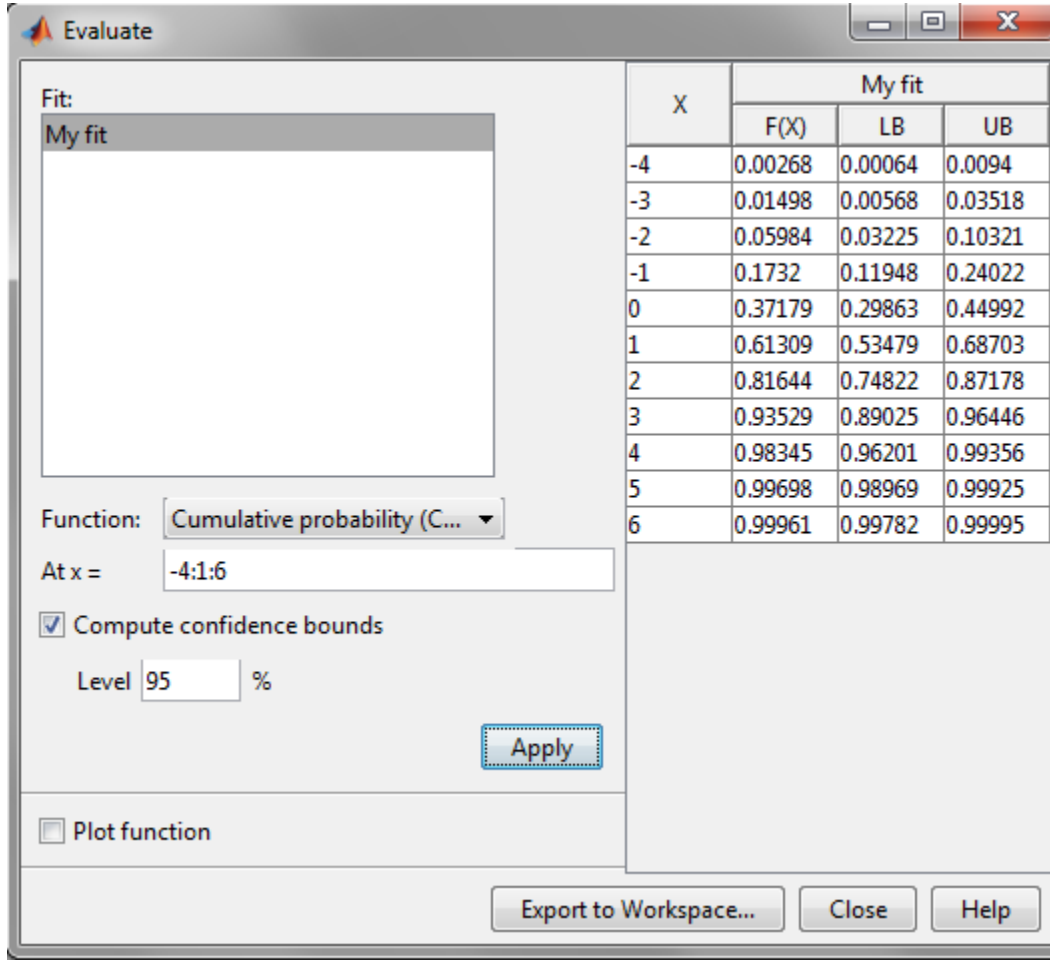
- **At x =** — Enter a vector of points or the name of a workspace variable containing a vector of points at which you want to evaluate the distribution function. If you change **Function** to `Quantile (inverse CDF)`, the field name changes to **At p =**, and you enter a vector of probability values.
- **Compute confidence bounds** — Select this box to compute confidence bounds for the selected fits. The check box is enabled only if you set **Function** to one of the following:

  - `Cumulative probability (CDF)`
  - `Quantile (inverse CDF)`
  - `Survivor function`
  - `Cumulative hazard`

  The Distribution Fitting app cannot compute confidence bounds for nonparametric fits and for some parametric fits. In these cases, it returns `NaN` for the bounds.
- **Level** — Set the level for the confidence bounds.
- **Plot function** — Select this box to display a plot of the distribution function, evaluated at the points you enter in the **At x =** field, in a new window.

Note The settings for **Compute confidence bounds**, **Level**, and **Plot function** do not affect the plots that are displayed in the main window of the Distribution Fitting app. The settings apply only to plots you create by clicking **Plot function** in the Evaluate window.

To apply these evaluation settings to the selected fit, click **Apply**. The following figure shows the results of evaluating the cumulative density function for the fit `My fit`, at the points in the vector `-4:1:6`.



X	My fit		
	F(X)	LB	UB
-4	0.00268	0.00064	0.0094
-3	0.01498	0.00568	0.03518
-2	0.05984	0.03225	0.10321
-1	0.1732	0.11948	0.24022
0	0.37179	0.29863	0.44992
1	0.61309	0.53479	0.68703
2	0.81644	0.74822	0.87178
3	0.93529	0.89025	0.96446
4	0.98345	0.96201	0.99356
5	0.99698	0.98969	0.99925
6	0.99961	0.99782	0.99995

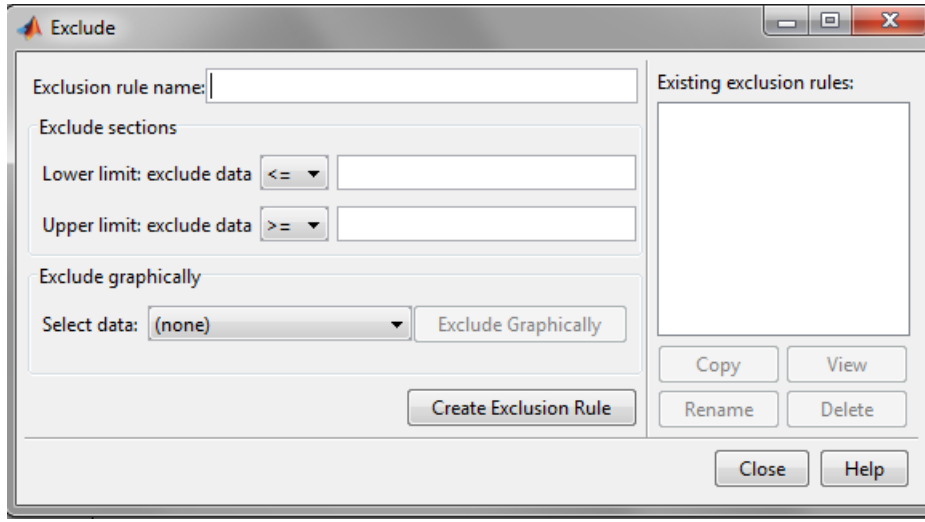
The columns of the table to the right of the **Fit** pane display the following values:

- X — The entries of the vector that you enter in **At x =** field.
- F(X)— The corresponding values of the CDF at the entries of X.
- LB — The lower bounds for the confidence interval, if you select **Compute confidence bounds**.
- UB — The upper bounds for the confidence interval, if you select **Compute confidence bounds**.

To save the data displayed in the table to a matrix in the MATLAB workspace, click **Export to Workspace**.

Exclude Data

To exclude values from fit, open the **Exclude** window by clicking the **Exclude** button. In the **Exclude** window, you can create rules for excluding specified data values. When you create a new fit in the **New Fit** window, you can use these rules to exclude data from the fit.

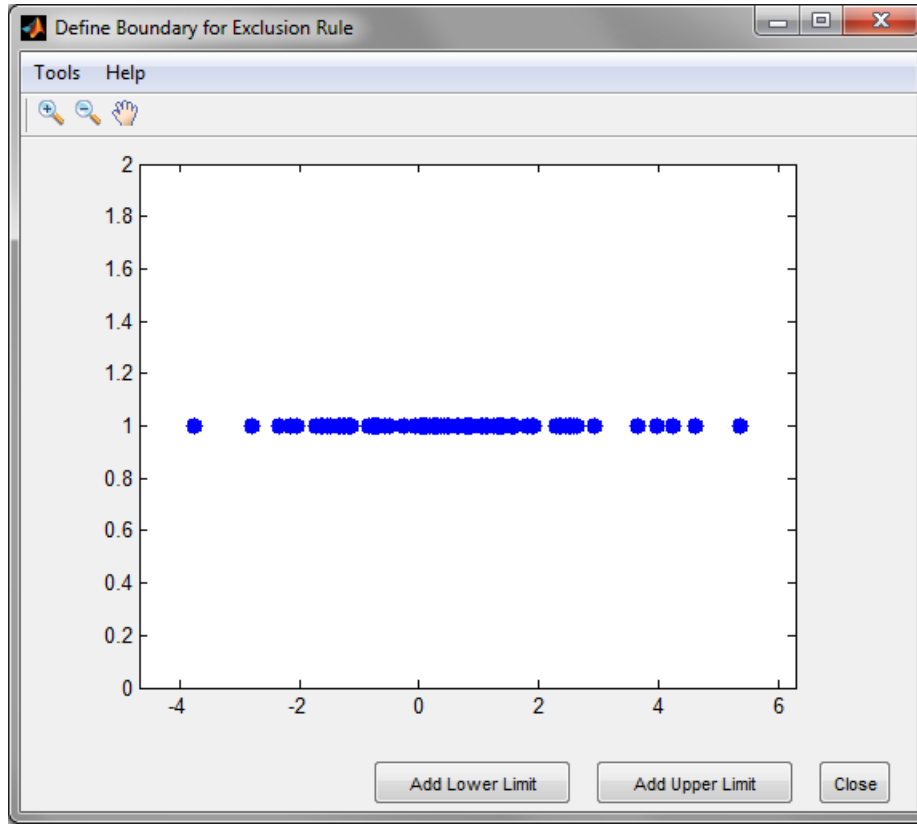


To create an exclusion rule:

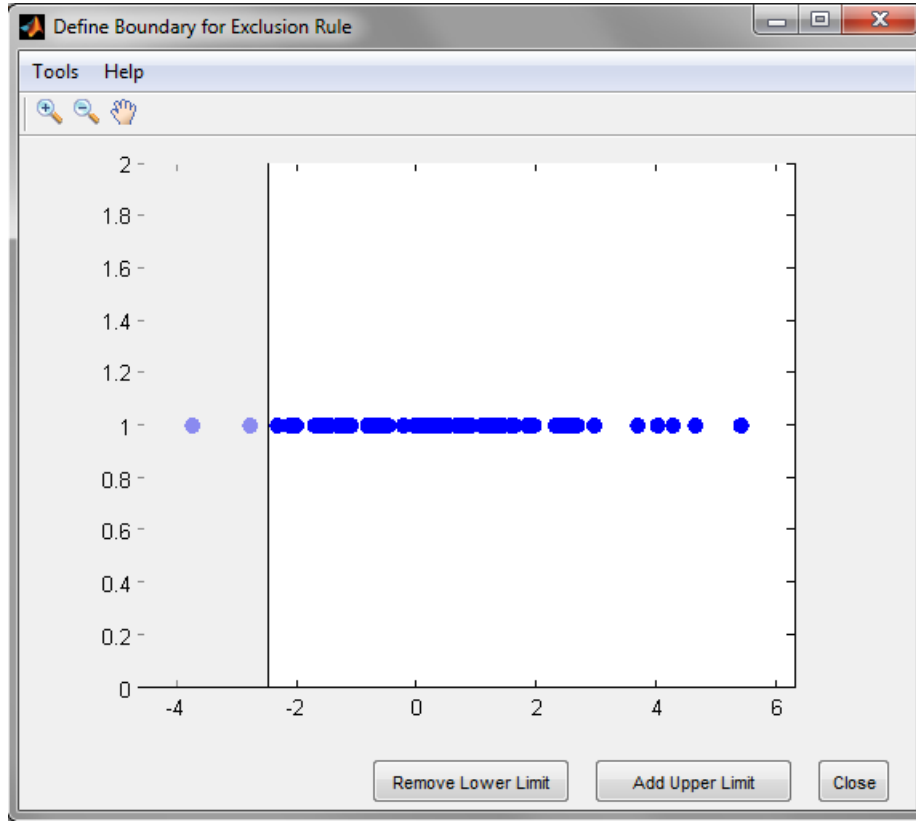
1. **Exclusion Rule Name**— Enter a name for the exclusion rule.
2. **Exclude Sections**— Specify bounds for the excluded data:
   - In the **Lower limit: exclude data** drop-down list, select <= or < and enter a scalar value in the field to the right. Depending on which operator you select, the app excludes from the fit any data values that are less than or equal to the scalar value, or less than the scalar value, respectively.
   - In the **Upper limit: exclude data** drop-down list, select >= or > and enter a scalar value in the field to the right. Depending on which operator you select, the app excludes from the fit any data values that are greater than or equal to the scalar value, or greater than the scalar value, respectively.

OR

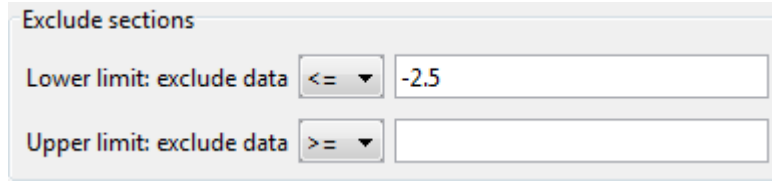
Click the **Exclude Graphically** button to define the exclusion rule by displaying a plot of the values in a data set and selecting the bounds for the excluded data. For example, if you created the data set `My data` as described in Create and Manage Data Sets, select it from the drop-down list next to **Exclude graphically**, and then click the **Exclude graphically** button. The app displays the values in `My data` in a new window.



To set a lower limit for the boundary of the excluded region, click **Add Lower Limit**. The app displays a vertical line on the left side of the plot window. Move the line to the point you where you want the lower limit, as shown in the following figure.



Move the vertical line to change the value displayed in the **Lower limit: exclude data** field in the **Exclude** window.



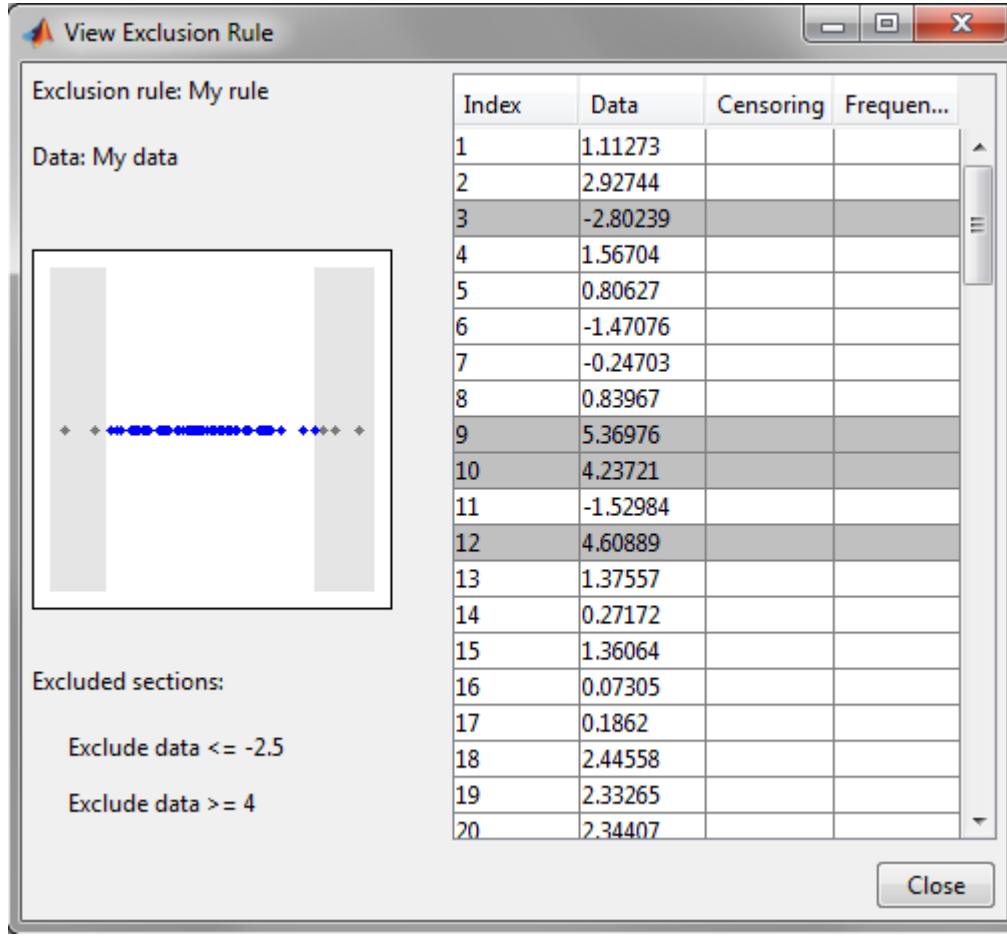
The value displayed corresponds to the x-coordinate of the vertical line.

Similarly, you can set the upper limit for the boundary of the excluded region by clicking **Add Upper Limit**, and then moving the vertical line that appears at the right side of the plot window. After setting the lower and upper limits, click **Close** and return to the Exclude window.

3 **Create Exclusion Rule**—Once you have set the lower and upper limits for the boundary of the excluded data, click **Create Exclusion Rule** to create the new rule. The name of the new rule appears in the **Existing exclusion rules** pane.

Selecting an exclusion rule in the **Existing exclusion rules** pane enables the following buttons:

- **Copy** — Creates a copy of the rule, which you can then modify. To save the modified rule under a different name, click **Create Exclusion Rule**.
- **View** — Opens a new window in which you can see the data points excluded by the rule. The following figure shows a typical example.



The shaded areas in the plot graphically display which data points are excluded. The table to the right lists all data points. The shaded rows indicate excluded points:

- **Rename** — Rename the rule.
- **Delete** — Delete the rule.

After you define an exclusion rule, you can use it when you fit a distribution to your data. The rule does not exclude points from the display of the data set.

Save and Load Sessions

Save your work in the current session, and then load it in a subsequent session, so that you can continue working where you left off.

Save a Session

To save the current session, from the **File** menu in the main window, select `Save Session`. A dialog box opens and prompts you to enter a file name, for example`my_session.dfit`. Click **Save** to save the following items created in the current session:

- Data sets
- Fits
- Exclusion rules
- Plot settings
- Bin width rules

Load a Session

To load a previously saved session, from the **File** menu in the main window, select `Load Session`. Enter the name of a previously saved session. Click **Open** to restore the information from the saved session to the current session.

Generate a File to Fit and Plot Distributions

Use the `Generate Code` option in the **File** to create a file that:

- Fits the distributions in the current session to any data vector in the MATLAB workspace.
- Plots the data and the fits.

After you end the current session, you can use the file to create plots in a standard MATLAB figure window, without reopening the Distribution Fitting app.

As an example, if you created the fit described in "Create a New Fit" on page 5-80, do the following steps:

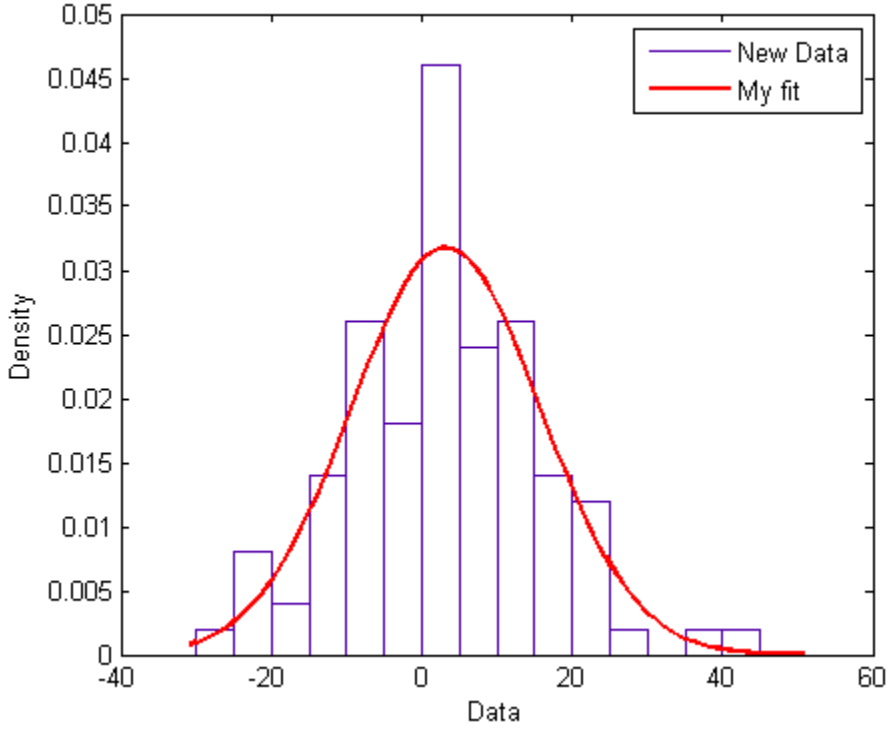
1. From the **File** menu, select `Generate Code`.
2. In the MATLAB Editor window, choose **File > Save as**. Save the file as `normal_fit.m` in a folder on the MATLAB path.

You can then apply the function `normal_fit` to any vector of data in the MATLAB workspace. For example, the following commands:

```
new_data = normrnd(4.1, 12.5, 100, 1);
newfit = normal_fit(new_data)
legend('New Data', 'My fit')
```

generate `newfit`, a fitted normal distribution of the data. The commands also generate a plot of the data and the fit.

```
newfit =

normal distribution

    mu = 3.19148
    sigma = 12.5631
```



Note By default, the file labels the data in the legend using the same name as the data set in the Distribution Fitting app. You can change the label using the `legend` command, as illustrated by the preceding example.

Fit a Distribution Using the Distribution Fitting App

This example shows how you can use the Distribution Fitting app to interactively fit a probability distribution to data.

In this section...

Step 1: Load Sample Data

Load the sample data.

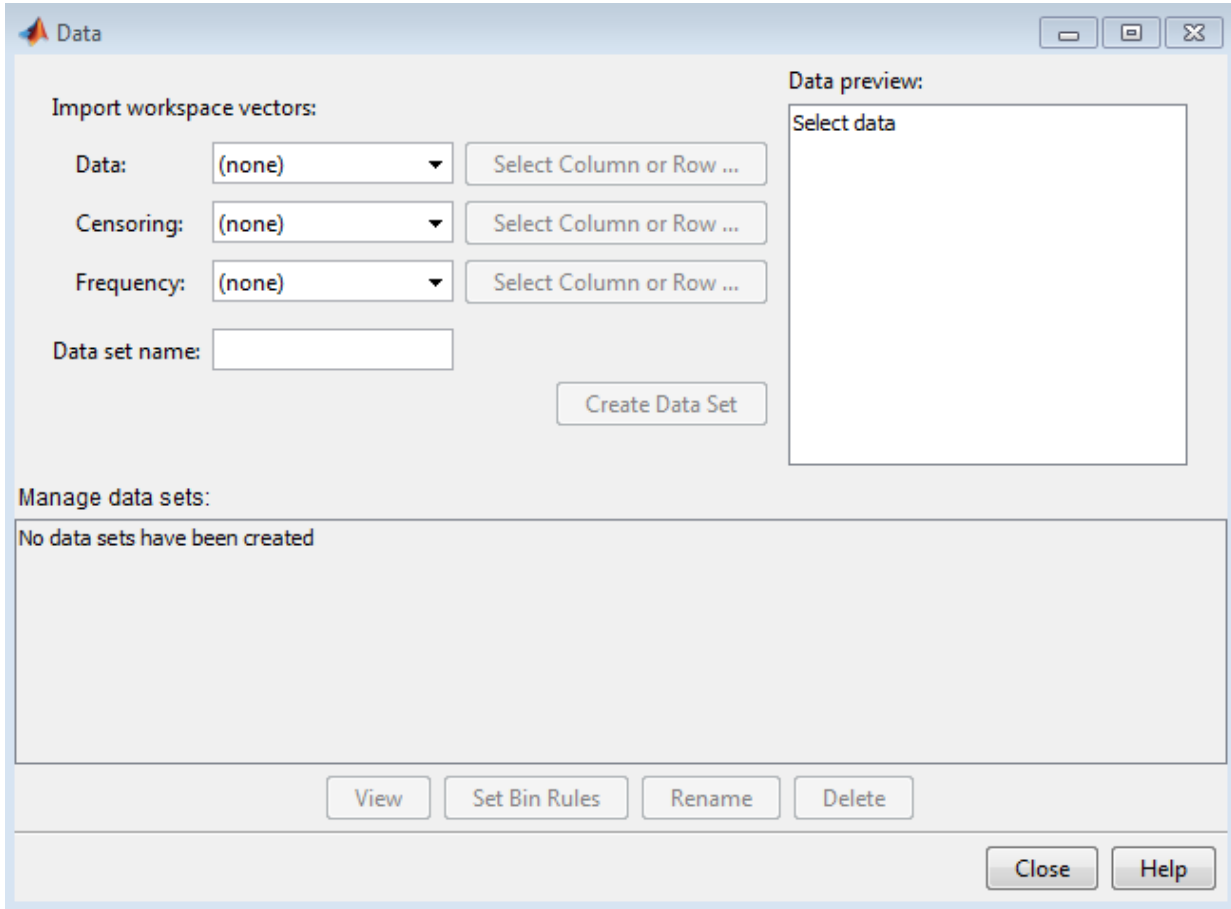
```
load carsmall
```

Step 2: Import Data

Open the distribution fitting tool.

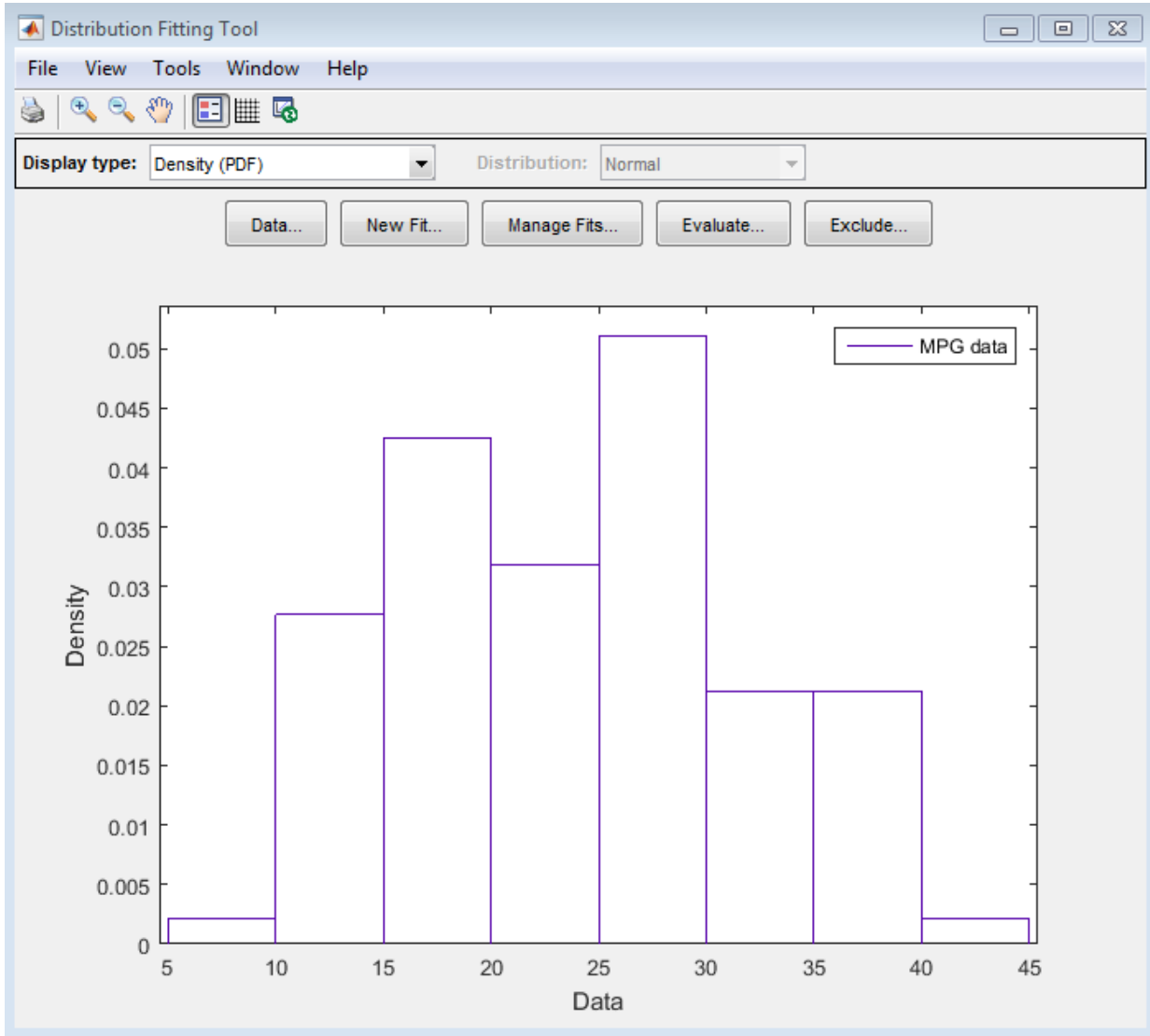
```
dfittool
```

To import the vector `MPG` into the Distribution Fitting app, click the **Data** button. The **Data** dialog box opens.



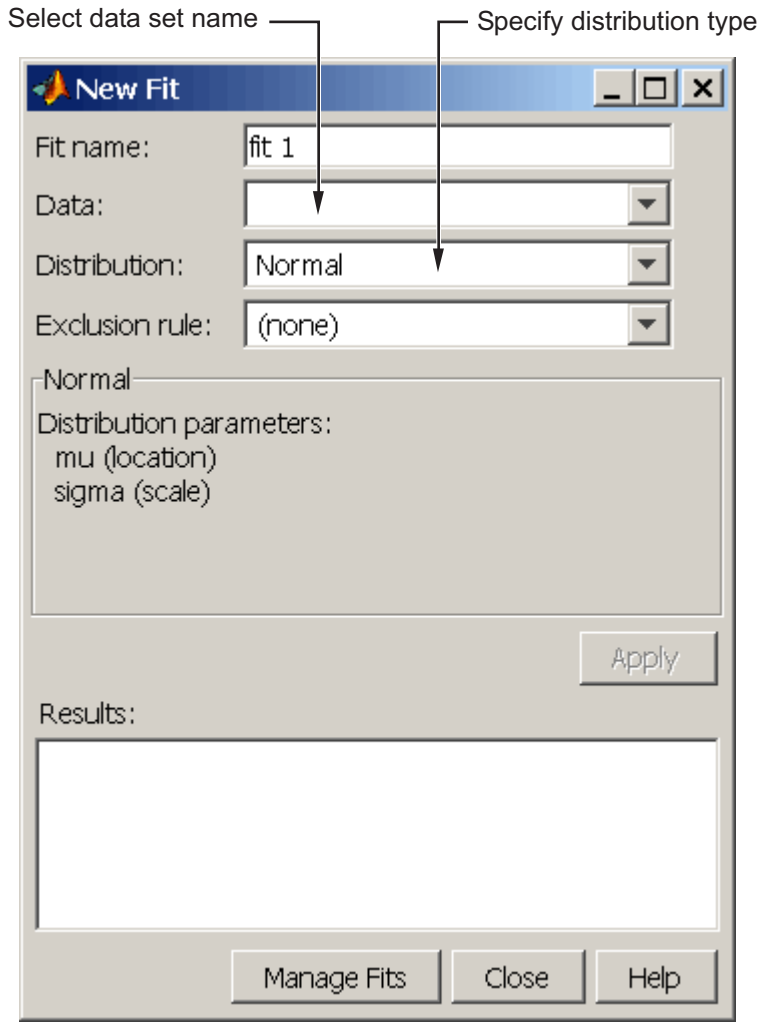
The **Data** field displays all numeric arrays in the MATLAB workspace. From the drop-down list, select `MPG`. A histogram of the selected data appears in the **Data preview** pane.

In the **Data set name** field, type a name for the data set, such as `MPG data`, and click **Create Data Set**. The main window of the Distribution Fitting app now displays a larger version of the histogram in the **Data preview** pane.



Step 3: Create a New Fit

To fit a distribution to the data, in the main window of the Distribution Fitting app, click **New Fit**.

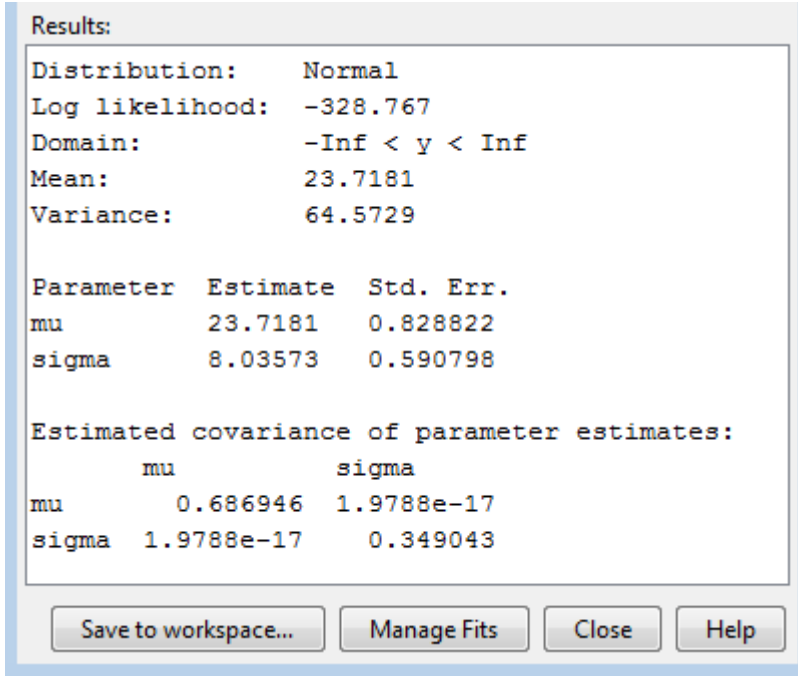


To fit a normal distribution to `My data`:

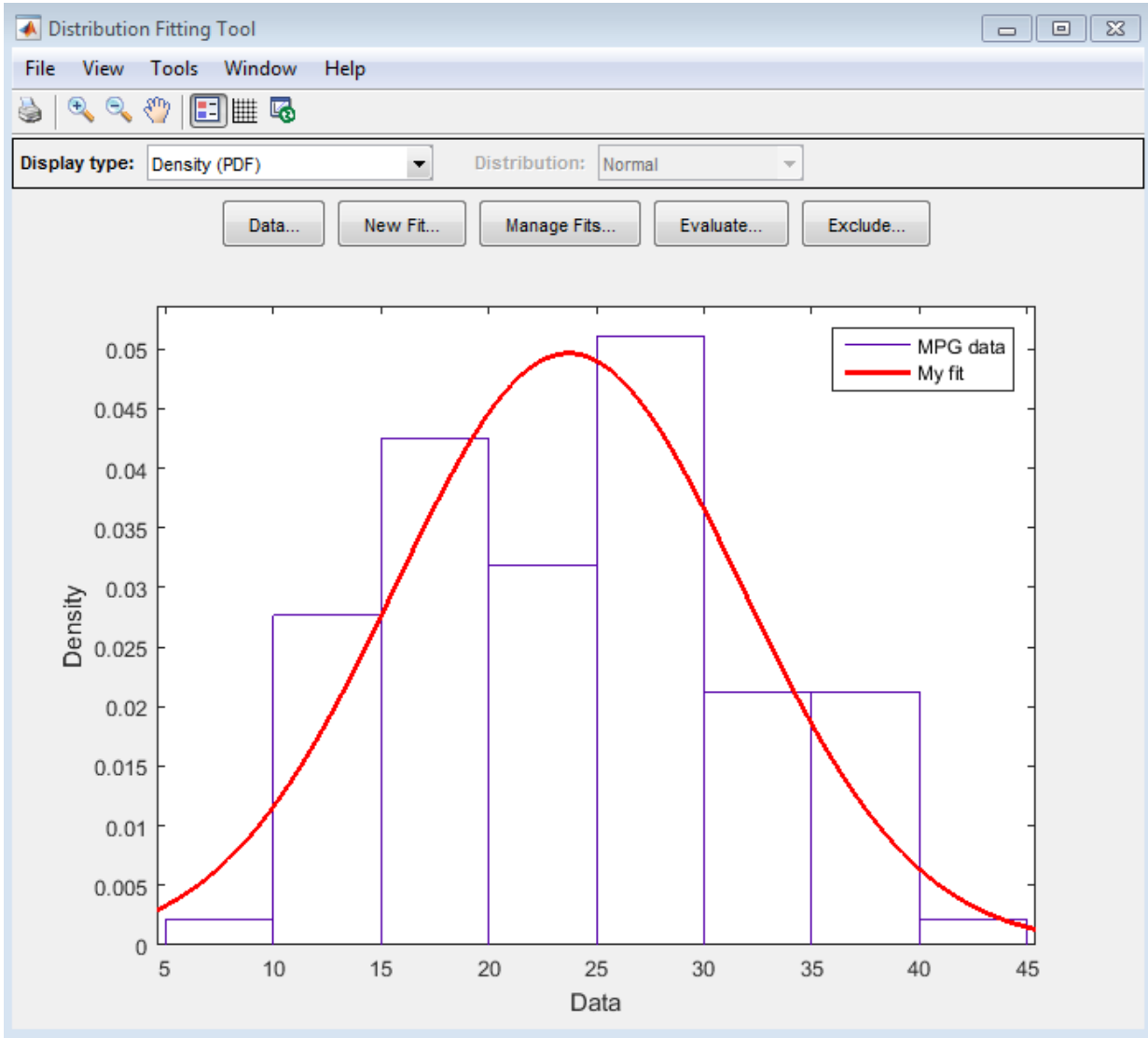
1. In the **Fit name** field, enter a name for the fit, such as `My fit`.
2. From the drop-down list in the **Data** field, select `MPG data`.
3. Confirm that `Normal` is selected from the drop-down menu in the **Distribution** field.

4 Click **Apply**.

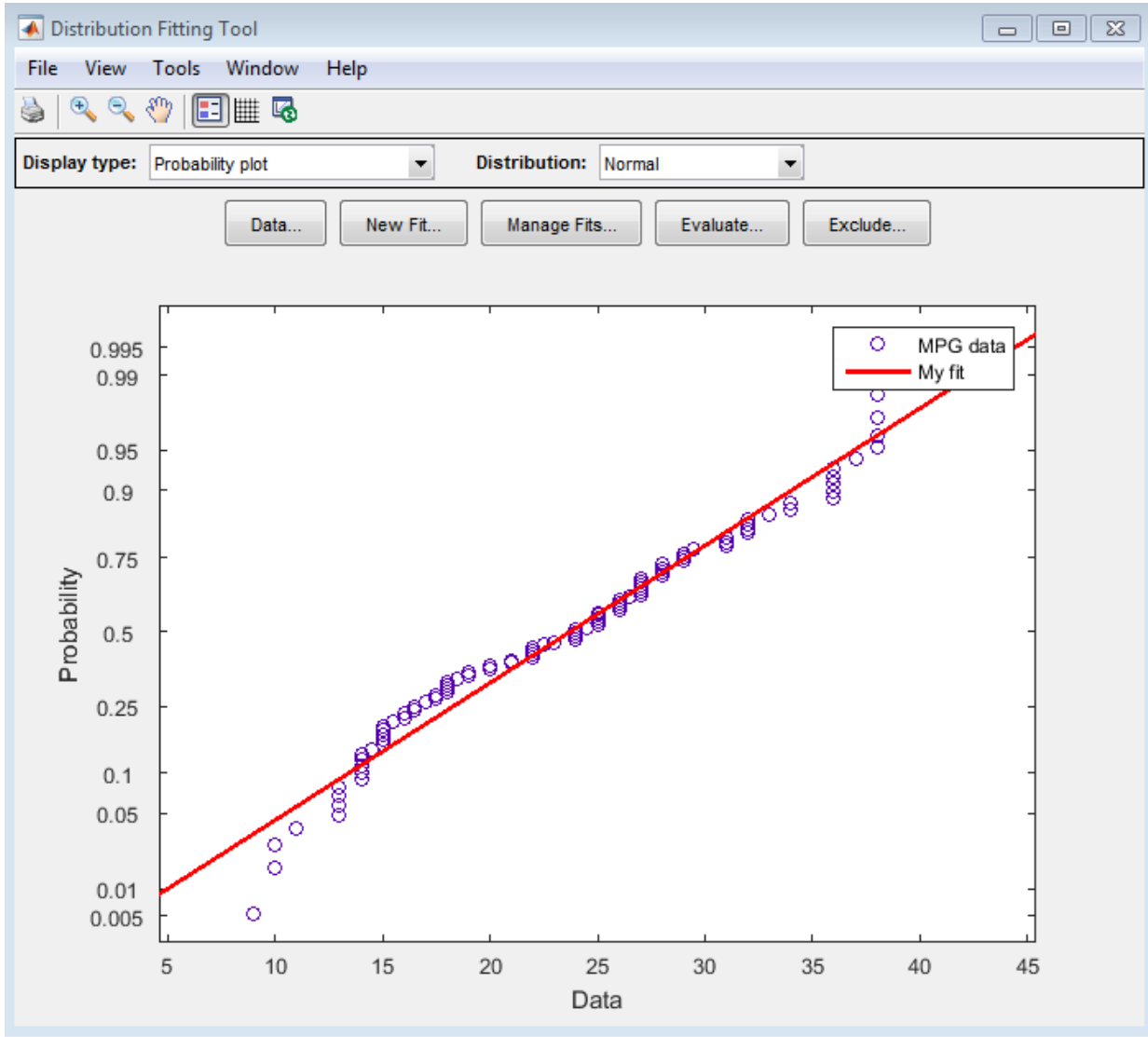
The **Results** pane displays the mean and standard deviation of the normal distribution that best fits `MPG data`.



The Distribution Fitting app main window displays a plot of the normal distribution with this mean and standard deviation.



Based on the plot, a normal distribution does not appear to provide a good fit for the `MPG` data. To obtain a better evaluation, select Probability plot from the **Display type** drop-down list. Confirm that the **Distribution** drop-down list is set to `Normal`. The main window displays the following figure.



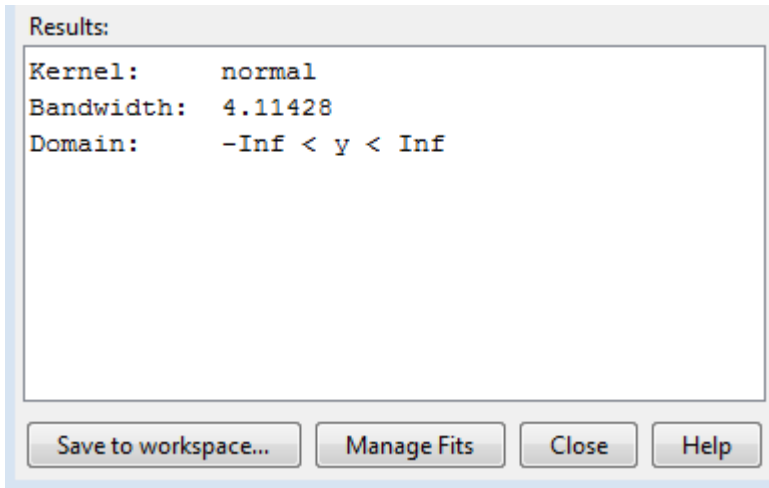
The normal probability plot shows that the data deviates from normal, especially in the tails.

Step 4: Create and Manage Additional Fits

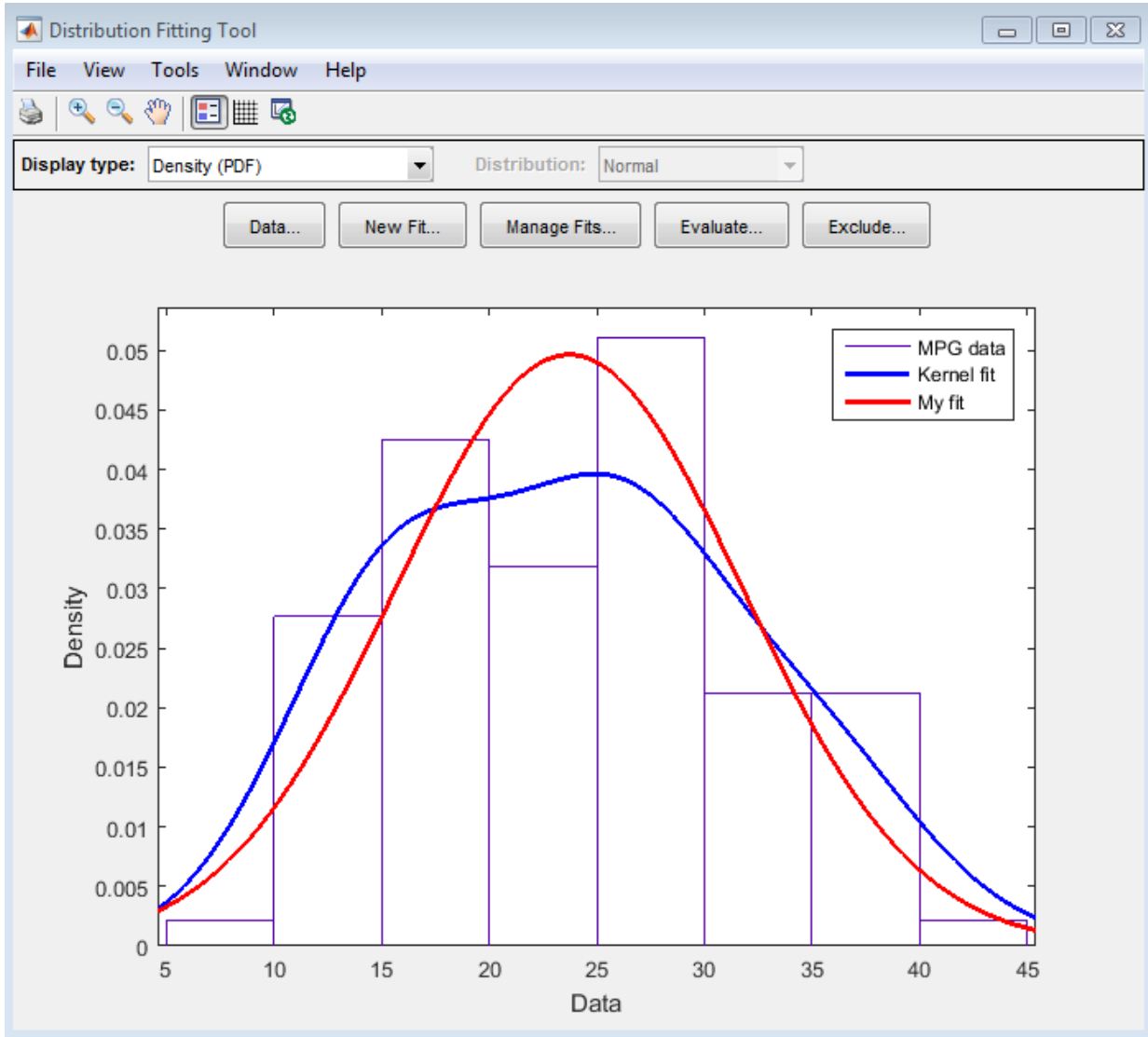
The `MPG` data pdf indicates that the data has two peaks. Try fitting a nonparametric kernel distribution to obtain a better fit for this data.

1. Click **Manage Fits**. In the dialog box, click **New Fit**.
2. In the **Fit name** field, enter a name for the fit, such as `Kernel fit`.
3. From the drop-down list in the **Data** field, select `MPG data`.
4. From the drop-down list in the **Distribution** field, select **Non-parametric**. This enables several options in the **Non-parametric** pane, including **Kernel**, **Bandwidth**, and **Domain**. For now, accept the default value to apply a normal kernel shape and automatically determine the kernel bandwidth (using `Auto`). For more information about nonparametric kernel distributions, see "Kernel Distribution" on page B-81.
5. Click **Apply**.

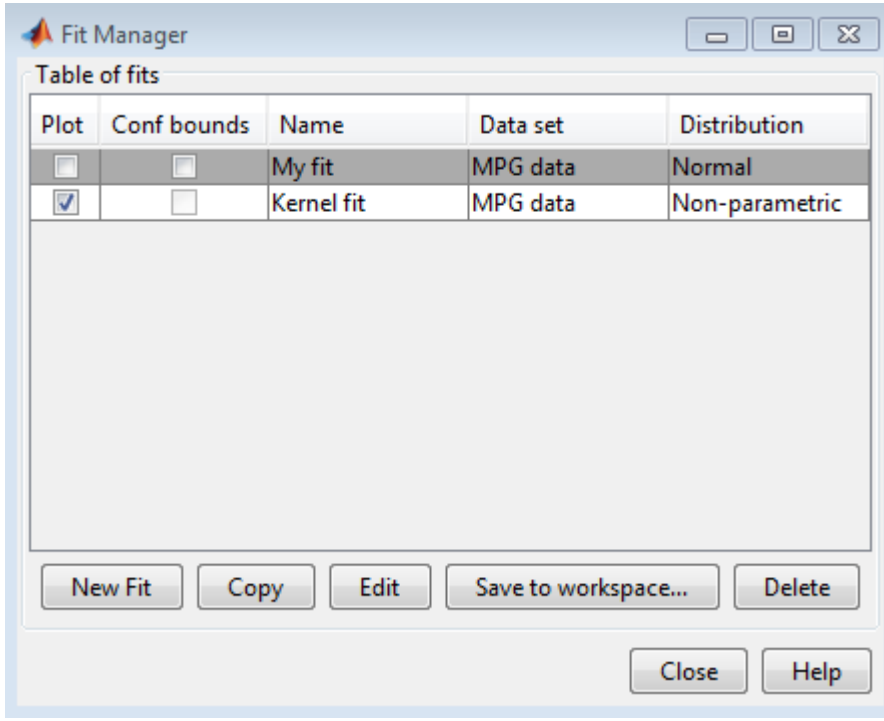
The **Results** pane displays the kernel type, bandwidth, and domain of the nonparametric distribution fit to `MPG data`.



The main window displays plots of the original `MPG data` with the normal distribution and nonparametric kernel distribution overlayed. To visually compare these two fits, select `Density (PDF)` from the **Display type** drop-down list.



To include only the nonparametric kernel fit line (`Kernel fit`) on the plot, click Manage Fits. In the **Table of fits** pane, locate the row for the normal distribution fit (`My fit`) and clear the box in the **Plot** column.


Fit Manager
Table of fits
Plot
Conf bounds
Name
Data set
Distribution
My fit
MPG data
Normal
Kernel fit
MPG data
Non-parametric
New Fit
Copy
Edit
Save to workspace...
Delete
Close
Help

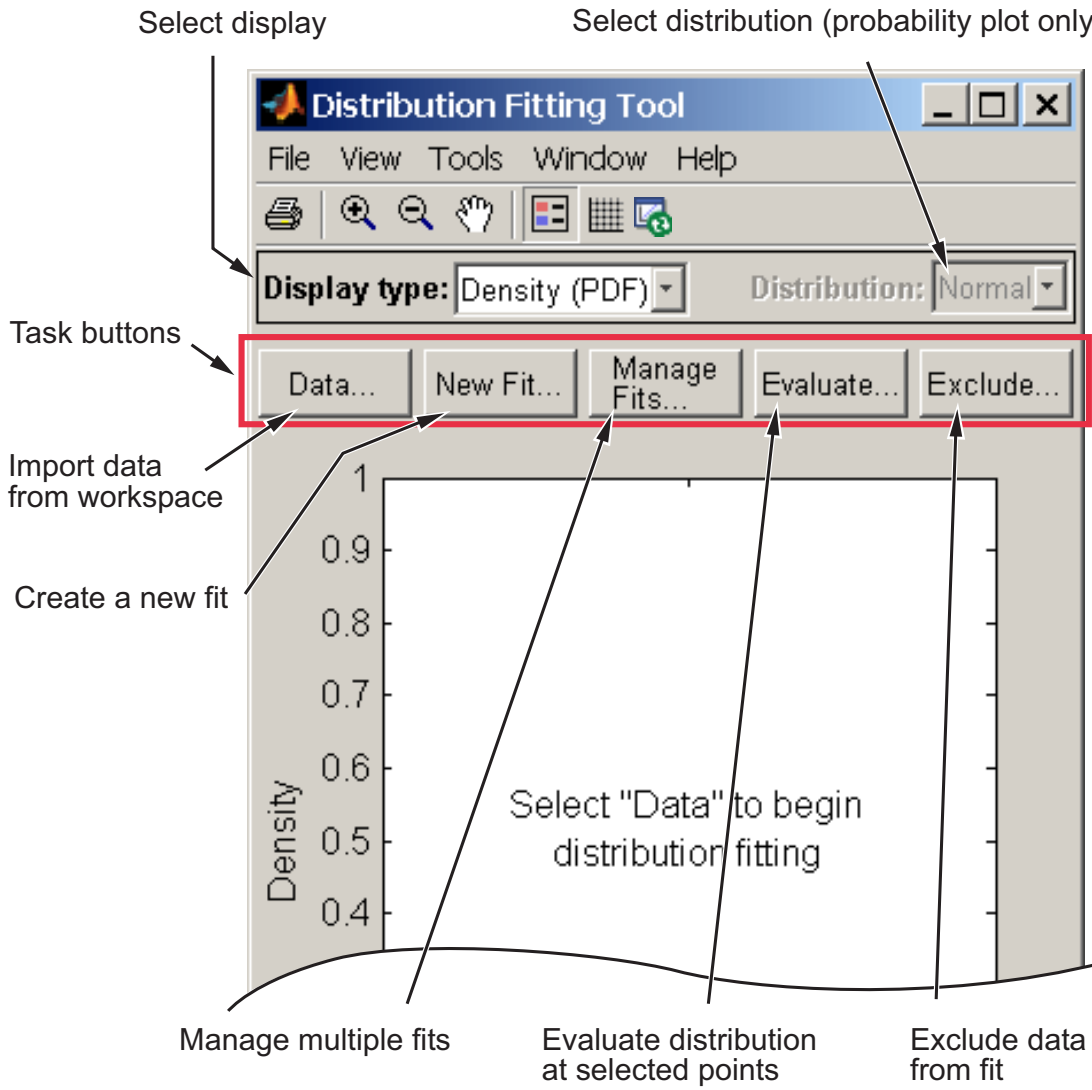
Custom Distributions Using the Distribution Fitting App

You can use the Distribution Fitting app to fit distributions not supported by the Statistics and Machine Learning Toolbox by defining a custom distribution.

Opening the Distribution Fitting App

To open the Distribution Fitting app, enter the command

```
dfittool
```



Alternatively, click Distribution Fitting on the Apps tab.

Defining Custom Distributions

To define a custom distribution, select `Define Custom Distribution` from the **File** menu. This opens a file template in the MATLAB editor. You then edit this file so that it computes the distribution you want.

The template includes example code that computes the Laplace distribution. Follow the instructions in the template to define your own custom distribution.

To save your custom distribution, create a directory called `+prob` on your path. Save the file in this directory using a name that matches your distribution name. If you save the template in a folder on the MATLAB path, under its default name `dfittooldists.m`, the Distribution Fitting app reads it in automatically when you start the tool. You can also save the template under a different name, such as `laplace.m`, and then import the custom distribution as described in the following section.

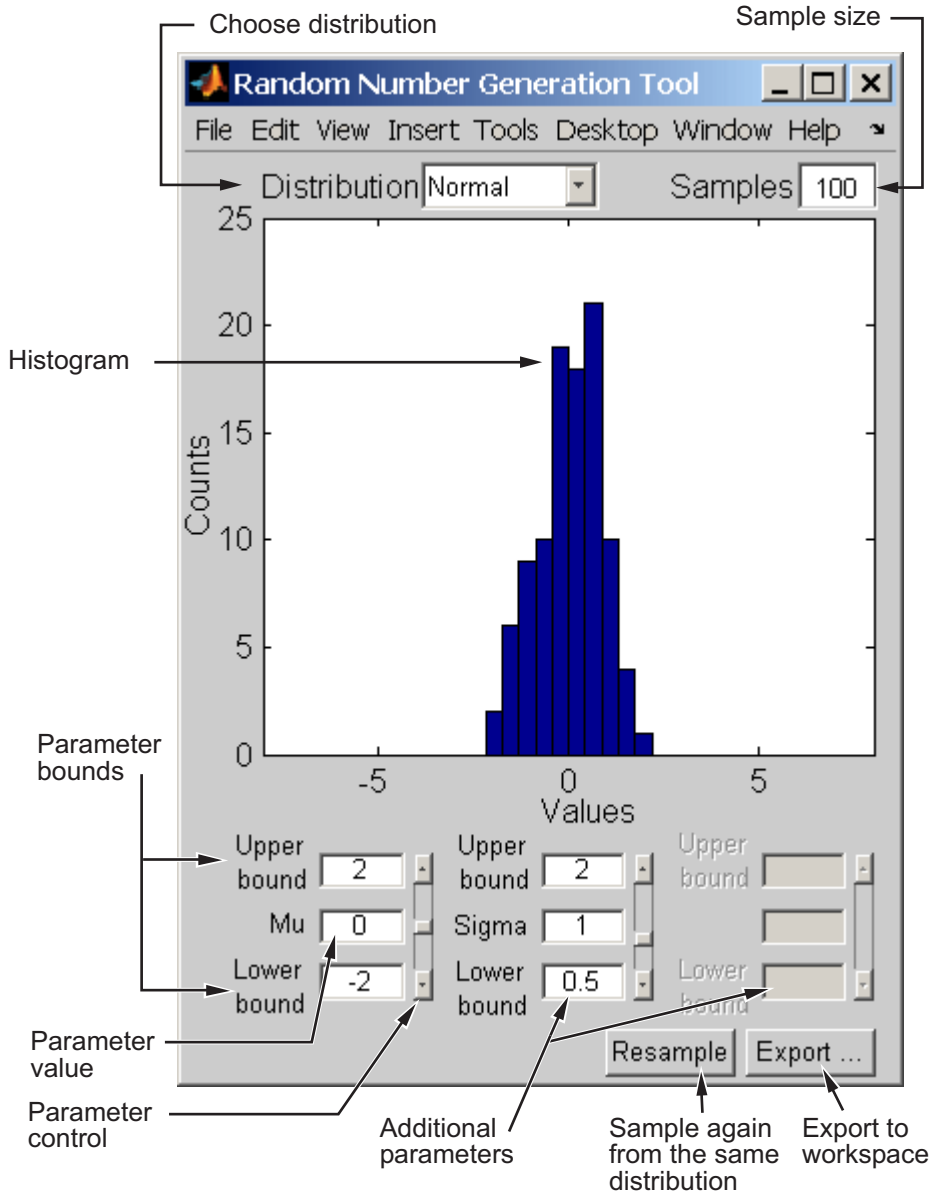
Importing Custom Distributions

To import a custom distribution, select `Import Custom Distributions` from the **File** menu. This opens a dialog box in which you can select the file that defines the distribution. For example, if you created the file `Laplace.m`, as described in the preceding section, the New Parametric Distribution List dialog that launches when you select `Import Custom Distributions` now includes `Laplace`. In addition, the **Distribution** field of the New Fit window also contains the option `Laplace`.

Explore the Random Number Generation UI

The Random Number Generation user interface (UI) generates random samples from specified probability distributions, and displays the samples as histograms. Use the interface to explore the effects of changing parameters and sample size on the distributions.

Run the user interface by typing `randtool` at the command line.



Start by selecting a distribution, then enter the desired sample size.

You can also

- Use the controls at the bottom of the window to set parameter values for the distribution and to change their upper and lower bounds.
- Draw another sample from the same distribution, with the same size and parameters.
- Export the current sample to your workspace. A dialog box enables you to provide a name for the sample.

Compare Multiple Distribution Fits

This example shows how to fit multiple probability distribution objects to the same set of sample data, and obtain a visual comparison of how well each distribution fits the data.

Step 1. Load sample data.

Load the sample data.

```
load carsmall;
```

This data contains miles per gallon (MPG) measurements for different makes and models of cars, grouped by country of origin (`Origin`), model year (`Model_Year`), and other vehicle characteristics.

Step 2. Create a nominal array.

Transform `Origin` into a nominal array and remove the Italian car from the sample data.

```
Origin = nominal(Origin);
MPG2 = MPG(Origin~='Italy');
Origin2 = Origin(Origin~='Italy');
Origin2 = droplevels(Origin2,'Italy');
```

Since there is only one Italian car, `fitdist` cannot fit a distribution to that group. Removing the Italian car from the sample data prevents `fitdist` from producing an error.

Step 3. Fit multiple distributions by group.

Use `fitdist` to fit Weibull, normal, logistic, and kernel distributions to each country of origin group in the MPG data.

```
[WeiByOrig,Country] = fitdist(MPG2,'weibull','by',Origin2);
[NormByOrig,Country] = fitdist(MPG2,'normal','by',Origin2);
[LogByOrig,Country] = fitdist(MPG2,'logistic','by',Origin2);
[KerByOrig,Country] = fitdist(MPG2,'kernel','by',Origin2);

WeiByOrig
Country

WeiByOrig =
```

```
  Column 1

    [1x1 prob.WeibullDistribution]

  Column 2

    [1x1 prob.WeibullDistribution]

  Column 3

    [1x1 prob.WeibullDistribution]

  Column 4

    [1x1 prob.WeibullDistribution]

  Column 5

    [1x1 prob.WeibullDistribution]


Country =

    'France'
    'Germany'
    'Japan'
    'Sweden'
    'USA'
```

Each country group now has four distribution objects associated with it. For example, the cell array `WeiByOrig` contains five Weibull distribution objects, one for each country represented in the sample data. Likewise, the cell array `NormByOrig` contains five normal distribution objects, and so on. Each object contains properties that hold information about the data, distribution, and parameters. The array `Country` lists the country of origin for each group in the same order as the distribution objects are stored in the cell arrays.

Step 4. Compute the pdf for each distribution.

Extract the four probability distribution objects for USA and compute the pdf for each distribution. As shown in Step 3, USA is in position 5 in each cell array.

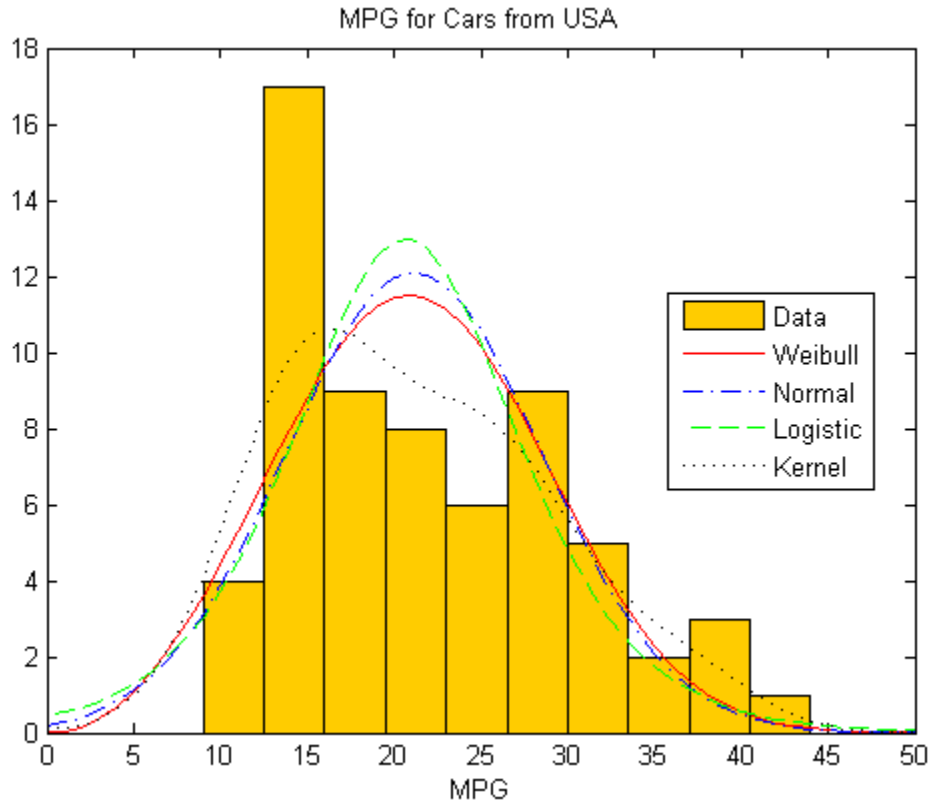
```
WeiUSA = WeiByOrig{5};
```

```
NormUSA = NormByOrig{5};
LogUSA = LogByOrig{5};
KerUSA = KerByOrig{5};

x = 0:1:50;
pdf_Wei = pdf(WeiUSA,x);
pdf_Norm = pdf(NormUSA,x);
pdf_Log = pdf(LogUSA,x);
pdf_Ker = pdf(KerUSA,x);
```

Step 5. Plot pdf the for each distribution.

Plot the pdf for each distribution fit to the USA data, superimposed on a histogram of the sample data. Scale the density by the histogram area for easier display.

```
% Create a histogram of the USA sample data
data = MPG(Origin2=='USA');
figure;
[n,y] = hist(data,10);
b = bar(y,n,'hist');
set(b,'FaceColor',[1,0.8,0]);

% Scale the density by the histogram area for easier display
area = sum(n)*(y(2)-y(1));
time = 0:50;
pdfWei = pdf(WeiUSA,time);
pdfNorm = pdf(NormUSA,time);
pdfLog = pdf(LogUSA,time);
pdfKer = pdf(KerUSA,time);

% Plot the pdf of each fitted distribution
line(x,pdfWei*area,'LineStyle','-','Color','r');
hold on;
line(x,pdfNorm*area,'LineStyle','-.','Color','b');
line(x,pdfLog*area,'LineStyle','--','Color','g');
line(x,pdfKer*area,'LineStyle',':','Color','k');
l = legend('Data','Weibull','Normal','Logistic','Kernel');
set(l,'Location','Best');
title('MPG for Cars from USA');
xlabel('MPG');
hold off;
```



Superimposing the pdf plots over a histogram of the sample data provides a visual comparison of how well each type of distribution fits the data. Only the nonparametric kernel distribution `KerUSA` comes close to revealing the two modes in the original data.

Step 6. Further group USA data by year.

To investigate the two modes revealed in Step 5, group the `MPG` data by both country of origin (`Origin`) and model year (`Model_Year`), and use `fitdist` to fit kernel distributions to each group.

```
[KerByYearOrig,Names] = fitdist(MPG,'Kernel','By',{Origin Model_Year});
```

Each unique combination of origin and model year now has a kernel distribution object associated with it.

Step 7. Compute the pdf for each group.

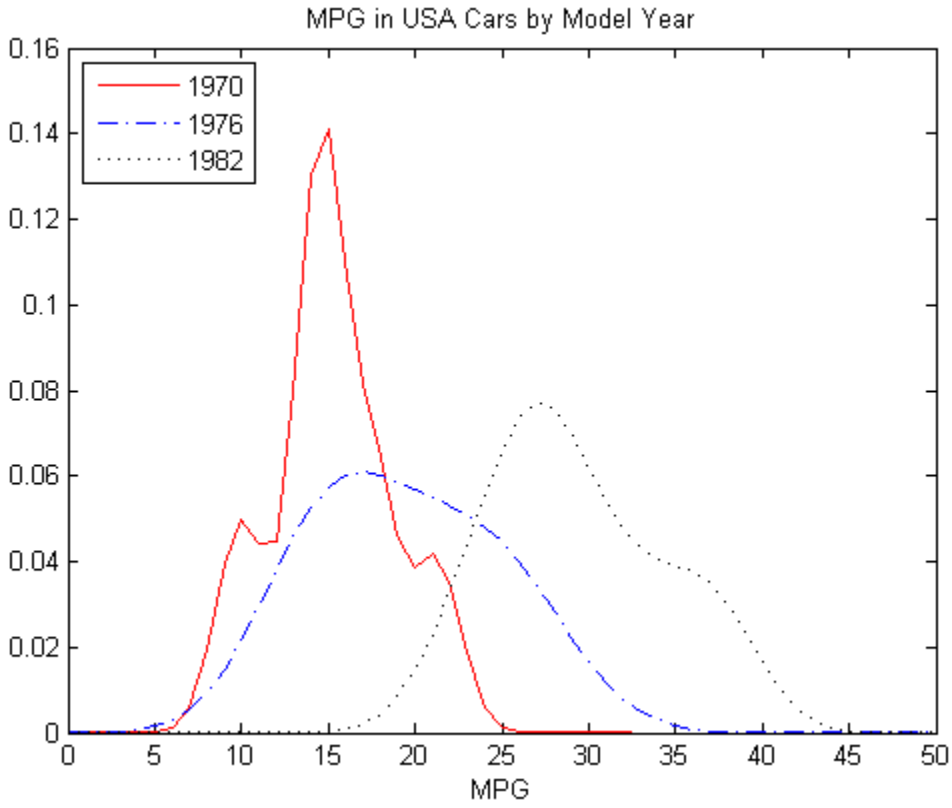
Extract the three probability distributions for each USA model year, which are in positions 12, 13, and 14 in the cell array `KerByYearOrig`. Compute each pdf.

```
USA70 = KerByYearOrig{12};
USA76 = KerByYearOrig{13};
USA82 = KerByYearOrig{14};

pdf70 = pdf(USA70,x);
pdf76 = pdf(USA76,x);
pdf82 = pdf(USA82,x);
```

Step 8. Plot pdf for each group.

Plot the pdf for each group on the same figure.

```
figure;
plot(x,pdf70,'r-');
hold on;
plot(x,pdf76,'b-.');
plot(x,pdf82,'k:');
legend({'1970','1976','1982'},'Location','NW');
title('MPG in USA Cars by Model Year');
xlabel('MPG');
hold off;
```



When further grouped by model year, the pdf plots reveal two distinct peaks in the `MPG` data for cars made in the USA — one for the model year 1970, and one for the model year 1982. This explains why the smooth curve produced by the kernel distribution for the combined USA miles per gallon data shows two peaks instead of one.

See Also

`fitdist`

Related Examples

- “Fit Probability Distribution Objects to Grouped Data” on page 5-124

More About

- "Grouping Variables" on page 2-52

Fit Probability Distribution Objects to Grouped Data

This example shows how to fit probability distribution objects to grouped sample data, and create a plot to visually compare the pdf of each group.

Step 1. Load sample data.

Load the sample data.

```
load carsmall;
```

The data contains miles per gallon (`MPG`) measurements for different makes and models of cars, grouped by country of origin (`Origin`), model year (`Model_Year`), and other vehicle characteristics.

Step 2. Create a nominal array.

Transform `Origin` into a nominal array and remove the Italian car from the sample data. Since there is only one Italian car, `fitdist` cannot fit a distribution to that group. Removing the Italian car from the sample data prevents `fitdist` from returning an error.

```
Origin = nominal(Origin);
MPG2 = MPG(Origin~='Italy');
Origin2 = Origin(Origin~='Italy');
Origin2 = droplevels(Origin2,'Italy');
```

Step 3. Fit kernel distributions to each group.

Use `fitdist` to fit kernel distributions to each country of origin group in the `MPG` data.

```
[KerByOrig,Country] = fitdist(MPG2,'Kernel','by',Origin2)
```

```
KerByOrig =

  Column 1

    [1x1 prob.KernelDistribution]

  Column 2

    [1x1 prob.KernelDistribution]
```

```
  Column 3

    [1x1 prob.KernelDistribution]

  Column 4

    [1x1 prob.KernelDistribution]

  Column 5

    [1x1 prob.KernelDistribution]


Country =

    'France'
    'Germany'
    'Japan'
    'Sweden'
    'USA'
```

The cell array `KerByOrig` contains five kernel distribution objects, one for each country represented in the sample data. Each object contains properties that hold information about the data, the distribution, and the parameters. The array `Country` lists the country of origin for each group in the same order as the distribution objects are stored in `KerByOrig`.

Step 4. Compute the pdf for each group.

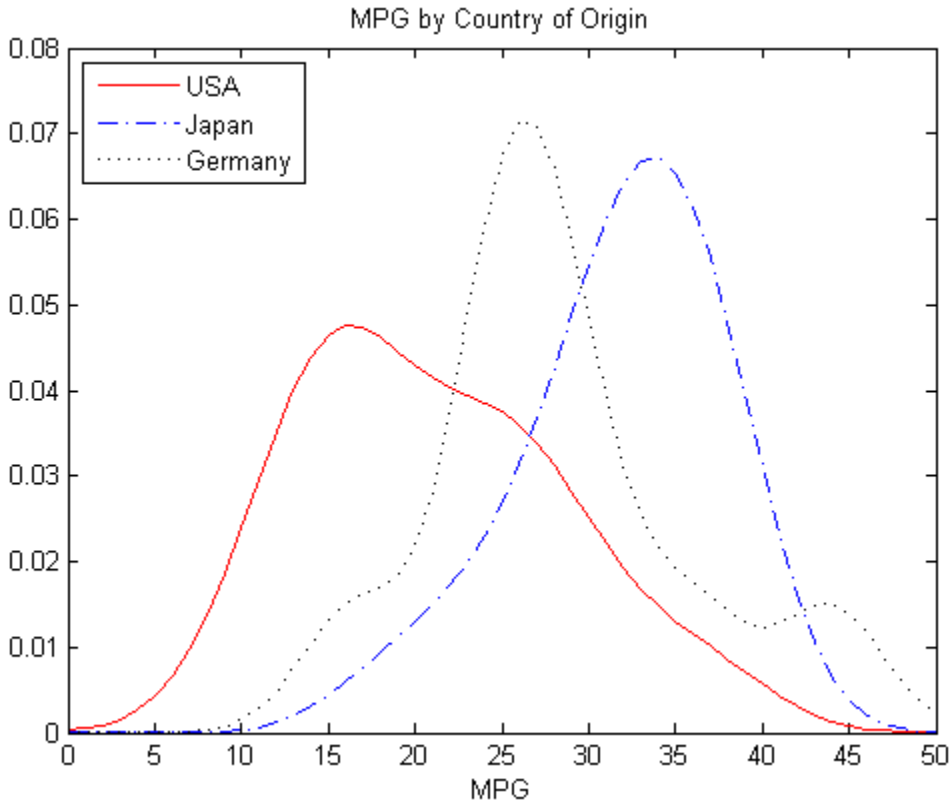
Extract the probability distribution objects for Germany, Japan, and USA. Use the positions of each country in `KerByOrig` shown in Step 3, which indicates that Germany is the second country, Japan is the third country, and USA is the fifth country. Compute the pdf for each group.

```
Germany = KerByOrig{2};
Japan = KerByOrig{3};
USA = KerByOrig{5};

x = 0:1:50;

USA_pdf = pdf(USA,x);
Japan_pdf = pdf(Japan,x);
Germany_pdf = pdf(Germany,x);
```

Step 5. Plot the pdf for each group.

Plot the pdf for each group on the same figure.

```
figure;
plot(x,USA_pdf,'r-');
hold on;
plot(x,Japan_pdf,'b-.');
plot(x,Germany_pdf,'k:');
legend({'USA','Japan','Germany'},'Location','NW');
title('MPG by Country of Origin');
xlabel('MPG');
```



The resulting plot shows how miles per gallon (`MPG`) performance differs by country of origin (`Origin`). Using this data, the USA has the widest distribution, and its peak is at the lowest `MPG` value of the three origins. Japan has the most regular distribution with a slightly heavier left tail, and its peak is at the highest `MPG` value of the three origins. The peak for Germany is between the USA and Japan, and the second bump near 44 miles per gallon suggests that there might be multiple modes in the data.

See Also

`fitdist` | `pdf`

Related Examples

- "Fit Distributions to Grouped Data Using ksdensity" on page 5-57

More About

- "Kernel Distribution" on page B-81
- "Grouping Variables" on page 2-52

Multinomial Probability Distribution Objects

This example shows how to generate random numbers, compute and plot the pdf, and compute descriptive statistics of a multinomial distribution using probability distribution objects.

Step 1. Define the distribution parameters.

Create a vector `p` containing the probability of each outcome. Outcome 1 has a probability of 1/2, outcome 2 has a probability of 1/3, and outcome 3 has a probability of 1/6. The number of trials `n` in each experiment is 5, and the number of repetitions `reps` of the experiment is 8.

```
p = [1/2 1/3 1/6];
n = 5;
reps = 8;
```

Step 2. Create a multinomial probability distribution object.

Create a multinomial probability distribution object using the specified value `p` for the `Probabilities` parameter.

```
pd = makedist('Multinomial','Probabilities',p)
```

```
pd =

  MultinomialDistribution

  Probabilities:
    0.5000    0.3333    0.1667
```

Step 3. Generate one random number.

Generate one random number from the multinomial distribution, which is the outcome of a single trial.

```
rng('default')  % For reproducibility
r = random(pd)
```

```
r =

     2
```

This trial resulted in outcome 2.

Step 4. Generate a matrix of random numbers.

You can also generate a matrix of random numbers from the multinomial distribution, which reports the results of multiple experiments that each contain multiple trials. Generate a matrix that contains the outcomes of an experiment with `n = 5` trials and `reps = 8` repetitions.

```
r = random(pd,reps,n)
```

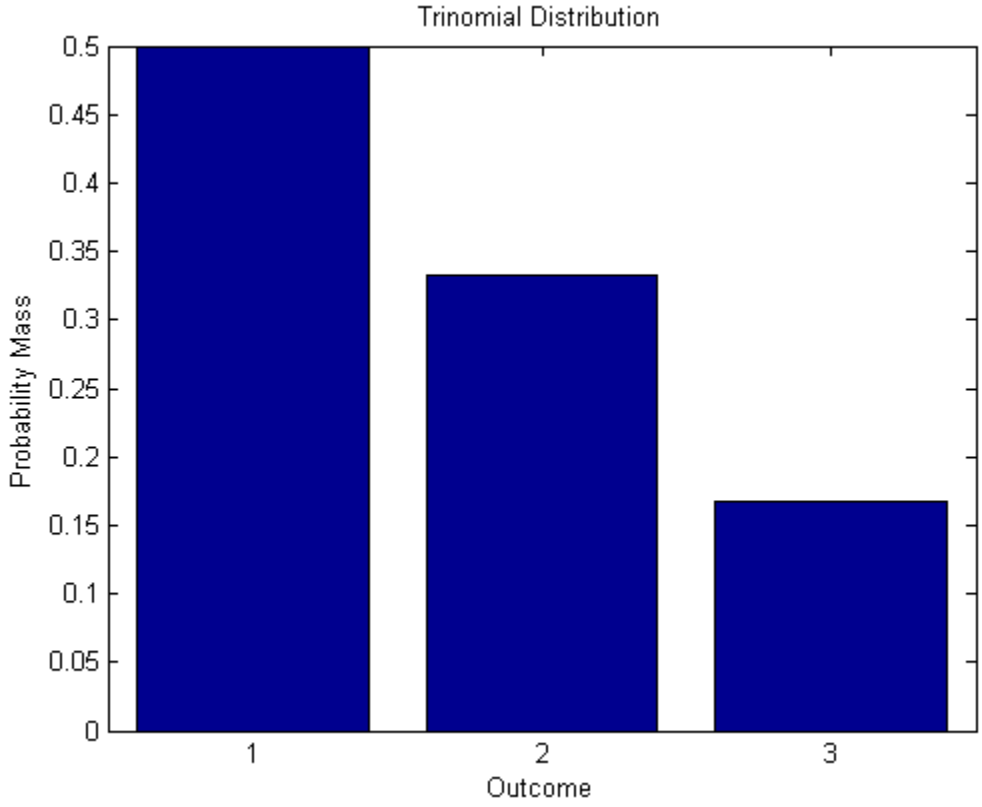
```
r =

     3     3     3     2     1
     1     1     2     2     1
     3     3     3     1     2
     2     3     2     2     2
     1     1     1     1     1
     1     2     3     2     3
     2     1     3     1     1
     3     1     2     1     1
```

Each element in the resulting matrix is the outcome of one trial. The columns correspond to the five trials in each experiment, and the rows correspond to the eight experiments. For example, in the first experiment (corresponding to the first row), one of the five trials resulted in outcome 1, one of the five trials resulted in outcome 2, and three of the five trials resulted in outcome 3.

Step 5. Compute and plot the pdf.

Compute the pdf of the distribution.

```
x = 1:3;
y = pdf(pd,x);
bar(x,y);
xlabel('Outcome');
ylabel('Probability Mass');
title('Trinomial Distribution');
```



The plot shows the probability mass for each k possible outcome. For this distribution, the pdf value for any `x` other than 1, 2, or 3 is 0.

Step 6. Compute descriptive statistics.

Compute the mean, median, and standard deviation of the distribution.

```
m = mean(pd)
med = median(pd)
s = std(pd)
```

```
m =

    1.6667
```

```
med =

     1

s =

    0.7454
```

Multinomial Probability Distribution Functions

This example shows how to generate random numbers and compute and plot the pdf of a multinomial distribution using probability distribution functions.

Step 1. Define the distribution parameters.

Create a vector `p` containing the probability of each outcome. Outcome 1 has a probability of 1/2, outcome 2 has a probability of 1/3, and outcome 3 has a probability of 1/6.
The number of trials in each experiment `n` is 5, and the number of repetitions of the experiment `reps` is 8.

```
p = [1/2 1/3 1/6];
n = 5;
reps = 8;
```

Step 2. Generate one random number.

Generate one random number from the multinomial distribution, which is the outcome of a single trial.

```
rng('default')  % For reproducibility
r = mnrnd(1,p,1)
```

```
r =

     0     1     0
```

The returned vector `r` contains three elements, which show the counts for each possible outcome. This single trial resulted in outcome 2.

Step 3. Generate a matrix of random numbers.

You can also generate a matrix of random numbers from the multinomial distribution, which reports the results of multiple experiments that each contain multiple trials. Generate a matrix that contains the outcomes of an experiment with `n = 5` trials and `reps = 8` repetitions.

```
r = mnrnd(n,p,reps)
```

```
r =
```

```
     1     1     3
     3     2     0
     1     1     3
     0     4     1
     5     0     0
     1     2     2
     3     1     1
     3     1     1
```

Each row in the resulting matrix contains counts for each of the k multinomial bins. For example, in the first experiment (corresponding to the first row), one of the five trials resulted in outcome 1, one of the five trials resulted in outcome 2, and three of the five trials resulted in outcome 3.

Step 4. Compute the pdf.

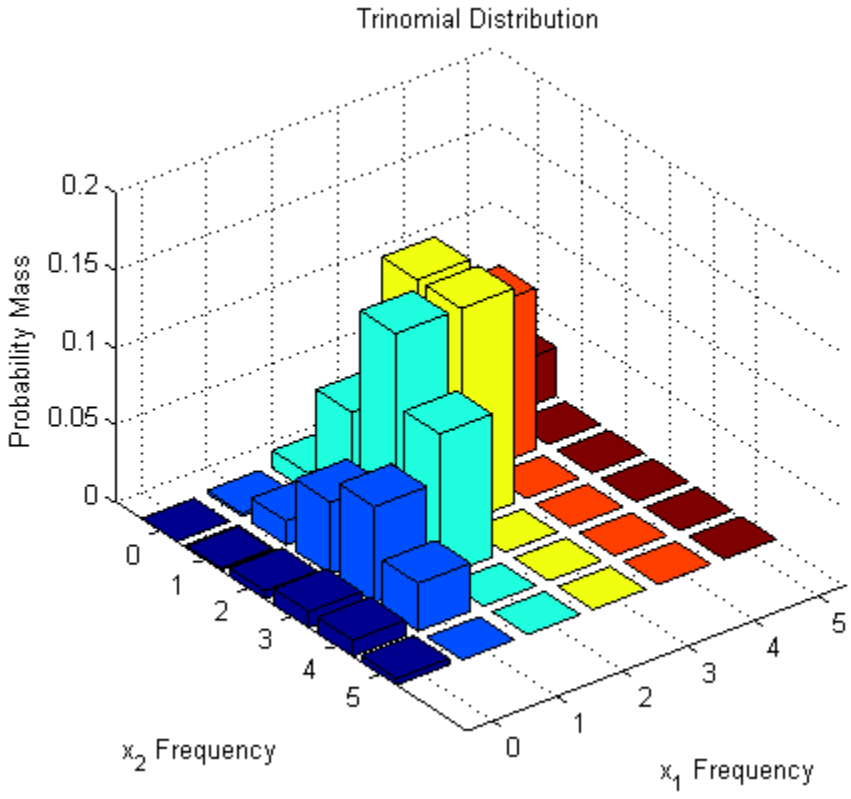
Since multinomial functions work with bin counts, create a multidimensional array of all possible outcome combinations, and compute the pdf using `mnpdf`.

```
count1 = 1:n;
count2 = 1:n;
[x1,x2] = meshgrid(count1,count2);
x3 = n-(x1+x2);
y = mnpdf([x1(:),x2(:),x3(:)],repmat(p,(n)^2,1));
```

Step 5. Plot the pdf.

Create a 3-D bar graph to visualize the pdf for each combination of outcome frequencies.

```
figure;
y = reshape(y,n,n);
bar3(y);
set(gca,'XTickLabel',1:n);
set(gca,'YTickLabel',1:n);
xlabel('x_1 Frequency');
ylabel('x_2 Frequency');
zlabel('Probability Mass');
```



The plot shows the probability mass for each possible combination of outcomes. It does not show x_3 , which is determined by the constraint $x_1 + x_2 + x_3 = n$.

Generate Random Numbers Using Uniform Distribution Inversion

This example shows how to generate random numbers using the uniform distribution inversion method. This is useful for distributions when it is possible to compute the inverse cumulative distribution function, but there is no support for sampling from the distribution directly.

Step 1. Generate random numbers from the standard uniform distribution.

Use `rand` to generate 1000 random numbers from the uniform distribution on the interval (0,1).

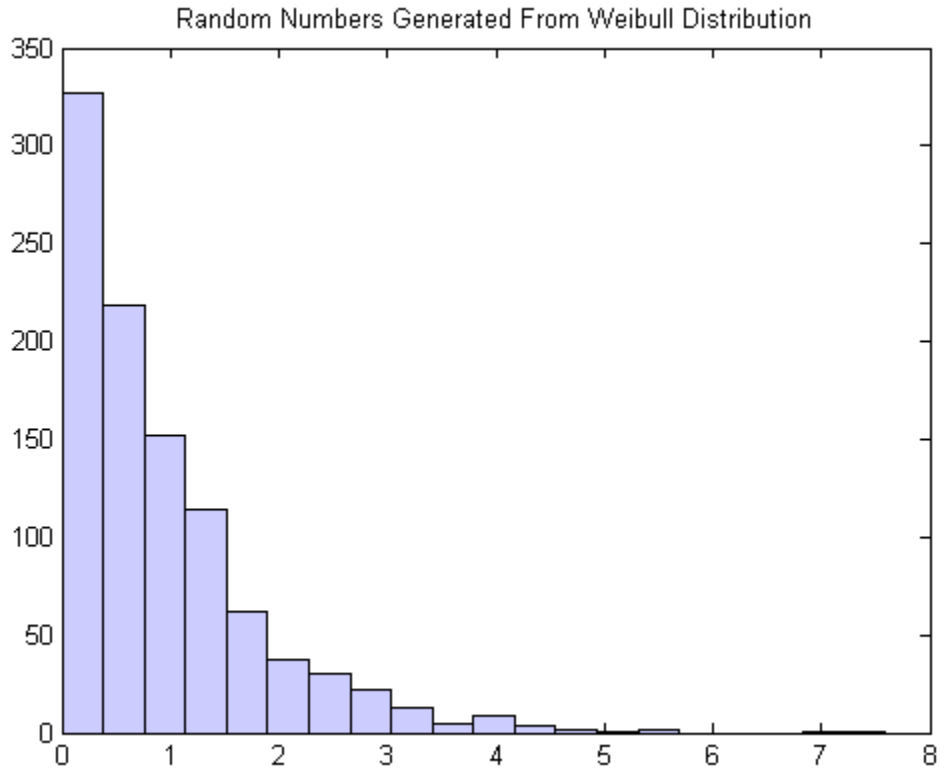
```
rng('default')  % For reproducibility
u = rand(1000,1);
```

The inversion method relies on the principle that continuous cumulative distribution functions (cdfs) range uniformly over the open interval (0,1). If u is a uniform random number on (0,1), then $x = F^{-1}(u)$ generates a random number x from any continuous distribution with the specified cdf `F`.

Step 2. Generate random numbers from the Weibull distribution.

Use the inverse cumulative distribution function to generate the random numbers from a Weibull distribution with parameters `A = 1` and `B = 1` that correspond to the probabilities in `u`. Plot the results.

```
figure;
x = wblinv(u,1,1);
hist(x,20);
```

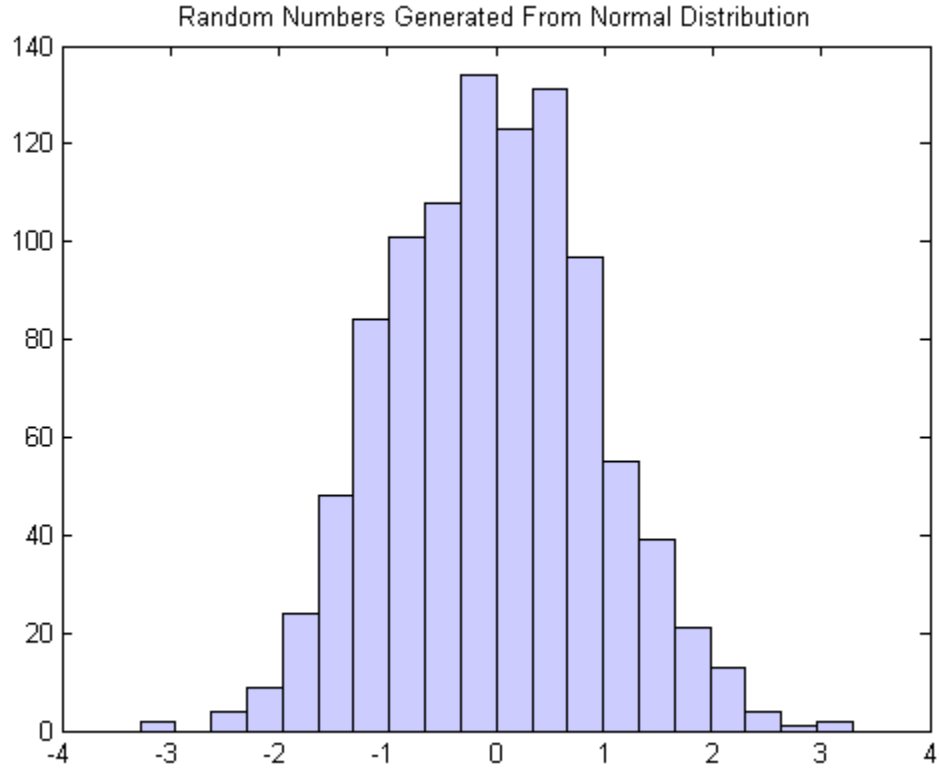


The histogram shows that the random numbers generated using the Weibull inverse cdf function `wblinv` have a Weibull distribution.

Step 3. Generate random numbers from the standard normal distribution.

The same values in `u` can generate random numbers from any distribution, for example the standard normal, by following the same procedure using the inverse cdf of the desired distribution.

```
figure;
x_norm = norminv(u,1,0);
hist = (x_norm,20);
```



The histogram shows that, by using the standard normal inverse cdf `norminv`, the random numbers generated from `u` now have a standard normal distribution.

See Also

`hist` | `norminv` | `rand` | `wblinv`

More About

- "Uniform Distribution (Continuous)" on page B-163
- "Weibull Distribution" on page B-172
- "Normal Distribution" on page B-130

Represent Cauchy Distribution Using *t* Location-Scale

This example shows how to use the *t* location-scale probability distribution object to work with a Cauchy distribution with nonstandard parameter values.

Step 1. Create a probability distribution object.

Create a *t* location-scale probability distribution object with degrees of freedom `nu = 1`. Specify `mu = 3` to set the location parameter equal to 3, and `sigma = 1` to set the scale parameter equal to 1.

```
pd = makedist('tLocationScale','mu',3,'sigma',1,'nu',1)
```

```
pd =

  tLocationScaleDistribution

  t Location-Scale distribution
       mu = 3
    sigma = 1
       nu = 1
```

Step 2. Compute descriptive statistics.

Use object functions to compute descriptive statistics for the Cauchy distribution.

```
med = median(pd)
r = iqr(pd)
m = mean(pd)
s = std(pd)
```

```
med =


     3

r =

     2


m =
```

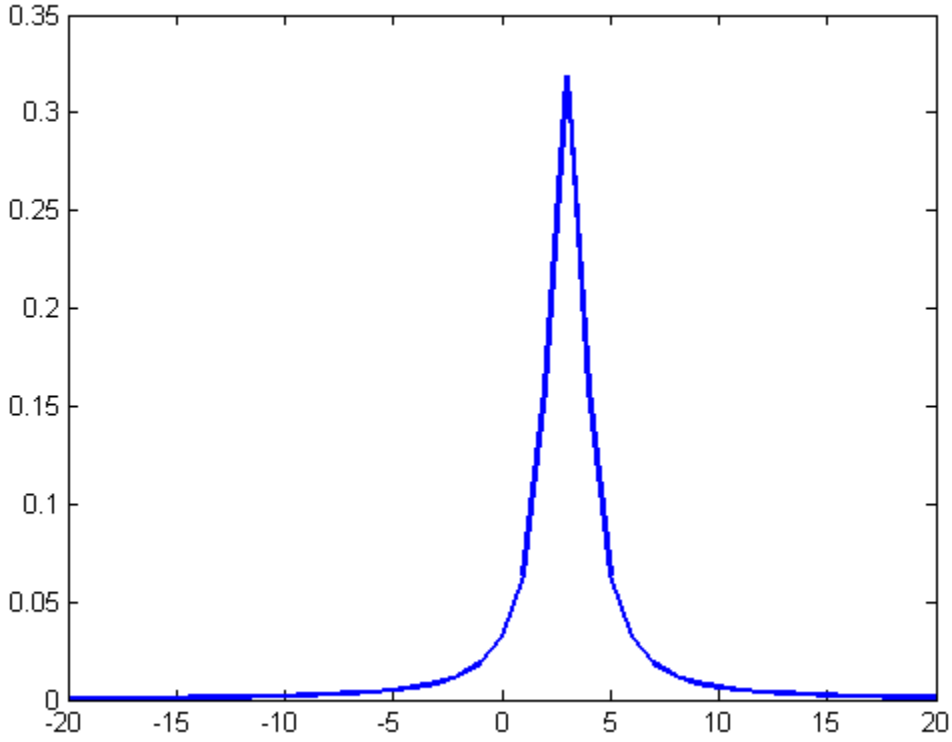
```
   NaN

s =

   Inf
```

The median of the Cauchy distribution is equal to its location parameter, and the interquartile range is equal to two times its scale parameter. Its mean and standard deviation are undefined.

Step 3. Compute and plot the pdf.

Compute and plot the pdf of the Cauchy distribution.

```
figure;
x = -20:1:20;
y = pdf(pd,x);
plot(x,y,'LineWidth',2);
```



The peak of the pdf is centered at the location parameter `mu = 3`.

Step 4. Generate a vector of Cauchy random numbers.

Generate a column vector containing 10 random numbers from the Cauchy distribution using the `random` function for the *t* location-scale probability distribution object.

```
rng('default');  % For reproducibility
r = random(pd,10,1)
```

```
r =

    3.2678
    4.6547
```

```
    2.0604
    4.7322
    3.1810
    1.6649
    1.8471
    4.2466
    5.4647
    8.8874
```

Step 5. Generate a matrix of Cauchy random numbers.

Generate a 5-by-5 matrix of Cauchy random numbers.

```
r = random(pd,5,5)
```

```
r =

    2.2867    2.9692   -1.7003    5.5949    1.9806
    2.7421    2.7180    3.2210    2.4233    3.1394
    3.5966    3.9806    1.0182    6.4180    5.1367
    5.4791   15.6472    0.7558    2.8908    5.9031
    1.6863    4.0985    2.9934   13.9506    4.8792
```

See Also

`makedist`

Related Examples

- "Generate Cauchy Random Numbers Using Student's *t*" on page 5-142

More About

- "t Location-Scale Distribution" on page B-154

Generate Cauchy Random Numbers Using Student's *t*

This example shows how to use the Student's *t* distribution to generate random numbers from a standard Cauchy distribution.

Step 1. Generate a vector of random numbers.

Generate a column vector containing 10 random numbers from a standard Cauchy distribution, which has a location parameter `mu = 0` and scale parameter `sigma = 1`. Use `trnd` with degrees of freedom `V = 1`.

```
rng('default');  % For reproducibility
r = trnd(1,10,1)
```

```
r =

    0.2678
    1.6547
   -0.9396
    1.7322
    0.1810
   -1.3351
   -1.1529
    1.2466
    2.4647
    5.8874
```

Step 2. Generate a matrix of random numbers.

Generate a 5-by-5 matrix of random numbers from a standard Cauchy distribution.

```
r = trnd(1,5,5)
```

```
r =

   -0.7133   -0.0308   -4.7003    2.5949   -1.0194
   -0.2579   -0.2820    0.2210   -0.5767    0.1394
    0.5966    0.9806   -1.9818    3.4180    2.1367
    2.4791   12.6472   -2.2442   -0.1092    2.9031
   -1.3137    1.0985   -0.0066   10.9506    1.8792
```

See Also

`trnd`

Related Examples

- "Represent Cauchy Distribution Using *t* Location-Scale" on page 5-138

More About

- "Student's t Distribution" on page B-146

Generate Correlated Data Using Rank Correlation

This example shows how to use a copula and rank correlation to generate correlated data from probability distributions that do not have an inverse cdf function available, such as the Pearson flexible distribution family.

Step 1. Generate Pearson random numbers.

Generate 1000 random numbers from two different Pearson distributions, using the `pearsrnd` function. The first distribution has the parameter values mu equal to 0, sigma equal to 1, skew equal to 1, and kurtosis equal to 4. The second distribution has the parameter values mu equal to 0, sigma equal to 1, skew equal to 0.75, and kurtosis equal to 3.

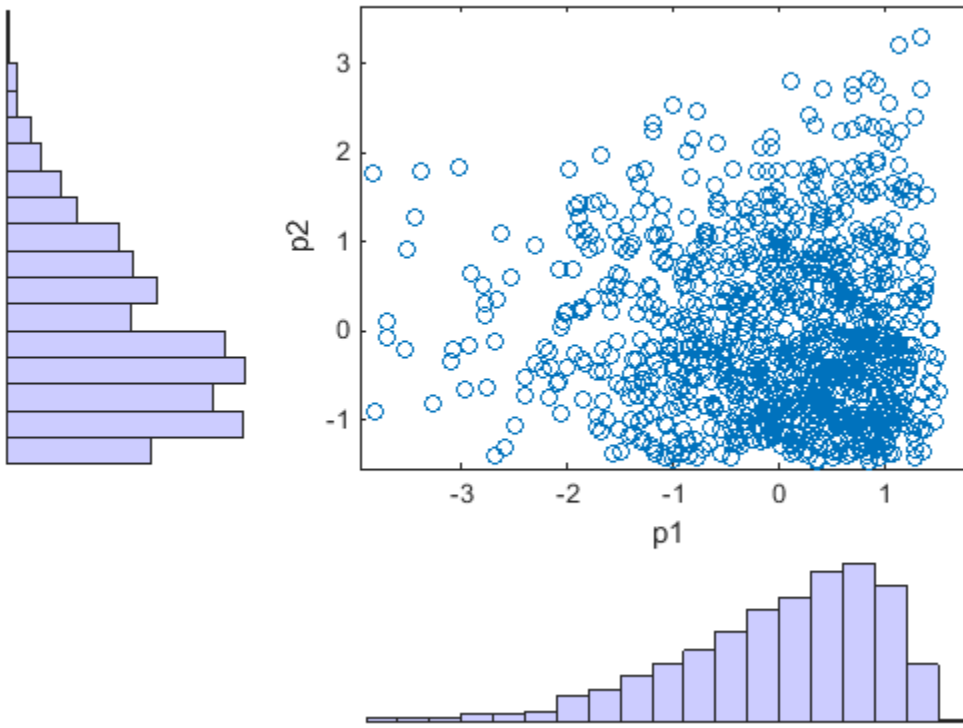
```
rng default  % For reproducibility
p1 = pearsrnd(0,1,-1,4,1000,1);
p2 = pearsrnd(0,1,0.75,3,1000,1);
```

At this stage, `p1` and `p2` are independent samples from their respective Pearson distributions, and are uncorrelated.

Step 2. Plot the Pearson random numbers.

Create a `scatterhist` plot to visualize the Pearson random numbers.

```
figure
scatterhist(p1,p2)
```

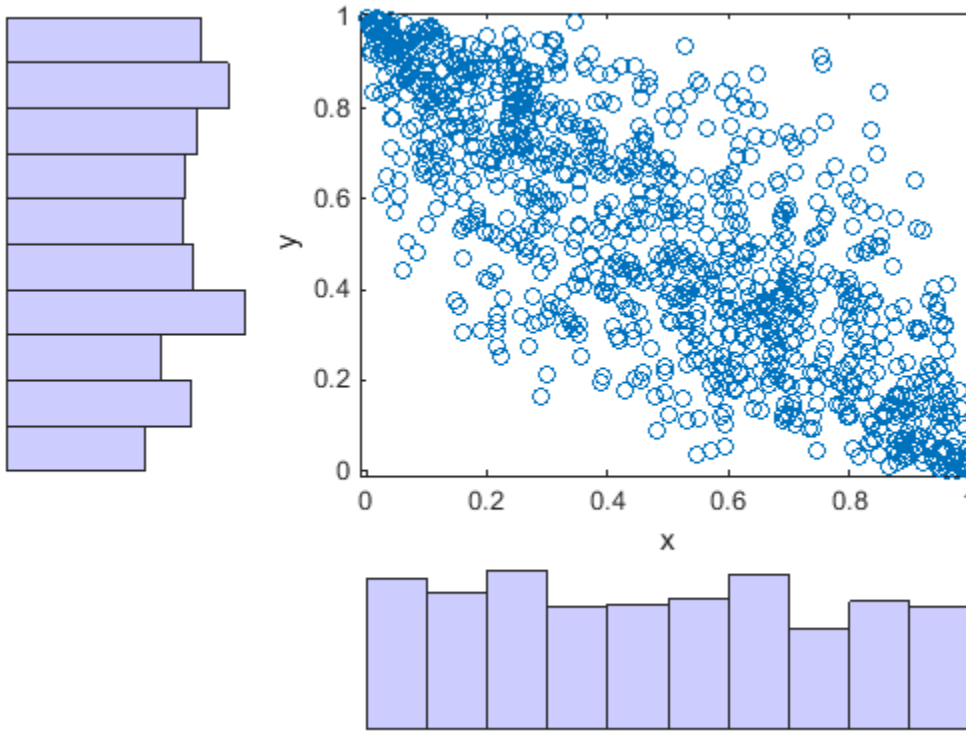


The histograms show the marginal distributions for `p1` and `p2`. The scatterplot shows the joint distribution for `p1` and `p2`. The lack of pattern to the scatterplot shows that `p1` and `p2` are independent.

Step 3. Generate random numbers using a Gaussian copula.

Use `copularnd` to generate 1000 correlated random numbers with a correlation coefficient equal to –0.8, using a Gaussian copula. Create a `scatterhist` plot to visualize the random numbers generated from the copula.

```
u = copularnd('Gaussian',-0.8,1000);
figure
scatterhist(u(:,1),u(:,2))
```



The histograms show that the data in each column of the copula have a marginal uniform distribution. The scatterplot shows that the data in the two columns are negatively correlated.

Step 4. Sort the copula random numbers.

Using Spearman's rank correlation, transform the two independent Pearson samples into correlated data.

Use the `sort` function to sort the copula random numbers from smallest to largest, and to return a vector of indices describing the rearranged order of the numbers.

```
[s1,i1] = sort(u(:,1));
```

```
[s2,i2] = sort(u(:,2));
```

`s1` and `s2` contain the numbers from the first and second columns of the copula, `u`, sorted in order from smallest to largest. `i1` and `i2` are index vectors that describe the rearranged order of the elements into `s1` and `s2`. For example, if the first value in the sorted vector `s1` is the third value in the original unsorted vector, then the first value in the index vector `i1` is 3.

Step 5. Transform the Pearson samples using Spearman's rank correlation.

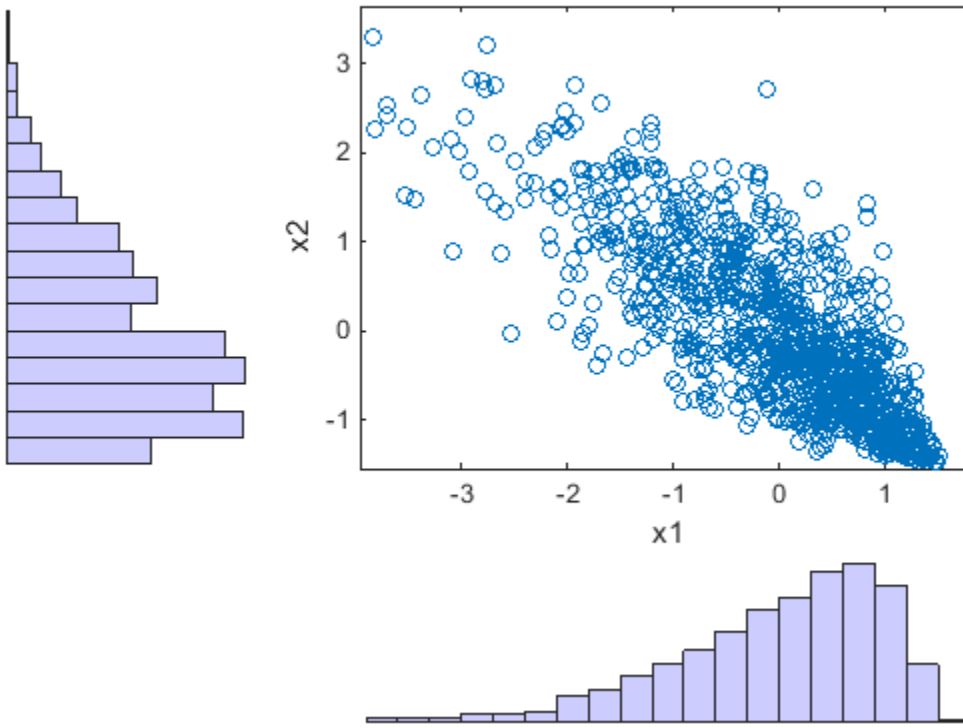
Create two vectors of zeros, `x1` and `x2`, that are the same size as the sorted copula vectors, `s1` and `s2`. Sort the values in `p1` and `p2` from smallest to largest. Place the values into `x1` and `x2`, in the same order as the indices `i1` and `i2` generated by sorting the copula random numbers.

```
x1 = zeros(size(s1));
x2 = zeros(size(s2));

x1(i1) = sort(p1);
x2(i2) = sort(p2);
```

Step 6. Plot the correlated Pearson random numbers.

Create a `scatterhist` plot to visualize the correlated Pearson data.

```
figure
scatterhist(x1,x2)
```



The histograms show the marginal Pearson distributions for each column of data. The scatterplot shows the joint distribution of `p1` and `p2`, and indicates that the data are now negatively correlated.

Step 7. Confirm Spearman rank correlation coefficient values.

Confirm that the Spearman rank correlation coefficient is the same for the copula random numbers and the correlated Pearson random numbers.

```
copula_corr = corr(u,'Type','spearman')
pearson_corr = corr([x1,x2],'Type','spearman')
```

```
copula_corr =
```

```
    1.0000   -0.7858
   -0.7858    1.0000


pearson_corr =

    1.0000   -0.7858
   -0.7858    1.0000
```

The Spearman rank correlation is the same for the copula and the Pearson random numbers.

See Also

`copularnd` | `corr` | `sort`

More About

- "Copulas: Generate Correlated Samples" on page 5-160

Gaussian Mixture Models

In this section...

Gaussian mixture models are formed by combining multivariate normal density components In Statistics and Machine Learning Toolbox software, use the `gmdistribution` class to fit data using an expectation maximization (EM) algorithm, which assigns posterior probabilities to each component density with respect to each observation. The fitting method uses an iterative algorithm that converges to a local optimum.

Clustering using Gaussian mixture models is sometimes considered a soft clustering method. The posterior probabilities for each point indicate that each data point has some probability of belonging to each cluster. For more information on clustering with Gaussian mixture models, see “Clustering Using Gaussian Mixture Models” on page 14-29. This section describes their creation.

Creating Gaussian Mixture Models

Specifying a Model

Use the `gmdistribution` constructor to create Gaussian mixture models with specified means, covariances, and mixture proportions.

First, define the means, covariances, and mixture proportions.

```
MU = [1 2;-3 -5]; % Means
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]); % Covariances
p = ones(1,2)/2; % Mixing proportions
```

Then, create an object of the `gmdistribution` class defining a two-component mixture of bivariate Gaussian distributions:

```
obj = gmdistribution(MU,SIGMA,p);
```

Display properties of the object with the MATLAB function `fieldnames`:

```
properties = fieldnames(obj)
```

```
properties =

    'NumVariables'
    'DistributionName'
    'NumComponents'
    'ComponentProportion'
    'SharedCovariance'
    'NumIterations'
    'RegularizationValue'
    'NegativeLogLikelihood'
    'CovarianceType'
    'mu'
    'Sigma'
    'AIC'
    'BIC'
    'Converged'
```

The `gmdistribution` reference page describes these properties. To access the value of a property, use dot indexing. For example, access the dimensions of the object.

```
dimension = obj.NDimensions
```

```
dimension =

     2
```

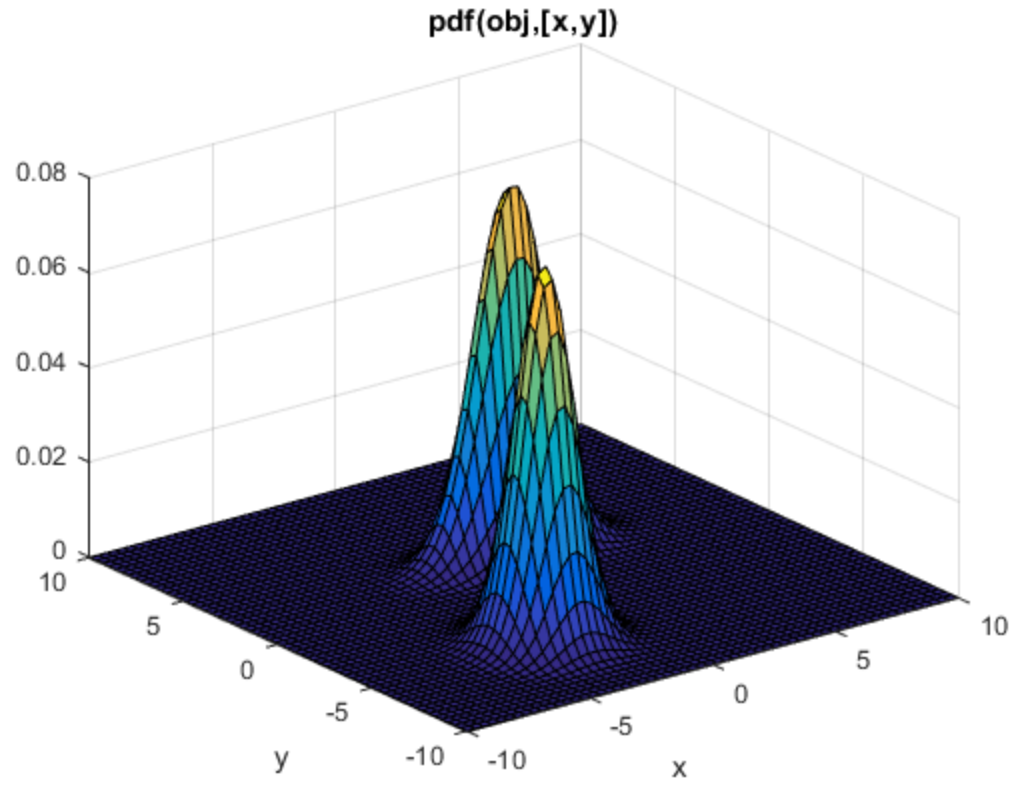
Access the distribution name.

```
name = obj.DistName
```

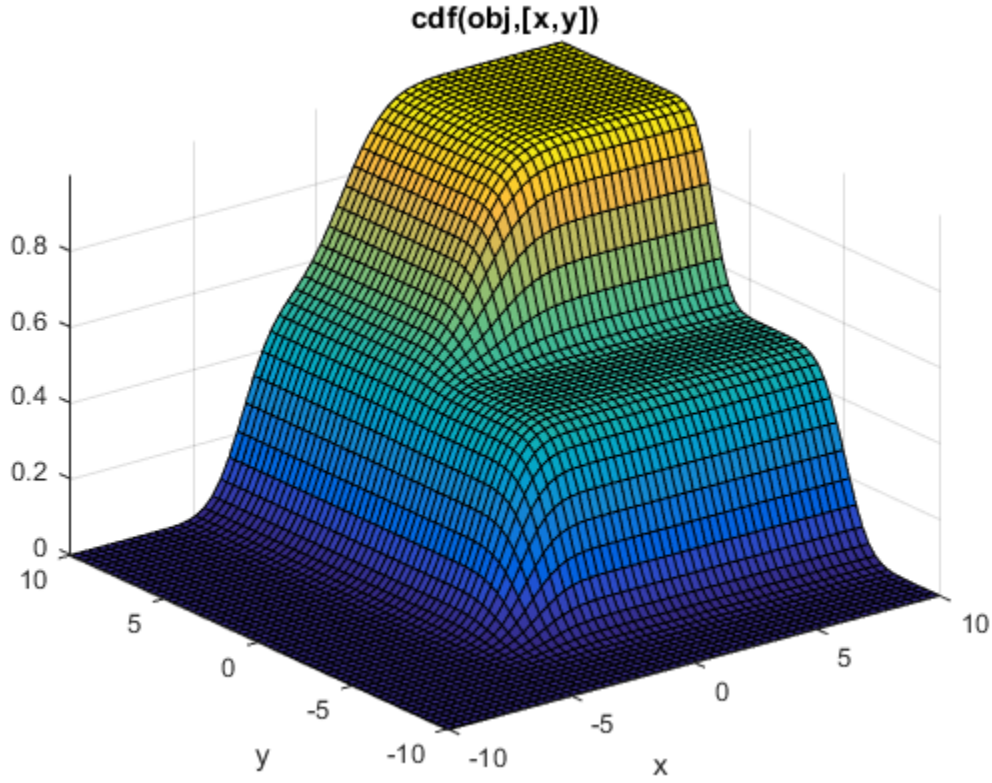
```
name =

gaussian mixture distribution
```

Use the methods `pdf` and `cdf` to compute values and visualize the object:

```
figure
ezsurf(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
```




```
figure
ezsurf(@(x,y)cdf(obj,[x y]),[-10 10],[-10 10])
```



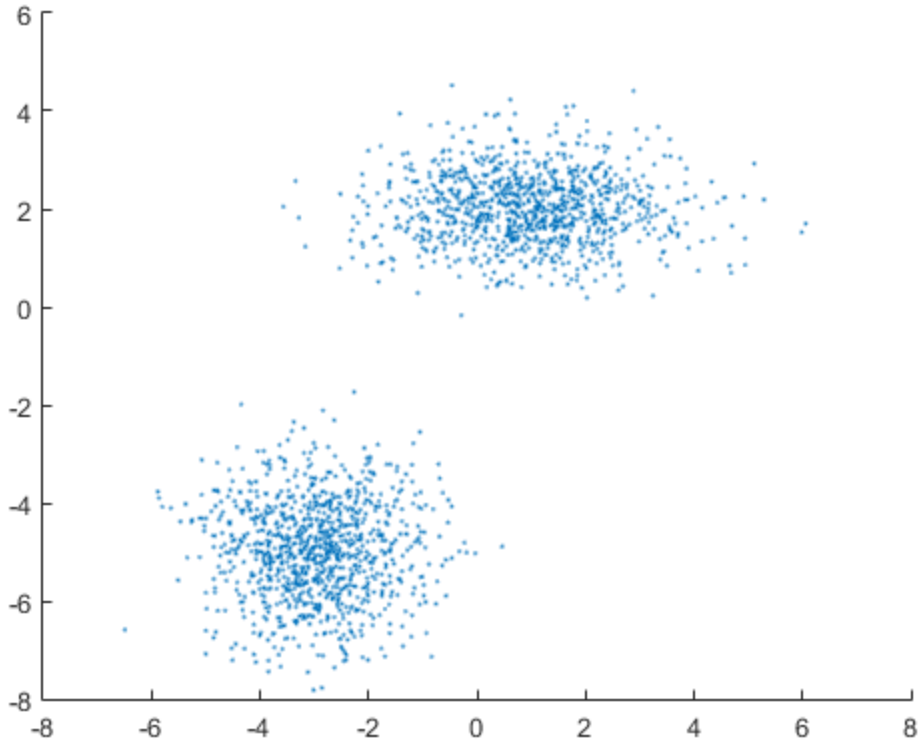
Fitting a Model to Data

You can also create Gaussian mixture models by fitting a parametric model with a specified number of components to data. `fitgmdist` uses the syntax `obj = fitgmdist(X,k)`, where `X` is a data matrix and `k` is the specified number of components. Choosing a suitable number of components `k` is essential for creating a useful model of the data—too few components fails to model the data accurately; too many components leads to an over-fit model with singular covariance matrices.

The following example illustrates this approach.

First, create some data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);
mvnrnd(MU2,SIGMA2,1000)];
figure
scatter(X(:,1),X(:,2),10,'.')
```

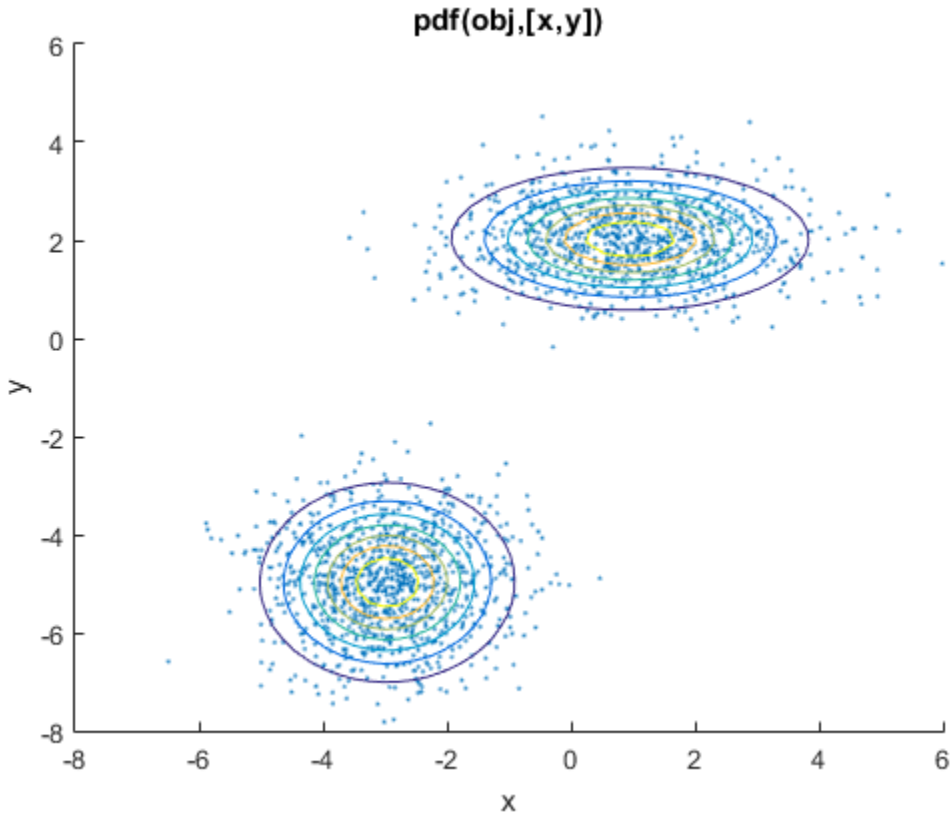


Next, fit a two-component Gaussian mixture model:

```
options = statset('Display','final');
obj = fitgmdist(X,2,'Options',options);
hold on
```

```
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
hold off
```

```
18 iterations, log-likelihood = -7058.35
```



Among the properties of the fit are the parameter estimates.

Display the estimates for mu, sigma, and mixture proportions

```
ComponentMeans = obj.mu
ComponentCovariances = obj.Sigma
MixtureProportions = obj.PComponents
```

```
ComponentMeans =
```

```
   -2.9617   -4.9727
    0.9539    2.0261


ComponentCovariances(:,:,1) =

    1.0100    0.0059
    0.0059    0.9897


ComponentCovariances(:,:,2) =

    1.9939   -0.0092
   -0.0092    0.4981


MixtureProportions =

    0.5000    0.5000
```

The two-component model minimizes the Akaike information:

```
AIC = zeros(1,4);
obj = cell(1,4);
for k = 1:4
    obj{k} = fitgmdist(X,k);
    AIC(k)= obj{k}.AIC;
end

[minAIC,numComponents] = min(AIC);
numComponents
```

```
numComponents =

     2
```

Display the model.

```
model = obj{2}
```

```
model =

Gaussian mixture distribution with 2 components in 2 dimensions
Component 1:
Mixing proportion: 0.500000
Mean:   -2.9617   -4.9727

Component 2:
Mixing proportion: 0.500000
Mean:    0.9539    2.0261
```

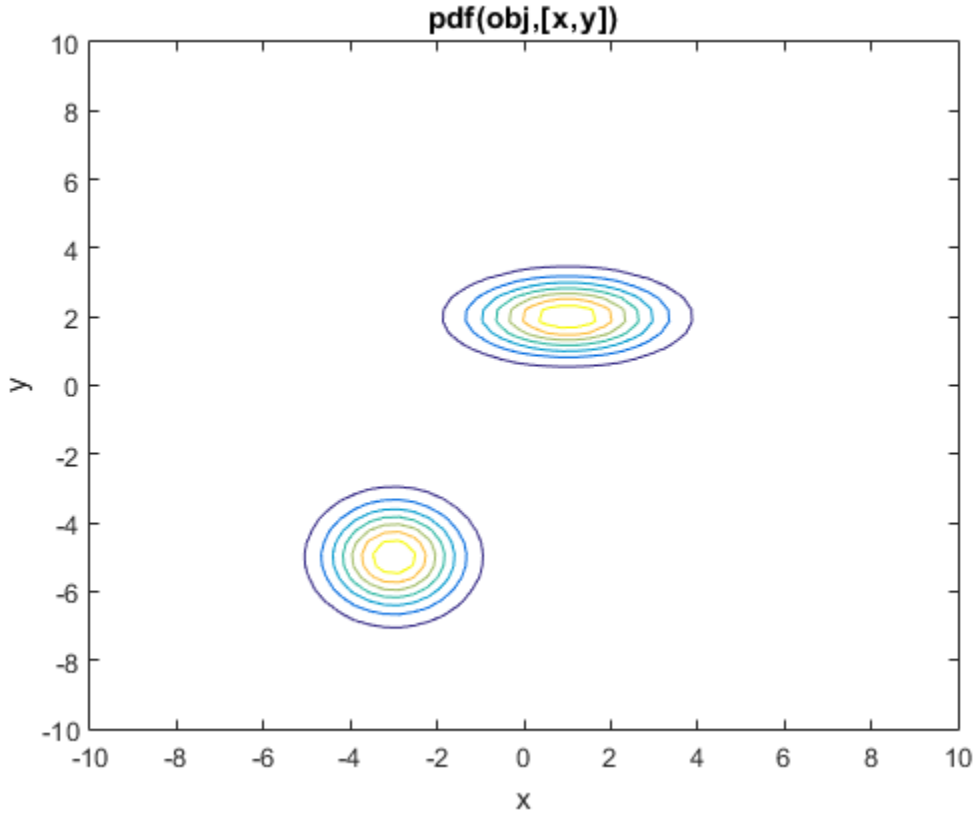
Both the Akaike and Bayes information are negative log-likelihoods for the data with penalty terms for the number of estimated parameters. You can use them to determine an appropriate number of components for a model when the number of components is unspecified.

Simulating Gaussian Mixtures

Use the method `random` of the `gmdistribution` class to generate random data from a Gaussian mixture model created with `gmdistribution` or `fitgmdist`.

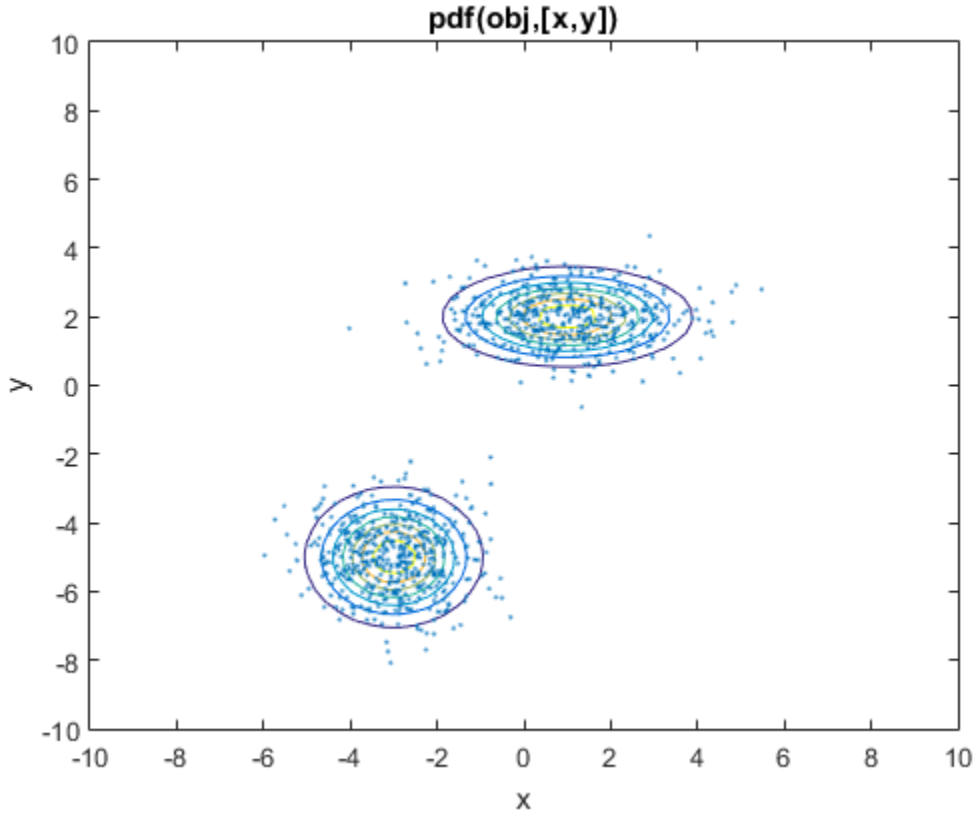
For example, the following specifies a `gmdistribution` object consisting of a two-component mixture of bivariate Gaussian distributions:

```
MU = [1 2;-3 -5];
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(MU,SIGMA,p);

figure
ezcontour(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
hold on
```



Use `random(gmdistribution)` to generate 1000 random values:

```
Y = random(obj,1000);
scatter(Y(:,1),Y(:,2),10,'.')
```


pdf(obj,[x,y])
10
8
6
4
2
0
-2
-4
-6
-8
-10
y
-10
-8
-6
-4
-2
0
2
4
6
8
10
x

Copulas: Generate Correlated Samples

In this section...

Copulas are functions that describe dependencies among variables, and provide a way to create distributions that model correlated multivariate data. Using a copula, you can construct a multivariate distribution by specifying marginal univariate distributions, and then choose a copula to provide a correlation structure between variables. Bivariate distributions, as well as distributions in higher dimensions, are possible.

Determining Dependence Between Simulation Inputs

One of the design decisions for a Monte Carlo simulation is a choice of probability distributions for the random inputs. Selecting a distribution for each individual variable is often straightforward, but deciding what dependencies should exist between the inputs may not be. Ideally, input data to a simulation should reflect what you know about dependence among the real quantities you are modeling. However, there may be little or no information on which to base any dependence in the simulation. In such cases, it is useful to experiment with different possibilities in order to determine the model's sensitivity.

It can be difficult to generate random inputs with dependence when they have distributions that are not from a standard multivariate distribution. Further, some of the standard multivariate distributions can model only limited types of dependence. It is always possible to make the inputs independent, and while that is a simple choice, it is not always sensible and can lead to the wrong conclusions.

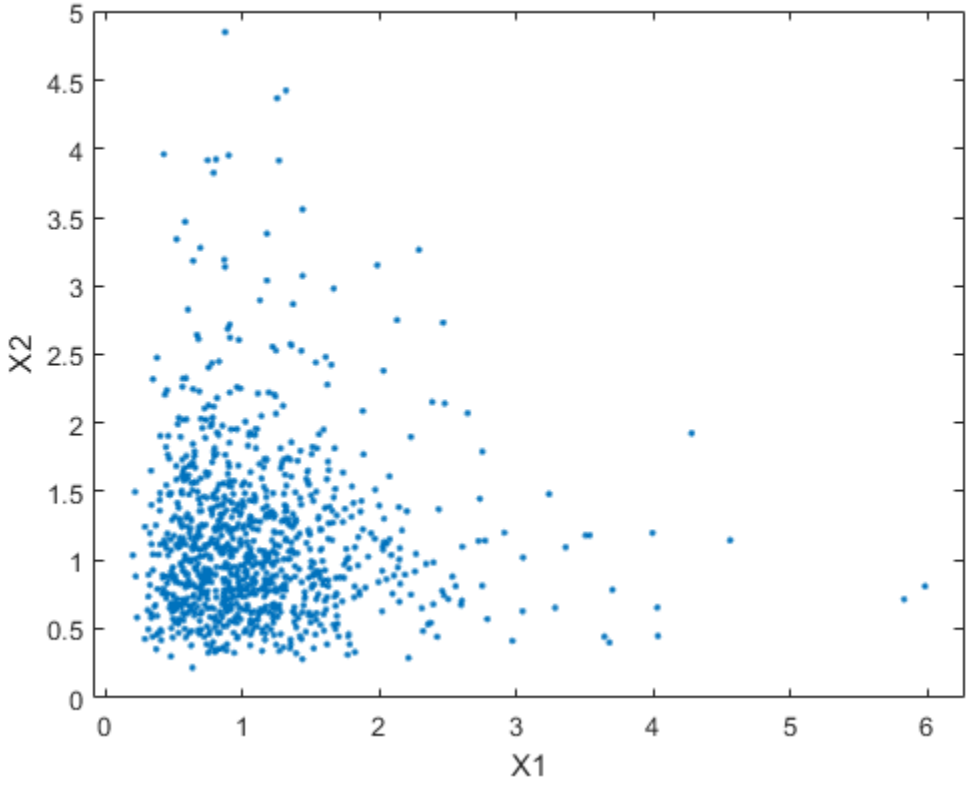
For example, a Monte-Carlo simulation of financial risk could have two random inputs that represent different sources of insurance losses. You could model these inputs as

lognormal random variables. A reasonable question to ask is how dependence between these two inputs affects the results of the simulation. Indeed, you might know from real data that the same random conditions affect both sources; ignoring that in the simulation could lead to the wrong conclusions.

Generate and Exponentiate Normal Random Variables

The `lognrnd` function simulates independent lognormal random variables. In the following example, the `mvnrnd` function generates `n` pairs of independent normal random variables, and then exponentiates them. Notice that the covariance matrix used here is diagonal.

```
n = 1000;

sigma = .5;
SigmaInd = sigma.^2 .* [1 0; 0 1]

rng('default');  % For reproducibility
ZInd = mvnrnd([0 0],SigmaInd,n);
XInd = exp(ZInd);

plot(XInd(:,1),XInd(:,2),'.')
axis([0 5 0 5])
axis equal
xlabel('X1')
ylabel('X2')


SigmaInd =

    0.2500         0
         0    0.2500
```



Dependent bivariate lognormal random variables are also easy to generate using a covariance matrix with nonzero off-diagonal terms.

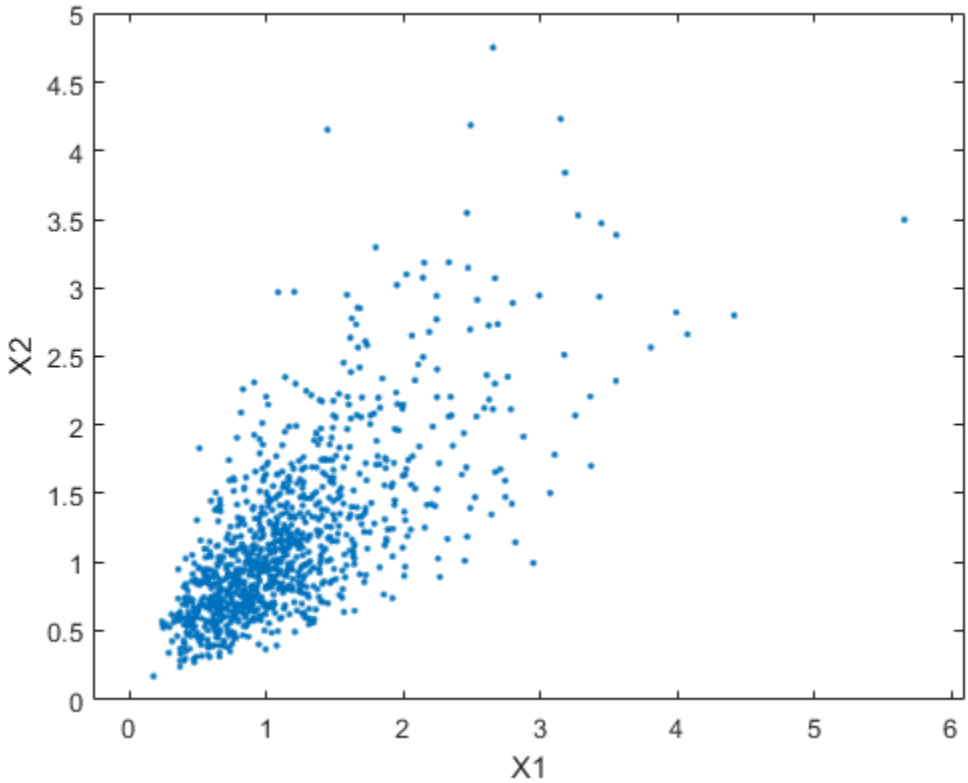
```
rho = .7;

SigmaDep = sigma.^2 .* [1 rho; rho 1]

ZDep = mvnrnd([0 0],SigmaDep,n);
XDep = exp(ZDep);
```

```
SigmaDep =

    0.2500    0.1750
```

```
    0.1750    0.2500
```

A second scatter plot demonstrates the difference between these two bivariate distributions.

```
plot(XDep(:,1),XDep(:,2),'.')
axis([0 5 0 5])
axis equal
xlabel('X1')
ylabel('X2')
```



It is clear that there is a tendency in the second data set for large values of `X1` to be associated with large values of `X2`, and similarly for small values. The correlation

parameter ρ of the underlying bivariate normal determines this dependence. The conclusions drawn from the simulation could well depend on whether you generate `X1` and `X2` with dependence. The bivariate lognormal distribution is a simple solution in this case; it easily generalizes to higher dimensions in cases where the marginal distributions are different lognormals.

Other multivariate distributions also exist. For example, the multivariate *t* and the Dirichlet distributions simulate dependent *t* and beta random variables, respectively. But the list of simple multivariate distributions is not long, and they only apply in cases where the marginals are all in the same family (or even the exact same distributions). This can be a serious limitation in many situations.

Constructing Dependent Bivariate Distributions

Although the construction discussed in the previous section creates a bivariate lognormal that is simple, it serves to illustrate a method that is more generally applicable.

1. Generate pairs of values from a bivariate normal distribution. There is statistical dependence between these two variables, and each has a normal marginal distribution.
2. Apply a transformation (the exponential function) separately to each variable, changing the marginal distributions into lognormals. The transformed variables still have a statistical dependence.

If a suitable transformation can be found, this method can be generalized to create dependent bivariate random vectors with other marginal distributions. In fact, a general method of constructing such a transformation does exist, although it is not as simple as exponentiation alone.

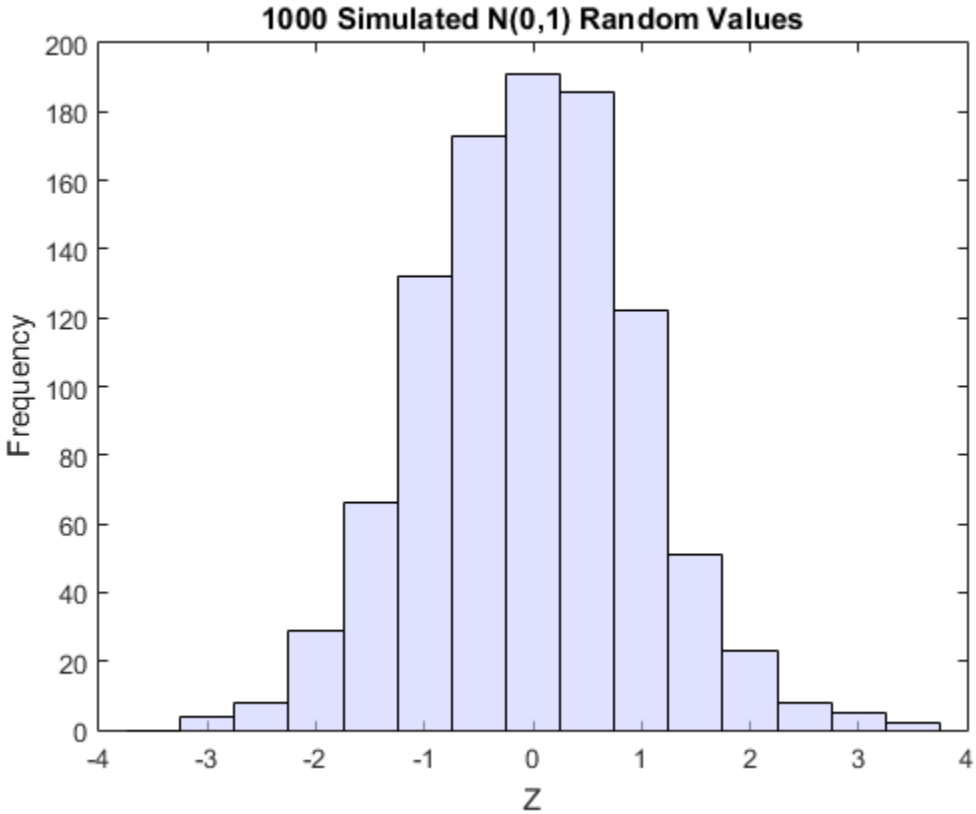
By definition, applying the normal cumulative distribution function (cdf), denoted here by Φ, to a standard normal random variable results in a random variable that is uniform on the interval [0,1]. To see this, if Z has a standard normal distribution, then the cdf of $U = \Phi(Z)$ is

$$\Pr\{U \le u\} = \Pr\{\Phi(Z) \le u\} = \Pr(Z \le \Phi^{-1}(u)\} = u$$

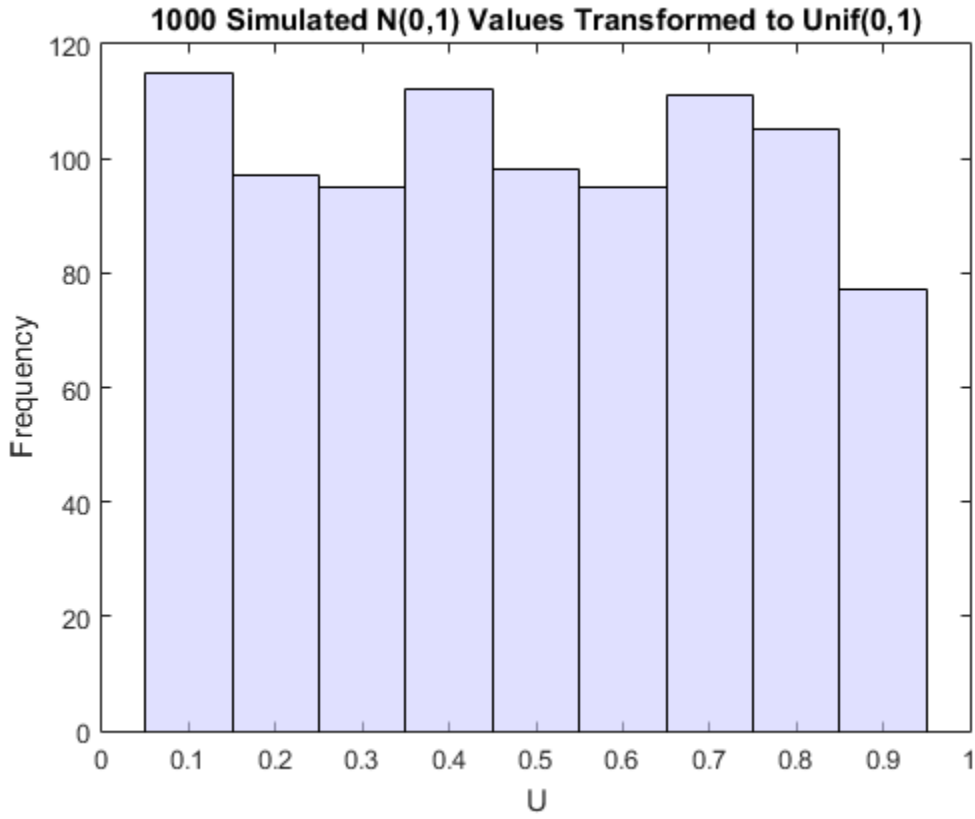
and that is the cdf of a Unif(0,1) random variable. Histograms of some simulated normal and transformed values demonstrate that fact:

```
n = 1000;
rng default % for reproducibility
```

```
z = normrnd(0,1,n,1); % generate standard normal data

histogram(z,-3.75:.5:3.75,'FaceColor',[.8 .8 1]) % plot the histogram of data
xlim([-4 4])
title('1000 Simulated N(0,1) Random Values')
xlabel('Z')
ylabel('Frequency')
```

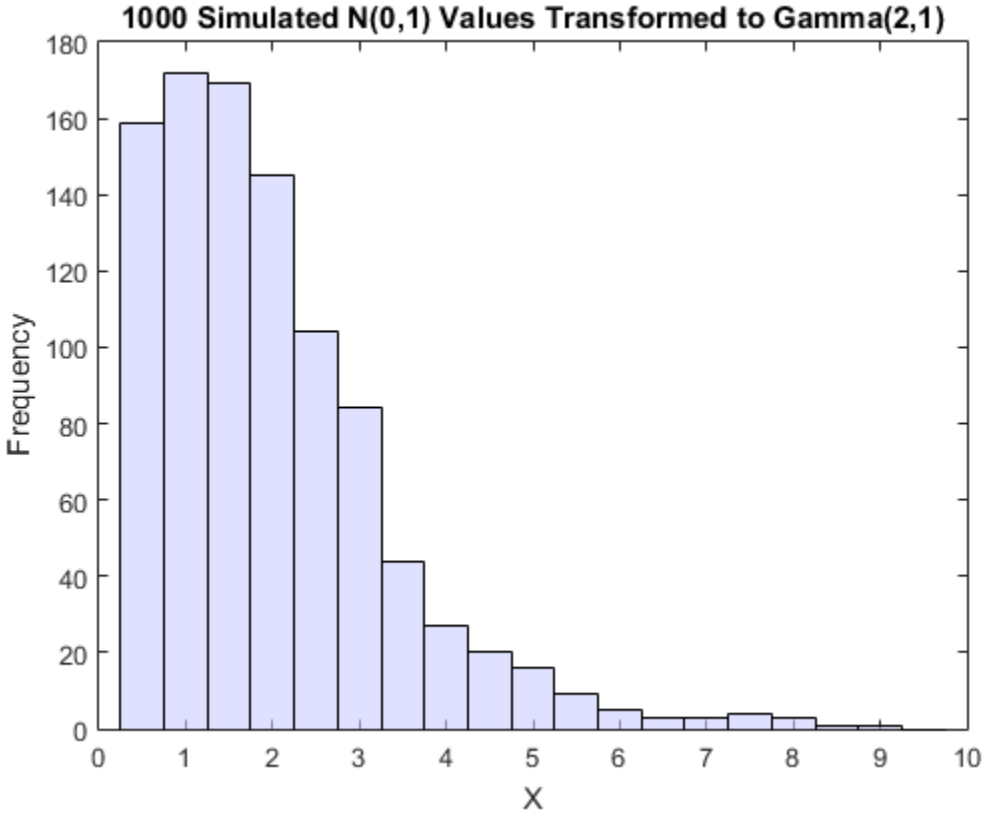



```
u = normcdf(z);  % compute the cdf values of the sample data

figure
histogram(u,.05:.1:.95,'FaceColor',[.8 .8 1]) % plot the histogram of the cdf values
title('1000 Simulated N(0,1) Values Transformed to Unif(0,1)')
xlabel('U')
ylabel('Frequency')
```



Borrowing from the theory of univariate random number generation, applying the inverse cdf of any distribution, *F*, to a Unif(0,1) random variable results in a random variable whose distribution is exactly *F* (see “Inversion Methods” on page 6-7). The proof is essentially the opposite of the preceding proof for the forward case. Another histogram illustrates the transformation to a gamma distribution:

```
x = gaminv(u,2,1); % transform to gamma values

figure
histogram(x,.25:.5:9.75,'FaceColor',[.8 .8 1]) % plot the histogram of gamma values
title('1000 Simulated N(0,1) Values Transformed to Gamma(2,1)')
xlabel('X')
ylabel('Frequency')
```

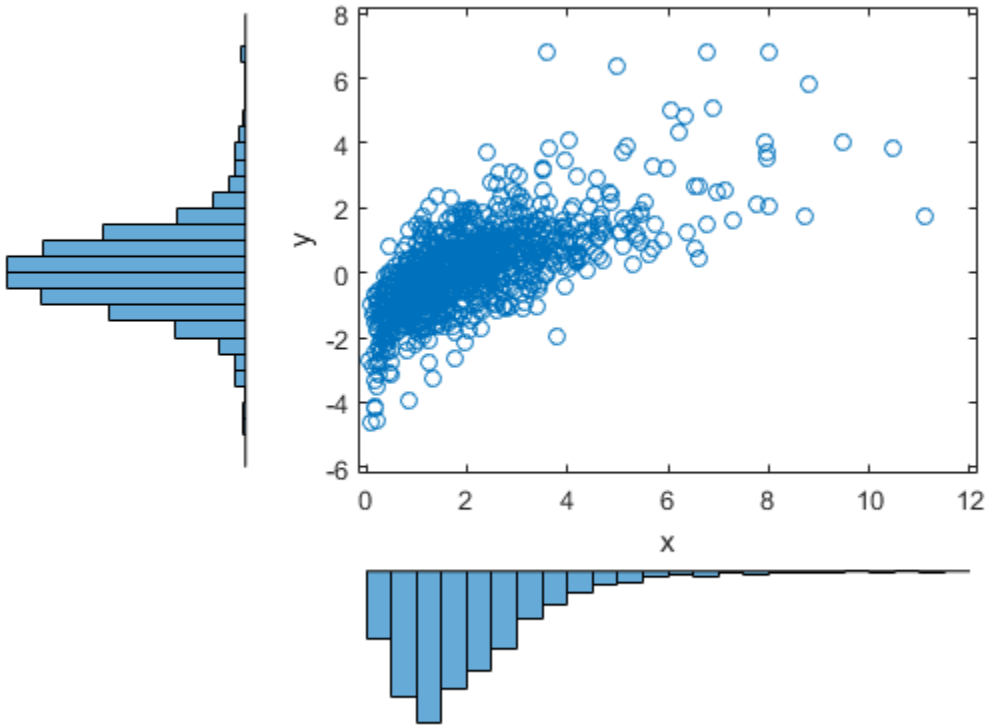


You can apply this two-step transformation to each variable of a standard bivariate normal, creating dependent random variables with arbitrary marginal distributions. Because the transformation works on each component separately, the two resulting random variables need not even have the same marginal distributions. The transformation is defined as:

$$Z = [Z_1, Z_2] \sim N\left([0,0], \begin{bmatrix} 1 & \rho \\ \rho & 1 \end{bmatrix}\right)$$
$$U = \left[\Phi(Z_1), \Phi(Z_2)\right]$$
$$X = \left[G_1(U_1), G_2(U_2)\right]$$

where G_1 and G_2 are inverse cdfs of two possibly different distributions. For example, the following generates random vectors from a bivariate distribution with t_5 and Gamma(2,1) marginals:

```
n = 1000; rho = .7;
Z = mvnrnd([0 0],[1 rho; rho 1],n);
U = normcdf(Z);
X = [gaminv(U(:,1),2,1) tinv(U(:,2),5)];

% draw the scatter plot of data with histograms
figure
scatterhist(X(:,1),X(:,2),'Direction','out')
```



This plot has histograms alongside a scatter plot to show both the marginal distributions, and the dependence.

Using Rank Correlation Coefficients

The correlation parameter, ρ, of the underlying bivariate normal determines the dependence between `X1` and `X2` in this construction. However, the linear correlation of `X1` and `X2` is not ρ. For example, in the original lognormal case, a closed form for that correlation is:

$$cor(X1, X2) = \frac{e^{\rho\sigma^2} - 1}{e^{\sigma^2} - 1}$$

which is strictly less than ρ, unless ρ is exactly 1. In more general cases such as the Gamma/*t* construction, the linear correlation between `X1` and `X2` is difficult or impossible to express in terms of ρ, but simulations show that the same effect happens.

That is because the linear correlation coefficient expresses the linear dependence between random variables, and when nonlinear transformations are applied to those random variables, linear correlation is not preserved. Instead, a rank correlation coefficient, such as Kendall's τ or Spearman's ρ, is more appropriate.

Roughly speaking, these rank correlations measure the degree to which large or small values of one random variable associate with large or small values of another. However, unlike the linear correlation coefficient, they measure the association only in terms of ranks. As a consequence, the rank correlation is preserved under any monotonic transformation. In particular, the transformation method just described preserves the rank correlation. Therefore, knowing the rank correlation of the bivariate normal Z exactly determines the rank correlation of the final transformed random variables, X. While the linear correlation coefficient, ρ, is still needed to parameterize the underlying bivariate normal, Kendall's τ or Spearman's ρ are more useful in describing the dependence between random variables, because they are invariant to the choice of marginal distribution.

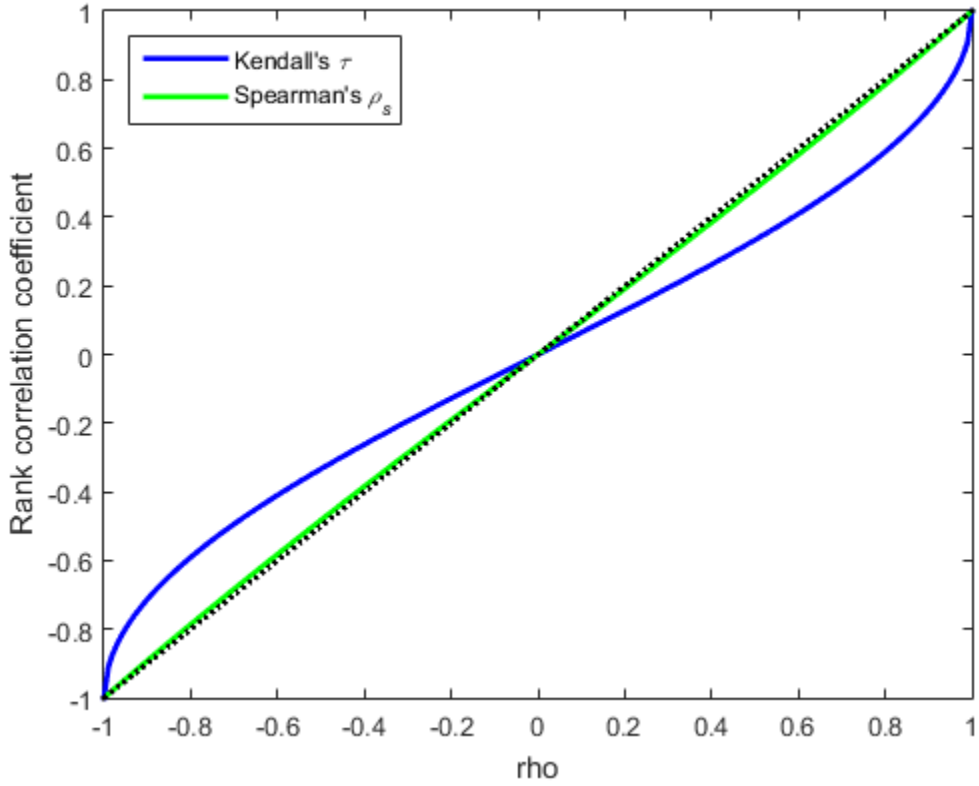
For the bivariate normal, there is a simple one-to-one mapping between Kendall's τ or Spearman's ρ, and the linear correlation coefficient ρ:

$$\tau = \frac{2}{\pi}\arcsin(\rho) \quad \text{or} \quad \rho = \sin\left(\tau\frac{\pi}{2}\right)$$

$$\rho_s = \frac{6}{\pi}\arcsin\left(\frac{\rho}{2}\right) \quad \text{or} \quad \rho = 2\sin\left(\rho_s\frac{\pi}{6}\right)$$

The following plot shows the relationship.

```
rho = -1:.01:1;
tau = 2.*asin(rho)./pi;
rho_s = 6.*asin(rho./2)./pi;

plot(rho,tau,'b-','LineWidth',2)
hold on
plot(rho,rho_s,'g-','LineWidth',2)
plot([-1 1],[-1 1],'k:','LineWidth',2)
axis([-1 1 -1 1])
xlabel('rho')
ylabel('Rank correlation coefficient')
legend('Kendall''s {\it\tau}', ...
       'Spearman''s {\it\rho_s}', ...
       'location','NW')
```



Thus, it is easy to create the desired rank correlation between `X1` and `X2`, regardless of their marginal distributions, by choosing the correct ρ parameter value for the linear correlation between `Z1` and `Z2`.

For the multivariate normal distribution, Spearman's rank correlation is almost identical to the linear correlation. However, this is not true once you transform to the final random variables.

Using Bivariate Copulas

The first step of the construction described in the previous section defines what is known as a bivariate Gaussian copula. A copula is a multivariate probability distribution, where each random variable has a uniform marginal distribution on the unit interval [0,1].

These variables may be completely independent, deterministically related (e.g., `U2 = U1`), or anything in between. Because of the possibility for dependence among variables, you can use a copula to construct a new multivariate distribution for dependent variables. By transforming each of the variables in the copula separately using the inversion method, possibly using different cdfs, the resulting distribution can have arbitrary marginal distributions. Such multivariate distributions are often useful in simulations, when you know that the different random inputs are not independent of each other.

Statistics and Machine Learning Toolbox functions compute:

- Probability density functions (`copulapdf`) and the cumulative distribution functions (`copulacdf`) for Gaussian copulas
- Rank correlations from linear correlations (`copulastat`) and vice versa (`copulaparam`)
- Random vectors (`copularnd`)
- Parameters for copulas fit to data (`copulafit`)

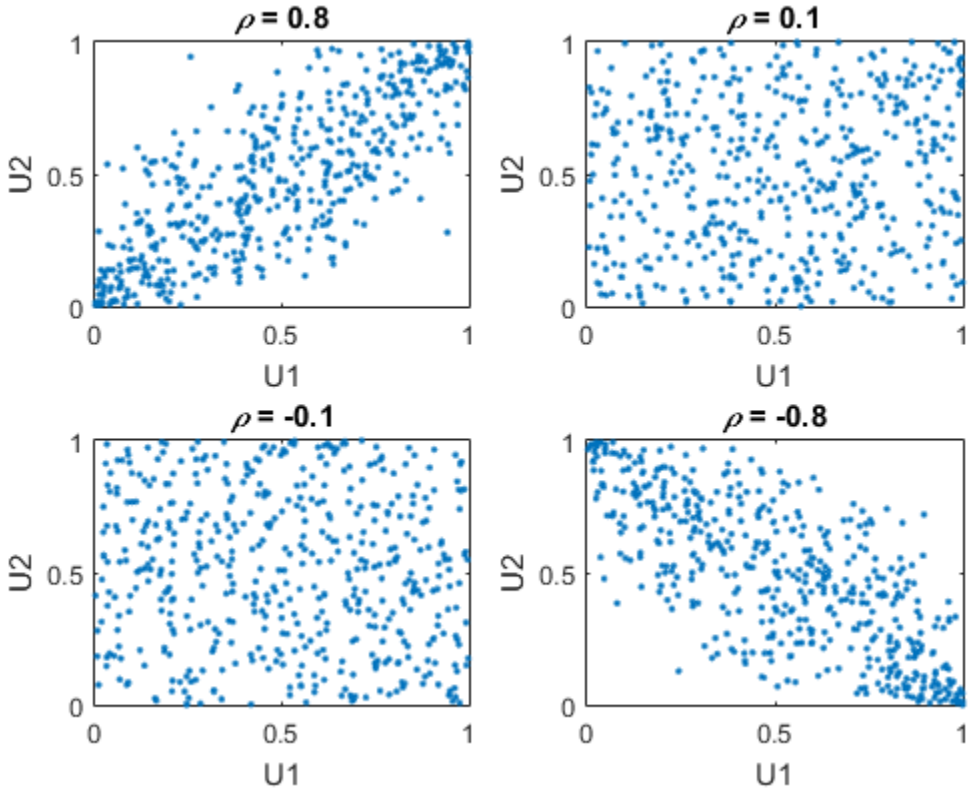
For example, use the `copularnd` function to create scatter plots of random values from a bivariate Gaussian copula for various levels of ρ, to illustrate the range of different dependence structures. The family of bivariate Gaussian copulas is parameterized by the linear correlation matrix:

$$P = \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}$$

`U1` and `U2` approach linear dependence as ρ approaches ±1, and approach complete independence as ρ approaches zero:

```
n = 500;

rng('default') % for reproducibility
U = copularnd('Gaussian',[1 .8; .8 1],n);
subplot(2,2,1)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.8')
xlabel('U1')
ylabel('U2')

U = copularnd('Gaussian',[1 .1; .1 1],n);
subplot(2,2,2)
```

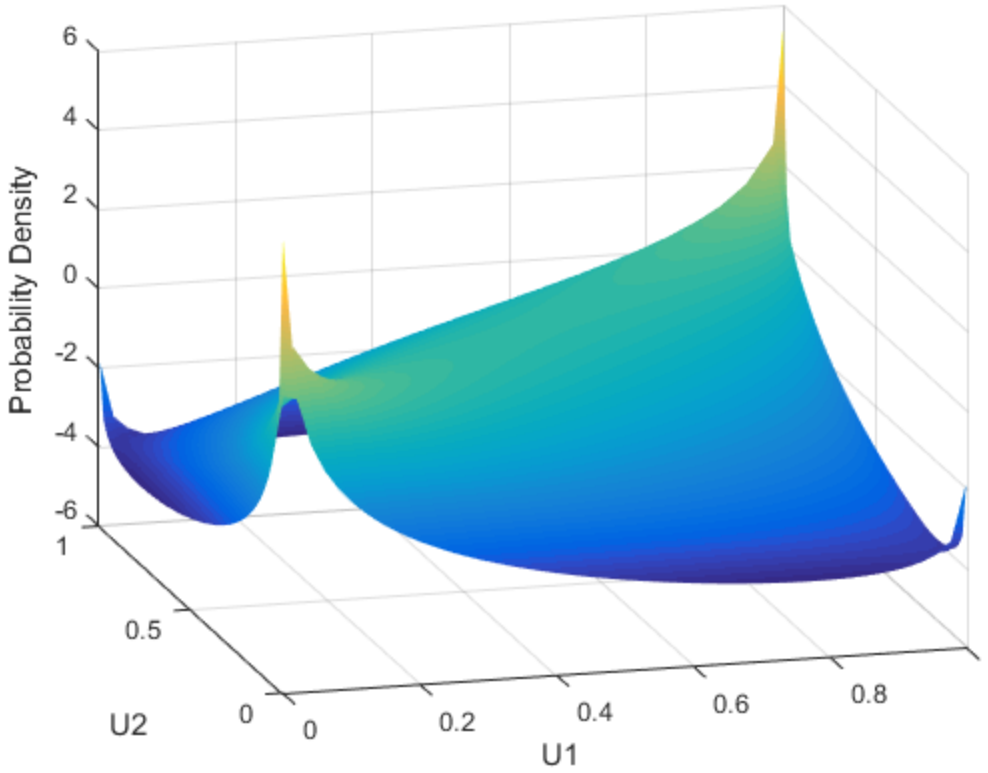
```
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('Gaussian',[1 -.1; -.1 1],n);
subplot(2,2,3)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('Gaussian',[1 -.8; -.8 1],n);
subplot(2,2,4)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.8')
xlabel('U1')
ylabel('U2')
```



The dependence between `U1` and `U2` is completely separate from the marginal distributions of `X1 = G(U1)` and `X2 = G(U2)`. `X1` and `X2` can be given any marginal distributions, and still have the same rank correlation. This is one of the main appeals of copulas—they allow this separate specification of dependence and marginal distribution. You can also compute the pdf (`copulapdf`) and the cdf (`copulacdf`) for a copula. For example, these plots show the pdf and cdf for $\rho = .8$:

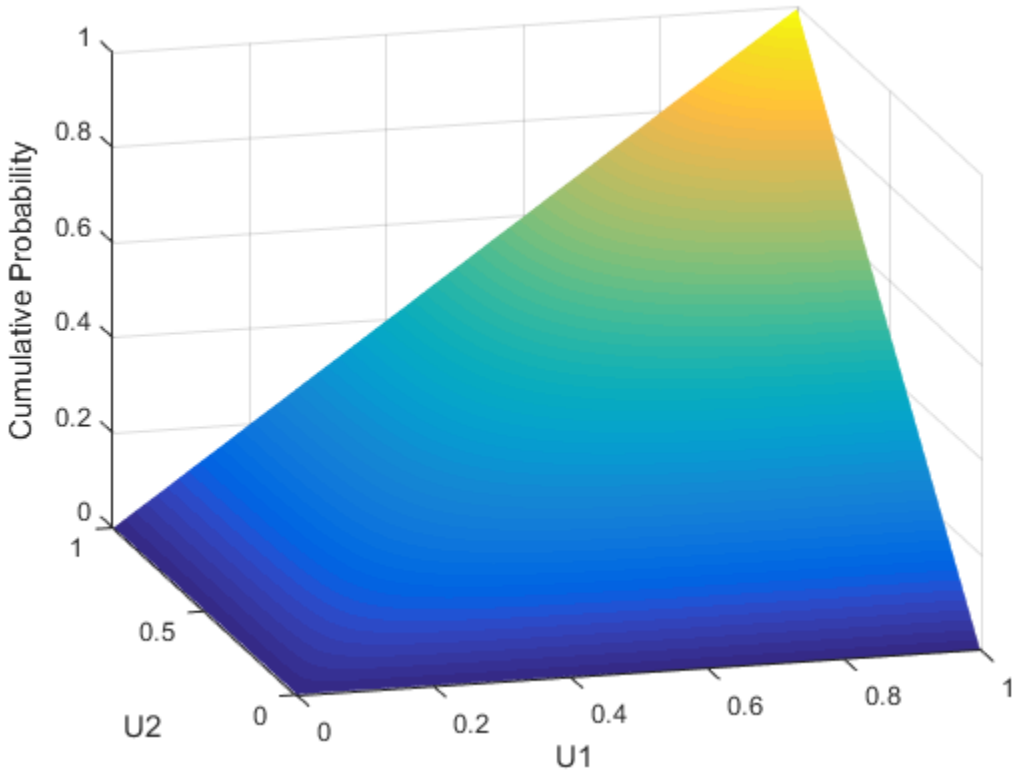
```
u1 = linspace(1e-3,1-1e-3,50);
u2 = linspace(1e-3,1-1e-3,50);
[U1,U2] = meshgrid(u1,u2);
Rho = [1 .8; .8 1];
f = copulapdf('t',[U1(:) U2(:)],Rho,5);
f = reshape(f,size(U1));
```

```
figure()
surf(u1,u2,log(f),'FaceColor','interp','EdgeColor','none')
view([-15,20])
xlabel('U1')
ylabel('U2')
zlabel('Probability Density')
```




```
u1 = linspace(1e-3,1-1e-3,50);
u2 = linspace(1e-3,1-1e-3,50);
[U1,U2] = meshgrid(u1,u2);
F = copulacdf('t',[U1(:) U2(:)],Rho,5);
F = reshape(F,size(U1));
```

```
figure()
surf(u1,u2,F,'FaceColor','interp','EdgeColor','none')
view([-15,20])
xlabel('U1')
ylabel('U2')
zlabel('Cumulative Probability')
```



A different family of copulas can be constructed by starting from a bivariate t distribution and transforming using the corresponding t cdf. The bivariate t distribution is parameterized with P, the linear correlation matrix, and ν, the degrees of freedom. Thus, for example, you can speak of a t_1 or a t_5 copula, based on the multivariate t with one and five degrees of freedom, respectively.

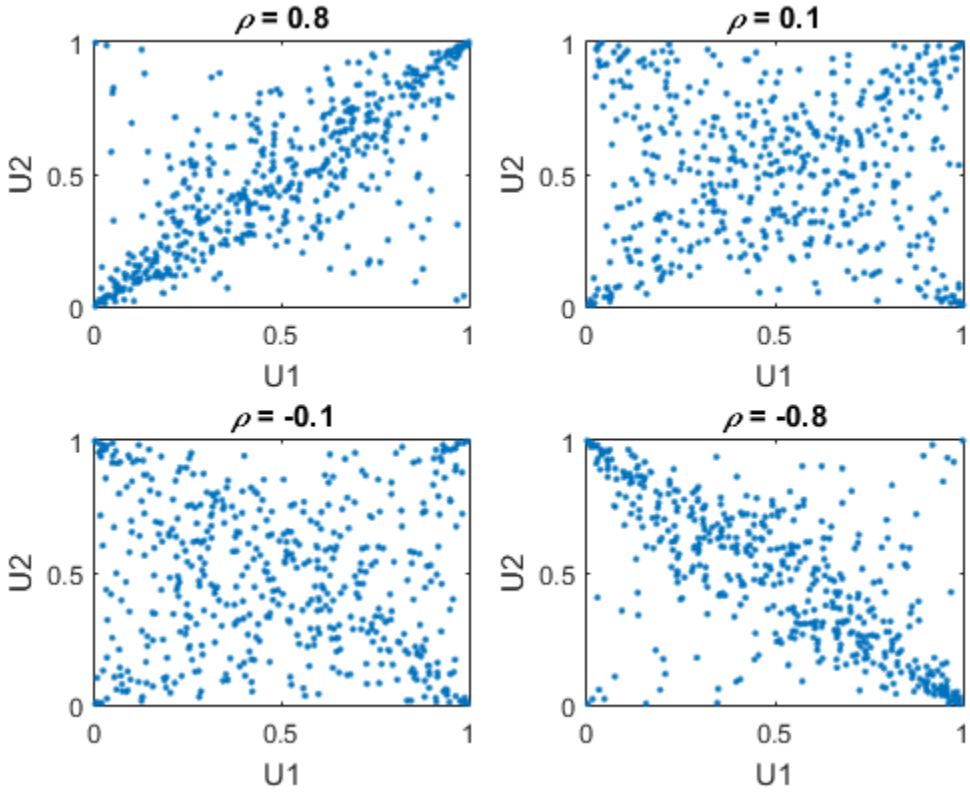
Just as for Gaussian copulas, Statistics and Machine Learning Toolbox functions for t copulas compute:

- Probability density functions (`copulapdf`) and the cumulative distribution functions (`copulacdf`) for Gaussian copulas
- Rank correlations from linear correlations (`copulastat`) and vice versa (`copulaparam`)
- Random vectors (`copularnd`)
- Parameters for copulas fit to data (`copulafit`)

For example, use the `copularnd` function to create scatter plots of random values from a bivariate t_1 copula for various levels of ρ, to illustrate the range of different dependence structures:

```
n = 500;
nu = 1;

rng('default') % for reproducibility
U = copularnd('t',[1 .8; .8 1],nu,n);
subplot(2,2,1)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.8')
xlabel('U1')
ylabel('U2')

U = copularnd('t',[1 .1; .1 1],nu,n);
subplot(2,2,2)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = 0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('t',[1 -.1; -.1 1],nu,n);
subplot(2,2,3)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.1')
xlabel('U1')
ylabel('U2')

U = copularnd('t',[1 -.8; -.8 1],nu, n);
subplot(2,2,4)
plot(U(:,1),U(:,2),'.')
title('{\it\rho} = -0.8')
```

```
xlabel('U1')
ylabel('U2')
```

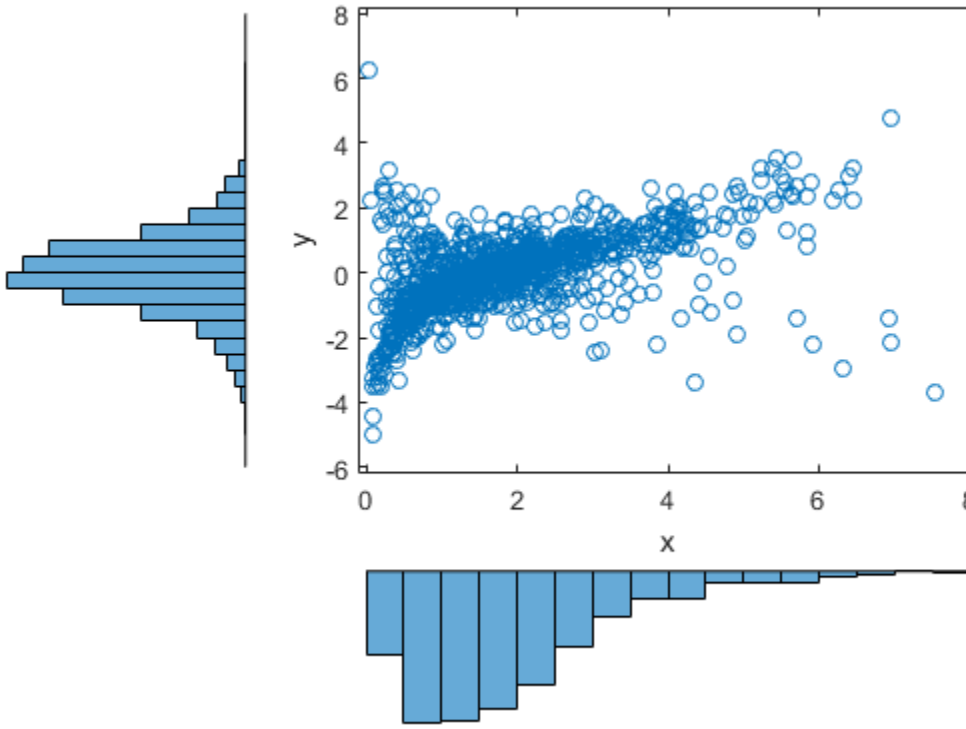


A t copula has uniform marginal distributions for `U1` and `U2`, just as a Gaussian copula does. The rank correlation τ or ρ_s between components in a t copula is also the same function of ρ as for a Gaussian. However, as these plots demonstrate, a t_1 copula differs quite a bit from a Gaussian copula, even when their components have the same rank correlation. The difference is in their dependence structure. Not surprisingly, as the degrees of freedom parameter ν is made larger, a t_ν copula approaches the corresponding Gaussian copula.

As with a Gaussian copula, any marginal distributions can be imposed over a t copula. For example, using a t copula with 1 degree of freedom, you can again generate

random vectors from a bivariate distribution with Gamma(2,1) and t_5 marginals using `copularnd`:

```
n = 1000;
rho = .7;
nu = 1;

rng('default') % for reproducibility
U = copularnd('t',[1 rho; rho 1],nu,n);
X = [gaminv(U(:,1),2,1) tinv(U(:,2),5)];

figure()
scatterhist(X(:,1),X(:,2),'Direction','out')
```



Compared to the bivariate Gamma/t distribution constructed earlier, which was based on a Gaussian copula, the distribution constructed here, based on a t_1 copula, has the same marginal distributions and the same rank correlation between variables but a very different dependence structure. This illustrates the fact that multivariate distributions are not uniquely defined by their marginal distributions, or by their correlations. The choice of a particular copula in an application may be based on actual observed data, or different copulas may be used as a way of determining the sensitivity of simulation results to the input distribution.

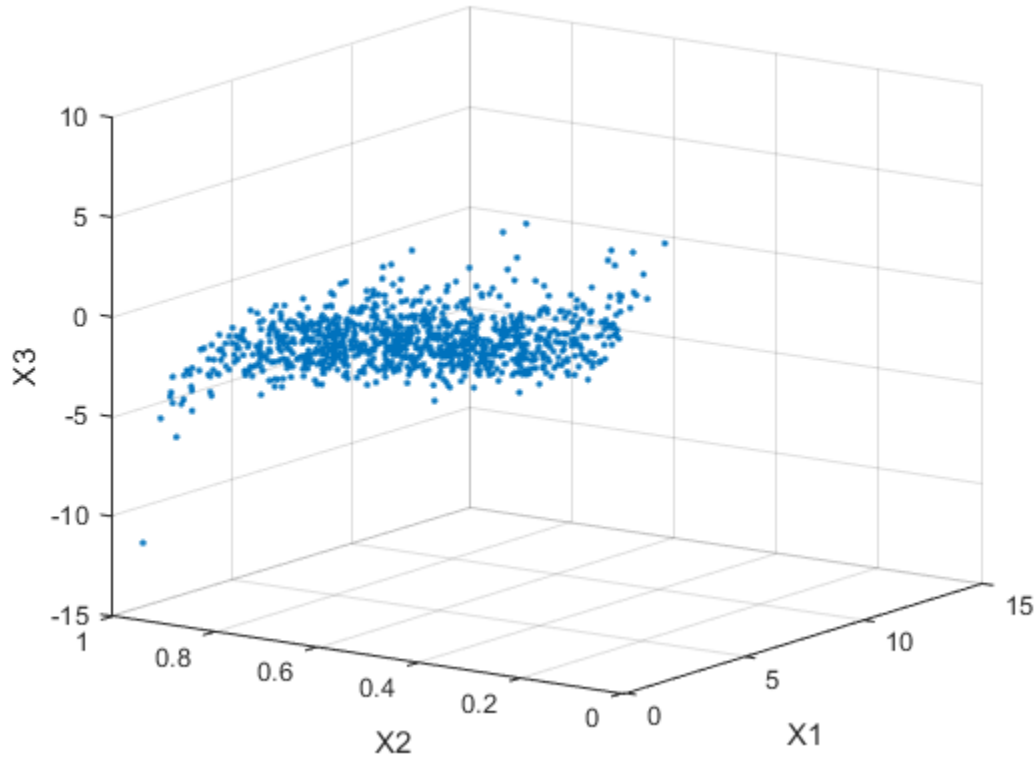
Higher Dimension Copulas

The Gaussian and t copulas are known as elliptical copulas. It is easy to generalize elliptical copulas to a higher number of dimensions. For example, simulate data from a trivariate distribution with Gamma(2,1), Beta(2,2), and t_5 marginals using a Gaussian copula and `copularnd`, as follows:

```
n = 1000;
Rho = [1 .4 .2; .4 1 -.8; .2 -.8 1];
rng('default') % for reproducibility
U = copularnd('Gaussian',Rho,n);
X = [gaminv(U(:,1),2,1) betainv(U(:,2),2,2) tinv(U(:,3),5)];
```

Plot the data.

```
subplot(1,1,1)
plot3(X(:,1),X(:,2),X(:,3),'.')
grid on
view([-55, 15])
xlabel('X1')
ylabel('X2')
zlabel('X3')
```



Notice that the relationship between the linear correlation parameter ρ and, for example, Kendall's τ, holds for each entry in the correlation matrix P used here. You can verify that the sample rank correlations of the data are approximately equal to the theoretical values:

```
tauTheoretical = 2.*asin(Rho)./pi
```

```
tauTheoretical =

    1.0000    0.2620    0.1282
    0.2620    1.0000   -0.5903
    0.1282   -0.5903    1.0000
```

```
tauSample = corr(X,'type','Kendall')


tauSample =

    1.0000    0.2581    0.1414
    0.2581    1.0000   -0.5790
    0.1414   -0.5790    1.0000
```

Archimedean Copulas

Statistics and Machine Learning Toolbox functions are available for three bivariate Archimedean copula families:

- Clayton copulas
- Frank copulas
- Gumbel copulas

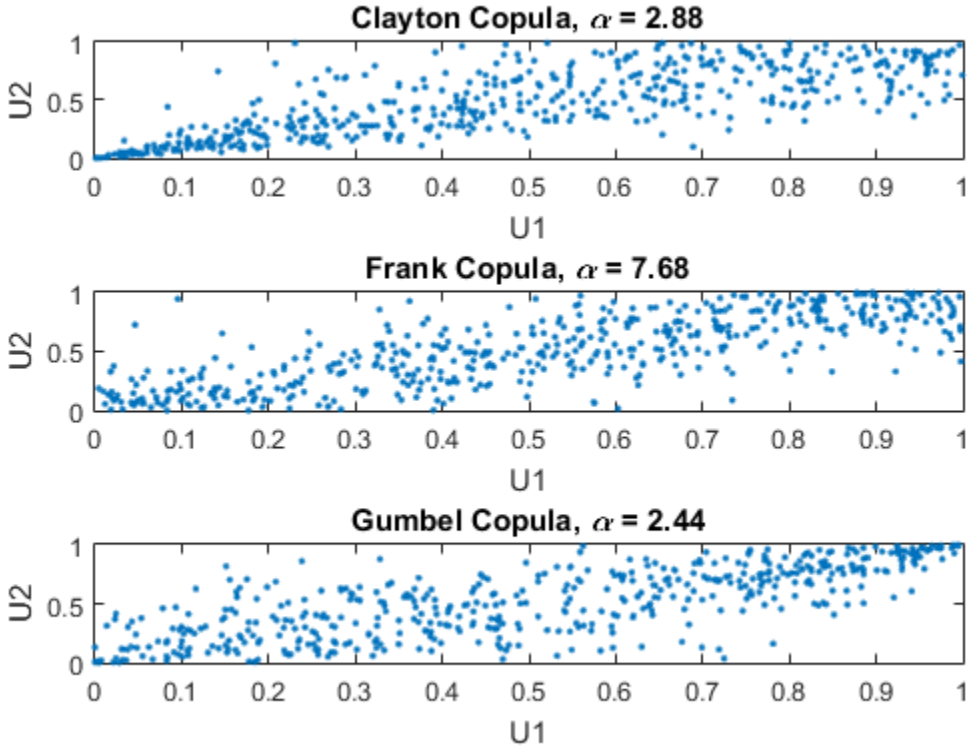
These are one-parameter families that are defined directly in terms of their cdfs, rather than being defined constructively using a standard multivariate distribution.

To compare these three Archimedean copulas to the Gaussian and *t* bivariate copulas, first use the `copulastat` function to find the rank correlation for a Gaussian or *t* copula with linear correlation parameter of 0.8, and then use the `copulaparam` function to find the Clayton copula parameter that corresponds to that rank correlation:

```
tau = copulastat('Gaussian',.8 ,'type','kendall')


tau =

    0.5903


alpha = copulaparam('Clayton',tau,'type','kendall')


alpha =

    2.8820
```

Finally, plot a random sample from the Clayton copula with `copularnd`. Repeat the same procedure for the Frank and Gumbel copulas:

```
n = 500;

U = copularnd('Clayton',alpha,n);
subplot(3,1,1)
plot(U(:,1),U(:,2),'.');
title(['Clayton Copula, {\it\alpha} = ',sprintf('%0.2f',alpha)])
xlabel('U1')
ylabel('U2')

alpha = copulaparam('Frank',tau,'type','kendall');
U = copularnd('Frank',alpha,n);
subplot(3,1,2)
plot(U(:,1),U(:,2),'.')
title(['Frank Copula, {\it\alpha} = ',sprintf('%0.2f',alpha)])
xlabel('U1')
ylabel('U2')

alpha = copulaparam('Gumbel',tau,'type','kendall');
U = copularnd('Gumbel',alpha,n);
subplot(3,1,3)
plot(U(:,1),U(:,2),'.')
title(['Gumbel Copula, {\it\alpha} = ',sprintf('%0.2f',alpha)])
xlabel('U1')
ylabel('U2')
```



Simulating Dependent Multivariate Data Using Copulas

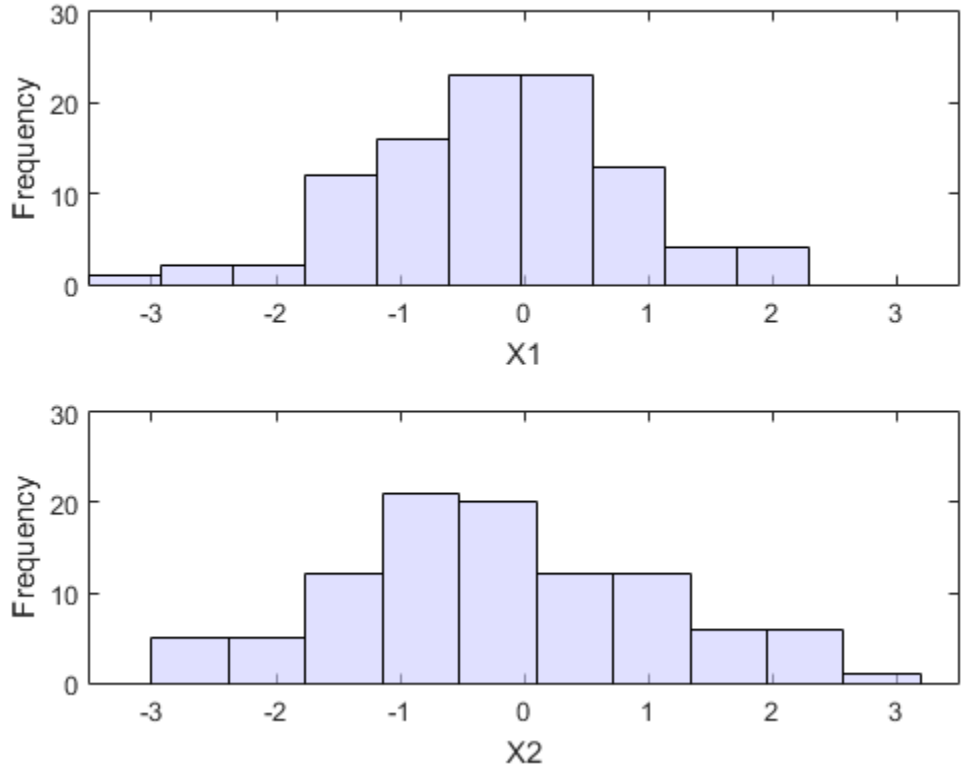
To simulate dependent multivariate data using a copula, you must specify each of the following:

- The copula family (and any shape parameters)
- The rank correlations among variables
- Marginal distributions for each variable

Suppose you have return data for two stocks and want to run a Monte Carlo simulation with inputs that follow the same distributions as the data:

```
load stockreturns
```

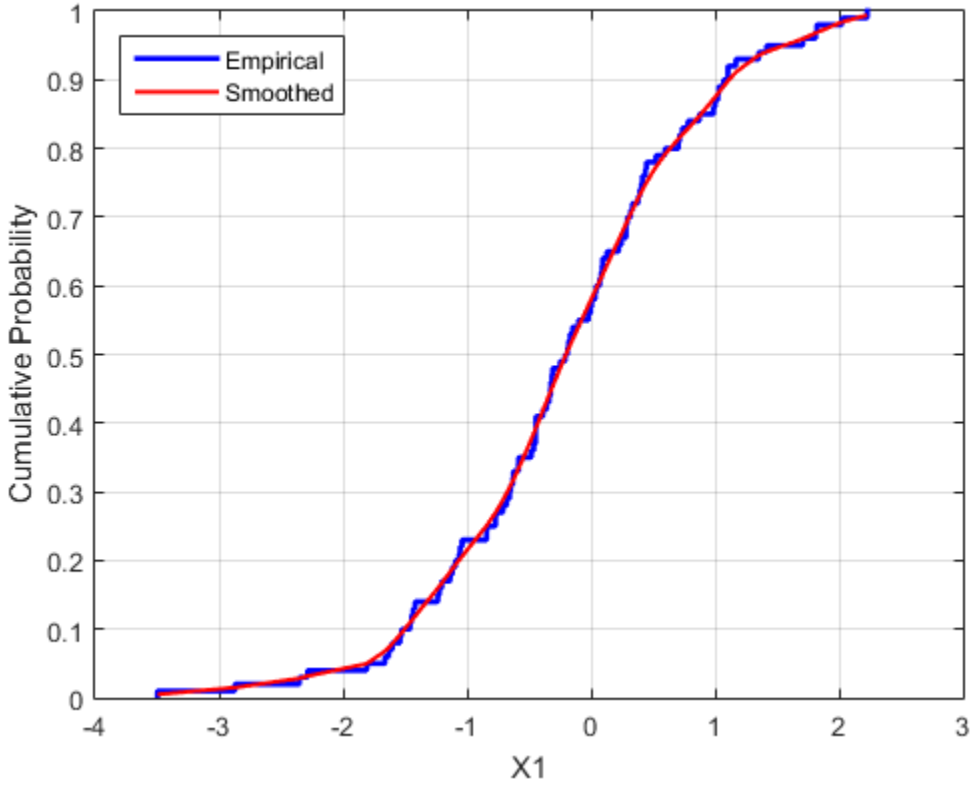
```
nobs = size(stocks,1);

subplot(2,1,1)
histogram(stocks(:,1),10,'FaceColor',[.8 .8 1])
xlim([-3.5 3.5])
xlabel('X1')
ylabel('Frequency')

subplot(2,1,2)
histogram(stocks(:,2),10,'FaceColor',[.8 .8 1])
xlim([-3.5 3.5])
xlabel('X2')
ylabel('Frequency')
```



You could fit a parametric model separately to each dataset, and use those estimates as the marginal distributions. However, a parametric model may not be sufficiently flexible. Instead, you can use a nonparametric model to transform to the marginal distributions. All that is needed is a way to compute the inverse cdf for the nonparametric model.

The simplest nonparametric model is the empirical cdf, as computed by the `ecdf` function. For a discrete marginal distribution, this is appropriate. However, for a continuous distribution, use a model that is smoother than the step function computed by `ecdf`. One way to do that is to estimate the empirical cdf and interpolate between the midpoints of the steps with a piecewise linear function. Another way is to use kernel smoothing with `ksdensity`. For example, compare the empirical cdf to a kernel smoothed cdf estimate for the first variable:

```
[Fi,xi] = ecdf(stocks(:,1));

figure()
stairs(xi,Fi,'b','LineWidth',2)
hold on

Fi_sm = ksdensity(stocks(:,1),xi,'function','cdf','width',.15);

plot(xi,Fi_sm,'r-','LineWidth',1.5)
xlabel('X1')
ylabel('Cumulative Probability')
legend('Empirical','Smoothed','Location','NW')
grid on
```



For the simulation, experiment with different copulas and correlations. Here, you will use a bivariate *t* copula with a fairly small degrees of freedom parameter. For the correlation parameter, you can compute the rank correlation of the data.

```
nu = 5;
tau = corr(stocks(:,1),stocks(:,2),'type','kendall')
```

```
tau =

    0.5180
```

Find the corresponding linear correlation parameter for the *t* copula using `copulaparam`.

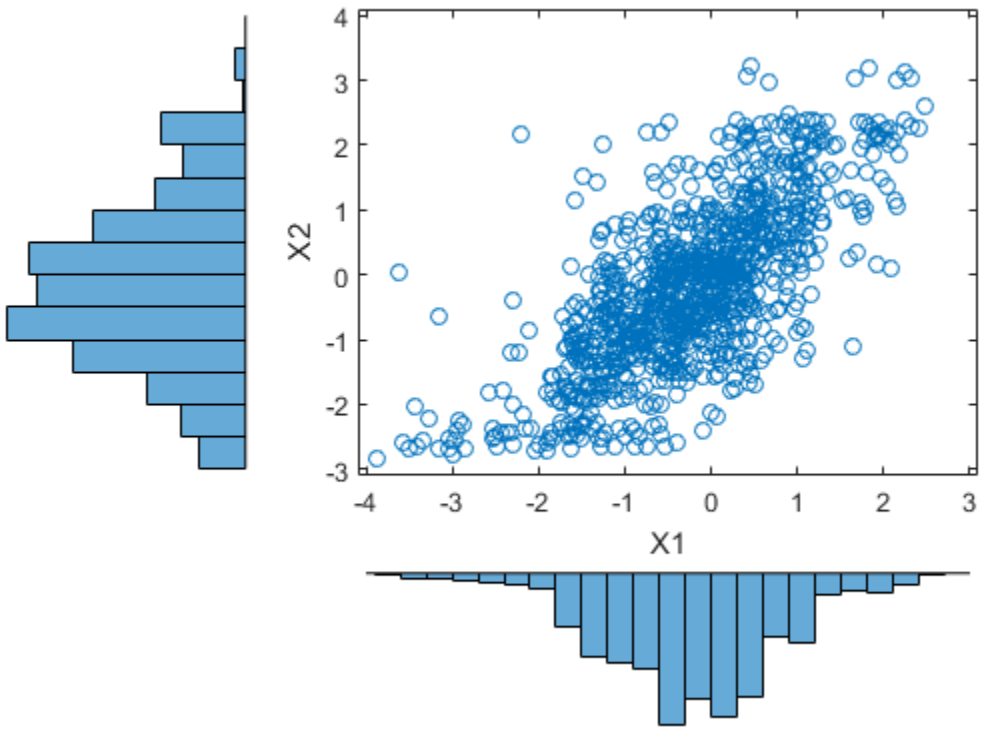
```
rho = copulaparam('t', tau, nu, 'type','kendall')


rho =

    0.7268
```

Next, use `copularnd` to generate random values from the *t* copula and transform using the nonparametric inverse cdfs. The `ksdensity` function allows you to make a kernel estimate of distribution and evaluate the inverse cdf at the copula points all in one step:

```
n = 1000;
U = copularnd('t',[1 rho; rho 1],nu,n);

X1 = ksdensity(stocks(:,1),U(:,1),...
               'function','icdf','width',.15);
X2 = ksdensity(stocks(:,2),U(:,2),...
               'function','icdf','width',.15);
```

Alternatively, when you have a large amount of data or need to simulate more than one set of values, it may be more efficient to compute the inverse cdf over a grid of values in the interval (0,1) and use interpolation to evaluate it at the copula points:

```
p = linspace(0.00001,0.99999,1000);
G1 = ksdensity(stocks(:,1),p,'function','icdf','width',0.15);
X1 = interp1(p,G1,U(:,1),'spline');
G2 = ksdensity(stocks(:,2),p,'function','icdf','width',0.15);
X2 = interp1(p,G2,U(:,2),'spline');

scatterhist(X1,X2,'Direction','out')
```



The marginal histograms of the simulated data are a smoothed version of the histograms for the original data. The amount of smoothing is controlled by the bandwidth input to `ksdensity`.

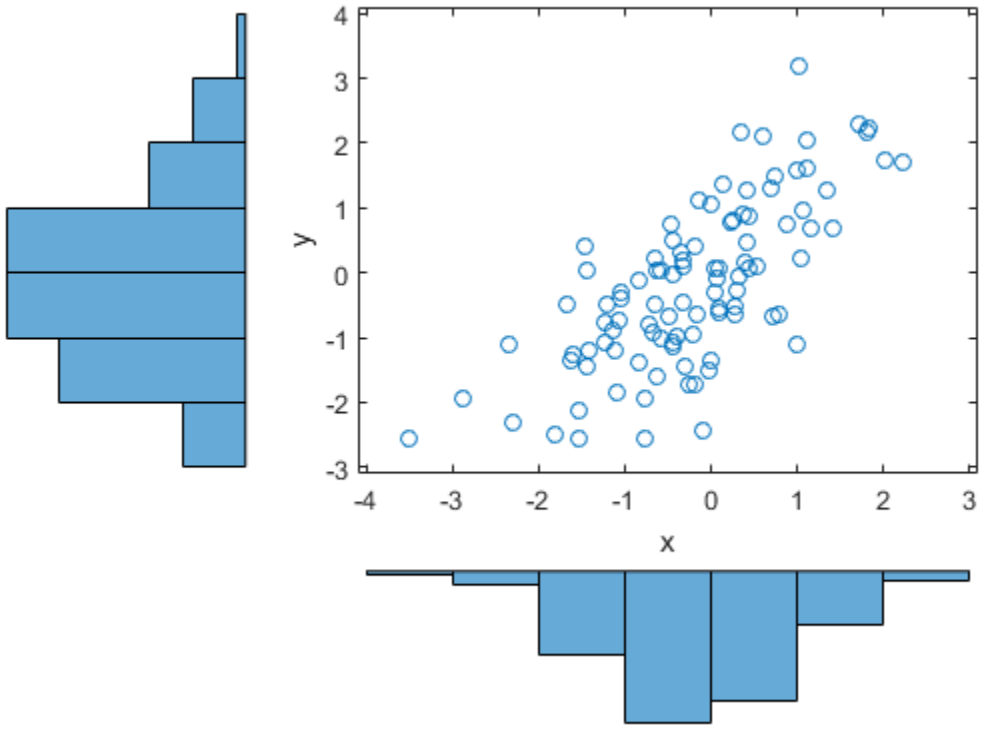
Fitting Copulas to Data

This example shows how to use `copulafit` to calibrate copulas with data. To generate data `Xsim` with a distribution "just like" (in terms of marginal distributions and correlations) the distribution of data in the matrix `X` , you need to fit marginal distributions to the columns of `X` , use appropriate cdf functions to transform `X` to `U` , so that `U` has values between 0 and 1, use `copulafit` to fit a copula to `U` , generate new

data `Usim` from the copula, and use appropriate inverse cdf functions to transform `Usim` to `Xsim` .

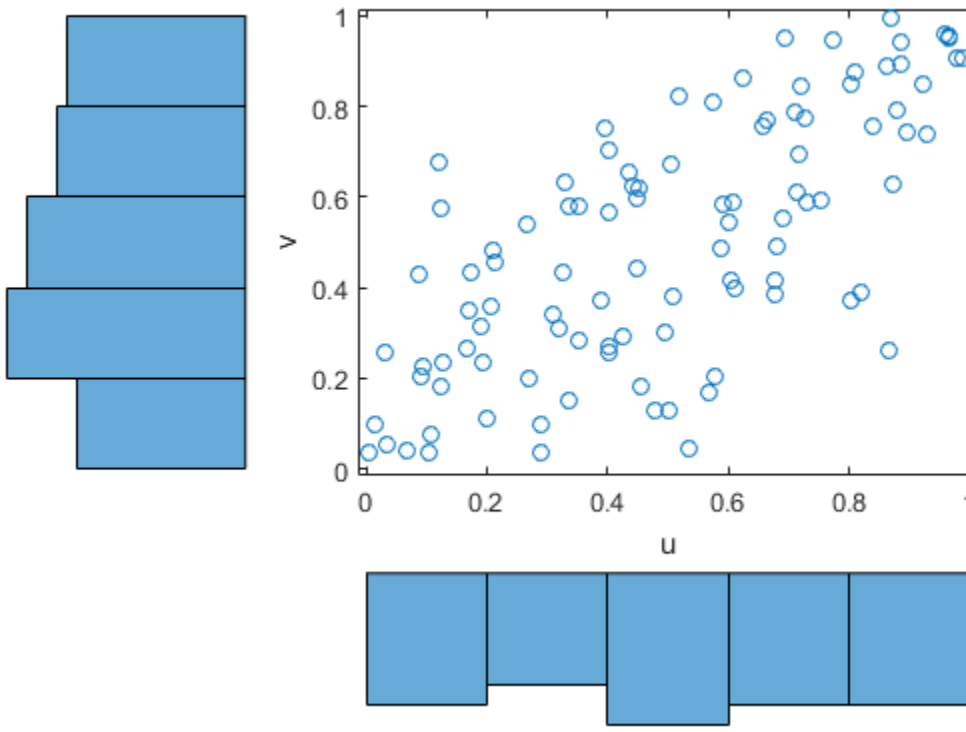
Load and plot the simulated stock return data.

```
load stockreturns
x = stocks(:,1);
y = stocks(:,2);

scatterhist(x,y,'Direction','out')
```



Transform the data to the copula scale (unit square) using a kernel estimator of the cumulative distribution function.

```
u = ksdensity(x,x,'function','cdf');
v = ksdensity(y,y,'function','cdf');

scatterhist(u,v,'Direction','out')
xlabel('u')
ylabel('v')
```



Fit a *t* copula.

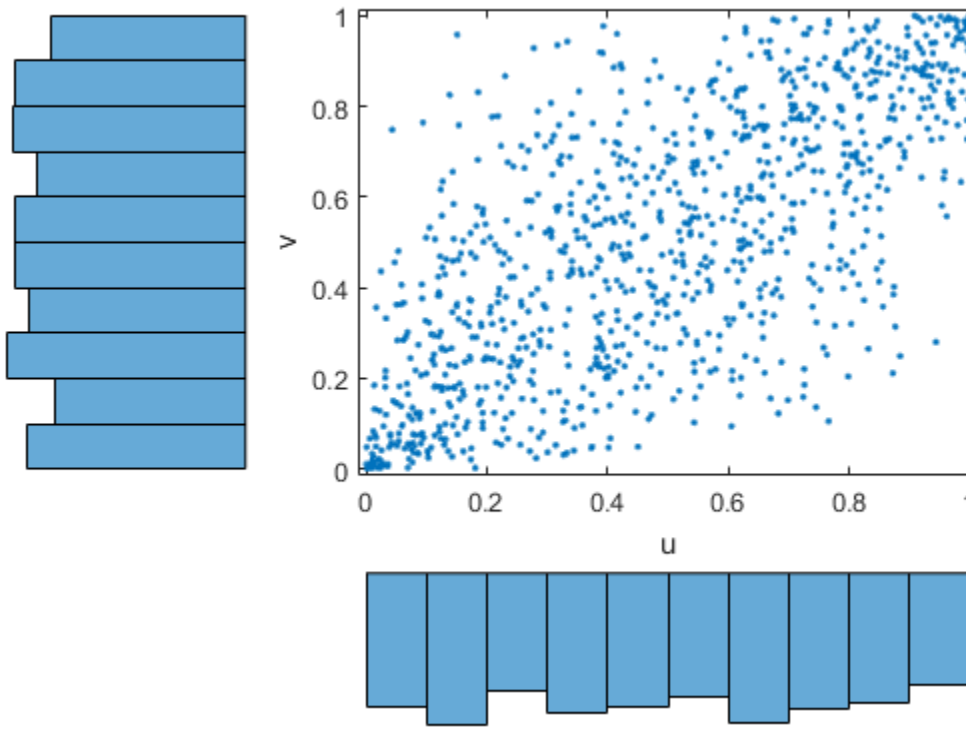
```
[Rho,nu] = copulafit('t',[u v],'Method','ApproximateML')
```

```
Rho =
```

```
    1.0000    0.7220
    0.7220    1.0000


nu =

   2.6133e+06
```

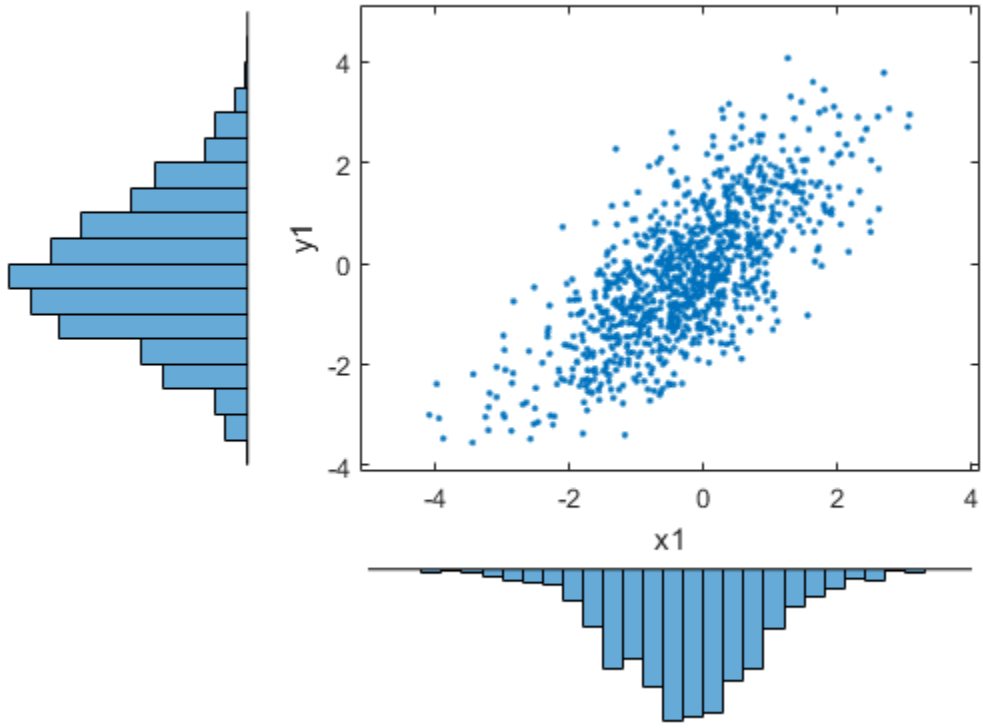
Generate a random sample from the *t* copula.

```
r = copularnd('t',Rho,nu,1000);
u1 = r(:,1);
v1 = r(:,2);

scatterhist(u1,v1,'Direction','out')
xlabel('u')
ylabel('v')
set(get(gca,'children'),'marker','.')
```



Transform the random sample back to the original scale of the data.

```
x1 = ksdensity(x,u1,'function','icdf');
y1 = ksdensity(y,v1,'function','icdf');

scatterhist(x1,y1,'Direction','out')
set(get(gca,'children'),'marker','.')
```



As the example illustrates, copulas integrate naturally with other distribution fitting functions.

6

Random Number Generation

Generating Random Data

Pseudorandom numbers are generated by deterministic algorithms. They are "random" in the sense that, on average, they pass statistical tests regarding their distribution and correlation. They differ from true random numbers in that they are generated by an algorithm, rather than a truly random process.

Random number generators (RNGs) like those in MATLAB are algorithms for generating pseudorandom numbers with a specified distribution.

For more information on the GUI for generating random numbers from supported distributions, see “Explore the Random Number Generation UI” on page 5-114.

Random Number Generation Functions

The following table lists the supported distributions and their respective random number generation functions.

Distribution	Random Number Generation Function
Beta	`betarnd`, `random`, `randtool`
Binomial	`binornd`, `random`, `randtool`
Chi-square	`chi2rnd`, `random`, `randtool`
Clayton copula	`copularnd`
Exponential	`exprnd`, `random`, `randtool`
Extreme value	`evrnd`, `random`, `randtool`
F	`frnd`, `random`, `randtool`
Frank copula	`copularnd`
Gamma	`gamrnd`, `randg`, `random`, `randtool`
Gaussian copula	`copularnd`
Gaussian mixture	`random`
Generalized extreme value	`gevrnd`, `random`, `randtool`
Generalized Pareto	`gprnd`, `random`, `randtool`
Geometric	`geornd`, `random`, `randtool`
Gumbel copula	`copularnd`
Hypergeometric	`hygernd`, `random`
Inverse Wishart	`iwishrnd`
Johnson system	`johnsrnd`
Lognormal	`lognrnd`, `random`, `randtool`
Multinomial	`mnrnd`
Multivariate normal	`mvnrnd`
Multivariate *t*	`mvtrnd`
Negative binomial	`nbinrnd`, `random`, `randtool`

Distribution	Random Number Generation Function
Noncentral chi-square	`ncx2rnd`, `random`, `randtool`
Noncentral F	`ncfrnd`, `random`, `randtool`
Noncentral t	`nctrnd`, `random`, `randtool`
Normal (Gaussian)	`normrnd`, `randn`, `random`, `randtool`
Pearson system	`pearsrnd`
Piecewise	`random`
Poisson	`poissrnd`, `random`, `randtool`
Rayleigh	`raylrnd`, `random`, `randtool`
Student's t	`trnd`, `random`, `randtool`
t copula	`copularnd`
Uniform (continuous)	`unifrnd`, `rand`, `random`
Uniform (discrete)	`unidrnd`, `random`, `randtool`
Weibull	`wblrnd`, `random`
Wishart	`wishrnd`

Common Generation Methods

In this section...

Methods for generating pseudorandom numbers usually start with uniform random numbers, like the MATLAB `rand` function produces. The methods described in this section detail how to produce random numbers from other distributions.

Direct Methods

Direct methods directly use the definition of the distribution.

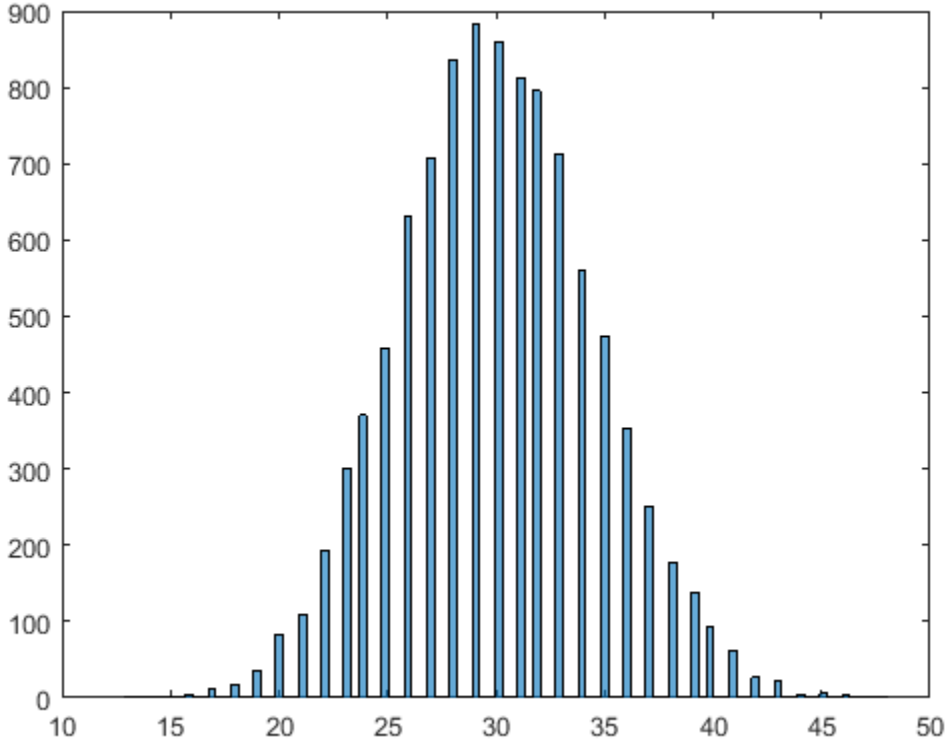
For example, consider binomial random numbers. A binomial random number is the number of heads in N tosses of a coin with probability p of a heads on any single toss. If you generate N uniform random numbers on the interval (0,1) and count the number less than p, then the count is a binomial random number with parameters N and p.

This function is a simple implementation of a binomial RNG using the direct approach:

```
function X = directbinornd(N,p,m,n)

X = zeros(m,n); % Preallocate memory
  for i = 1:m*n
    u = rand(N,1);
    X(i) = sum(u < p);
 end

end
```

For example:

```
X = directbinornd(100,0.3,1e4,1);
histogram(X,101)
```



The Statistics and Machine Learning Toolbox function `binornd` uses a modified direct method, based on the definition of a binomial random variable as the sum of Bernoulli random variables.

You can easily convert the previous method to a random number generator for the Poisson distribution with parameter λ. The Poisson distribution is the limiting case of the binomial distribution as N approaches infinity, p approaches zero, and Np is held fixed at λ. To generate Poisson random numbers, create a version of the previous generator that inputs λ rather than N and p, and internally sets N to some large number and p to λ/N.

The Statistics and Machine Learning Toolbox function `poissrnd` actually uses two direct methods:

- A waiting time method for small values of λ
- A method due to Ahrens and Dieter for larger values of λ

Inversion Methods

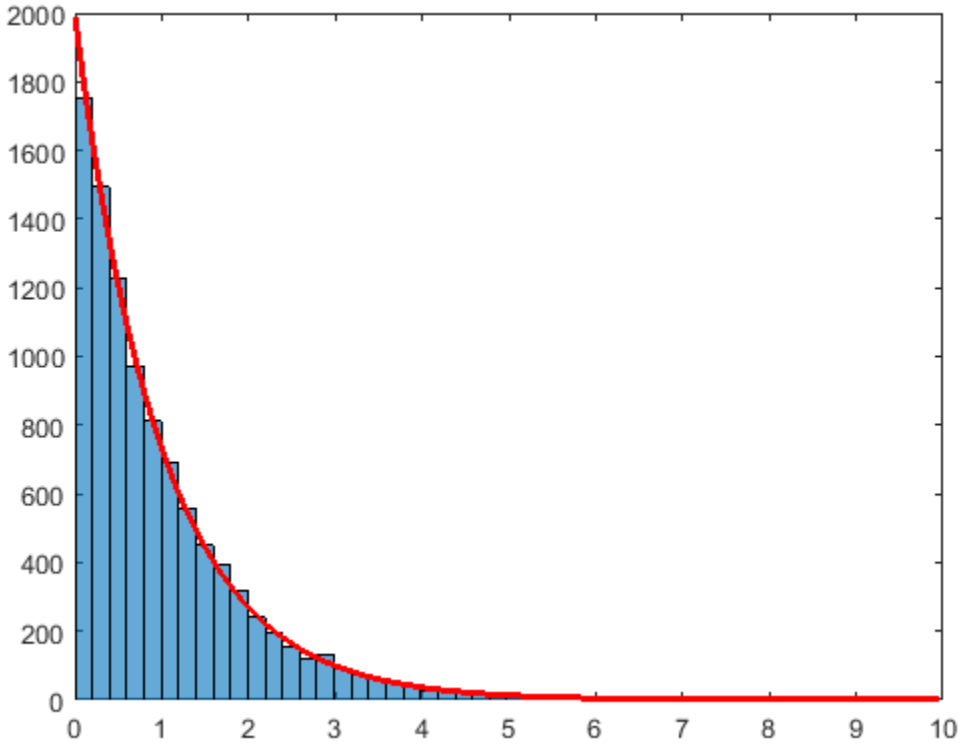
Inversion methods are based on the observation that continuous cumulative distribution functions (cdfs) range uniformly over the interval (0,1). If u is a uniform random number on (0,1), then using $X = F^{-1}(U)$ generates a random number X from a continuous distribution with specified cdf F.

For example, the following code generates random numbers from a specific exponential distribution using the inverse cdf and the MATLAB uniform random number generator `rand`:

```
mu = 1;
X = expinv(rand(1e4,1),mu);
```

Compare the distribution of the generated random numbers to the pdf of the specified exponential by scaling the pdf to the area of the histogram used to display the distribution:

```
numbins = 50;
h = histogram(X,numbins)
hold on

histarea = h.BinWidth*sum(h.Values);

x = h.BinEdges(1):0.001:h.BinEdges(end);
y = exppdf(x,mu);
plot(x,histarea*y,'r','LineWidth',2)
```



Inversion methods also work for discrete distributions. To generate a random number X from a discrete distribution with probability mass vector $P(X=x_i) = p_i$ where $x_0<x_1< x_2<...$, generate a uniform random number u on (0,1) and then set $X = x_i$ if $F(x_{i-1})<u<F(x_i)$.

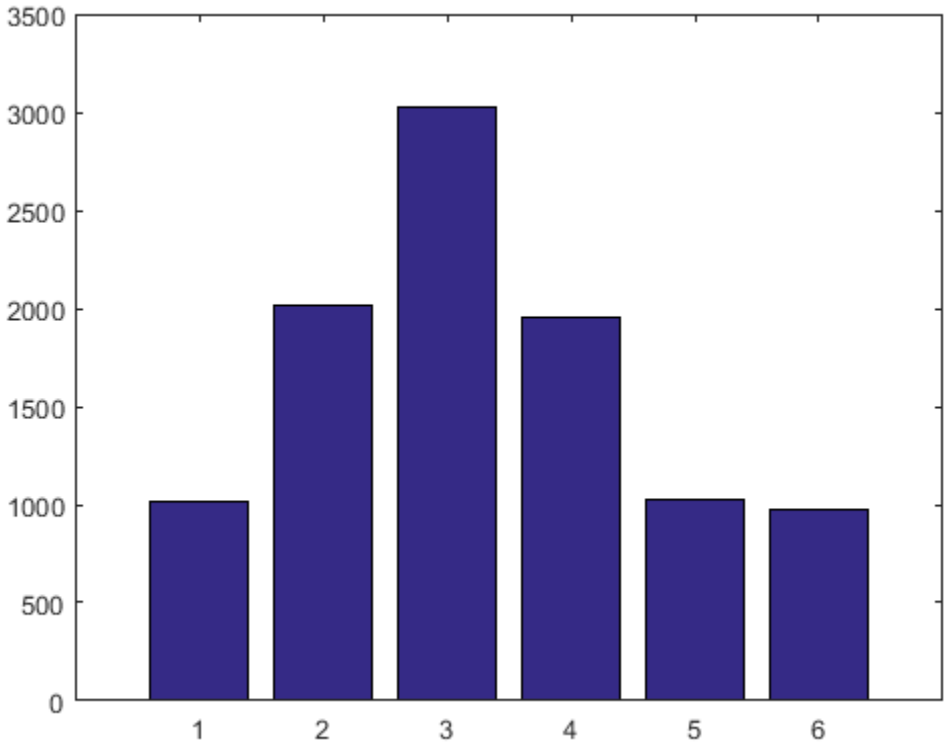
For example, the following function implements an inversion method for a discrete distribution with probability mass vector p:

```
function X = discreteinvrnd(p,m,n)

  X = zeros(m,n); % Preallocate memory
  for i = 1:m*n
    u = rand;
    I = find(u < cumsum(p));
    X(i) = min(I);
```

```
  end

end
```

Use the function to generate random numbers from any discrete distribution:

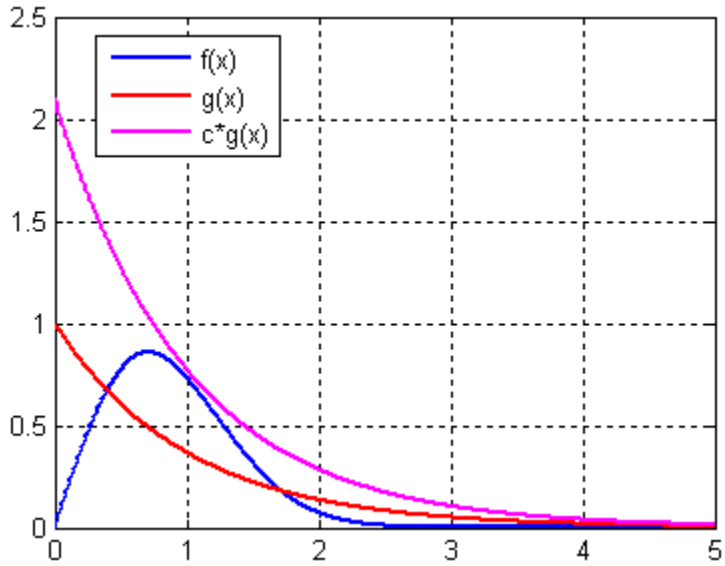
```
p = [0.1 0.2 0.3 0.2 0.1 0.1]; % Probability mass vector
X = discreteinvrnd(p,1e4,1);
h = histogram(X,length(p));
bar(1:length(p),h.Values)
```



Acceptance-Rejection Methods

The functional form of some distributions makes it difficult or time-consuming to generate random numbers using direct or inversion methods. Acceptance-rejection methods provide an alternative in these cases.

Acceptance-rejection methods begin with uniform random numbers, but require an additional random number generator. If your goal is to generate a random number from a continuous distribution with pdf f, acceptance-rejection methods first generate a random number from a continuous distribution with pdf g satisfying $f(x) \le cg(x)$ for some c and all x.



A continuous acceptance-rejection RNG proceeds as follows:

1. Chooses a density g.
2. Finds a constant c such that $f(x)/g(x) \le c$ for all x.
3. Generates a uniform random number u.
4. Generates a random number v from g.
5. If $cu \le f(v)/g(v)$, accepts and returns v.

6 Otherwise, rejects v and goes to step 3.

For efficiency, a "cheap" method is necessary for generating random numbers from g, and the scalar c should be small. The expected number of iterations to produce a single random number is c.

The following function implements an acceptance-rejection method for generating random numbers from pdf f, given f, g, the RNG `grnd` for g, and the constant c:

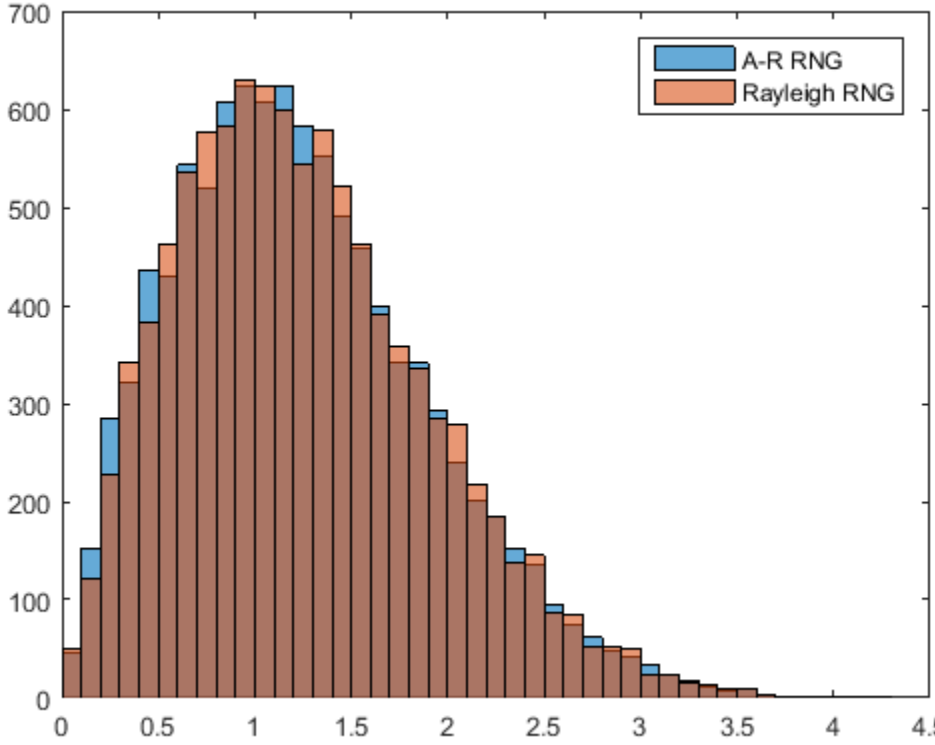
```
function X = accrejrnd(f,g,grnd,c,m,n)

X = zeros(m,n); % Preallocate memory
for i = 1:m*n
    accept = false;
    while accept == false
        u = rand();
        v = grnd();
        if c*u <= f(v)/g(v)
           X(i) = v;
           accept = true;
        end
    end
end
```

For example, the function $f(x) = xe^{-x^2/2}$ satisfies the conditions for a pdf on $[0,\infty)$ (nonnegative and integrates to 1). The exponential pdf with mean 1, $f(x) = e^{-x}$, dominates g for c greater than about 2.2. Thus, you can use `rand` and `exprnd` to generate random numbers from f:

```
f = @(x)x.*exp(-(x.^2)/2);
g = @(x)exp(-x);
grnd = @()exprnd(1);
X = accrejrnd(f,g,grnd,2.2,1e4,1);
```

The pdf f is actually a Rayleigh distribution with shape parameter 1. This example compares the distribution of random numbers generated by the acceptance-rejection method with those generated by `raylrnd`:

```
Y = raylrnd(1,1e4,1);
histogram(X)
hold on
histogram(Y)
legend('A-R RNG','Rayleigh RNG')
```



The Statistics and Machine Learning Toolbox function `raylrnd` uses a transformation method, expressing a Rayleigh random variable in terms of a chi-square random variable, which you compute using `randn`.

Acceptance-rejection methods also work for discrete distributions. In this case, the goal is to generate random numbers from a distribution with probability mass $P_p(X = i) = p_i$, assuming that you have a method for generating random numbers from a distribution with probability mass $P_q(X = i) = q_i$. The RNG proceeds as follows:

1. Chooses a density P_q.
2. Finds a constant c such that $p_i/q_i \leq c$ for all i .
3. Generates a uniform random number u.

4. Generates a random number v from P_q.
5. If $cu \le p_v/q_v$, accepts and returns v.
6. Otherwise, rejects v and goes to step 3.

Representing Sampling Distributions Using Markov Chain Samplers

In this section...

The methods in "Common Generation Methods" on page 6-5 might be inadequate when sampling distributions are difficult to represent in computations. Such distributions arise, for example, in Bayesian data analysis and in the large combinatorial problems of Markov chain Monte Carlo (MCMC) simulations. An alternative is to construct a Markov chain with a stationary distribution equal to the target sampling distribution, using the states of the chain to generate random numbers after an initial burn-in period in which the state distribution converges to the target.

Using the Metropolis-Hastings Algorithm

The Metropolis-Hastings algorithm draws samples from a distribution that is only known up to a constant. Random numbers are generated from a distribution with a probability density function that is equal to or proportional to a proposal function.

To generate random numbers:

1. Assume an initial value $x(t)$.
2. Draw a sample, $y(t)$, from a proposal distribution $q(y \mid x(t))$.
3. Accept $y(t)$ as the next sample $x(t + 1)$ with probability $r(x(t),y(t))$, and keep $x(t)$ as the next sample $x(t + 1)$ with probability $1 - r(x(t),y(t))$, where:

$$r(x,y) = min\left\{\frac{f(y)}{f(x)}\frac{q(x \mid y)}{q(y \mid x)}, 1\right\}$$

4. Increment $t \rightarrow t + 1$, and repeat steps 2 and 3 until you get the desired number of samples.

Generate random numbers using the Metropolis-Hastings method with the `mhsample` function. To produce quality samples efficiently with the Metropolis-Hastings algorithm, it is crucial to select a good proposal distribution. If it is difficult to find an efficient

proposal distribution, use the slice sampling algorithm (`slicesample`) without explicitly specifying a proposal distribution.

Using Slice Sampling

In instances where it is difficult to find an efficient Metropolis-Hastings proposal distribution, the slice sampling algorithm does not require an explicit specification. The slice sampling algorithm draws samples from the region under the density function using a sequence of vertical and horizontal steps. First, it selects a height at random from 0 to the density function $f(x)$. Then, it selects a new x value at random by sampling from the horizontal "slice" of the density above the selected height. A similar slice sampling algorithm is used for a multivariate distribution.

If a function $f(x)$ proportional to the density function is given, then do the following to generate random numbers:

1. Assume an initial value $x(t)$ within the domain of $f(x)$.
2. Draw a real value y uniformly from $(0, f(x(t)))$, thereby defining a horizontal "slice" as $S = \{x: y < f(x)\}$.
3. Find an interval $I = (L, R)$ around $x(t)$ that contains all, or much of the "slice" S.
4. Draw the new point $x(t + 1)$ within this interval.
5. Increment $t \rightarrow t + 1$ and repeat steps 2 through 4 until you get the desired number of samples.

Slice sampling can generate random numbers from a distribution with an arbitrary form of the density function, provided that an efficient numerical procedure is available to find the interval $I = (L,R)$, which is the "slice" of the density.

Generate random numbers using the slice sampling method with the `slicesample` function.

Generating Quasi-Random Numbers

In this section...

Quasi-Random Sequences

Quasi-random number generators (QRNGs) produce highly uniform samples of the unit hypercube. QRNGs minimize the *discrepancy* between the distribution of generated points and a distribution with equal proportions of points in each sub-cube of a uniform partition of the hypercube. As a result, QRNGs systematically fill the "holes" in any initial segment of the generated quasi-random sequence.

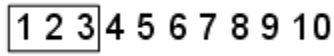
Unlike the pseudorandom sequences described in "Common Generation Methods" on page 6-5, quasi-random sequences fail many statistical tests for randomness. Approximating true randomness, however, is not their goal. Quasi-random sequences seek to fill space uniformly, and to do so in such a way that initial segments approximate this behavior up to a specified density.

QRNG applications include:

- **Quasi-Monte Carlo (QMC) integration.** Monte Carlo techniques are often used to evaluate difficult, multi-dimensional integrals without a closed-form solution. QMC uses quasi-random sequences to improve the convergence properties of these techniques.
- **Space-filling experimental designs.** In many experimental settings, taking measurements at every factor setting is expensive or infeasible. Quasi-random sequences provide efficient, uniform sampling of the design space.
- **Global optimization.** Optimization algorithms typically find a local optimum in the neighborhood of an initial value. By using a quasi-random sequence of initial values, searches for global optima uniformly sample the basins of attraction of all local minima.

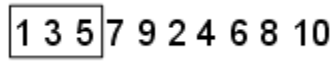
Example: Using Scramble, Leap, and Skip

Imagine a simple 1-D sequence that produces the integers from 1 to 10. This is the basic sequence and the first three points are `[1,2,3]`:

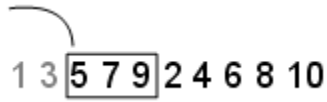


Now look at how `Scramble`, `Leap`, and `Skip` work together:

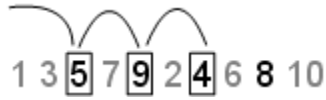
- `Scramble` — Scrambling shuffles the points in one of several different ways. In this example, assume a scramble turns the sequence into `1,3,5,7,9,2,4,6,8,10`. The first three points are now `[1,3,5]`:



- `Skip` — A `Skip` value specifies the number of initial points to ignore. In this example, set the `Skip` value to 2. The sequence is now `5,7,9,2,4,6,8,10` and the first three points are `[5,7,9]`:



- `Leap` — A `Leap` value specifies the number of points to ignore for each one you take. Continuing the example with the `Skip` set to 2, if you set the `Leap` to 1, the sequence uses every other point. In this example, the sequence is now `5,9,4,8` and the first three points are `[5,9,4]`:



Quasi-Random Point Sets

Statistics and Machine Learning Toolbox functions support these quasi-random sequences:

- **Halton sequences.** Produced by the `haltonset` function. These sequences use different prime bases to form successively finer uniform partitions of the unit interval in each dimension.

- **Sobol sequences.** Produced by the `sobolset` function. These sequences use a base of 2 to form successively finer uniform partitions of the unit interval, and then reorder the coordinates in each dimension.
- **Latin hypercube sequences.** Produced by the `lhsdesign` function. Though not quasi-random in the sense of minimizing discrepancy, these sequences nevertheless produce sparse uniform samples useful in experimental designs.

Quasi-random sequences are functions from the positive integers to the unit hypercube. To be useful in application, an initial *point set* of a sequence must be generated. Point sets are matrices of size n-by-d, where n is the number of points and d is the dimension of the hypercube being sampled. The functions `haltonset` and `sobolset` construct point sets with properties of a specified quasi-random sequence. Initial segments of the point sets are generated by the `net` method of the `qrandset` class (parent class of the `haltonset` class and `sobolset` class), but points can be generated and accessed more generally using parenthesis indexing.

Because of the way in which quasi-random sequences are generated, they may contain undesirable correlations, especially in their initial segments, and especially in higher dimensions. To address this issue, quasi-random point sets often *skip*, *leap* over, or *scramble* values in a sequence. The `haltonset` and `sobolset` functions allow you to specify both a `Skip` and a `Leap` property of a quasi-random sequence, and the `scramble` method of the `qrandset` class allows you apply a variety of scrambling techniques. Scrambling reduces correlations while also improving uniformity.

Generate a Quasi-Random Point Set

This example shows how to use `haltonset` to construct a 2-D Halton quasi-random point set.

Create a `haltonset` object `p`, that skips the first 1000 values of the sequence and then retains every 101st point.

```
rng default  % For reproducibility
p = haltonset(2,'Skip',1e3,'Leap',1e2)


p =

Halton point set in 2 dimensions (89180190640991 points)

Properties:
```

```
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

The object `p` encapsulates properties of the specified quasi-random sequence. The point set is finite, with a length determined by the `Skip` and `Leap` properties and by limits on the size of point set indices.

Use `scramble` to apply reverse-radix scrambling.

```
p = scramble(p,'RR2')
```

```
p =

Halton point set in 2 dimensions (89180190640991 points)

Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first 500 points.

```
X0 = net(p,500);
```

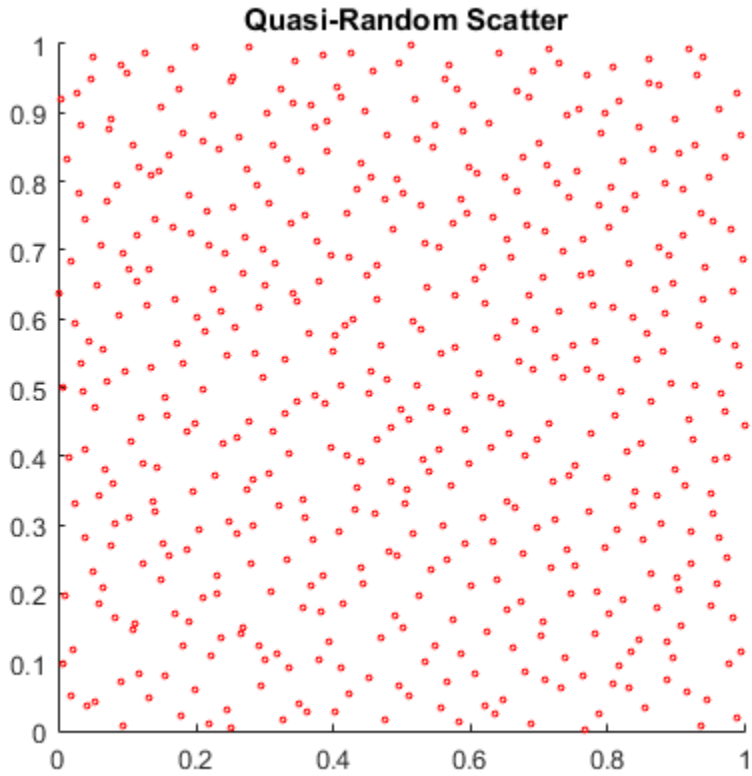
This is equivalent to

```
X0 = p(1:500,:);
```

Values of the point set `X0` are not generated and stored in memory until you access `p` using `net` or parenthesis indexing.

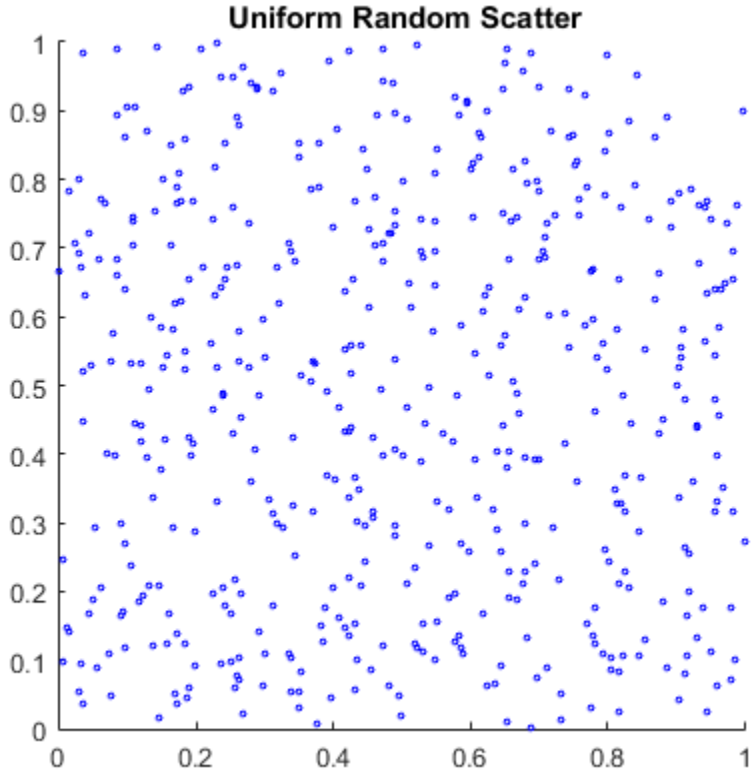
To appreciate the nature of quasi-random numbers, create a scatter plot of the two dimensions in `X0`.

```
scatter(X0(:,1),X0(:,2),5,'r')
axis square
title('{\bf Quasi-Random Scatter}')
```



Compare this to a scatter of uniform pseudorandom numbers generated by the `rand` function.

```
X = rand(500,2);
scatter(X(:,1),X(:,2),5,'b')
axis square
title('{\bf Uniform Random Scatter}')
```

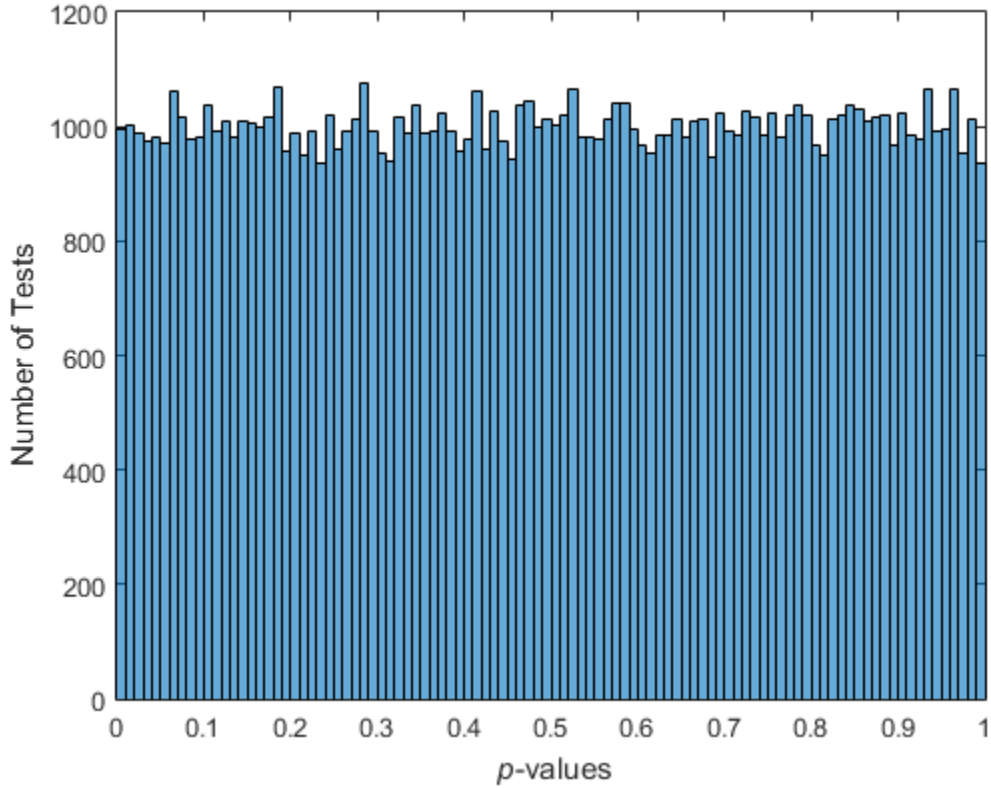


The quasi-random scatter appears more uniform, avoiding the clumping in the pseudorandom scatter.

In a statistical sense, quasi-random numbers are too uniform to pass traditional tests of randomness. For example, a Kolmogorov-Smirnov test, performed by `kstest`, is used to assess whether or not a point set has a uniform random distribution. When performed repeatedly on uniform pseudorandom samples, such as those generated by `rand`, the test produces a uniform distribution of *p*-values.

```
nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
    x = rand(sampSize,1);
```

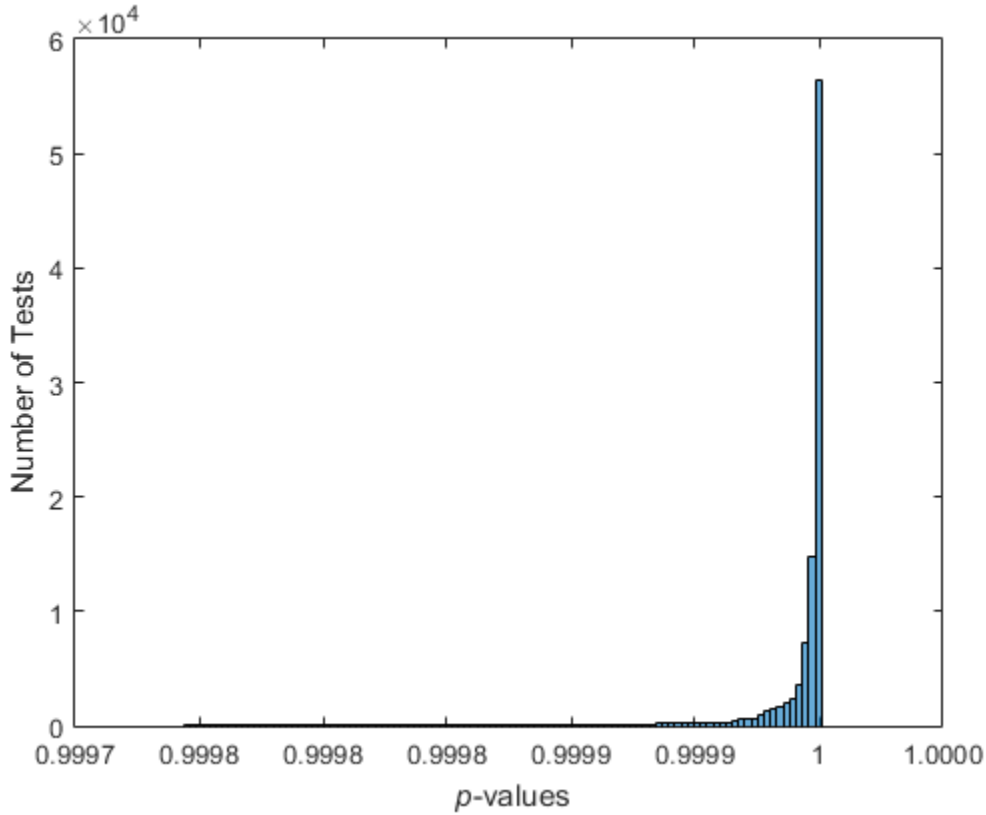
```
    [h,pval] = kstest(x,[x,x]);
    PVALS(test) = pval;
end

histogram(PVALS,100)
h = findobj(gca,'Type','patch');
xlabel('{\it p}-values')
ylabel('Number of Tests')
```



The results are quite different when the test is performed repeatedly on uniform quasi-random samples.

```
p = haltonset(1,'Skip',1e3,'Leap',1e2);
```

```
p = scramble(p,'RR2');

nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
    x = p(test:test+(sampSize-1),:);
    [h,pval] = kstest(x,[x,x]);
    PVALS(test) = pval;
end

histogram(PVALS,100)
xlabel('{\it p}-values')
ylabel('Number of Tests')
```



Small *p*-values call into question the null hypothesis that the data are uniformly distributed. If the hypothesis is true, about 5% of the *p*-values are expected to fall below 0.05. The results are remarkably consistent in their failure to challenge the hypothesis.

Quasi-Random Streams

Quasi-random *streams*, produced by the `qrandstream` function, are used to generate sequential quasi-random outputs, rather than point sets of a specific size. Streams are used like pseudoRNGS, such as `rand`, when client applications require a source of quasi-random numbers of indefinite size that can be accessed intermittently. Properties of a quasi-random stream, such as its type (Halton or Sobol), dimension, skip, leap, and scramble, are set when the stream is constructed.

In implementation, quasi-random streams are essentially very large quasi-random point sets, though they are accessed differently. The *state* of a quasi-random stream is the scalar index of the next point to be taken from the stream. Use the `qrand` method of the `qrandstream` class to generate points from the stream, starting from the current state. Use the `reset` method to reset the state to `1`. Unlike point sets, streams do not support parenthesis indexing.

Generate a Quasi-Random Stream

This example shows how to generate samples from a quasi-random point set.

Use `haltonset` to create a quasi-random point set `p`, then repeatedly increment the index into the point set `test` to generate different samples.

```
p = haltonset(1,'Skip',1e3,'Leap',1e2);
p = scramble(p,'RR2');

nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
    x = p(test:test+(sampSize-1),:);
    [h,pval] = kstest(x,[x,x]);
    PVALS(test) = pval;
end
```

The same results are obtained by using `qrandstream` to construct a quasi-random stream `q` based on the point set `p` and letting the stream take care of increments to the index.

```
p = haltonset(1,'Skip',1e3,'Leap',1e2);
p = scramble(p,'RR2');
q = qrandstream(p);

nTests = 1e5;
sampSize = 50;
PVALS = zeros(nTests,1);
for test = 1:nTests
    X = qrand(q,sampSize);
    [h,pval] = kstest(X,[X,X]);
    PVALS(test) = pval;
end
```

Generating Data Using Flexible Families of Distributions

In this section...

Pearson and Johnson Systems

As described in "Working with Probability Distributions" on page 5-3, choosing an appropriate parametric family of distributions to model your data can be based on *a priori* or *a posteriori* knowledge of the data-producing process, but the choice is often difficult. The *Pearson and Johnson systems* can make such a choice unnecessary. Each system is a flexible parametric family of distributions that includes a wide range of distribution shapes, and it is often possible to find a distribution within one of these two systems that provides a good match to your data.

Data Input

The following parameters define each member of the Pearson and Johnson systems

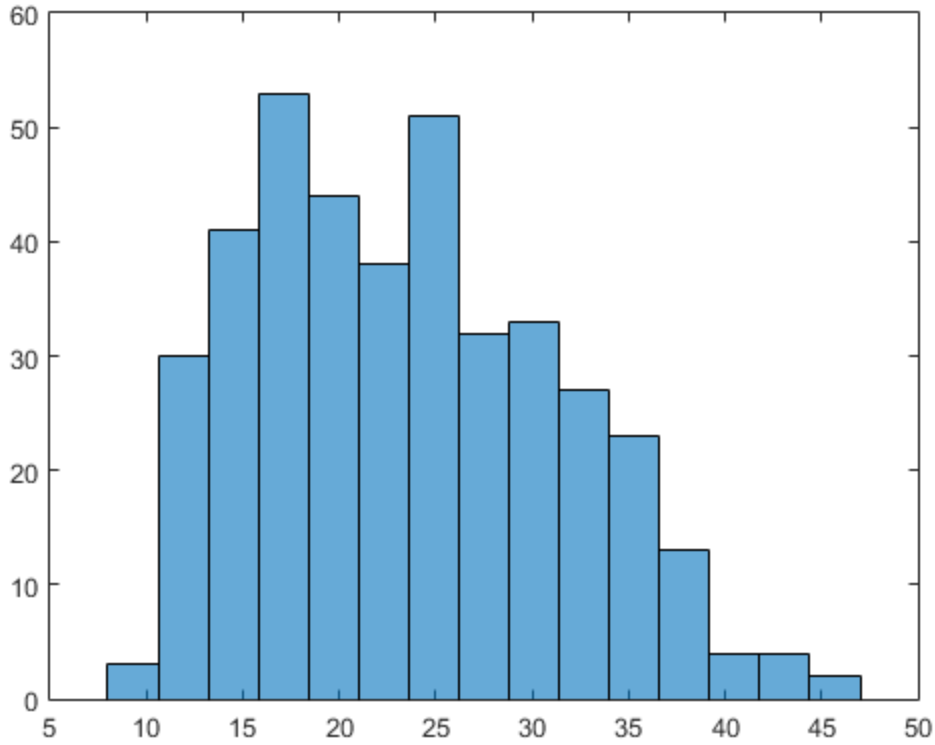
- Mean — Estimated by `mean`
- Standard deviation — Estimated by `std`
- Skewness — Estimated by `skewness`
- Kurtosis — Estimated by `kurtosis`

These statistics can also be computed with the `moment` function. The Johnson system, while based on these four parameters, is more naturally described using quantiles, estimated by the `quantile` function.

The Statistics and Machine Learning Toolbox functions `pearsrnd` and `johnsrnd` take input arguments defining a distribution (parameters or quantiles, respectively) and return the type and the coefficients of the distribution in the corresponding system. Both functions also generate random numbers from the specified distribution.

As an example, load the data in `carbig.mat`, which includes a variable `MPG` containing measurements of the gas mileage for each car.

```
load carbig
MPG = MPG(~isnan(MPG));
histogram(MPG,15)
```



The following two sections model the distribution with members of the Pearson and Johnson systems, respectively.

Generating Data Using the Pearson System

The statistician Karl Pearson devised a system, or family, of distributions that includes a unique distribution corresponding to every valid combination of mean, standard deviation, skewness, and kurtosis. If you compute sample values for each of these

moments from data, it is easy to find the distribution in the Pearson system that matches these four moments and to generate a random sample.

The Pearson system embeds seven basic types of distribution together in a single parametric framework. It includes common distributions such as the normal and *t* distributions, simple transformations of standard distributions such as a shifted and scaled beta distribution and the inverse gamma distribution, and one distribution—the Type IV—that is not a simple transformation of any standard distribution.

For a given set of moments, there are distributions that are not in the system that also have those same first four moments, and the distribution in the Pearson system may not be a good match to your data, particularly if the data are multimodal. But the system does cover a wide range of distribution shapes, including both symmetric and skewed distributions.

To generate a sample from the Pearson distribution that closely matches the `MPG` data, simply compute the four sample moments and treat those as distribution parameters.

```
moments = {mean(MPG),std(MPG),skewness(MPG),kurtosis(MPG)};
rng default  % For reproducibility
[r,type] = pearsrnd(moments{:},10000,1);
```

The optional second output from `pearsrnd` indicates which type of distribution within the Pearson system matches the combination of moments.

```
type
```

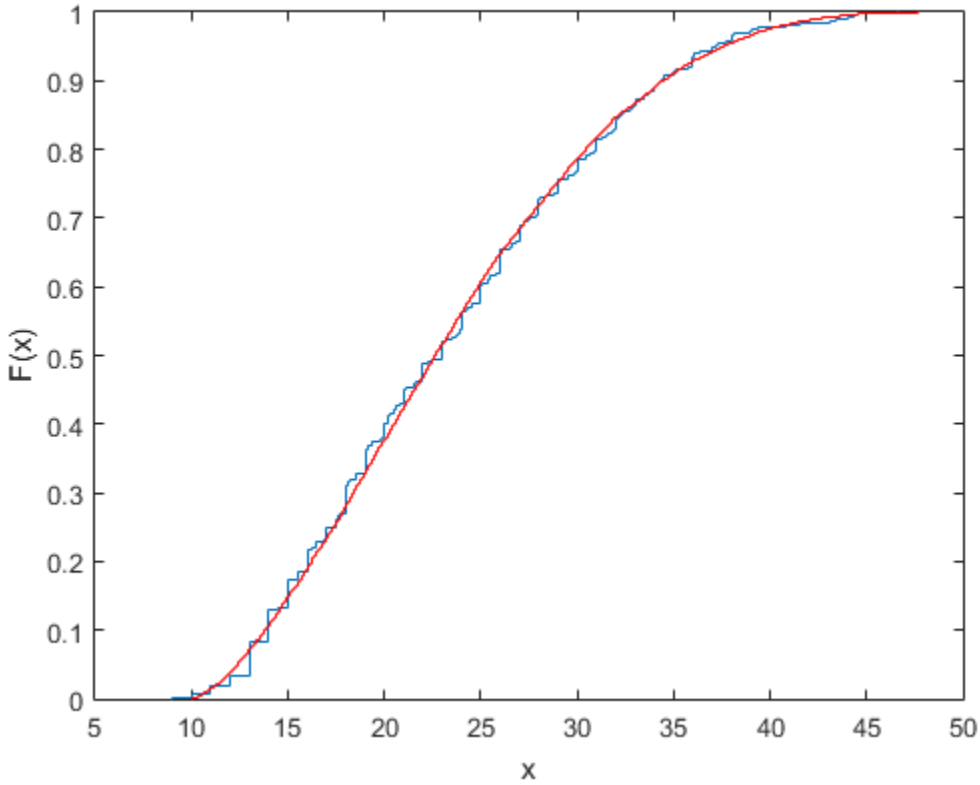
```
type =

     1
```

In this case, `pearsrnd` has determined that the data are best described with a Type I Pearson distribution, which is a shifted, scaled beta distribution.

Verify that the sample resembles the original data by overlaying the empirical cumulative distribution functions.

```
ecdf(MPG);
[Fi,xi] = ecdf(r);
hold on;
stairs(xi,Fi,'r');
```

```
hold off
```



Generating Data Using the Johnson System

Statistician Norman Johnson devised a different system of distributions that also includes a unique distribution for every valid combination of mean, standard deviation, skewness, and kurtosis. However, since it is more natural to describe distributions in the Johnson system using quantiles, working with this system is different than working with the Pearson system.

The Johnson system is based on three possible transformations of a normal random variable, plus the identity transformation. The three nontrivial cases are known as SL,

SU, and SB, corresponding to exponential, logistic, and hyperbolic sine transformations. All three can be written as

$$X = \gamma + \delta \cdot \Gamma\left(\frac{(Z-\xi)}{\lambda}\right)$$

where Z is a standard normal random variable, Γ is the transformation, and γ, δ, ξ, and λ are scale and location parameters. The fourth case, SN, is the identity transformation.

To generate a sample from the Johnson distribution that matches the MPG data, first define the four quantiles to which the four evenly spaced standard normal quantiles of -1.5, -0.5, 0.5, and 1.5 should be transformed. That is, you compute the sample quantiles of the data for the cumulative probabilities of 0.067, 0.309, 0.691, and 0.933.

```
probs = normcdf([-1.5 -0.5 0.5 1.5])
```

```
probs =

    0.0668    0.3085    0.6915    0.9332
```

```
quantiles = quantile(MPG,probs)
```

```
quantiles =

   13.0000   18.0000   27.2000   36.0000
```

Then treat those quantiles as distribution parameters.

```
[r1,type] = johnsrnd(quantiles,10000,1);
```

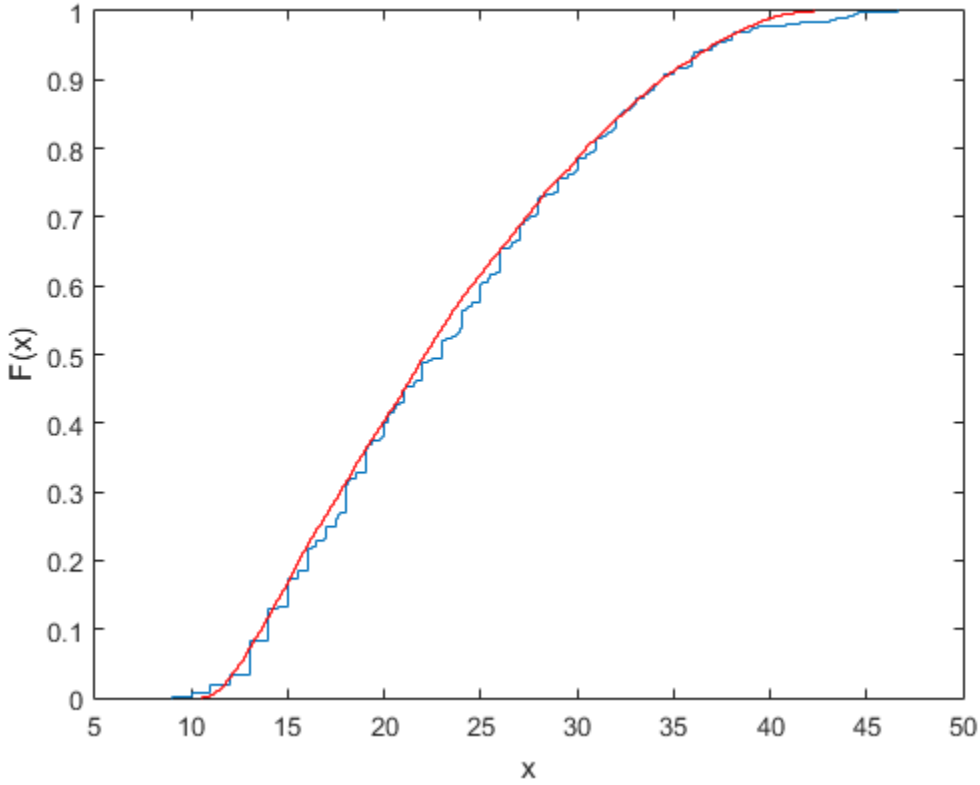
The optional second output from `johnsrnd` indicates which type of distribution within the Johnson system matches the quantiles.

```
type
```

```
type =

SB
```

You can verify that the sample resembles the original data by overlaying the empirical cumulative distribution functions.

```
ecdf(MPG);
[Fi,xi] = ecdf(r1);
hold on;
stairs(xi,Fi,'r');
hold off
```

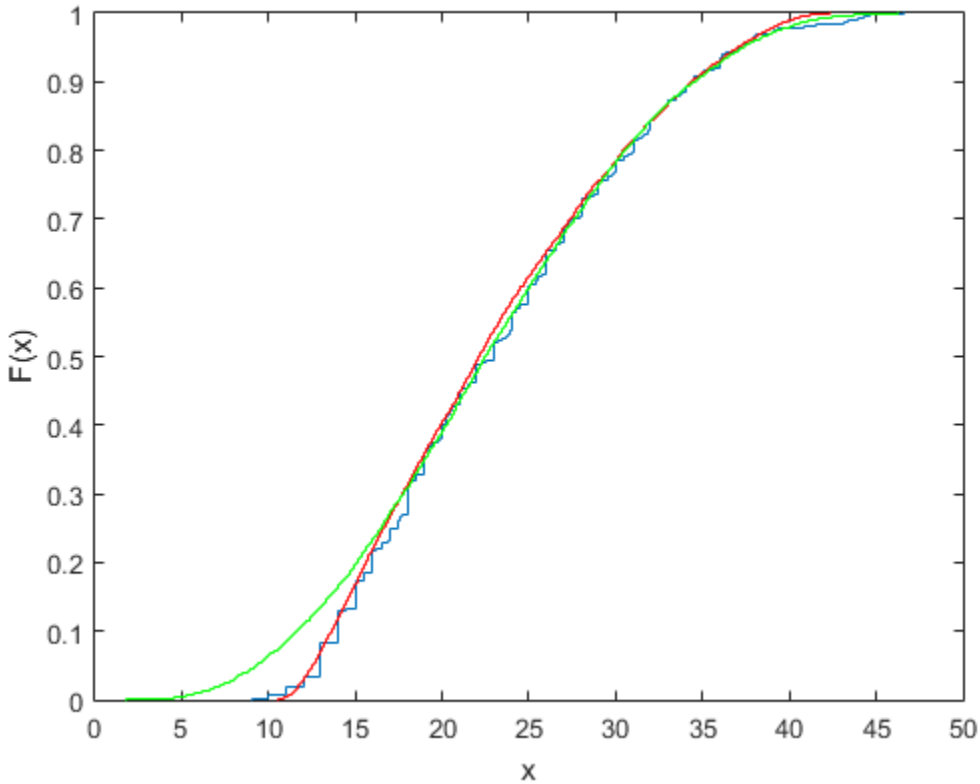


In some applications, it may be important to match the quantiles better in some regions of the data than in others. To do that, specify four evenly spaced standard normal quantiles at which you want to match the data, instead of the default -1.5, -0.5, 0.5, and 1.5. For example, you might care more about matching the data in the right tail than in the left, and so you specify standard normal quantiles that emphasizes the right tail.

```
qnorm = [-.5 .25 1 1.75];
probs = normcdf(qnorm);
qemp = quantile(MPG,probs);
r2 = johnsrnd([qnorm; qemp],10000,1);
```

However, while the new sample matches the original data better in the right tail, it matches much worse in the left tail.

```
[Fj,xj] = ecdf(r2);
hold on;
stairs(xj,Fj,'g');
hold off
```



7

Hypothesis Tests

Introduction to Hypothesis Tests

Hypothesis testing is a common method of drawing inferences about a population based on statistical evidence from a sample.

As an example, suppose someone says that at a certain time in the state of Massachusetts the average price of a gallon of regular unleaded gas was $1.15. How could you determine the truth of the statement? You could try to find prices at every gas station in the state at the time. That approach would be definitive, but it could be time-consuming, costly, or even impossible.

A simpler approach would be to find prices at a small number of randomly selected gas stations around the state, and then compute the sample average.

Sample averages differ from one another due to chance variability in the selection process. Suppose your sample average comes out to be $1.18. Is the $0.03 difference an artifact of random sampling or significant evidence that the average price of a gallon of gas was in fact greater than $1.15? Hypothesis testing is a statistical method for making such decisions.

Hypothesis Test Terminology

All hypothesis tests share the same basic terminology and structure.

- A *null hypothesis* is an assertion about a population that you would like to test. It is "null" in the sense that it often represents a status quo belief, such as the absence of a characteristic or the lack of an effect. It may be formalized by asserting that a population parameter, or a combination of population parameters, has a certain value. In the example given in the "Introduction to Hypothesis Tests" on page 7-2, the null hypothesis would be that the average price of gas across the state was \$1.15. This is written H_0: $\mu = 1.15$.
- An *alternative hypothesis* is a contrasting assertion about the population that can be tested against the null hypothesis. In the example given in the "Introduction to Hypothesis Tests" on page 7-2, possible alternative hypotheses are:

  H_1: $\mu \neq 1.15$ — State average was different from \$1.15 (two-tailed test)

  H_1: $\mu > 1.15$ — State average was greater than \$1.15 (right-tail test)

  H_1: $\mu < 1.15$ — State average was less than \$1.15 (left-tail test)
- To conduct a hypothesis test, a random sample from the population is collected and a relevant *test statistic* is computed to summarize the sample. This statistic varies with the type of test, but its distribution under the null hypothesis must be known (or assumed).
- The *p value* of a test is the probability, under the null hypothesis, of obtaining a value of the test statistic as extreme or more extreme than the value computed from the sample.
- The *significance level* of a test is a threshold of probability α agreed to before the test is conducted. A typical value of α is 0.05. If the p value of a test is less than α, the test rejects the null hypothesis. If the p value is greater than α, there is insufficient evidence to reject the null hypothesis. Note that lack of evidence for rejecting the null hypothesis is not evidence for accepting the null hypothesis. Also note that substantive "significance" of an alternative cannot be inferred from the statistical significance of a test.
- The significance level α can be interpreted as the probability of rejecting the null hypothesis when it is actually true—a *type I error*. The distribution of the test statistic under the null hypothesis determines the probability α of a type I error. Even if the null hypothesis is not rejected, it may still be false—a *type II error*. The distribution of the test statistic under the alternative hypothesis determines the probability β of a

type II error. Type II errors are often due to small sample sizes. The *power* of a test, $1 - \beta$, is the probability of correctly rejecting a false null hypothesis.

- Results of hypothesis tests are often communicated with a *confidence interval*. A confidence interval is an estimated range of values with a specified probability of containing the true population value of a parameter. Upper and lower bounds for confidence intervals are computed from the sample estimate of the parameter and the known (or assumed) sampling distribution of the estimator. A typical assumption is that estimates will be normally distributed with repeated sampling (as dictated by the Central Limit Theorem). Wider confidence intervals correspond to poor estimates (smaller samples); narrow intervals correspond to better estimates (larger samples). If the null hypothesis asserts the value of a population parameter, the test rejects the null hypothesis when the hypothesized value lies outside the computed confidence interval for the parameter.

Hypothesis Test Assumptions

Different hypothesis tests make different assumptions about the distribution of the random variable being sampled in the data. These assumptions must be considered when choosing a test and when interpreting the results.

For example, the *z*-test (`ztest`) and the *t*-test (`ttest`) both assume that the data are independently sampled from a normal distribution. Statistics and Machine Learning Toolbox functions are available for testing this assumption, such as `chi2gof`, `jbtest`, `lillietest`, and `normplot`.

Both the *z*-test and the *t*-test are relatively robust with respect to departures from this assumption, so long as the sample size n is large enough. Both tests compute a sample mean $\bar{x}$, which, by the Central Limit Theorem, has an approximately normal sampling distribution with mean equal to the population mean μ, regardless of the population distribution being sampled.

The difference between the *z*-test and the *t*-test is in the assumption of the standard deviation σ of the underlying normal distribution. A *z*-test assumes that σ is known; a *t*-test does not. As a result, a *t*-test must compute an estimate s of the standard deviation from the sample.

Test statistics for the *z*-test and the *t*-test are, respectively,

$$z = \frac{\bar{x} - \mu}{\sigma / \sqrt{n}}$$

$$t = \frac{\bar{x} - \mu}{s / \sqrt{n}}$$

Under the null hypothesis that the population is distributed with mean μ, the *z*-statistic has a standard normal distribution, $N(0,1)$. Under the same null hypothesis, the *t*-statistic has Student's *t* distribution with $n - 1$ degrees of freedom. For small sample sizes, Student's *t* distribution is flatter and wider than $N(0,1)$, compensating for the decreased confidence in the estimate s. As sample size increases, however, Student's *t* distribution approaches the standard normal distribution, and the two tests become essentially equivalent.

Knowing the distribution of the test statistic under the null hypothesis allows for accurate calculation of *p*-values. Interpreting *p*-values in the context of the test assumptions allows for critical analysis of test results.

Assumptions underlying Statistics and Machine Learning Toolbox hypothesis tests are given in the reference pages for implementing functions.

Hypothesis Testing

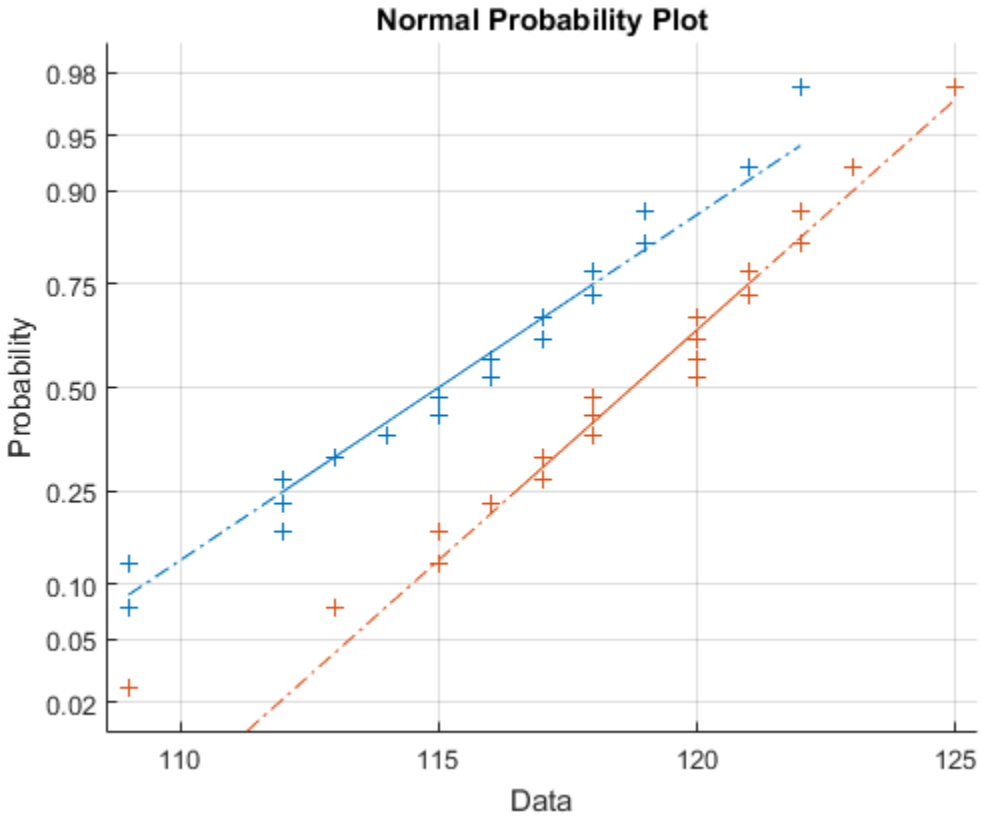
This example shows how to use hypothesis testing to analyze gas prices measured across the state of Massachusetts during two separate months.

This example uses the gas price data in the file `gas.mat`. The file contains two random samples of prices for a gallon of gas around the state of Massachusetts in 1993. The first sample, `price1`, contains 20 random observations around the state on a single day in January. The second sample, `price2`, contains 20 random observations around the state one month later.

```
load gas
prices = [price1 price2];
```

As a first step, you might want to test the assumption that the samples come from normal distributions. A normal probability plot gives a quick idea.

```
normplot(prices)
```



Both scatters approximately follow straight lines through the first and third quartiles of the samples, indicating approximate normal distributions. The February sample (the right-hand line) shows a slight departure from normality in the lower tail. A shift in the mean from January to February is evident. A hypothesis test is used to quantify the test of normality. Since each sample is relatively small, a Lilliefors test is recommended.

```
lillietest(price1)
lillietest(price2)
```

```
ans =

     0
```

```
ans =

     0
```

The default significance level of `lillietest` is 5%. The logical 0 returned by each test indicates a failure to reject the null hypothesis that the samples are normally distributed. This failure may reflect normality in the population or it may reflect a lack of strong evidence against the null hypothesis due to the small sample size.

Now compute the sample means.

```
sample_means = mean(prices)


sample_means =

  115.1500  118.5000
```

You might want to test the null hypothesis that the mean price across the state on the day of the January sample was $1.15. If you know that the standard deviation in prices across the state has historically, and consistently, been $0.04, then a *z*-test is appropriate.

```
[h,pvalue,ci] = ztest(price1/100,1.15,0.04)


h =

     0


pvalue =

    0.8668


ci =

    1.1340
    1.1690
```

The logical output `h = 0` indicates a failure to reject the null hypothesis at the default significance level of 5%. This is a consequence of the high probability under the null hypothesis, indicated by the *p* value, of observing a value as extreme or more extreme of the *z*-statistic computed from the sample. The 95% confidence interval on the mean [1.1340 1.1690] includes the hypothesized population mean of $1.15.

Does the later sample offer stronger evidence for rejecting a null hypothesis of a state-wide average price of $1.15 in February? The shift shown in the probability plot and the difference in the computed sample means suggest this. The shift might indicate a significant fluctuation in the market, raising questions about the validity of using the historical standard deviation. If a known standard deviation cannot be assumed, a *t*-test is more appropriate.

```
[h,pvalue,ci] = ttest(price2/100,1.15)
```

```
h =

     1


pvalue =

   4.9517e-04


ci =

    1.1675
    1.2025
```

The logical output `h = 1` indicates a rejection of the null hypothesis at the default significance level of 5%. In this case, the 95% confidence interval on the mean does not include the hypothesized population mean of $1.15.

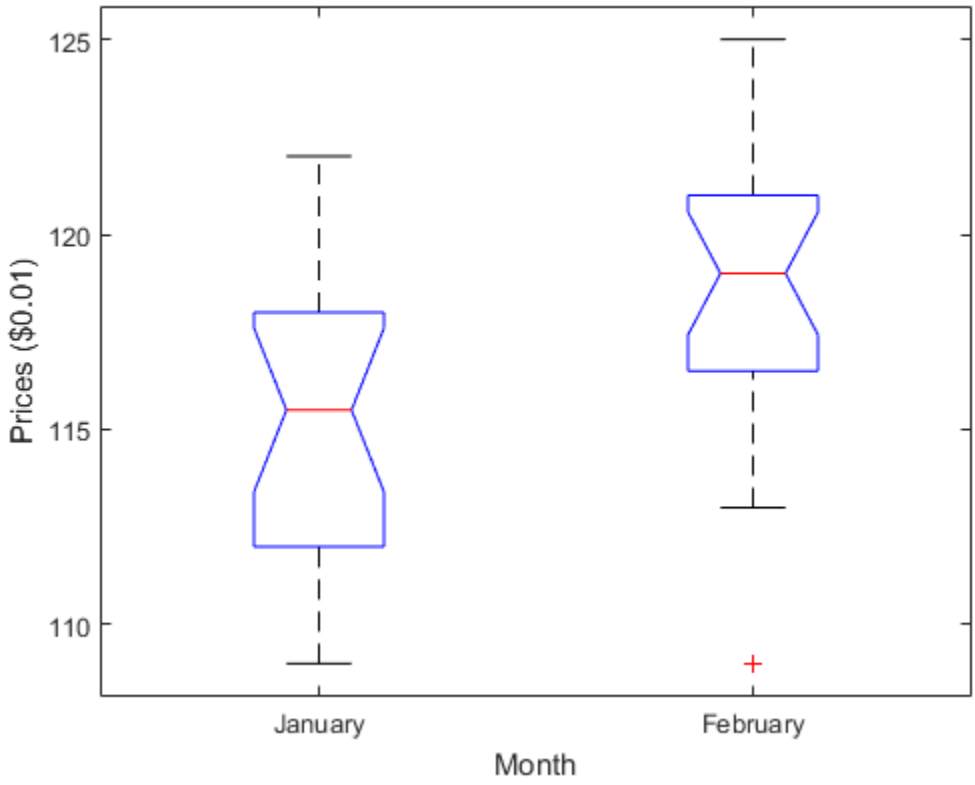
You might want to investigate the shift in prices a little more closely. The function `ttest2` tests if two independent samples come from normal distributions with equal but unknown standard deviations and the same mean, against the alternative that the means are unequal.

```
[h,sig,ci] = ttest2(price1,price2)
```

```
h =

     1


sig =

    0.0083


ci =

   -5.7845
   -0.9155
```

The null hypothesis is rejected at the default 5% significance level, and the confidence interval on the difference of means does not include the hypothesized value of 0. A notched box plot is another way to visualize the shift.

```
boxplot(prices,1)
h = gca;
h.XTick = [1 2];
h.XTickLabel = {'January','February'};
xlabel('Month')
ylabel('Prices ($0.01)')
```



The plot displays the distribution of the samples around their medians. The heights of the notches in each box are computed so that the side-by-side boxes have nonoverlapping notches when their medians are different at a default 5% significance level. The computation is based on an assumption of normality in the data, but the comparison is reasonably robust for other distributions. The side-by-side plots provide a kind of visual hypothesis test, comparing medians rather than means. The plot above appears to barely reject the null hypothesis of equal medians.

The nonparametric Wilcoxon rank sum test, implemented by the function `ranksum`, can be used to quantify the test of equal medians. It tests if two independent samples come from identical continuous (not necessarily normal) distributions with equal medians, against the alternative that they do not have equal medians.

```
[p,h] = ranksum(price1,price2)

p =

    0.0095

h =

     1
```

The test rejects the null hypothesis of equal medians at the default 5% significance level.

Available Hypothesis Tests

Function	Description
`ansaribradley`	Ansari-Bradley test. Tests if two independent samples come from the same distribution, against the alternative that they come from distributions that have the same median and shape but different variances.
`barttest`	Bartlett's test. Tests if the variances of the data values along each principal component are equal, against the alternative that the variances are not all equal.
`chi2gof`	Chi-square goodness-of-fit test. Tests if a sample comes from a specified distribution, against the alternative that it does not come from that distribution.
`dwtest`	Durbin-Watson test. Tests if the residuals from a linear regression are uncorrelated, against the alternative that there is autocorrelation among them.
`friedman`	Friedman's test. Tests if the column effects in a two-way layout are all the same, against the alternative that the column effects are not all the same.
`jbtest`	Jarque-Bera test. Tests if a sample comes from a normal distribution with unknown mean and variance, against the alternative that it does not come from a normal distribution.
`kruskalwallis`	Kruskal-Wallis test. Tests if multiple samples are all drawn from the same populations (or equivalently, from different populations with the same distribution), against the alternative that they are not all drawn from the same population.
`kstest`	One-sample Kolmogorov-Smirnov test. Tests if a sample comes from a continuous distribution with specified parameters, against the alternative that it does not come from that distribution.
`kstest2`	Two-sample Kolmogorov-Smirnov test. Tests if two samples come from the same continuous distribution, against the alternative that they do not come from the same distribution.
`lillietest`	Lilliefors test. Tests if a sample comes from a distribution in the normal family, against the alternative that it does not come from a normal distribution.

Function	Description
`linhyptest`	Linear hypothesis test. Tests if `H*b = c` for parameter estimates `b` with estimated covariance `H` and specified `c`, against the alternative that `H*b ≠ c`.
`ranksum`	Wilcoxon rank sum test. Tests if two independent samples come from identical continuous distributions with equal medians, against the alternative that they do not have equal medians.
`runstest`	Runs test. Tests if a sequence of values comes in random order, against the alternative that the ordering is not random.
`signrank`	One-sample or paired-sample Wilcoxon signed rank test. Tests if a sample comes from a continuous distribution symmetric about a specified median, against the alternative that it does not have that median.
`signtest`	One-sample or paired-sample sign test. Tests if a sample comes from an arbitrary continuous distribution with a specified median, against the alternative that it does not have that median.
`ttest`	One-sample or paired-sample *t*-test. Tests if a sample comes from a normal distribution with unknown variance and a specified mean, against the alternative that it does not have that mean.
`ttest2`	Two-sample *t*-test. Tests if two independent samples come from normal distributions with unknown but equal (or, optionally, unequal) variances and the same mean, against the alternative that the means are unequal.
`vartest`	One-sample chi-square variance test. Tests if a sample comes from a normal distribution with specified variance, against the alternative that it comes from a normal distribution with a different variance.
`vartest2`	Two-sample *F*-test for equal variances. Tests if two independent samples come from normal distributions with the same variance, against the alternative that they come from normal distributions with different variances.
`vartestn`	Bartlett multiple-sample test for equal variances. Tests if multiple samples come from normal distributions with the same variance, against the alternative that they come from normal distributions with different variances.

Function	Description
`ztest`	One-sample *z*-test. Tests if a sample comes from a normal distribution with known variance and specified mean, against the alternative that it does not have that mean.

Note: In addition to the previous functions, Statistics and Machine Learning Toolbox functions are available for analysis of variance (ANOVA), which perform hypothesis tests in the context of linear modeling.

8

Analysis of Variance

Introduction to Analysis of Variance

Analysis of variance (ANOVA) is a procedure for assigning sample variance to different sources and deciding whether the variation arises within or among different population groups. Samples are described in terms of variation around group means and variation of group means around an overall mean. If variations within groups are small relative to variations between groups, a difference in group means may be inferred. Hypothesis tests are used to quantify decisions.

One-Way ANOVA

In this section...

Introduction to One-Way ANOVA

You can use the Statistics and Machine Learning Toolbox function `anova1` to perform one-way analysis of variance (ANOVA). The purpose of one-way ANOVA is to determine whether data from several groups (levels) of a factor have a common mean. That is, one-way ANOVA enables you to find out whether different groups of an independent variable have different effects on the response variable y. Suppose, a hospital wants to determine if the two new proposed scheduling methods reduce patient wait times more than the old way of scheduling appointments. In this case, the independent variable is the scheduling method, and the response variable is the waiting time of the patients.

One-way ANOVA is a simple special case of the linear model. The one-way ANOVA form of the model is

$$y_{ij} = \alpha_{.j} + \varepsilon_{ij}$$

with the following assumptions:

- y_{ij} is an observation, in which i represents the observation number, and j represents a different group (level) of the predictor variable y. All y_{ij} are independent.
- α_j represents the population mean for the jth group (level or treatment).
- ε_{ij} is the random error, independent and normally distributed, with zero mean and constant variance, i.e., $\varepsilon_{ij} \sim N(0,\sigma^2)$.

This model is also called the *means model*. The model assumes that the columns of y are the constant α_j plus the error component ε_{ij}. ANOVA helps determine if the constants are all the same.

ANOVA tests the hypothesis that all group means are equal versus the alternative hypothesis that at least one group is different from the others.

$H_0 : \alpha_1 = \alpha_2 = ... = \alpha_k$
H_1 : not all group means are equal

`anova1(y)` tests the equality of column means for the data in matrix `y`, where each column is a different group and has the same number of observations (i.e., a balanced design). `anova1(y,group)` tests the equality of group means, specified in `group`, for the data in vector or matrix `y`. In this case, each group or column can have a different number of observations (i.e., an unbalanced design).

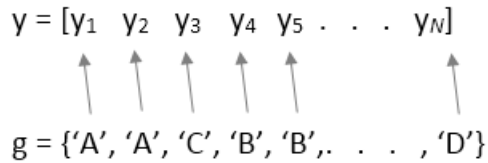
ANOVA is based on the assumption that all sample populations are normally distributed. It is known to be robust to modest violations of this assumption. You can check the normality assumption visually by using a normality plot (`normplot`). Alternatively, you can use one of the Statistics and Machine Learning Toolbox functions that checks for normality: the Anderson-Darling test (`adtest`), the chi-squared goodness of fit test (`chi2gof`), the Jarque-Bera test (`jbtest`), or the Lilliefors test (`lillietest`).

Prepare Data for One-Way ANOVA

You can provide sample data as a vector or a matrix.

- If the sample data is in a vector, y, then you must provide grouping information using the `group` input variable: `anova1(y,group)`.

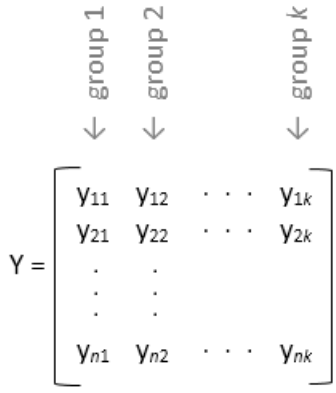
  group must be a categorical variable, numeric vector, logical vector, string array, or cell array of strings, with one name for each element of y. The `anova1` function treats the y values corresponding to the same value of group as part of the same group. For example,

  Use this design when groups have different numbers of elements (unbalanced ANOVA).

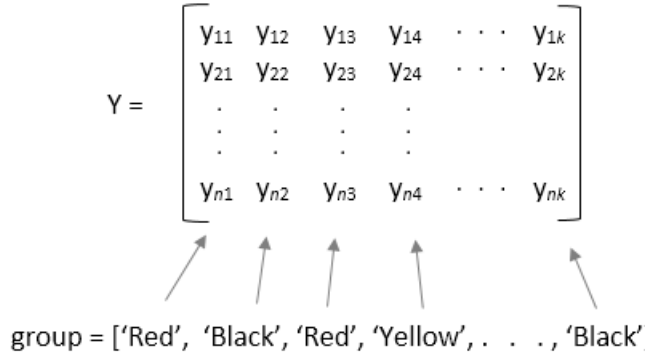
- If the sample data is in a matrix, y, providing the group information is optional.

- If you do not specify the input variable `group`, then `anova1` treats each column of y as a separate group, and evaluates whether the population means of the columns are equal. For example,



  Use this form of design when each group has the same number of elements (balanced ANOVA).

- If you specify the input variable group, then group must be a character array or cell array of strings, with one name for each column of y. The `anova1` function treats the columns with the same group name as part of the same group. For example,



If group contains empty or `NaN` valued cells or strings, `anova1` disregards the corresponding observations in y.

Perform One-Way ANOVA

This example shows how to perform one-way ANOVA to determine whether data from several groups have a common mean.

Load and display the sample data.

```
load hogg
hogg
```

```
hogg =

    24    14    11     7    19
    15     7     9     7    24
    21    12     7     4    19
    27    17    13     7    15
    33    14    12    12    10
    23    16    18    18    20
```

The data comes from a Hogg and Ledolter (1987) study on bacteria counts in shipments of milk. The columns of the matrix `hogg` represent different shipments. The rows are bacteria counts from cartons of milk chosen randomly from each shipment.

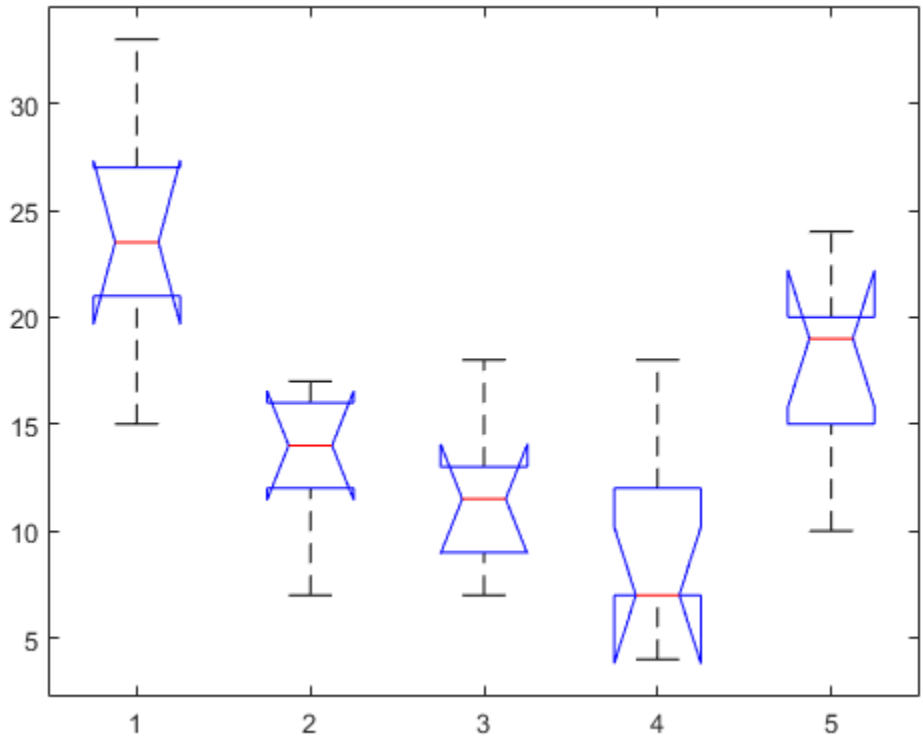
Test if some shipments have higher counts than others. By default, anova1 returns two figures. One is the standard ANOVA table, and the other one is the box plots of data by group.

```
[p,tbl,stats] = anova1(hogg);
p
```

```
p =

   1.1971e-04
```

ANOVA Table

Source	SS	df	MS	F	Prob>F
Columns	803	4	200.75	9.01	0.0001
Error	557.17	25	22.287		
Total	1360.17	29			



The small p-value of about 0.0001 indicates that the bacteria counts from the different shipments are not the same.

You can get some graphical assurance that the means are different by looking at the box plots. The notches, however, compare the medians, not the means. For more information on this display, see boxplot.

View the standard ANOVA table. `anova1` saves the standard ANOVA table as a cell array in the output argument `tbl`.

```
tbl
```

```
tbl =
```

```
    'Source'     'SS'            'df'    'MS'          'F'         'Prob>F'
    'Columns'    [  803.0000]    [ 4]    [200.7500]    [9.0076]    [1.1971e-04]
    'Error'      [  557.1667]    [25]    [ 22.2867]          []              []
    'Total'      [1.3602e+03]    [29]            []          []              []
```

Save the F-statistic value in the variable `Fstat`.

```
Fstat = tbl{2,5}
```

```
Fstat =

    9.0076
```

View the statistics necessary to make a multiple pairwise comparison of group means. `anova1` saves these statistics in the structure `stats`.

```
stats
```

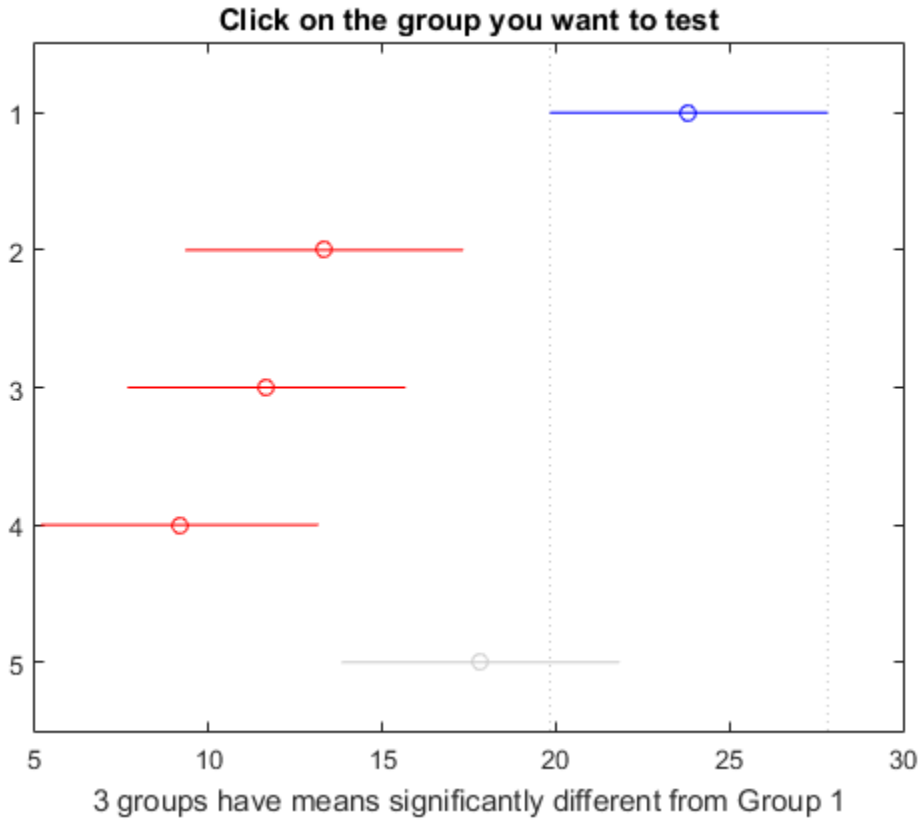
```
stats =

    gnames: [5x1 char]
         n: [6 6 6 6 6]
    source: 'anova1'
     means: [23.8333 13.3333 11.6667 9.1667 17.8333]
        df: 25
         s: 4.7209
```

ANOVA rejects the null hypothesis that all group means are equal, so you can use the multiple comparisons to determine which group means are different from others. To conduct multiple comparison tests, use the function multcompare, which accepts `stats` as an input argument. In this example, `anova1` rejects the null hypothesis that the mean bacteria counts from all four shipments are equal to each other, i.e., $H_0 : \mu_1 = \mu_2 = \mu_3 = \mu_4$.

Perform a multiple comparison test to determine which shipments are different than the others in terms of mean bacteria counts.

```
multcompare(stats)
```

```
ans =

    1.0000    2.0000    2.4953   10.5000   18.5047    0.0059
    1.0000    3.0000    4.1619   12.1667   20.1714    0.0013
    1.0000    4.0000    6.6619   14.6667   22.6714    0.0001
    1.0000    5.0000   -2.0047    6.0000   14.0047    0.2119
    2.0000    3.0000   -6.3381    1.6667    9.6714    0.9719
    2.0000    4.0000   -3.8381    4.1667   12.1714    0.5544
    2.0000    5.0000  -12.5047   -4.5000    3.5047    0.4806
    3.0000    4.0000   -5.5047    2.5000   10.5047    0.8876
    3.0000    5.0000  -14.1714   -6.1667    1.8381    0.1905
    4.0000    5.0000  -16.6714   -8.6667   -0.6619    0.0292
```



The first two columns show which group means are compared with each other. For example, the first row compares the means for groups 1 and 2. The last column shows the *p*-values for the tests. The *p*-values 0.0059, 0.0013, and 0.0001 indicate that the mean bacteria counts in the milk from the first shipment is different from the ones from the second, third, and fourth shipments. The *p*-value of 0.0292 indicates that the mean bacteria counts in the milk from the fourth shipment is different from the ones from the fifth. The procedure fails to reject the hypotheses that the other group means are different from each other.

The figure also illustrates the same result. The blue bar shows the comparison interval for the first group mean, which does not overlap with the comparison intervals for the second, third, and fourth group means, shown in red. The comparison interval for the mean of fifth group, shown in gray, overlaps with the comparison interval for the first group mean. Hence, the group means for the first and fifth groups are not significantly different from each other.

Mathematical Details

ANOVA tests for the difference in the group means by partitioning the total variation in the data into two components:

- Variation of group means from the overall mean, i.e., $\bar{y}_{\cdot j} - \bar{y}_{\cdot\cdot}$ (variation between groups), where $\bar{y}_{\cdot j}$ is the sample mean of group j, and $\bar{y}_{\cdot\cdot}$ is the overall sample mean.
- Variation of observations in each group from their group mean estimates, $y_{ij} - \bar{y}_{\cdot j}$ (variation within group).

In other words, ANOVA partitions the total sum of squares (SST) into sum of squares due to between-groups effect (SSR) and sum of squared errors(SSE).

$$\underbrace{\sum_i \sum_j \left(y_{ij} - \bar{y}_{\cdot\cdot}\right)^2}_{SST} = \underbrace{\sum_j n_j \left(\bar{y}_{\cdot j} - \bar{y}_{\cdot\cdot}\right)^2}_{SSR} + \underbrace{\sum_i \sum_j \left(y_{ij} - \bar{y}_{\cdot j}\right)^2}_{SSE},$$

where n_j is the sample size for the jth group, $j = 1, 2, \ldots, k$.

Then ANOVA compares the variation between groups to the variation within groups. If the ratio of within-group variation to between-group variation is significantly high,

then you can conclude that the group means are significantly different from each other. You can measure this using a test statistic that has an F-distribution with $(k-1, N-k)$ degrees of freedom:

$$F = \frac{SSR/k-1}{SSE/N-k} = \frac{MSR}{MSE} \sim F_{k-1,N-k},$$

where MSR is the mean squared treatment, MSE is the mean squared error, k is the number of groups, and N is the total number of observations. If the p-value for the F-statistic is smaller than the significance level, then the test rejects the null hypothesis that all group means are equal and concludes that at least one of the group means is different from the others. The most common significance levels are 0.05 and 0.01.

ANOVA Table

The ANOVA table captures the variability in the model by source, the F-statistic for testing the significance of this variability, and the p-value for deciding on the significance of this variability. The p-value returned by `anova1` depends on assumptions about the random disturbances ε_{ij} in the model equation. For the p-value to be correct, these disturbances need to be independent, normally distributed, and have constant variance. The standard ANOVA table has this form:

Source	SS	df	MS	F	p-value
Group (Between)	SSR	$k-1$	MSR = SSR/$(k-1)$	MSR/MSE	$P(F_{k-1,N-k}) > F$
Error (Within)	SSE	$N-k$	MSE = SSE/$(N-k)$		
Total	SST	$N-1$			

`anova1` returns the standard ANOVA table as a cell array with six columns.

Column	Definition
`Source`	Source of the variability.
`SS`	Sum of squares due to each source.
`df`	Degrees of freedom associated with each source. Suppose N is the total number of observations and k is the number of groups. Then, $N-k$ is the within-groups degrees

Column	Definition
	of freedom (`Error`), $k-1$ is the between-groups degrees of freedom (`Columns`), and $N-1$ is the total degrees of freedom: $N-1 = (N-k) + (k-1)$.
`MS`	Mean squares for each source, which is the ratio `SS/df`.
`F`	F-statistic, which is the ratio of the mean squares.
`Prob>F`	p-value, which is the probability that the F-statistic can take a value larger than the computed test-statistic value. `anova1` derives this probability from the cdf of the F-distribution.

The rows of the ANOVA table show the variability in the data, divided by the source.

Row (Source)	Definition
`Groups` or `Columns`	Variability due to the differences among the group means (variability *between* groups)
`Error`	Variability due to the differences between the data in each group and the group mean (variability *within* groups)
`Total`	Total variability

References

[1] Wu, C. F. J., and M. Hamada. *Experiments: Planning, Analysis, and Parameter Design Optimization*, 2000.

[2] Neter, J., M. H. Kutner, C. J. Nachtsheim, and W. Wasserman. 4th ed. *Applied Linear Statistical Models*. Irwin Press, 1996.

See Also

`anova1` | `kruskalwallis` | `multcompare`

More About

- "Two-Way ANOVA" on page 8-15
- "N-Way ANOVA" on page 8-36
- "Multiple Comparisons" on page 8-26
- "Nonparametric Methods" on page 8-67

Two-Way ANOVA

In this section...

Introduction to Two-Way ANOVA

You can use the Statistics and Machine Learning Toolbox function `anova2` to perform a balanced two-way analysis of variance (ANOVA). To perform two-way ANOVA for an unbalanced design, use `anovan`. For an example, see "Two-Way ANOVA for Unbalanced Design" on page 22-88.

As in one-way ANOVA, the data for a two-way ANOVA study can be experimental or observational. The difference between one-way and two-way ANOVA is that in two-way ANOVA, the effects of two factors on a response variable are of interest. These two factors can be independent, and have no interaction effect, or the impact of one factor on the response variable can depend on the group (level) of the other factor. If the two factors have no interactions, the model is called an *additive* model.

Suppose an automobile company has two factories, and each factory makes the same three car models. The gas mileage in the cars can vary from factory to factory and from model to model. These two factors, factory and model, explain the differences in mileage, that is, the response. One measure of interest is the difference in mileage due to the production methods between factories. Another measure of interest is the difference in the mileage of the models (irrespective of the factory) due to different design specifications. The effects of these measures of interest are *additive*. In addition, suppose only one model has different gas mileage between factories, while the mileage of the other two models is the same between factories. This is called an *interaction* effect. To measure an interaction effect, there must be multiple observations for some combination of factory and car model. These multiple observations are called *replications*.

Two-way ANOVA is a special case of the linear model. The two-way ANOVA form of the model is

$$y_{ijr} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijr}$$

where,

- y_{ijr} is an observation of the response variable.
  - i represents group i of row factor A, $i = 1, 2, ..., I$
  - j represents group j of column factor B, $j = 1, 2, ..., J$
  - r represents the replication number, $r = 1, 2, ..., R$

  There are a total of $N = I*J*R$ observations.
- μ is the overall mean.
- α_i are the deviations of groups of row factor A from the overall mean μ due to row factor B. The values of α_i sum to 0, i.e., $\sum_{i=1}^{I} \alpha_i = 0$.
- β_j are the deviations of groups in column factor B from the overall mean μ due to row factor B. All values in a given column of β_j are identical, and the values of β_j sum to 0, i.e., $\sum_{j=1}^{J} \beta_j = 0$.
- $\alpha\beta_{ij}$ are the interactions. The values in each row and in each column of $\alpha\beta_{ij}$ sum to 0, i.e., $\sum_{i=1}^{I} (\alpha\beta)_{ij} = \sum_{j=1}^{J} (\alpha\beta)_{ij} = 0$.
- ε_{ijr} are the random disturbances. They are assumed to be independent, normally distributed, and have constant variance.

In the mileage example:

- y_{ijr} are the gas mileage observations, μ is the overall mean gas mileage.
- α_i are the deviations of each car's gas mileage from the mean gas mileage μ due to the car's *model*.
- β_j are the deviations of each car's gas mileage from the mean gas mileage μ due to the car's *factory*.

`anova2` requires that data be balanced, so each combination of model and factory must have the same number of cars.

Two-way ANOVA tests hypotheses about the effects of factors A and B, and their interaction on the response variable y. The hypotheses about the equality of the mean response for groups of row factor A are

$$H_0 : \alpha_1 = \alpha_2 \cdots = \alpha_I$$
$$H_1 : \text{ at least one } \alpha_i \text{ is different, } i = 1,\ 2,\ ...,\ I.$$

The hypotheses about the equality of the mean response for groups of column factor B are

$$H_0 : \beta_1 = \beta_2 = \cdots = \beta_J$$
$$H_1 : \text{ at least one } \beta_j \text{ is different, } j = 1,\ 2,\ ...,\ J.$$

The hypotheses about the interaction of the column and row factors are

$$H_0 : (\alpha\beta)_{ij} = 0$$
$$H_1 : \text{at least one } (\alpha\beta)_{ij} \neq 0$$

Prepare Data for Balanced Two-Way ANOVA

To perform balanced two-way ANOVA using `anova2`, you must arrange data in a specific matrix form. The columns of the matrix must correspond to groups of the column factor, B. The rows must correspond to the groups of the row factor, A, with the same number of replications for each combination of the groups of factors A and B.

Suppose that row factor A has three groups, and column factor B has two groups (levels). Also suppose that each combination of factors A and B has two measurements or observations (`reps = 2`). Then, each group of factor A has six observations and each group of factor B four observations.

$$\begin{array}{cc} B=1 & B=2 \\ \left[\begin{array}{cc} y_{111} & y_{121} \\ y_{112} & y_{122} \end{array}\right] & \} A=1 \\ \left[\begin{array}{cc} y_{211} & y_{221} \\ y_{212} & y_{222} \end{array}\right] & \} A=2 \\ \left[\begin{array}{cc} y_{311} & y_{321} \\ y_{312} & y_{322} \end{array}\right] & \} A=3 \end{array}$$

The subscripts indicate row, column, and replication, respectively. For example, y_{221} corresponds to the measurement for the second group of factor A, the second group of factor B, and the first replication for this combination.

Perform Two-Way ANOVA

This example shows how to perform two-way ANOVA to determine the effect of car model and factory on the mileage rating of cars.

Load and display the sample data.

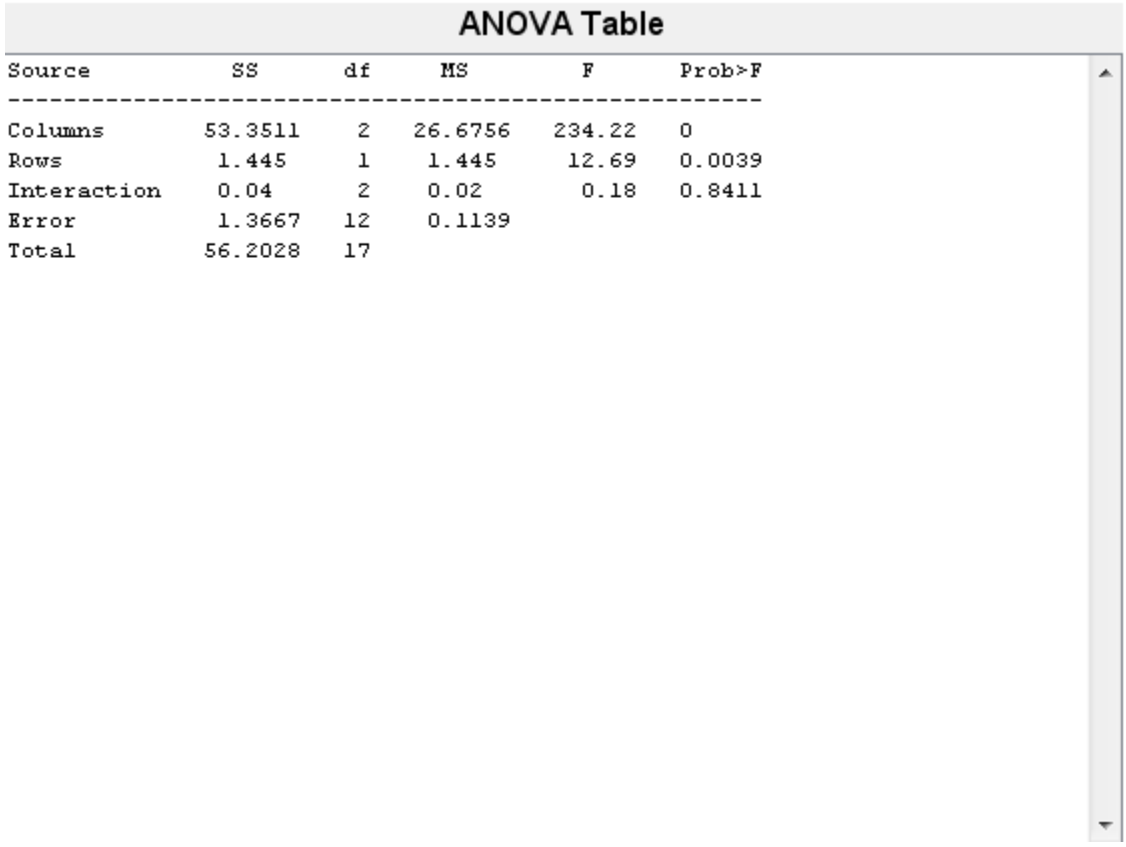
```
load mileage
mileage
```

```
mileage =

   33.3000   34.5000   37.4000
   33.4000   34.8000   36.8000
   32.9000   33.8000   37.6000
   32.6000   33.4000   36.6000
   32.5000   33.7000   37.0000
   33.0000   33.9000   36.7000
```

There are three car models (columns) and two factories (rows). The data has six mileage rows because each factory provided three cars of each model for the study (i.e, the replication number is three). The data from the first factory is in the first three rows, and the data from the second factory is in the last three rows.

Perform two-way ANOVA. Return the structure of statistics, `stats`, to use in multiple comparisons.

```
nmbcars = 3; % Number of cars from each model, i.e., number of replications
[~,~,stats] = anova2(mileage,nmbcars);
```



You can use the *F*-statistics to do hypotheses tests to find out if the mileage is the same across models, factories, and model - factory pairs. Before performing these tests, you must adjust for the additive effects. `anova2` ret rns the *p*-value from these tests.

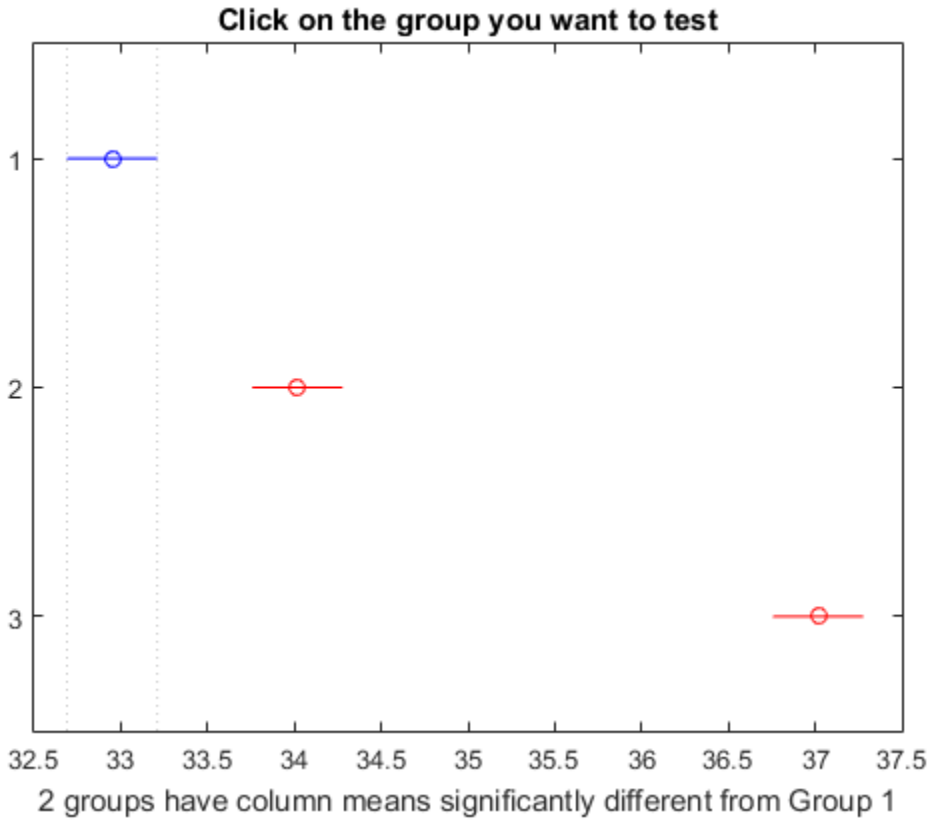
The *p*-value for the model effect (`Columns`) is zero to four decimal places. This result is a strong indication that the mileage varies from one model to another.

The *p*-value for the factory effect (`Rows`) is 0.0039, which is also highly significant. This value indicates that one factory is out-performing the other in the gas mileage of the cars it produces. The observed *p*-value indicates that an *F*-statistic as extreme as the observed *F* occurs by chance about four out of 1000 times, if the gas mileage were truly equal from factory to factory.

The factories and models appear to have no interaction. The *p*-value, 0.8411, means that the observed result is likely (84 out 100 times), given that there is no interaction.

Perform "Multiple Comparisons" to find out which pair of the three car models is significantly different.

```
c = multcompare(stats)

Note: Your model includes an interaction term.  A test of main effects can be
difficult to interpret when the model includes interactions.

c =

    1.0000    2.0000   -1.5865   -1.0667   -0.5469    0.0004
    1.0000    3.0000   -4.5865   -4.0667   -3.5469    0.0000
    2.0000    3.0000   -3.5198   -3.0000   -2.4802    0.0000
```



In the matrix `c`, the first two columns show the pairs of car models that are compared. By default, multcompare uses Tukey's honestly significant difference procedure. The last column shows the *p*-values for the test. All *p*-values are small (0.0004, 0, and 0), which indicates that the mean mileage of all car models are significantly different from each other.

In the figure the blue bar is the comparison interval for the mean mileage of the first car model. The red bars are the comparison intervals for the mean mileage of the second and third car models. None of the second and third comparison intervals overlap with the first comparison interval, indicating that the mean mileage of the first car model is different from the mean mileage of the second and the third car models. If you click on one of the other bars, you can test for the other car models. None of the comparison

intervals overlap, indicating that the mean mileage of each car model is significantly different from the other two.

Mathematical Details

The two-factor ANOVA partitions the total variation into the following components:

- Variation of row factor group means from the overall mean, $\bar{y}_{i..} - \bar{y}_{...}$
- Variation of column factor group means from the overall mean, $\bar{y}_{.j.} - \bar{y}_{...}$
- Variation of overall mean plus the replication mean from the column factor group mean plus row factor group mean, $\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...}$
- Variation of observations from the replication means, $y_{ijk} - \bar{y}_{ij.}$

ANOVA partitions the total sum of squares (SST) into the sum of squares due to row factor A (SS_A), the sum of squares due to column factor B (SS_B), the sum of squares due to interaction between A and B (SS_{AB}), and the sum of squares error (SSE).

$$\underbrace{\sum_{i=1}^{m}\sum_{j=1}^{k}\sum_{r=1}^{R}\left(y_{ijk}-\bar{y}_{...}\right)^2}_{SST} = \underbrace{kR\sum_{i=1}^{m}\left(\bar{y}_{i..}-\bar{y}_{...}\right)^2}_{SS_B} + \underbrace{mR\sum_{j=1}^{k}\left(\bar{y}_{.j.}-\bar{y}_{...}\right)^2}_{SS_A}$$
$$+ \underbrace{R\sum_{i=1}^{m}\sum_{j=1}^{k}\left(\bar{y}_{ij.}-\bar{y}_{i..}-\bar{y}_{.j.}+\bar{y}_{...}\right)^2}_{SS_{AB}} + \underbrace{\sum_{i=1}^{m}\sum_{j=1}^{k}\sum_{r=1}^{R}\left(y_{ijk}-\bar{y}_{ij.}\right)^2}_{SSE}$$

ANOVA takes the variation due to the factor or interaction and compares it to the variation due to error. If the ratio of the two variations is high, then the effect of the factor or the interaction effect is statistically significant. You can measure the statistical significance using a test statistic that has an F-distribution.

For the null hypothesis that the mean response for groups of the row factor A are equal, the test statistic is

$$F = \frac{SS_B \big/ (m-1)}{SSE \big/ mk(R-1)} \sim F_{m-1,mk(R-1)}.$$

For the null hypothesis that the mean response for groups of the column factor B are equal, the test statistic is

$$F = \frac{SS_A / (k-1)}{SSE / mk(R-1)} \sim F_{k-1,mk(R-1)}.$$

For the null hypothesis that the interaction of the column and row factors are equal to zero, the test statistic is

$$F = \frac{SS_{AB} / (m-1)(k-1)}{SSE / mk(R-1)} \sim F_{(m-1)(k-1),mk(R-1)}.$$

If the p-value for the F-statistic is smaller than the significance level, then ANOVA rejects the null hypothesis. The most common significance levels are 0.01 and 0.05.

ANOVA Table

The ANOVA table captures the variability in the model by the source, the F-statistic for testing the significance of this variability, and the p-value for deciding on the significance of this variability. The p-value returned by `anova2` depends on assumptions about the random disturbances, ε_{ij}, in the model equation. For the p-value to be correct, these disturbances need to be independent, normally distributed, and have constant variance. The standard ANOVA table has this form:

Source	SS	df	MS	F	p-value
Columns	SS_A	k - 1	MS_A	MS_A/MSE	$P(F_{k-1,mk(R-1)}) > F$
Rows	SS_B	m - 1	MS_B	MS_B/MSE	$P(F_{m-1,mk(R-1)}) > F$
Interaction	SS_{AB}	$(m-1)(k-1)$	MS_{AB}	MS_{AB}/MSE	$P(F_{(m-1)(k-1),mk(R-1)}) > F$
Error	SSE	$mk(R-1)$	MSE		
Total	SST	mkR - 1			

`anova2` returns the standard ANOVA table as a cell array with six columns.

Column	Definition
`Source`	The source of the variability.
`SS`	The sum of squares due to each source.
`df`	The degrees of freedom associated with each source. Suppose J is the number of groups in the column factor, I is the number of groups in the row factor, and R is the number of replications. Then, the total number of observations is IJR and the total degrees of freedom is $IJR - 1$. $I - 1$ is the degrees of freedom for the row factor,$J - 1$ is the degrees of freedom for the column factor, $(I - 1)(J - 1)$ is the interaction degrees of freedom, and $IJ(R - 1)$ is the error degrees of freedom.
`MS`	The mean squares for each source, which is the ratio `SS/df`.
`F`	F-statistic, which is the ratio of the mean squares.
`Prob>F`	The p-value, which is the probability that the F-statistic can take a value larger than the computed test-statistic value. `anova2` derives this probability from the cdf of the F-distribution.

The rows of the ANOVA table show the variability in the data that is divided by the source.

Row (Source)	Definition
`Columns`	Variability due to the column factor
`Rows`	Variability due to the row factor
`Interaction`	Variability due to the interaction of the row and column factors
`Error`	Variability due to the differences between the data in each group and the group mean (variability *within* groups)

Row (Source)	Definition
`Total`	Total variability

References

[1] Wu, C. F. J., and M. Hamada. *Experiments: Planning, Analysis, and Parameter Design Optimization*, 2000.

[2] Neter, J., M. H. Kutner, C. J. Nachtsheim, and W. Wasserman. 4th ed. *Applied Linear Statistical Models*. Irwin Press, 1996.

See Also

`anova1` | `anova2` | `anovan` | `multcompare`

Related Examples

- "Two-Way ANOVA for Unbalanced Design" on page 22-88

More About

- "One-Way ANOVA" on page 8-3
- "N-Way ANOVA" on page 8-36
- "Multiple Comparisons" on page 8-26
- "Nonparametric Methods" on page 8-67

Multiple Comparisons

In this section...

Introduction

Analysis of variance (ANOVA) techniques test whether a set of group means (treatment effects) are equal or not. Rejection of the null hypothesis leads to the conclusion that not all group means are the same. This result, however, does not provide further information on which group means are different.

Performing a series of *t*-tests to determine which pairs of means are significantly different is not recommended. When you perform multiple *t*-tests, the probability that the means appear significant, and significant difference results might be due to large number of tests. These *t*-tests use the data from the same sample, hence they are not independent. This fact makes it more difficult to quantify the level of significance for multiple tests.

Suppose that in a single *t*-test, the probability that the null hypothesis (H_0) is rejected when it is actually true is a small value, say 0.05. Suppose also that you conduct six independent *t*-tests. If the significance level for each test is 0.05, then the probability that the tests correctly fail to reject H_0, when H_0 is true for each case, is $(0.95)^6 = 0.735$. And the probability that one of the tests incorrectly rejects the null hypothesis is $1 - 0.735 = 0.265$, which is much higher than 0.05.

To compensate for multiple tests, you can use multiple comparison procedures. The Statistics and Machine Learning Toolbox function `multcompare` performs multiple pairwise comparison of the group means, or treatment effects. The options are Tukey's honestly significant difference criterion, the Bonferroni method, Scheffe's procedure, Fisher's least significant differences (lsd) method, and Dunn & Sidak's approach to *t*-test.

To perform multiple comparisons of group means, provide the structure `stats` as an input for `multcompare`. You can obtain `stats` from one of the following functions :

- `anova1` — One-way ANOVA
- `anova2` — Two-way ANOVA
- `anovan` — *N*-way ANOVA
- `aoctool` — Interactive ANCOVA
- `kruskalwallis` — Nonparametric method for one-way layout
- `friedman` — Nonparametric method for two-way layout

For multiple comparison procedure options for repeated measures, see `multcompare` (`RepeatedMeasuresModel`).

Multiple Comparisons Using One-Way ANOVA

Load the sample data.

```
load carsmall
```

`MPG` represents the miles per gallon for each car, and `Cylinders` represents the number of cylinders in each car, either 4, 6, or 8 cylinders.

Test if the mean miles per gallon (mpg) is different across cars that have different numbers of cylinders. Also compute the statistics needed for multiple comparison tests.

```
[p,~,stats] = anova1(MPG,Cylinders,'off');
p
```

```
p =

   4.4902e-24
```

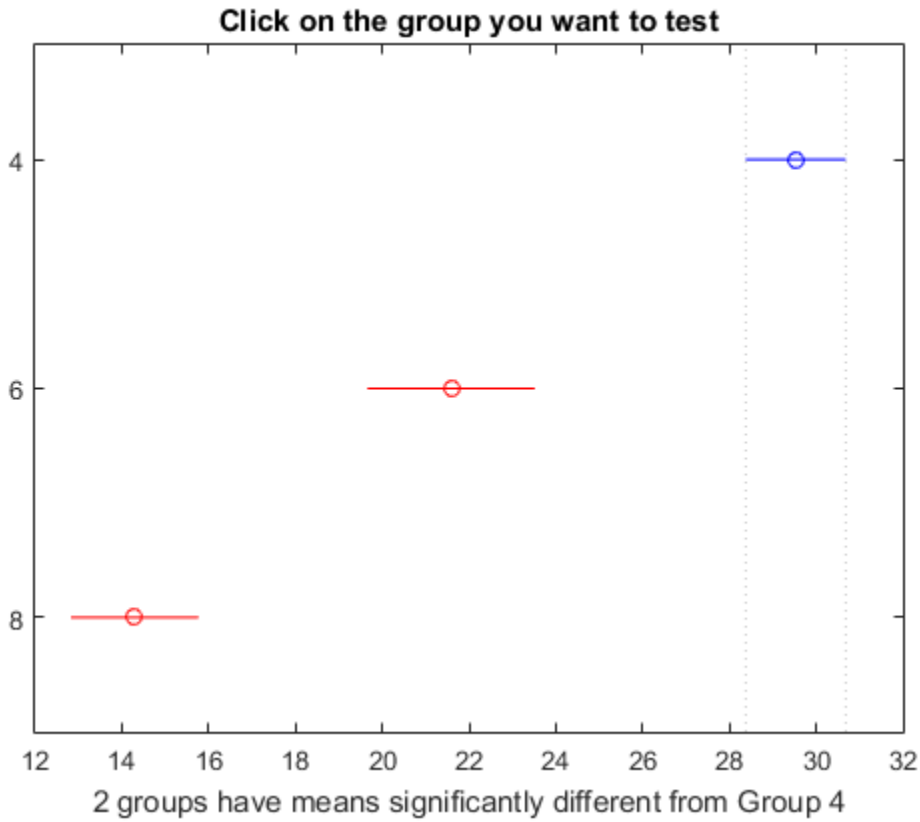
The small *p*-value of about 0 is a strong indication that mean miles per gallon is significantly different across cars with different numbers of cylinders.

Perform a multiple comparison test, using the Bonferroni method, to determine which numbers of cylinders make a difference in the performance of the cars.

```
[results,means] = multcompare(stats,'CType','bonferroni')
```

```
results =
```

```
    1.0000    2.0000    4.8605    7.9418   11.0230    0.0000
    1.0000    3.0000   12.6127   15.2337   17.8548    0.0000
    2.0000    3.0000    3.8940    7.2919   10.6899    0.0000

means =

   29.5300    0.6363
   21.5882    1.0913
   14.2963    0.8660
```



In the `results` matrix, 1, 2, and 3 correspond to cars with 4, 6, and 8 cylinders, respectively. The first two columns show which groups are compared. For example, the

first row compares the cars with 4 and 6 cylinders. The fourth column shows the mean mpg difference for the compared groups. The third and fifth columns show the lower and upper limits for a 95% confidence interval for the difference in the group means. The last column shows the *p*-values for the tests. All *p*-values are zero, which indicates that the mean mpg for all groups differ across all groups.

In the figure the blue bar represents the group of cars with 4 cylinders. The red bars represent the other groups. None of the red comparison intervals for the mean mpg of cars overlap, which means that the mean mpg is significantly different for cars having 4, 6, or 8 cylinders.

The first column of the `means` matrix has the mean mpg estimates for each group of cars. The second column contains the standard errors of the estimates.

Multiple Comparisons for Three-Way ANOVA

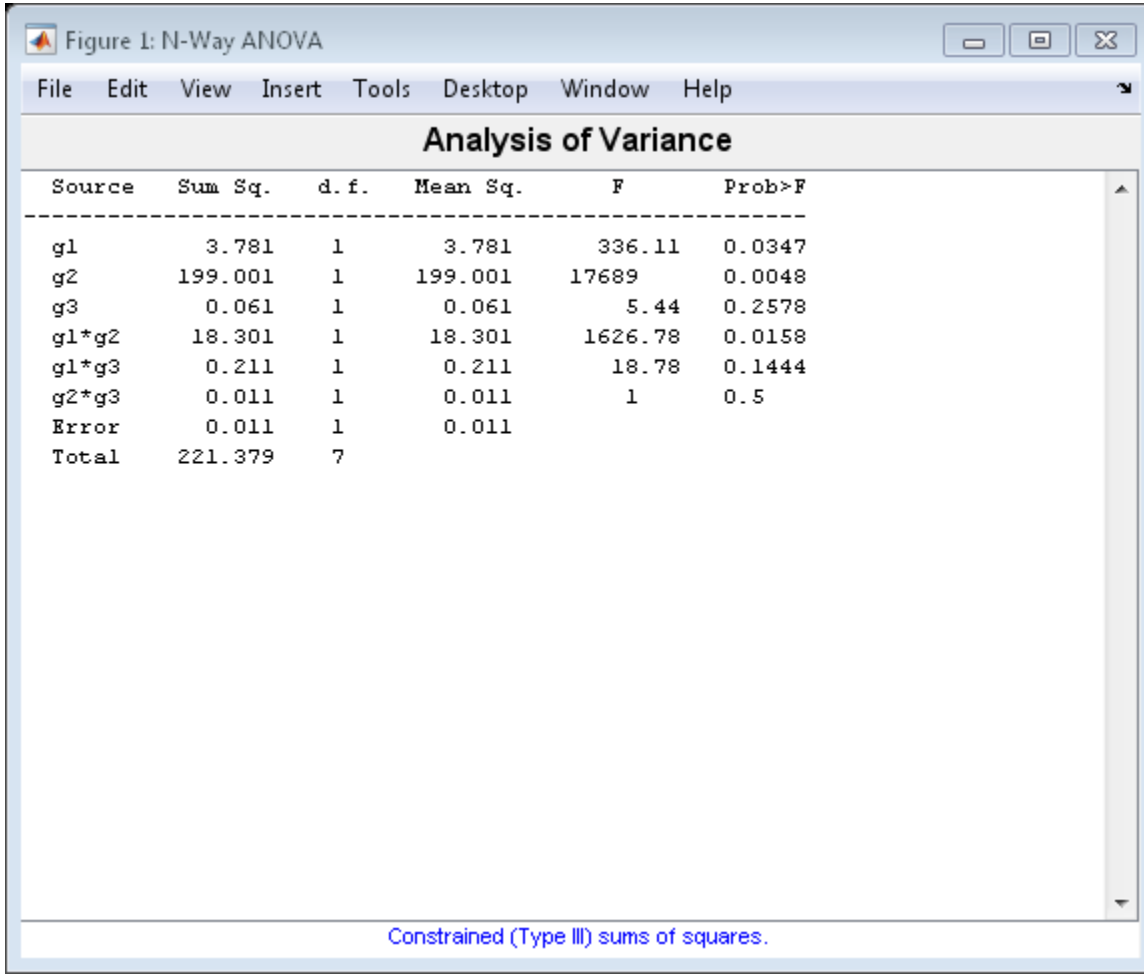
Load the sample data.

```
y = [52.7 57.5 45.9 44.5 53.0 57.0 45.9 44.0]';
g1 = [1 2 1 2 1 2 1 2];
g2 = {'hi';'hi';'lo';'lo';'hi';'hi';'lo';'lo'};
g3 = {'may';'may';'may';'may';'june';'june';'june';'june'};
```

`y` is the response vector and `g1`, `g2`, and `g3` are the grouping variables (factors). Each factor has two levels, and every observation in `y` is identified by a combination of factor levels. For example, observation `y(1)` is associated with level 1 of factor `g1`, level `'hi'` of factor `g2`, and level `'may'` of factor `g3`. Similarly, observation `y(6)` is associated with level 2 of factor `g1`, level `'hi'` of factor `g2`, and level `'june'` of factor `g3`.

Test if the response is the same for all factor levels. Also compute the statistics required for multiple comparison tests.

```
[~,~,stats] = anovan(y,{g1 g2 g3},'model','interaction',...
    'varnames',{'g1','g2','g3'});
```

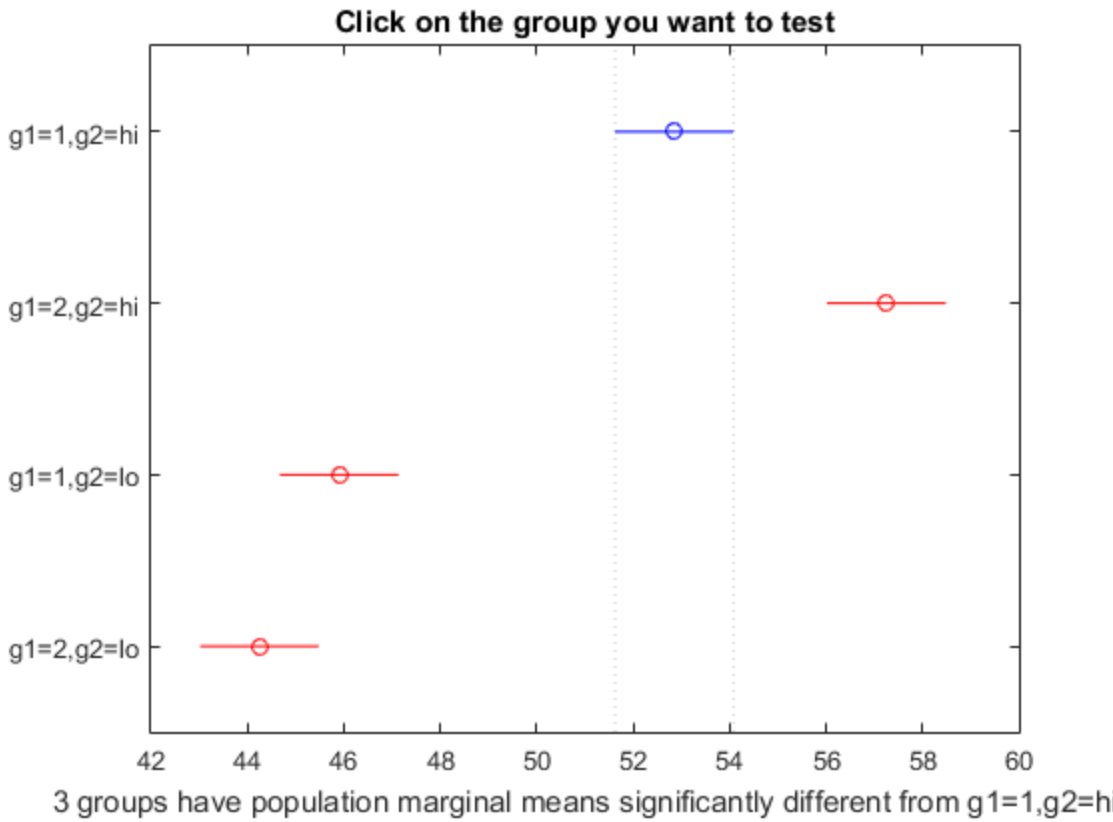


The p-value of 0.2578 indicates that the mean responses for levels `'may'` and `'june'` of factor `g3` are not significantly different. The p-value of 0.0347 indicates that the mean responses for levels `1` and `2` of factor `g1` are significantly different. Similarly, the p-value of 0.0048 indicates that the mean responses for levels `'hi'` and `'lo'` of factor `g2` are significantly different.

Perform multiple comparison tests to find out which groups of the factors `g1` and `g2` are significantly different.

```
results = multcompare(stats,'Dimension',[1 2])
```

```
results =

    1.0000    2.0000   -6.8604   -4.4000   -1.9396    0.0280
    1.0000    3.0000    4.4896    6.9500    9.4104    0.0177
    1.0000    4.0000    6.1396    8.6000   11.0604    0.0143
    2.0000    3.0000    8.8896   11.3500   13.8104    0.0108
    2.0000    4.0000   10.5396   13.0000   15.4604    0.0095
    3.0000    4.0000   -0.8104    1.6500    4.1104    0.0745
```



multcompare compares the combinations of groups (levels) of the two grouping variables, g1 and g2. In the results matrix, the number 1 corresponds to the combination of level 1 of g1 and level hi of g2, the number 2 corresponds to the combination of level 2 of g1 and level hi of g2. Similarly, the number 3 corresponds to the combination of level 1 of g1 and level lo of g2, and the number 4 corresponds to the combination of level 2 of g1 and level lo of g2. The last column of the matrix contains the *p*-values.

For example, the first row of the matrix shows that the combination of level 1 of g1 and level hi of g2 has the same mean response values as the combination of level 2 of g1 and level hi of g2. The *p*-value corresponding to this test is 0.0280, which indicates that the mean responses are significantly different. You can also see this result in the figure. The blue bar shows the comparison interval for the mean response for the combination of level 1 of g1 and level hi of g2. The red bars are the comparison intervals for the mean response for other group combinations. None of the red bars overlap with the blue bar, which means the mean response for the combination of level 1 of g1 and level hi of g2 is significantly different from the mean response for other group combinations.

You can test the other groups by clicking on the corresponding comparison interval for the group. The bar you click on turns to blue. The bars for the groups that are significantly different are red. The bars for the groups that are not significantly different are gray. For example, if you click on the comparison interval for the combination of level 1 of g1 and level lo of g2, the comparison interval for the combination of level 2 of g1 and level lo of g2 overlaps, and is therefore gray. Conversely, the other comparison intervals are red, indicating significant difference.

Multiple Comparison Procedures

To specify the multiple comparison procedure you want multcompare to conduct use the 'CType' name-value pair argument. multcompare provides the following procedures:

- “Tukey’s Honestly Significant Difference Procedure” on page 8-33
- “Bonferroni Method” on page 8-33
- “Dunn & Sidák’s Approach” on page 8-34
- “Least Significant Difference” on page 8-34
- “Scheffe’s Procedure” on page 8-35

Tukey's Honestly Significant Difference Procedure

You can specify Tukey's honestly significant difference procedure using the `'CType','Tukey-Kramer'` or `'CType','hsd'` name-value pair argument. The test is based on studentized range distribution. Reject H_0:$a_i = a_j$ if

$$|t| = \frac{\left|\bar{y}_i - \bar{y}_j\right|}{\sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}} > \frac{1}{\sqrt{2}} q_{\alpha,k,N-k},$$

where $q_{\alpha,k,N-k}$ is the upper 100*(1 – α)th percentile of the studentized range distribution with parameter k and $N – k$ degrees of freedom. k is the number of groups (treatments or marginal means) and N is the total number of observations.

Tukey's honestly significant difference procedure is optimal for balanced one-way ANOVA and similar procedures with equal sample sizes. It has been proven to be conservative for one-way ANOVA with different sample sizes. According to the unproven Tukey-Kramer conjecture, it is also accurate for problems where the quantities being compared are correlated, as in analysis of covariance with unbalanced covariate values.

Bonferroni Method

You can specify the Bonferroni method using the `'CType','bonferroni'` name-value pair. This method uses critical values from Student's t-distribution after an adjustment to compensate for multiple comparisons. The test rejects H_0:$a_i = a_j$ at the $\alpha \Big/ 2\binom{k}{2}$ significance level, where k is the number of groups if

$$|t| = \frac{\left|\bar{y}_i - \bar{y}_j\right|}{\sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}} > t_{\alpha \Big/ 2\binom{k}{2},N-k},$$

where N is the total number of observations and k is the number of groups (marginal means). This procedure is conservative, but usually less so than the Scheffé procedure.

Dunn & Sidák's Approach

You can specify Dunn & Sidak's approach using the `'CType','dunn-sidak'` name-value pair argument. It uses critical values from the t-distribution, after an adjustment for multiple comparisons that was proposed by Dunn and proved accurate by Sidák. This test rejects $H_0{:}a_i = a_j$ if

$$|t| = \frac{\left|\bar{y}_i - \bar{y}_j\right|}{\sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}} > t_{1-\eta/2,v},$$

where

$$\eta = 1 - (1-\alpha)^{1/\binom{k}{2}}$$

and k is the number of groups. This procedure is similar to, but less conservative than, the Bonferroni procedure.

Least Significant Difference

You can specify the least significance difference procedure using the `'CType','lsd'` name-value pair argument. This test uses the test statistic

$$t = \frac{\bar{y}_i - \bar{y}_j}{\sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}}.$$

It rejects $H_0{:}a_i = a_j$ if

$$\left|\bar{y}_i - \bar{y}_j\right| > \underbrace{t_{\alpha/2,N-k}\sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}}_{LSD}.$$

Fisher suggests a protection against multiple comparisons by performing LSD only when the null hypothesis H_0: $a_1 = a_2 = \ldots = a_k$ is rejected by ANOVA F-test. Even in this case,

LSD might not reject any of the individual hypotheses. It is also possible that ANOVA does not reject H_0, even when there are differences between some group means. This behavior occurs because the equality of the remaining group means can cause the *F*-test statistic to be nonsignificant. Without any condition, LSD does not provide any protection against the multiple comparison problem.

Scheffe's Procedure

You can specify Scheffe's procedure using the `'CType','scheffe'` name-value pair argument. The critical values are derived from the *F* distribution. The test rejects H_0:$a_i = a_j$ if

$$\frac{\left|\bar{y}_i - \bar{y}_j\right|}{\sqrt{MSE\left(\frac{1}{n_i}+\frac{1}{n_j}\right)}} > \sqrt{(k-1)F_{k-1,N-k,\alpha}}$$

This procedure provides a simultaneous confidence level for comparisons of all linear combinations of the means. It is conservative for comparisons of simple differences of pairs.

References

[1] Milliken G. A. and D. E. Johnson. *Analysis of Messy Data. Volume I: Designed Experiments*. Boca Raton, FL: Chapman & Hall/CRC Press, 1992.

[2] Neter J., M. H. Kutner, C. J. Nachtsheim, W. Wasserman. 4th ed. *Applied Linear Statistical Models*.Irwin Press, 1996.

[3] Hochberg, Y., and A. C. Tamhane. *Multiple Comparison Procedures*. Hoboken, NJ: John Wiley & Sons, 1987.

See Also

`anova1` | `anova2` | `anovan` | `aoctool` | `friedman` | `kruskalwallis` | `multcompare`

Related Examples

- "Perform One-Way ANOVA" on page 8-6
- "Perform Two-Way ANOVA" on page 8-18

N-Way ANOVA

In this section...

Introduction to N-Way ANOVA

You can use the Statistics and Machine Learning Toolbox function `anovan` to perform N-way ANOVA. Use N-way ANOVA to determine if the means in a set of data differ with respect to groups (levels) of multiple factors. By default, `anovan` treats all grouping variables as fixed effects. For an example of ANOVA with random effects, see "ANOVA with Random Effects" on page 8-48.

N-way ANOVA is a generalization of two-way ANOVA. For three factors, for example, the model can be written as

$$y_{ijkr} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \varepsilon_{ijkr},$$

where

- y_{ijkr} is an observation of the response variable. i represents group i of factor A, $i = 1, 2, ..., I$, j represents group j of factor B, $j = 1, 2, ..., J$, k represents group k of factor C, and r represents the replication number, $r = 1, 2, ..., R$. For constant R, there are a total of $N = I*J*K*R$ observations, but the number of observations does not have to be the same for each combination of groups of factors.
- μ is the overall mean.
- α_i are the deviations of groups of factor A from the overall mean μ due to factor A. The values of α_i sum to 0, i.e., $\sum_{i=1}^{I} \alpha_i = 0$.
- β_j are the deviations of groups in factor B from the overall mean μ due to factor B. The values of β_j sum to 0, i.e., $\sum_{j=1}^{J} \beta_j = 0$.

- γ_k are the deviations of groups in factor C from the overall mean μ due to factor C. The values of γ_k sum to 0, i.e., $\sum_{k=1}^{K}\gamma_k = 0$.
- $(\alpha\beta)_{ij}$ is the interaction term between factors A and B. $(\alpha\beta)_{ij}$ sum to 0 over either index, i.e., $\sum_{i=1}^{I}(\alpha\beta)_{ij} = \sum_{j=1}^{J}(\alpha\beta)_{ij} = 0$.
- $(\alpha\gamma)_{ik}$ is the interaction term between factors A and C. The values of $(\alpha\gamma)_{ik}$ sum to 0 over either index, i.e., $\sum_{i=1}^{I}(\alpha\gamma)_{ik} = \sum_{k=1}^{K}(\alpha\gamma)_{ik} = 0$.
- $(\beta\gamma)_{jk}$ is the interaction term between factors B and C. The values of $(\beta\gamma)_{jk}$ sum to 0 over either index, i.e., $\sum_{j=1}^{J}(\beta\gamma)_{jk} = \sum_{k=1}^{K}(\beta\gamma)_{jk} = 0$.
- $(\alpha\beta\gamma)_{ijk}$ is the three-way interaction term between factors A, B, and C. The values of $(\alpha\beta\gamma)_{ijk}$ sum to 0 over any index, i.e., $\sum_{i=1}^{I}(\alpha\beta\gamma)_{ijk} = \sum_{j=1}^{J}(\alpha\beta\gamma)_{ijk} = \sum_{k=1}^{K}(\alpha\beta\gamma)_{ijk} = 0$.
- ε_{ijkr} are the random disturbances. They are assumed to be independent, normally distributed, and have constant variance.

Three-way ANOVA tests hypotheses about the effects of factors A, B, C, and their interactions on the response variable y. The hypotheses about the equality of the mean responses for groups of factor A are

$$H_0 : \alpha_1 = \alpha_2 \cdots = \alpha_I$$
$$H_1 : \text{ at least one } \alpha_i \text{ is different, } i = 1,\ 2,\ \ldots,\ I.$$

The hypotheses about the equality of the mean response for groups of factor B are

$$H_0 : \beta_1 = \beta_2 = \cdots = \beta_J$$
$$H_1 : \text{ at least one } \beta_j \text{ is different, } j = 1,\ 2,\ \ldots,\ J.$$

The hypotheses about the equality of the mean response for groups of factor C are

$$H_0 : \gamma_1 = \gamma_2 = \cdots = \gamma_K$$
$$H_1 : \text{ at least one } \gamma_k \text{ is different, } k = 1,\ 2,\ \ldots,\ K.$$

The hypotheses about the interaction of the factors are

$$H_0 : (\alpha\beta)_{ij} = 0$$
$$H_1 : \text{at least one } (\alpha\beta)_{ij} \neq 0$$

$$H_0 : (\alpha\gamma)_{ik} = 0$$
$$H_1 : \text{at least one } (\alpha\gamma)_{ik} \neq 0$$

$$H_0 : (\beta\gamma)_{jk} = 0$$
$$H_1 : \text{at least one } (\beta\gamma)_{jk} \neq 0$$

$$H_0 : (\alpha\beta\gamma)_{ijk} = 0$$
$$H_1 : \text{at least one } (\alpha\beta\gamma)_{ijk} \neq 0$$

In this notation parameters with two subscripts, such as $(\alpha\beta)_{ij}$, represent the interaction effect of two factors. The parameter $(\alpha\beta\gamma)_{ijk}$ represents the three-way interaction. An ANOVA model can have the full set of parameters or any subset, but conventionally it does not include complex interaction terms unless it also includes all simpler terms for those factors. For example, one would generally not include the three-way interaction without also including all two-way interactions.

Prepare Data for N-Way ANOVA

Unlike `anova1` and `anova2`, `anovan` does not expect data in a tabular form. Instead, it expects a vector of response measurements and a separate vector (or text array) containing the values corresponding to each factor. This input data format is more convenient than matrices when there are more than two factors or when the number of measurements per factor combination is not constant.

$$\begin{array}{lcl}
y & = & [\ \underset{\uparrow}{y_1},\ \underset{\uparrow}{y_2},\ \underset{\uparrow}{y_3},\ \underset{\uparrow}{y_4},\ \underset{\uparrow}{y_5},\ \cdots,\ \underset{\uparrow}{y_N}\ ]' \\
g1 & = & \{\ 'A',\ 'A',\ 'C',\ 'B',\ 'B',\ \cdots,\ 'D'\ \} \\
g2 & = & [\ 1\ \ 2\ \ 1\ \ 3\ \ 1\ \ \cdots,\ 2\ ] \\
g3 & = & \{\ \text{'hi'},\ \text{'mid'},\ \text{'low'},\ \text{'mid'},\ \text{'hi'},\ \cdots,\ \text{'low'}\ \}
\end{array}$$

Perform N-Way ANOVA

This example shows how to perform N-way ANOVA on car data with mileage and other information on 406 cars made between 1970 and 1982.

Load the sample data.

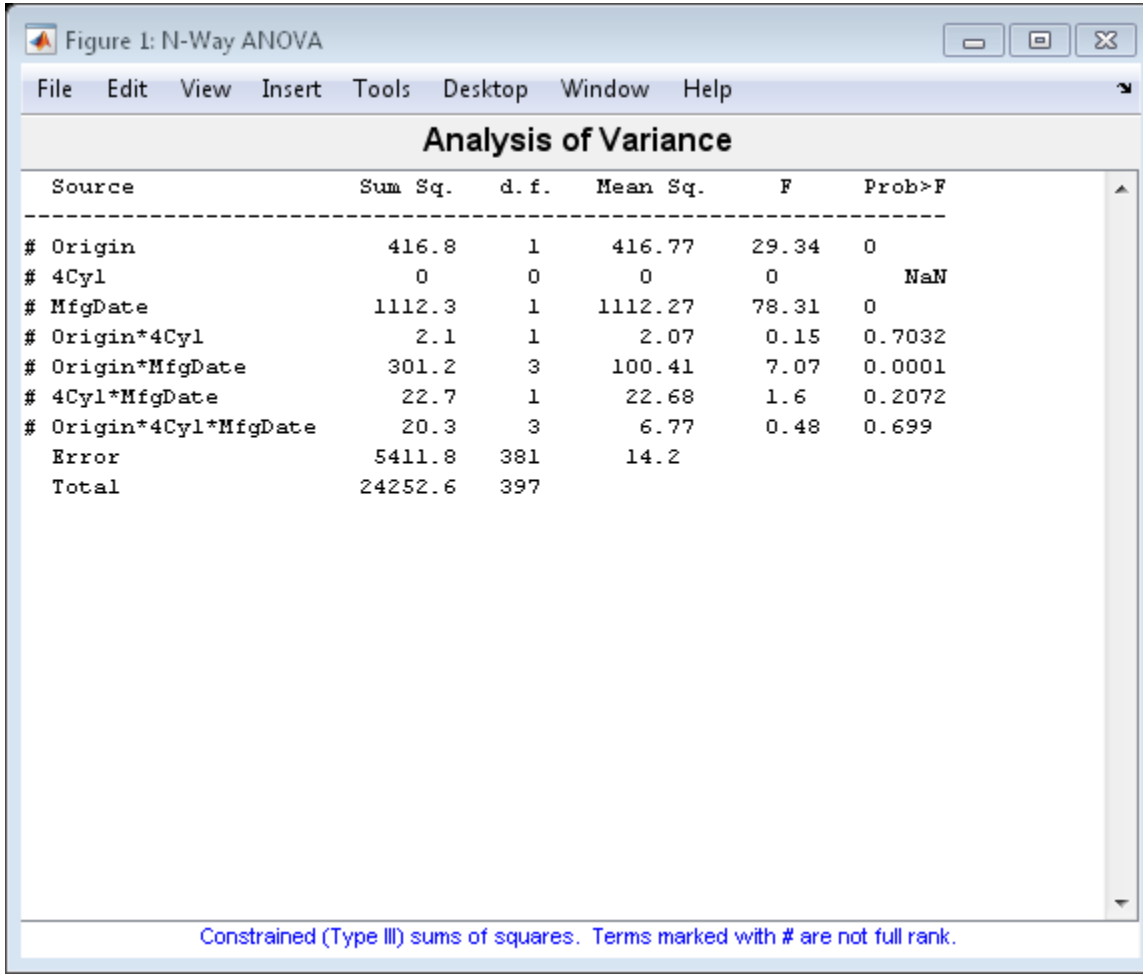
```
load carbig
```

The example focusses on four variables. `MPG` is the number of miles per gallon for each of 406 cars (though some have missing values coded as `NaN`). The other three variables are factors: `cyl4` (four-cylinder car or not), `org` (car originated in Europe, Japan, or the USA), and `when` (car was built early in the period, in the middle of the period, or late in the period).

Fit the full model, requesting up to three-way interactions and Type 3 sums-of-squares.

```
varnames = {'Origin';'4Cyl';'MfgDate'};
anovan(MPG,{org cyl4 when},3,3,varnames)
```

```
ans =

    0.0000
       NaN
    0.0000
    0.7032
    0.0001
    0.2072
    0.6990
```



Note that many terms are marked by a # symbol as not having full rank, and one of them has zero degrees of freedom and is missing a *p*-value. This can happen when there are missing factor combinations and the model has higher-order terms. In this case, the cross-tabulation below shows that there are no cars made in Europe during the early part of the period with other than four cylinders, as indicated by the 0 in `tbl(2,1,1)`.

```
[tbl,chi2,p,factorvals] = crosstab(org,when,cyl4)
```

```
tbl(:,:,1) =

    82    75    25
     0     4     3
     3     3     4


tbl(:,:,2) =

    12    22    38
    23    26    17
    12    25    32


chi2 =

  207.7689


p =

   8.0973e-38


factorvals =

    'USA'       'Early'    'Other'
    'Europe'    'Mid'      'Four'
    'Japan'     'Late'          []
```

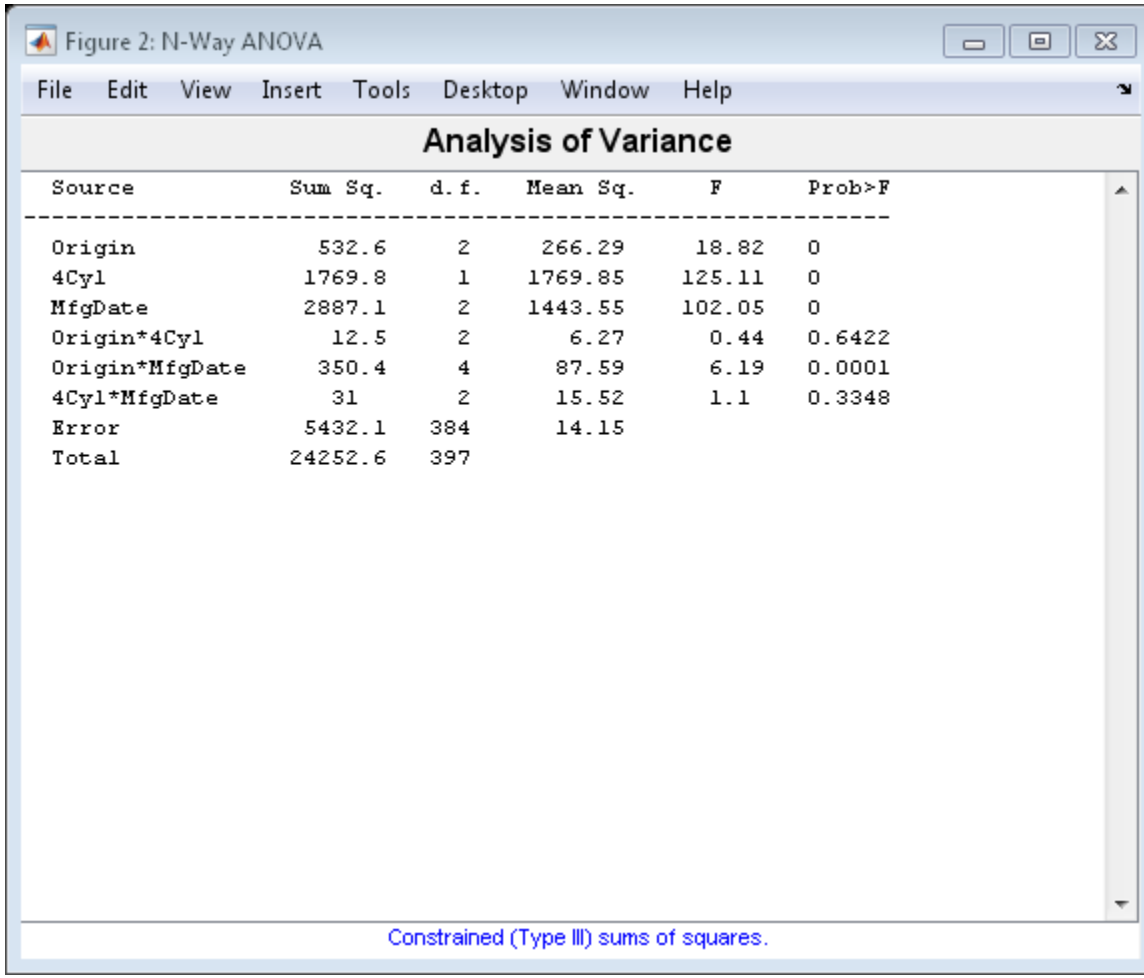
Consequently it is impossible to estimate the three-way interaction effects, and including the three-way interaction term in the model makes the fit singular.

Using even the limited information available in the ANOVA table, you can see that the three-way interaction has a *p*-value of 0.699, so it is not significant.

Examine only two-way interactions.

```
[p,tbl2,stats,terms] = anovan(MPG,{org cyl4 when},2,3,varnames);
terms


terms =
```

```
     1     0     0
     0     1     0
     0     0     1
     1     1     0
     1     0     1
     0     1     1
```



Now all terms are estimable. The *p*-values for interaction term 4 (`Origin*4Cyl`) and interaction term 6 (`4Cyl*MfgDate`) are much larger than a typical cutoff value of 0.05,

indicating these terms are not significant. You could choose to omit these terms and pool their effects into the error term. The output `terms` variable returns a matrix of codes, each of which is a bit pattern representing a term.

Omit terms from the model by deleting their entries from `terms`.

```
terms([4 6],:) = []
```

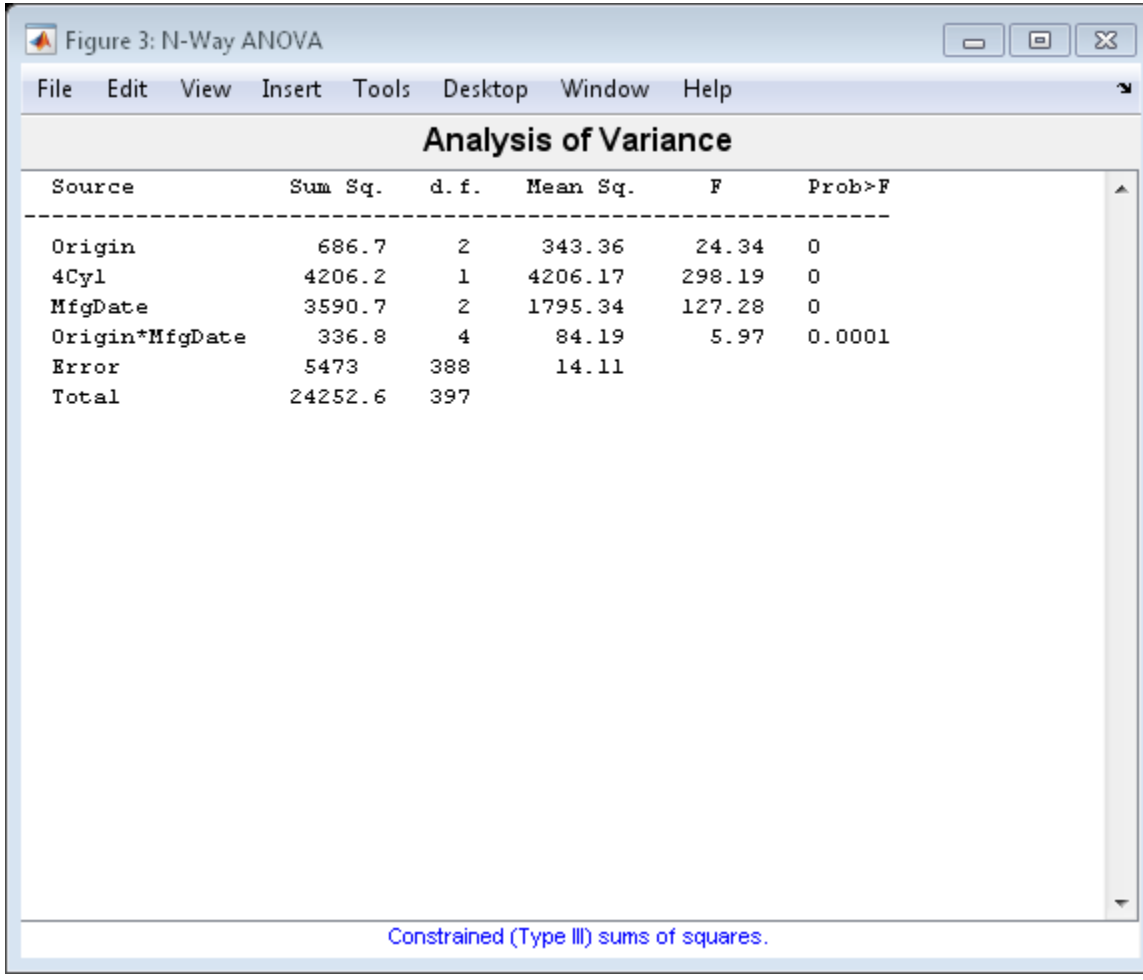
```
terms =

     1     0     0
     0     1     0
     0     0     1
     1     0     1
```

Run `anovan` again, this time supplying the resulting vector as the model argument. Also return the statistics required for multiple comparisons of factors.

```
[~,~,stats] = anovan(MPG,{org cyl4 when},terms,3,varnames)
```

```
stats =

         source: 'anovan'
          resid: [1x406 double]
         coeffs: [18x1 double]
            Rtr: [10x10 double]
       rowbasis: [10x18 double]
            dfe: 388
            mse: 14.1056
    nullproject: [18x10 double]
          terms: [4x3 double]
        nlevels: [3x1 double]
     continuous: [0 0 0]
          vmeans: [3x1 double]
       termcols: [5x1 double]
     coeffnames: {18x1 cell}
           vars: [18x3 double]
       varnames: {3x1 cell}
       grpnames: {3x1 cell}
        vnested: []
            ems: []
```

```
      denom: []
    dfdenom: []
    msdenom: []
     varest: []
      varci: []
   txtdenom: []
     txtems: []
    rtnames: []
```

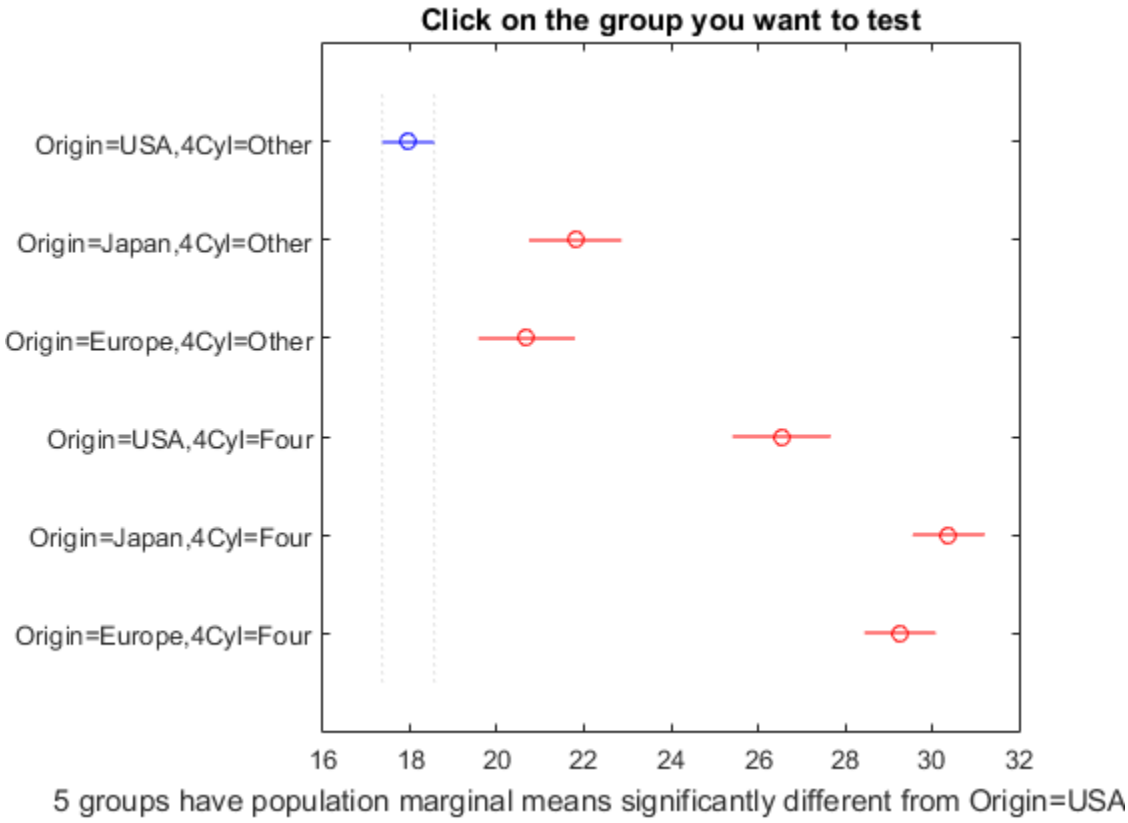


Now you have a more parsimonious model indicating that the mileage of these cars seems to be related to all three factors, and that the effect of the manufacturing date depends on where the car was made.

Perform multiple comparisons for Origin and Cylinder.

```
results = multcompare(stats,'Dimension',[1,2])
```

```
results =

    1.0000    2.0000   -5.4891   -3.8412   -2.1932    0.0000
    1.0000    3.0000   -4.4146   -2.7251   -1.0356    0.0001
    1.0000    4.0000   -9.9992   -8.5828   -7.1664    0.0000
    1.0000    5.0000  -14.0237  -12.4240  -10.8242    0.0000
    1.0000    6.0000  -12.8980  -11.3080   -9.7180    0.0000
    2.0000    3.0000   -0.7171    1.1160    2.9492    0.5085
    2.0000    4.0000   -7.3655   -4.7417   -2.1179    0.0000
    2.0000    5.0000   -9.9992   -8.5828   -7.1664    0.0000
    2.0000    6.0000   -9.7464   -7.4668   -5.1872    0.0000
    3.0000    4.0000   -8.5396   -5.8577   -3.1757    0.0000
    3.0000    5.0000  -12.0518   -9.6988   -7.3459    0.0000
    3.0000    6.0000   -9.9992   -8.5828   -7.1664    0.0000
    4.0000    5.0000   -5.4891   -3.8412   -2.1932    0.0000
    4.0000    6.0000   -4.4146   -2.7251   -1.0356    0.0001
    5.0000    6.0000   -0.7171    1.1160    2.9492    0.5085
```



See Also

`anova1` | `anovan` | `kruskalwallis` | `multcompare`

Related Examples

- "ANOVA with Random Effects" on page 8-48

More About

- "One-Way ANOVA" on page 8-3
- "Two-Way ANOVA" on page 8-15
- "Multiple Comparisons" on page 8-26

- “Nonparametric Methods” on page 8-67

ANOVA with Random Effects

This example shows how to use anovan to fit models where a factor's levels represent a random selection from a larger (infinite) set of possible levels.

In an ordinary ANOVA model, each grouping variable represents a fixed factor. The levels of that factor are a fixed set of values. The goal is to determine whether different factor levels lead to different response values.

Set Up the Model

Load the sample data.

```
load mileage
```

The anova2 function works only with balanced data, and it infers the values of the grouping variables from the row and column numbers of the input matrix. The anovan function, on the other hand, requires you to explicitly create vectors of grouping variable values. Create these vectors in the following way.

Create an array indicating the factory for each value in mileage. This array is 1 for the first column, 2 for the second, and 3 for the third.

```
factory  = repmat(1:3,6,1);
```

Create an array indicating the car model for each mileage value. This array is 1 for the first three rows of mileage, and 2 for the remaining three rows.

```
carmod = [ones(3,3); 2*ones(3,3)];
```

Turn these matrices into vectors and display them.

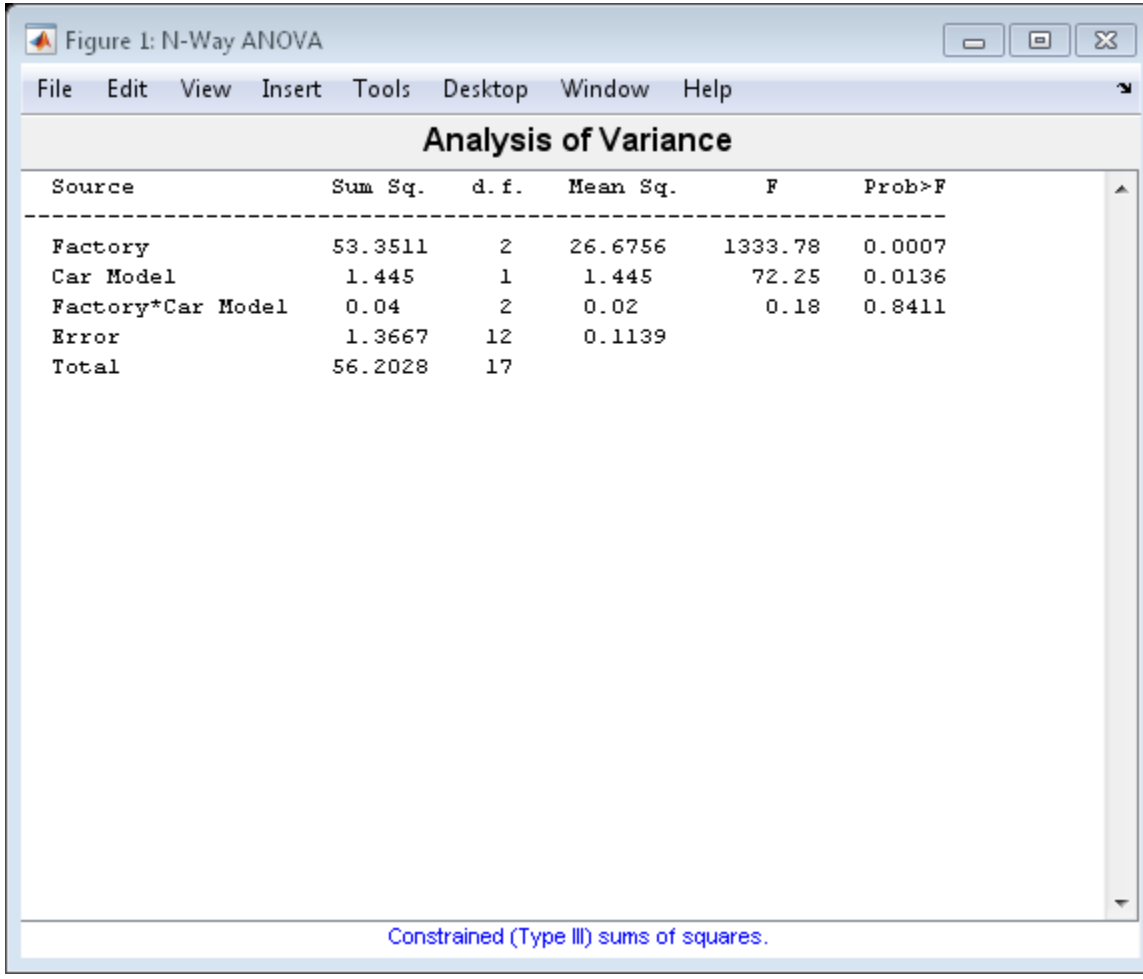
```
mileage = mileage(:);
factory = factory(:);
carmod = carmod(:);
[mileage factory carmod]


ans =

   33.3000    1.0000    1.0000
   33.4000    1.0000    1.0000
```

```
   32.9000    1.0000    1.0000
   32.6000    1.0000    2.0000
   32.5000    1.0000    2.0000
   33.0000    1.0000    2.0000
   34.5000    2.0000    1.0000
   34.8000    2.0000    1.0000
   33.8000    2.0000    1.0000
   33.4000    2.0000    2.0000
   33.7000    2.0000    2.0000
   33.9000    2.0000    2.0000
   37.4000    3.0000    1.0000
   36.8000    3.0000    1.0000
   37.6000    3.0000    1.0000
   36.6000    3.0000    2.0000
   37.0000    3.0000    2.0000
   36.7000    3.0000    2.0000
```

Fit a Random Effects Model

Suppose you are studying a few factories but you want information about what would happen if you build these same car models in a different factory, either one that you already have or another that you might construct. To get this information, fit the analysis of variance model, specifying a model that includes an interaction term and that the factory factor is random.

```
[pvals,tbl,stats] = anovan(mileage, {factory carmod}, ...
'model',2, 'random',1,'varnames',{'Factory' 'Car Model'});
```



In the fixed effects version of this fit, which you get by omitting the inputs `'random',1` in the preceding code, the effect of car model is significant, with a p -value of 0.0039. But in this example, which takes into account the random variation of the effect of the variable `'Car Model'` from one factory to another, the effect is still significant, but with a higher p -value of 0.0136.

F-Statistics for Models with Random Effects

The F -statistic in a model having random effects is defined differently than in a model having all fixed effects. In the fixed effects model, you compute the F -statistic for any term by taking the ratio of the mean square for that term with the mean square for error. In a random effects model, however, some F -statistics use a different mean square in the denominator.

In the example described in **Setting Up the Model** , the effect of the variable `'Factory'` could vary across car models. In this case, the interaction mean square takes the place of the error mean square in the F -statistic.

Find the F -statistic.

```
F = 26.6756 / 0.02
```

```
F =

   1.3338e+03
```

The degrees of freedom for the statistic are the degrees of freedom for the numerator (2) and denominator (2) mean squares.

Find the p -value.

```
pval = 1 - fcdf(F,2,2)
```

```
pval =

   7.4919e-04
```

With random effects, the expected value of each mean square depends not only on the variance of the error term, but also on the variances contributed by the random effects. You can see these dependencies by writing the expected values as linear combinations of contributions from the various model terms.

Find the coefficients of these linear combinations.

```
stats.ems
```

```
ans =

    6.0000    0.0000    3.0000    1.0000
    0.0000    9.0000    3.0000    1.0000
    0.0000    0.0000    3.0000    1.0000
         0         0         0    1.0000
```

```
This returns the |ems| field of the |stats| structure.
```

Display text representations of the linear combinations.

```
stats.txtems
```

```
ans =

    '6*V(Factory)+3*V(Factory*Car Model)+V(Error)'
    '9*Q(Car Model)+3*V(Factory*Car Model)+V(Error)'
    '3*V(Factory*Car Model)+V(Error)'
    'V(Error)'
```

The expected value for the mean square due to car model (second term) includes contributions from a quadratic function of the car model effects, plus three times the variance of the interaction term's effect, plus the variance of the error term. Notice that if the car model effects were all zero, the expression would reduce to the expected mean square for the third term (the interaction term). That is why the F -statistic for the car model effect uses the interaction mean square in the denominator.

In some cases there is no single term whose expected value matches the one required for the denominator of the F -statistic. In that case, the denominator is a linear combination of mean squares. The stats structure contains fields giving the definitions of the denominators for each F -statistic. The `txtdenom` field, `stats.txtdenom` , contains a text representation, and the `denom` field contains a matrix that defines a linear combination of the variances of terms in the model. For balanced models like this one, the `denom` matrix, `stats.denom` , contains zeros and ones, because the denominator is just a single term's mean square.

Display the `txtdenom` field.

```
stats.txtdenom
```

```
ans =

    'MS(Factory*Car Model)'
    'MS(Factory*Car Model)'
    'MS(Error)'
```

Display the `denom` field.

```
stats.denom
```

```
ans =

    0.0000    1.0000    0.0000
    0.0000    1.0000   -0.0000
    0.0000         0    1.0000
```

Variance Components

For the model described in **Setting Up the Model** , consider the mileage for a particular car of a particular model made at a random factory. The variance of that car is the sum of components, or contributions, one from each of the random terms.

Display the names of the random terms.

```
stats.rtnames
```

```
ans =

    'Factory'
    'Factory*Car Model'
    'Error'
```

You do not know the variances, but you can estimate them from the data. Recall that the `ems` field of the `stats` structure expresses the expected value of each term's mean square as a linear combination of unknown variances for random terms, and unknown quadratic forms for fixed terms. If you take the expected mean square expressions for the random terms, and equate those expected values to the computed mean squares, you get a system of equations that you can solve for the unknown variances. These solutions are the variance component estimates.

Display the variance component estimate for each term.

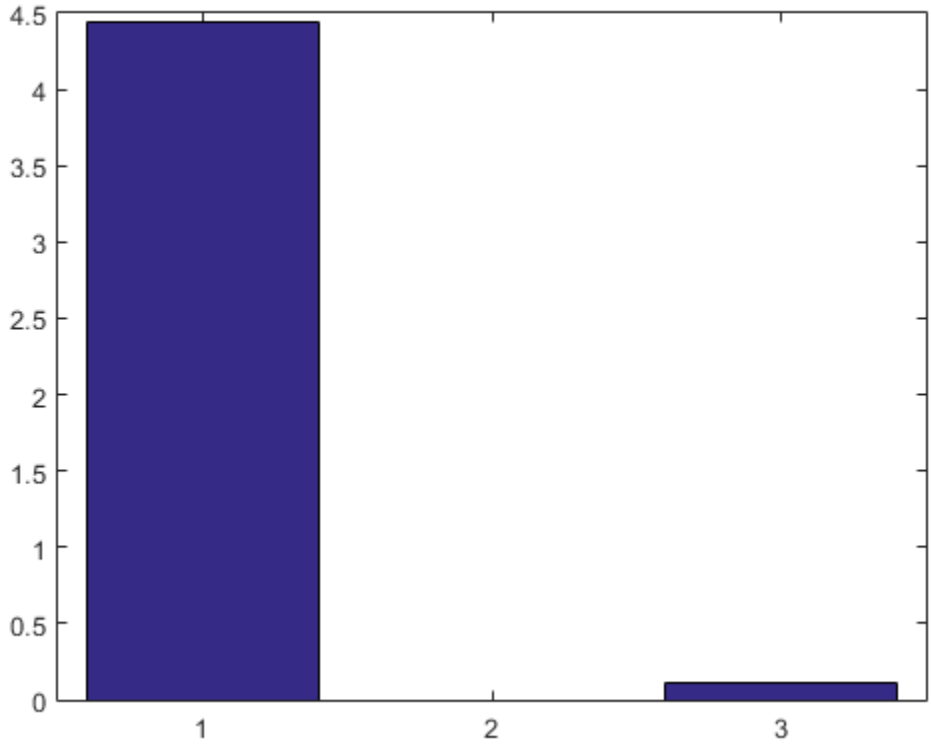
```
stats.varest
```

```
ans =

    4.4426
   -0.0313
    0.1139
```

Under some conditions, the variability attributed to a term is unusually low, and that term's variance component estimate is negative. In those cases it is common to set the estimate to zero, which you might do, for example, to create a bar graph of the components.

Create a bar graph of the components.

```
bar(max(0,stats.varest))
gca.xtick = 1:3;
gca.xticklabel = stats.rtnames;
```



You can also compute confidence bounds for the variance estimate. The `anovan` function does this by computing confidence bounds for the variance expected mean squares, and finding lower and upper limits on each variance component containing all of these bounds. This procedure leads to a set of bounds that is conservative for balanced data. (That is, 95% confidence bounds will have a probability of at least 95% of containing the true variances if the number of observations for each combination of grouping variables is the same.) For unbalanced data, these are approximations that are not guaranteed to be conservative.

Display the variance estimates and the confidence limits for the variance estimates of each component.

```
[{'Term' 'Estimate' 'Lower' 'Upper'};
```

```
 stats.rtnames, num2cell([stats.varest stats.varci])]

ans =

    'Term'                 'Estimate'    'Lower'     'Upper'
    'Factory'              [  4.4426]    [1.0736]    [175.6038]
    'Factory*Car Model'    [ -0.0313]    [   NaN]    [     NaN]
    'Error'                [  0.1139]    [0.0586]    [  0.3103]
```

Other ANOVA Models

The `anovan` function also has arguments that enable you to specify two other types of model terms. First, the `'nested'` argument specifies a matrix that indicates which factors are nested within other factors. A nested factor is one that takes different values within each level its nested factor.

For example, the mileage data from the previous section assumed that the two car models produced in each factory were the same. Suppose instead, each factory produced two distinct car models for a total of six car models, and we numbered them 1 and 2 for each factory for convenience. Then, the car model is nested in factory. A more accurate and less ambiguous numbering of car model would be as follows:

Factory	Car Model
1	1
1	2
2	3
2	4
3	5
3	6

However, it is common with nested models to number the nested factor the same way in each nested factor.

Second, the `'continuous'` argument specifies that some factors are to be treated as continuous variables. The remaining factors are categorical variables. Although the `anovan` function can fit models with multiple continuous and categorical predictors, the simplest model that combines one predictor of each type is known as an *analysis of covariance* model. The next section describes a specialized tool for fitting this model.

Analysis of Covariance

In this section...

Introduction to Analysis of Covariance

Analysis of covariance is a technique for analyzing grouped data having a response (y, the variable to be predicted) and a predictor (x, the variable used to do the prediction). Using analysis of covariance, you can model y as a linear function of x, with the coefficients of the line possibly varying from group to group.

Analysis of Covariance Tool

The `aoctool` function opens an interactive graphical environment for fitting and prediction with analysis of covariance (ANOCOVA) models. It fits the following models for the ith group:

Same mean	$y = \alpha + \varepsilon$
Separate means	$y = (\alpha + \alpha_i) + \varepsilon$
Same line	$y = \alpha + \beta x + \varepsilon$
Parallel lines	$y = (\alpha + \alpha_i) + \beta x + \varepsilon$
Separate lines	$y = (\alpha + \alpha_i) + (\beta + \beta_i)x + \varepsilon$

For example, in the parallel lines model the intercept varies from one group to the next, but the slope is the same for each group. In the same mean model, there is a common intercept and no slope. In order to make the group coefficients well determined, the tool imposes the constraints

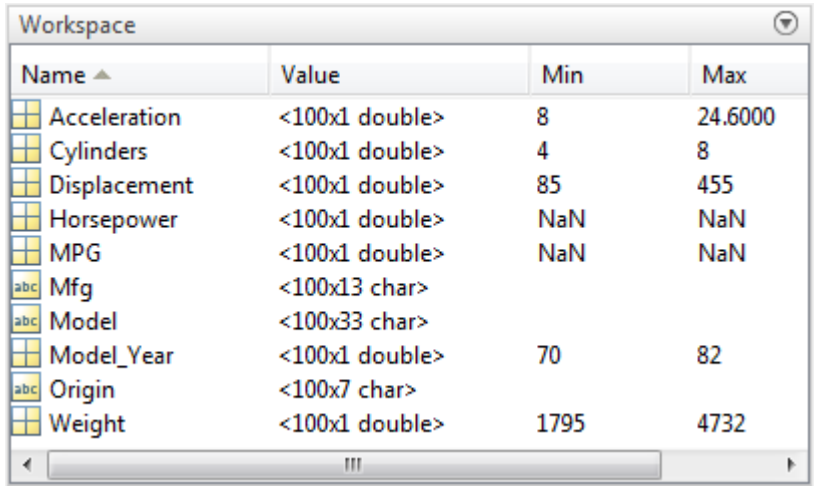
$$\sum \alpha_j = \sum \beta_j = 0$$

The following steps describe the use of `aoctool`.

1 **Load the data.** The Statistics and Machine Learning Toolbox data set `carsmall.mat` contains information on cars from the years 1970, 1976, and 1982. This example studies the relationship between the weight of a car and its mileage, and whether this relationship has changed over the years. To start the demonstration, load the data set.

```
load carsmall
```

The Workspace Browser shows the variables in the data set.



You can also use `aoctool` with your own data.

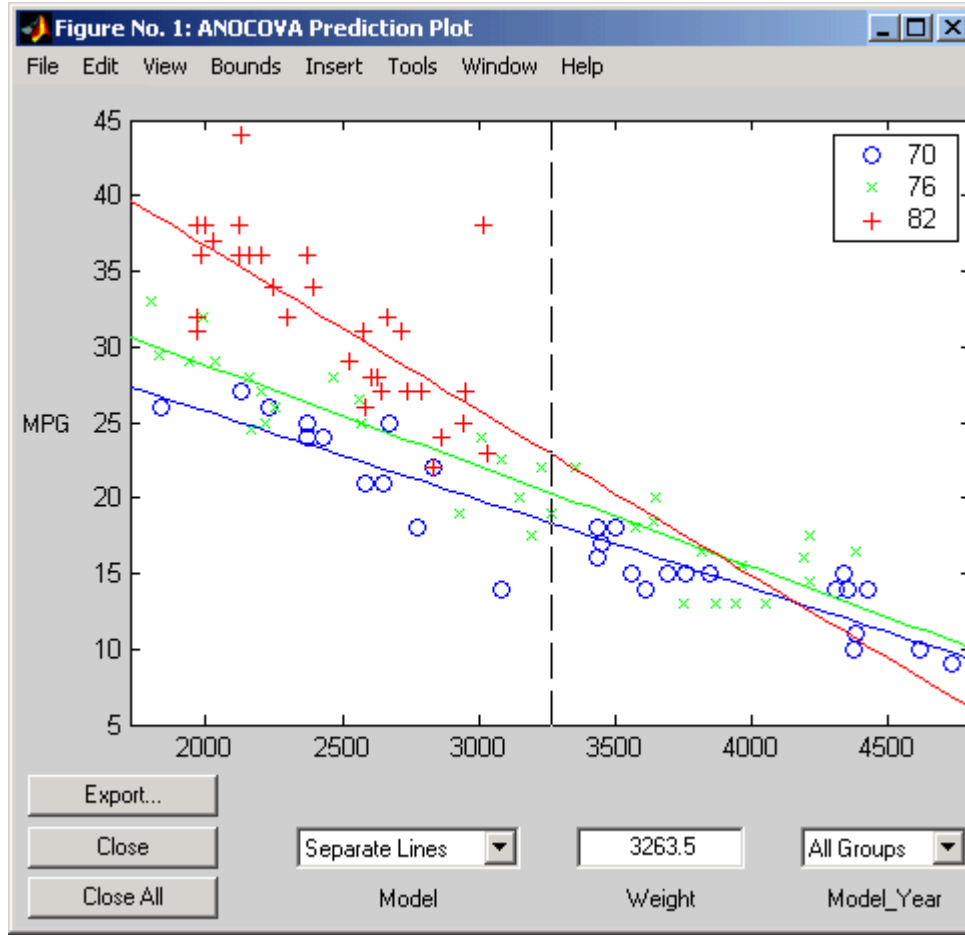
2 **Start the tool.** The following command calls `aoctool` to fit a separate line to the column vectors `Weight` and `MPG` for each of the three model group defined in `Model_Year`. The initial fit models the *y* variable, `MPG`, as a linear function of the *x* variable, `Weight`.

```
[h,atab,ctab,stats] = aoctool(Weight,MPG,Model_Year);
```

See the `aoctool` function reference page for detailed information about calling `aoctool`.

3 **Examine the output.** The graphical output consists of a main window with a plot, a table of coefficient estimates, and an analysis of variance table. In the plot, each

`Model_Year` group has a separate line. The data points for each group are coded with the same color and symbol, and the fit for each group has the same color as the data points.



The coefficients of the three lines appear in the figure titled ANOCOVA Coefficients. You can see that the slopes are roughly –0.0078, with a small deviation for each group:

- Model year 1970: $y = (45.9798 - 8.5805) + (-0.0078 + 0.002)x + \varepsilon$

- Model year 1976: $y = (45.9798 - 3.8902) + (-0.0078 + 0.0011)x + \varepsilon$
- Model year 1982: $y = (45.9798 + 12.4707) + (-0.0078 - 0.0031)x + \varepsilon$

Figure No. 3: ANOCOVA Coefficients

File Edit View Insert Tools Window Help

Coefficient Estimates

Term	Estimate	Std. Err.	T	Prob>|T|
Intercept	45.9798	1.52085	30.23	0
70	-8.5805	1.96186	-4.37	0
76	-3.8902	1.86864	-2.08	0.0403
82	12.4707	2.5568	4.88	0
Slope	-0.0078	0.00056	-14	0
70	0.002	0.00066	2.96	0.0039
76	0.0011	0.00065	1.74	0.0849
82	-0.0031	0.001	-3.1	0.0026

Because the three fitted lines have slopes that are roughly similar, you may wonder if they really are the same. The `Model_Year*Weight` interaction expresses the difference in slopes, and the ANOVA table shows a test for the significance of this term. With an F statistic of 5.23 and a p value of 0.0072, the slopes are significantly different.

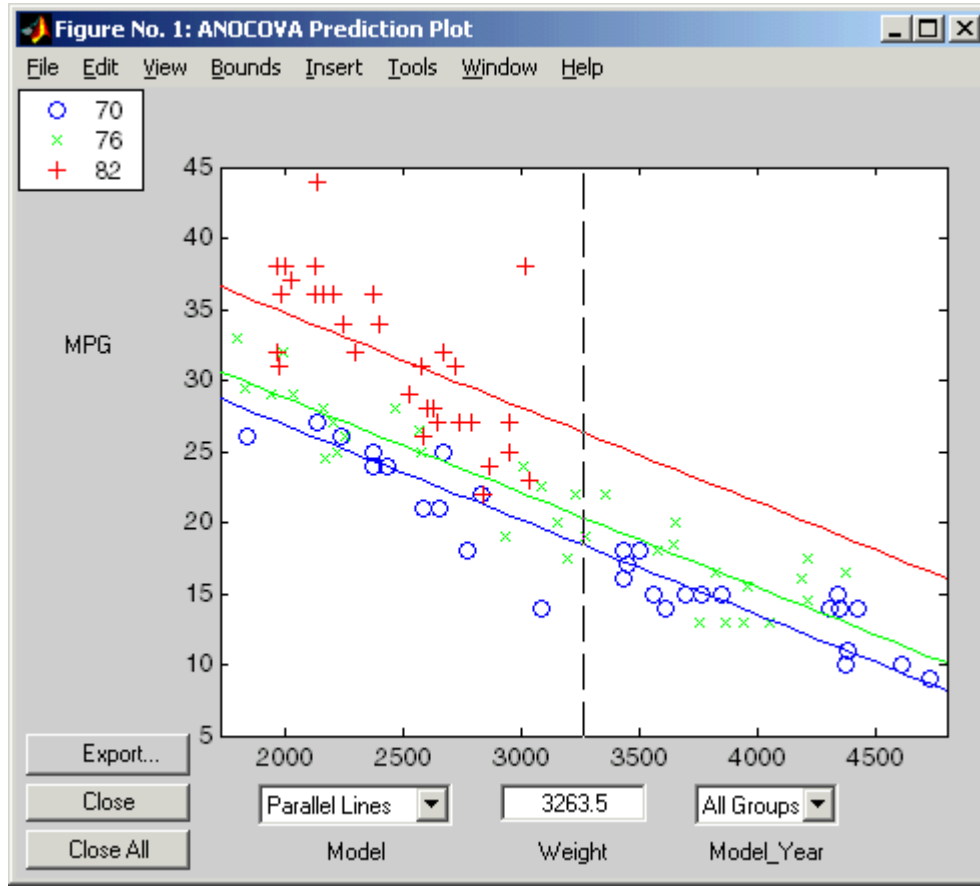
Figure No. 2: ANOCOVA Test Results

File Edit View Insert Tools Window Help

ANOVA Table

Source	d.f	Sum Sq	Mean Sq	F	Prob>F
Model_Year	2	807.69	403.84	51.98	0
Weight	1	2050.2	2050.2	263.87	0
Model_Year*Weigh	2	81.22	40.61	5.23	0.0072
Error	88	683.74	7.77		

4 **Constrain the slopes to be the same.** To examine the fits when the slopes are constrained to be the same, return to the ANOCOVA Prediction Plot window and use the **Model** pop-up menu to select a `Parallel Lines` model. The window updates to show the following graph.

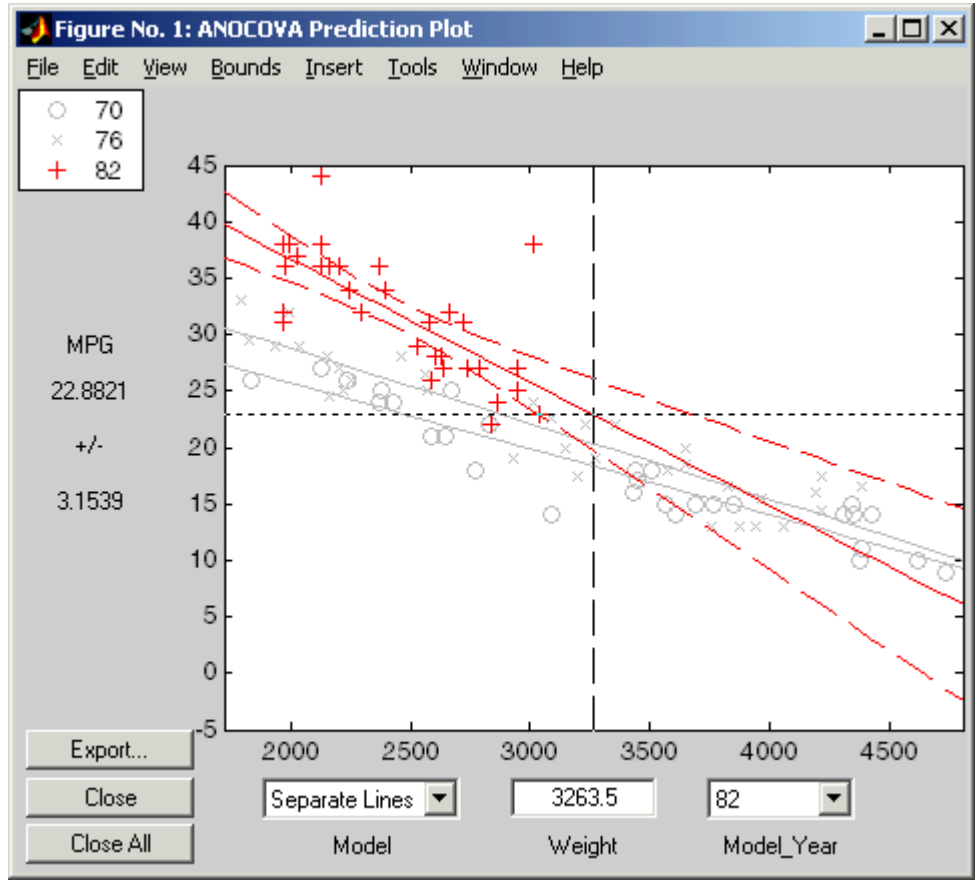


Though this fit looks reasonable, it is significantly worse than the `Separate Lines` model. Use the **Model** pop-up menu again to return to the original model.

Confidence Bounds

The example in "Analysis of Covariance Tool" on page 8-58 provides estimates of the relationship between `MPG` and `Weight` for each `Model_Year`, but how accurate are these estimates? To find out, you can superimpose confidence bounds on the fits by examining them one group at a time.

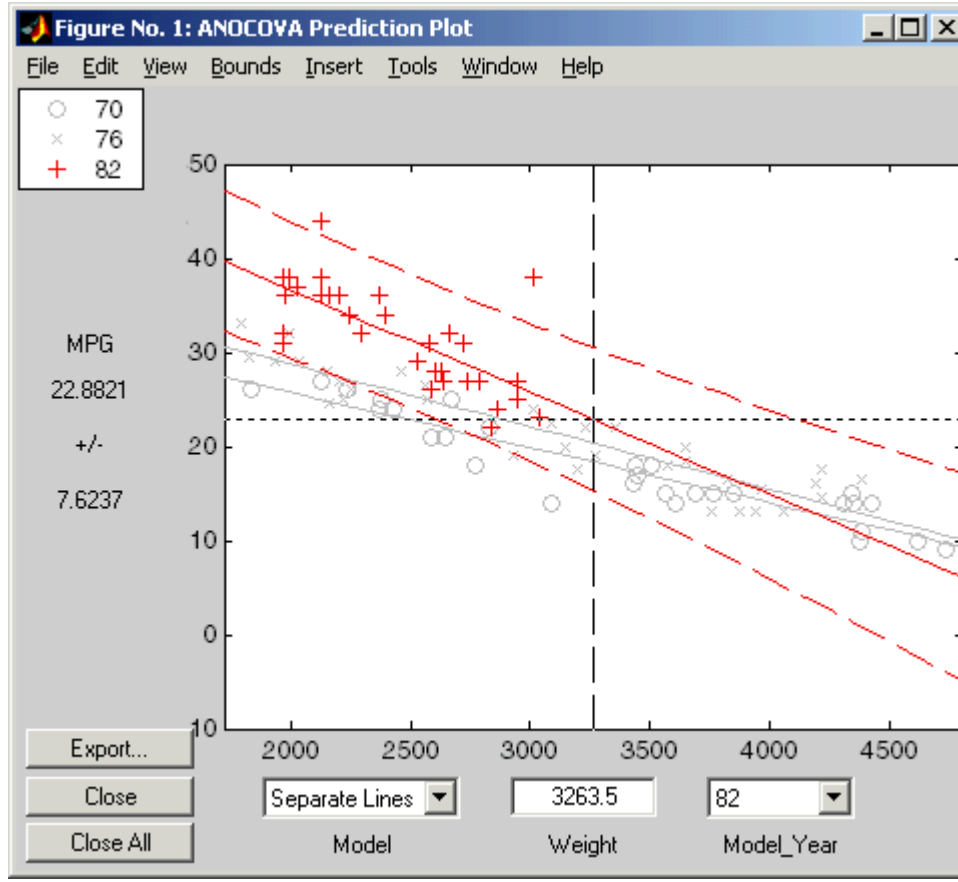
1 In the **Model_Year** menu at the lower right of the figure, change the setting from `All Groups` to 82. The data and fits for the other groups are dimmed, and confidence bounds appear around the 82 fit.



The dashed lines form an envelope around the fitted line for model year 82. Under the assumption that the true relationship is linear, these bounds provide a 95% confidence region for the true line. Note that the fits for the other model years are well outside these confidence bounds for `Weight` values between `2000` and `3000`.

2 Sometimes it is more valuable to be able to predict the response value for a new observation, not just estimate the average response value. Use the `aoctool` function **Bounds** menu to change the definition of the confidence bounds from

`Line` to `Observation`. The resulting wider intervals reflect the uncertainty in the parameter estimates as well as the randomness of a new observation.



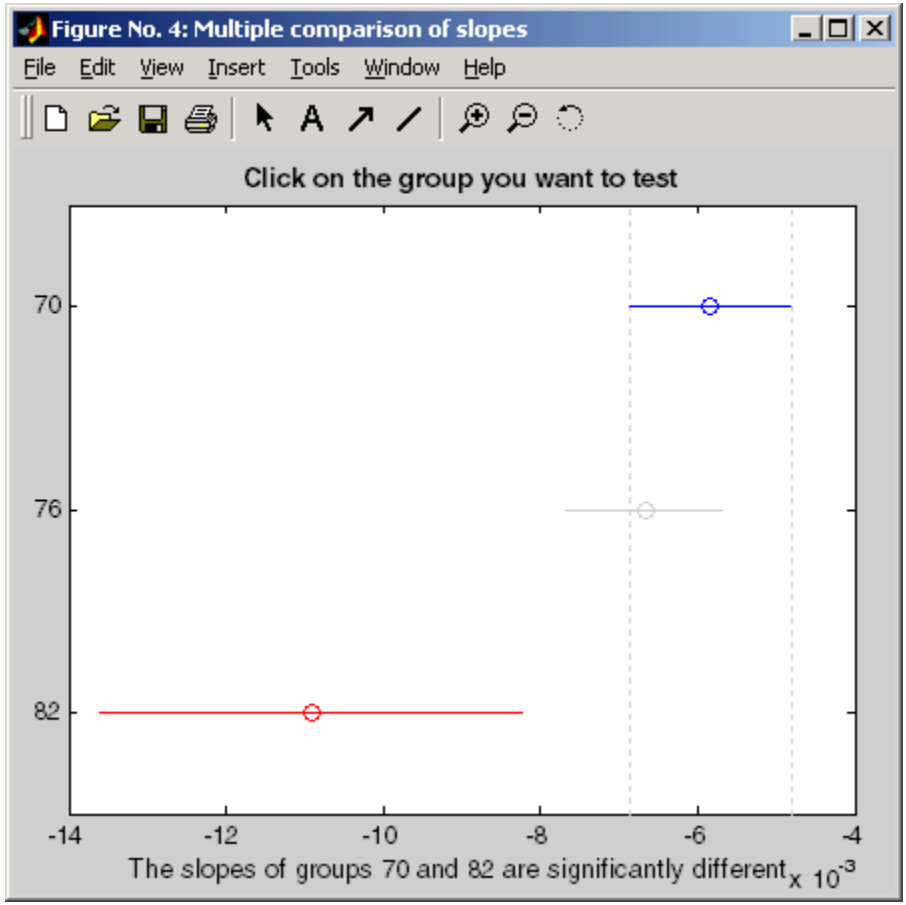
Like the `polytool` function, the `aoctool` function has cross hairs that you can use to manipulate the `Weight` and watch the estimate and confidence bounds along the *y*-axis update. These values appear only when a single group is selected, not when `All Groups` is selected.

Multiple Comparisons

You can perform a multiple comparison test by using the `stats` output structure from `aoctool` as input to the `multcompare` function. The `multcompare` function can test either slopes, intercepts, or population marginal means (the predicted MPG of the mean weight for each group). The example in "Analysis of Covariance Tool" on page 8-58 shows that the slopes are not all the same, but could it be that two are the same and only the other one is different? You can test that hypothesis.

```
multcompare(stats,0.05,'on','','s')

ans =
    1.0000    2.0000   -0.0012    0.0008    0.0029
    1.0000    3.0000    0.0013    0.0051    0.0088
    2.0000    3.0000    0.0005    0.0042    0.0079
```

This matrix shows that the estimated difference between the intercepts of groups 1 and 2 (1970 and 1976) is 0.0008, and a confidence interval for the difference is [–0.0012, 0.0029]. There is no significant difference between the two. There are significant differences, however, between the intercept for 1982 and each of the other two. The graph shows the same information.



Note that the `stats` structure was created in the initial call to the `aoctool` function, so it is based on the initial model fit (typically a separate-lines model). If you change the model interactively and want to base your multiple comparisons on the new model, you need to run `aoctool` again to get another `stats` structure, this time specifying your new model as the initial model.

Nonparametric Methods

In this section...

Introduction to Nonparametric Methods

Statistics and Machine Learning Toolbox functions include nonparametric versions of one-way and two-way analysis of variance. Unlike classical tests, nonparametric tests make only mild assumptions about the data, and are appropriate when the distribution of the data is non-normal. On the other hand, they are less powerful than classical methods for normally distributed data.

Both of the nonparametric functions described here will return a `stats` structure that can be used as an input to the `multcompare` function for multiple comparisons.

Kruskal-Wallis Test

The example “Perform One-Way ANOVA” on page 8-6 uses one-way analysis of variance to determine if the bacteria counts of milk varied from shipment to shipment. The one-way analysis rests on the assumption that the measurements are independent, and that each has a normal distribution with a common variance and with a mean that was constant in each column. You can conclude that the column means were not all the same. The following example repeats that analysis using a nonparametric procedure.

The Kruskal-Wallis test is a nonparametric version of one-way analysis of variance. The assumption behind this test is that the measurements come from a continuous distribution, but not necessarily a normal distribution. The test is based on an analysis of variance using the ranks of the data values, not the data values themselves. Output includes a table similar to an ANOVA table, and a box plot.

You can run this test as follows:

```
load hogg

p = kruskalwallis(hogg)
```

```
p =
    0.0020
```

The low p value means the Kruskal-Wallis test results agree with the one-way analysis of variance results.

Friedman's Test

"Perform Two-Way ANOVA" on page 8-18 uses two-way analysis of variance to study the effect of car model and factory on car mileage. The example tests whether either of these factors has a significant effect on mileage, and whether there is an interaction between these factors. The conclusion of the example is there is no interaction, but that each individual factor has a significant effect. The next example examines whether a nonparametric analysis leads to the same conclusion.

Friedman's test is a nonparametric test for data having a two-way layout (data grouped by two categorical factors). Unlike two-way analysis of variance, Friedman's test does not treat the two factors symmetrically and it does not test for an interaction between them. Instead, it is a test for whether the columns are different after adjusting for possible row differences. The test is based on an analysis of variance using the ranks of the data across categories of the row factor. Output includes a table similar to an ANOVA table.

You can run Friedman's test as follows.

```
load mileage
p = friedman(mileage,3)
p =
  7.4659e-004
```

Recall the classical analysis of variance gave a p value to test column effects, row effects, and interaction effects. This p value is for column effects. Using either this p value or the p value from ANOVA ($p < 0.0001$), you conclude that there are significant column effects.

In order to test for row effects, you need to rearrange the data to swap the roles of the rows in columns. For a data matrix `x` with no replications, you could simply transpose the data and type

```
p = friedman(x')
```

With replicated data it is slightly more complicated. A simple way is to transform the matrix into a three-dimensional array with the first dimension representing the replicates, swapping the other two dimensions, and restoring the two-dimensional shape.

```
x = reshape(mileage, [3 2 3]);
x = permute(x,[1 3 2]);
x = reshape(x,[9 2])
x =
   33.3000   32.6000
   33.4000   32.5000
   32.9000   33.0000
   34.5000   33.4000
   34.8000   33.7000
   33.8000   33.9000
   37.4000   36.6000
   36.8000   37.0000
   37.6000   36.7000

friedman(x,3)
ans =
    0.0082
```

Again, the conclusion is similar to that of the classical analysis of variance. Both this p value and the one from ANOVA ($p = 0.0039$) lead you to conclude that there are significant row effects.

You cannot use Friedman's test to test for interactions between the row and column factors.

MANOVA

In this section...

Introduction to MANOVA

The analysis of variance technique in “Perform One-Way ANOVA” on page 8-6 takes a set of grouped data and determine whether the mean of a variable differs significantly among groups. Often there are multiple response variables, and you are interested in determining whether the entire set of means is different from one group to the next. There is a multivariate version of analysis of variance that can address the problem.

ANOVA with Multiple Responses

The `carsmall` data set has measurements on a variety of car models from the years 1970, 1976, and 1982. Suppose you are interested in whether the characteristics of the cars have changed over time.

Load the sample data.

```
load carsmall
whos
```

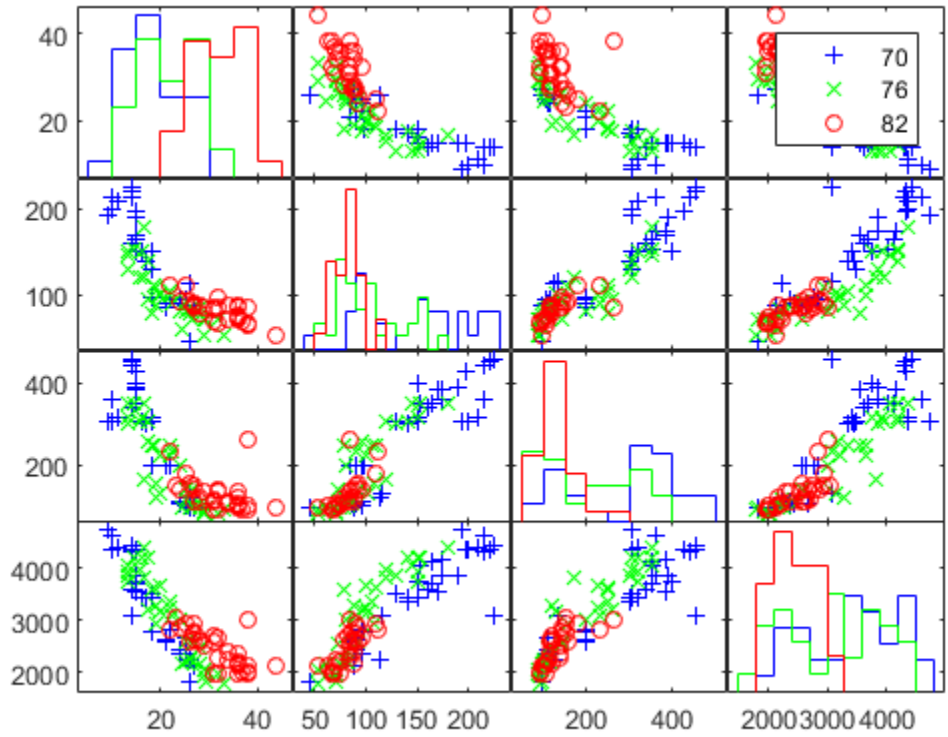
```
  Name               Size            Bytes  Class     Attributes

  Acceleration      100x1               800  double
  Cylinders         100x1               800  double
  Displacement      100x1               800  double
  Horsepower        100x1               800  double
  MPG               100x1               800  double
  Mfg               100x13             2600  char
  Model             100x33             6600  char
  Model_Year        100x1               800  double
  Origin            100x7              1400  char
  Weight            100x1               800  double
```

Four of these variables (`Acceleration`, `Displacement`, `Horsepower`, and `MPG`) are continuous measurements on individual car models. The variable `Model_Year` indicates

the year in which the car was made. You can create a grouped plot matrix of these variables using the `gplotmatrix` function.

Create a grouped plot matrix of these variables using the gplotmatrix function.

```
x = [MPG Horsepower Displacement Weight];
gplotmatrix(x,[],Model_Year,[],'+xo')
```



(When the second argument of `gplotmatrix` is empty, the function graphs the columns of the `x` argument against each other, and places histograms along the diagonals. The empty fourth argument produces a graph with the default colors. The fifth argument controls the symbols used to distinguish between groups.)

It appears the cars do differ from year to year. The upper right plot, for example, is a graph of `MPG` versus `Weight`. The 1982 cars appear to have higher mileage than the older cars, and they appear to weigh less on average. But as a group, are the three years significantly different from one another? The `manova1` function can answer that question.

```
[d,p,stats] = manova1(x,Model_Year)


d =

     2


p =

   1.0e-06 *

    0.0000
    0.1141


stats =

          W: [4x4 double]
          B: [4x4 double]
          T: [4x4 double]
        dfW: 90
        dfB: 2
        dfT: 92
     lambda: [2x1 double]
      chisq: [2x1 double]
    chisqdf: [2x1 double]
   eigenval: [4x1 double]
   eigenvec: [4x4 double]
      canon: [100x4 double]
      mdist: [1x100 double]
     gmdist: [3x3 double]
     gnames: {3x1 cell}
```

The `manova1` function produces three outputs:

- The first output, `d`, is an estimate of the dimension of the group means. If the means were all the same, the dimension would be 0, indicating that the means are at the same point. If the means differed but fell along a line, the dimension would be 1. In the example the dimension is 2, indicating that the group means fall in a plane but not along a line. This is the largest possible dimension for the means of three groups.
- The second output, `p`, is a vector of *p*-values for a sequence of tests. The first *p* value tests whether the dimension is 0, the next whether the dimension is 1, and so on. In this case both *p*-values are small. That's why the estimated dimension is 2.
- The third output, `stats`, is a structure containing several fields, described in the following section.

The Fields of the stats Structure

The `W`, `B`, and `T` fields are matrix analogs to the within, between, and total sums of squares in ordinary one-way analysis of variance. The next three fields are the degrees of freedom for these matrices. Fields `lambda`, `chisq`, and `chisqdf` are the ingredients of the test for the dimensionality of the group means. (The *p*-values for these tests are the first output argument of `manova1`.)

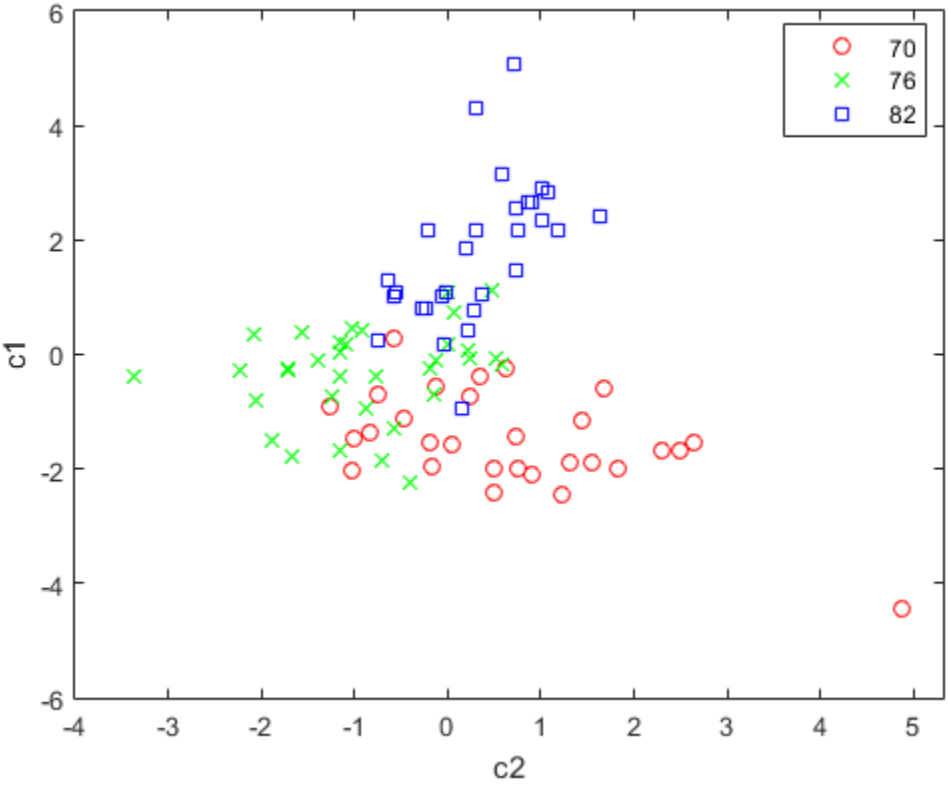
The next three fields are used to do a canonical analysis. Recall that in principal components analysis (“Principal Component Analysis (PCA)” on page 13-75) you look for the combination of the original variables that has the largest possible variation. In multivariate analysis of variance, you instead look for the linear combination of the original variables that has the largest separation between groups. It is the single variable that would give the most significant result in a univariate one-way analysis of variance. Having found that combination, you next look for the combination with the second highest separation, and so on.

The `eigenvec` field is a matrix that defines the coefficients of the linear combinations of the original variables. The `eigenval` field is a vector measuring the ratio of the between-group variance to the within-group variance for the corresponding linear combination. The `canon` field is a matrix of the canonical variable values. Each column is a linear combination of the mean-centered original variables, using coefficients from the `eigenvec` matrix.

```
c1 = stats.canon(:,1);
c2 = stats.canon(:,2);
```

Plot the grouped scatter plot of the first two canonical variables.

```
figure()
gscatter(c2,c1,Model_Year,[],'oxs')
```



A grouped scatter plot of the first two canonical variables shows more separation between groups then a grouped scatter plot of any pair of original variables. In this example, it shows three clouds of points, overlapping but with distinct centers. One point in the bottom right sits apart from the others. You can mark this point on the plot using the `gname` function.

Roughly speaking, the first canonical variable, `c1`, separates the 1982 cars (which have high values of `c1`) from the older cars. The second canonical variable, `c2`, reveals some separation between the 1970 and 1976 cars.

The final two fields of the `stats` structure are Mahalanobis distances. The `mdist` field measures the distance from each point to its group mean. Points with large values may be outliers. In this data set, the largest outlier is the one in the scatter plot, the Buick

Estate station wagon. (Note that you could have supplied the model name to the `gname` function above if you wanted to label the point with its model name rather than its row number.)

Find the largest distance from the group mean.

```
max(stats.mdist)
```

```
ans =

   31.5273
```

Find the point that has the largest distance from the group mean.

```
find(stats.mdist == ans)
```

```
ans =

    20
```

Find the car model that corresponds to the largest distance from the group mean.

```
Model(20,:)
```

```
ans =

buick estate wagon (sw)
```

The `gmdist` field measures the distances between each pair of group means. Examine the group means using `grpstats`.

```
grpstats(x, Model_Year)
```

```
ans =

   1.0e+03 *

    0.0177    0.1489    0.2869    3.4413
```

```
    0.0216    0.1011    0.1978    3.0787
    0.0317    0.0815    0.1289    2.4535
```

Find the distances between the each pair of group means.

```
stats.gmdist
```

```
ans =

         0    3.8277   11.1106
    3.8277         0    6.1374
   11.1106    6.1374         0
```

As might be expected, the multivariate distance between the extreme years 1970 and 1982 (11.1) is larger than the difference between more closely spaced years (3.8 and 6.1). This is consistent with the scatter plots, where the points seem to follow a progression as the year changes from 1970 through 1976 to 1982. If you had more groups, you might find it instructive to use the `manovacluster` function to draw a diagram that presents clusters of the groups, formed using the distances between their means.

Model Specification for Repeated Measures Models

Model specification for a repeated measures model is a string representing a formula in the form
`'y1-yk ~ terms'`,
where the responses and terms are in Wilkinson notation.

For example, if you have five repeated measures $y1$, $y2$, $y3$, $y4$, and $y5$, and you include the terms $X1$, $X2$, $X3$, $X4$, and $X3$:$X4$ in your linear model, then you can specify `modelspec` as follows:

Wilkinson Notation

Wilkinson notation describes the factors present in models. It does not describe the multipliers (coefficients) of those factors.

Use these rules to specify the responses in modelspec.

Wilkinson Notation	Description
`Y1,Y2,Y3`	Specific list of variables
`Y1-Y5`	All table variables from `Y1` through `Y5`

The following rules are for specifying terms in modelspec.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1*X2`
`X1:X2`	`X1*X2` only
`-X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

See Also

`fitrm`

Compound Symmetry Assumption and Epsilon Corrections

The regular p-value calculations in the repeated measures anova (`ranova`) are accurate if the theoretical distribution of the response variables has compound symmetry. This means that all response variables have the same variance, and each pair of response variables share a common correlation. That is,

$$\Sigma = \sigma^2 \begin{pmatrix} 1 & \rho & \cdots & \rho \\ \rho & 1 & \cdots & \rho \\ \vdots & \vdots & \ddots & \vdots \\ \rho & \rho & \cdots & 1 \end{pmatrix}.$$

Under the compound symmetry assumption, the F-statistics in the repeated measures anova table have an F-distribution with degrees of freedom (v_1, v_2). Here, v_1 is the rank of the contrast being tested, and v_2 is the degrees of freedom for error. If the compound symmetry assumption is not true, the F-statistic has an approximate F-distribution with degrees of freedom (εv_1, εv_2), where ε is the correction factor. Then, the p-value must be computed using the adjusted values. The three different correction factor computations are as follows:

- **Greenhouse-Geisser approximation**

$$\varepsilon_{GG} = \frac{\left(\sum_{i=1}^{p} \lambda_i\right)^2}{d\sum_{i=1}^{p} \lambda_i^2},$$

  where λ_i i = 1, 2, .., p are the eigenvalues of the covariance matrix. p is the number of variables, and d is equal to p-1.

- **Huynh-Feldt approximation**

$$\varepsilon_{HF} = \min\left(1, \frac{nd\varepsilon_{GG} - 2}{d(n - rx) - d^2\varepsilon_{GG}}\right),$$

where n is the number of rows in the design matrix and r is the rank of the design matrix.

- **Lower bound on the true *p*-value**

$$\varepsilon_{LB} = \frac{1}{d}.$$

References

[1] Huynh, H., and L. S. Feldt. "Estimation of the Box Correction for Degrees of Freedom from Sample Data in Randomized Block and Split-Plot Designs." *Journal of Educational Statistics*. Vol. 1, 1976, pp. 69–82.

[2] Greenhouse, S. W., and S. Geisser. "An Extension of Box's Result on the Use of *F*-Distribution in Multivariate Analysis." *Annals of Mathematical Statistics*. Vol. 29, 1958, pp. 885–891.

See Also

`epsilon` | `mauchly` | `ranova`

More About

- "Mauchly's Test of Sphericity" on page 8-81

Mauchly's Test of Sphericity

The regular p-value calculations in the repeated measures anova (`ranova`) are accurate if the theoretical distribution of the response variables have compound symmetry. This means that all response variables have the same variance, and each pair of response variables share a common correlation. That is,

$$\Sigma = \sigma^2 \begin{pmatrix} 1 & \rho & \cdots & \rho \\ \rho & 1 & \cdots & \rho \\ \vdots & \vdots & \ddots & \vdots \\ \rho & \rho & \cdots & 1 \end{pmatrix}.$$

If the compound symmetry assumption is false, then the degrees of freedom for the repeated measures anova test must be adjusted by a factor ε, and the p-value must be computed using the adjusted values.

Compound symmetry implies sphericity.

For a repeated measures model with responses $y1$, $y2$, ..., sphericity means that all pairwise differences $y1 - y2$, $y1 - y3$, ... have the same theoretical variance. Mauchly's test is the most accepted test for sphericity.

Mauchly's W statistic is

$$W = \frac{|T|}{\left(trace(T)/\ p\right)^d},$$

where

$$T = M' \Sigma M.$$

M is a p-by-d orthogonal contrast matrix, Σ is the covariance matrix, p is the number of variables, and $d = p - 1$.

A chi-square test statistic assesses the significance of W. If n is the number of rows in the design matrix, and r is the rank of the design matrix, then the chi-square statistic is

$$C = -(n - r)\log(W)D,$$

where

$$D = 1 - \frac{2d^2 + d + 2}{6d(n - r)}.$$

The C test statistic has a chi-square distribution with $(p(p-1)/2) - 1$ degrees of freedom. A small p-value for the Mauchly's test indicates that the sphericity assumption does not hold.

The `rmanova` method computes the p-values for the repeated measures anova based on the results of the Mauchly's test and each epsilon value.

References

[1] Mauchly, J. W. "Significance Test for Sphericity of a Normal n-Variate Distribution. *The Annals of Mathematical Statistics*. Vol. 11, 1940, pp. 204–209.

See Also

`epsilon` | `mauchly` | `ranova`

More About

- "Compound Symmetry Assumption and Epsilon Corrections" on page 8-79

Multivariate Analysis of Variance for Repeated Measures

Multivariate analysis of variance analysis is a test of the form `A*B*C = D`, where `B` is the p-by-r matrix of coefficients. p is the number of terms, such as the constant, linear predictors, dummy variables for categorical predictors, and products and powers, r is the number of repeated measures, and n is the number of subjects. `A` is an a-by-p matrix, with rank $a \le p$, defining hypotheses based on the between-subjects model. `C` is an r-by-c matrix, with rank $c \le r \le n - p$, defining hypotheses based on the within-subjects model, and `D` is an a-by-c matrix, containing the hypothesized value.

`manova` tests if the model terms are significant in their effect on the response by measuring how they contribute to the overall covariance. It includes all terms in the between-subjects model. `manova` always takes `D` as zero. The multivariate response for each observation (subject) is the vector of repeated measures.

`manova` uses four different methods to measure these contributions: Wilks' lambda, Pillai's trace, Hotelling-Lawley trace, Roy's maximum root statistic. Define

$$T = A\hat{B}C - D,$$
$$Z = A(X'X)^{-1}A'.$$

Then, the hypotheses sum of squares and products matrix is

$$Q_h = T'Z^{-1}T,$$

and the residuals sum of squares and products matrix is

$$Q_e = C'(R'R)C,$$

where

$$R = Y - X\hat{B}.$$

The matrix Q_h is analogous to the numerator of a univariate F-test, and Q_e is analogous to the error sum of squares. Hence, the four statistics `manova` uses are:

- **Wilks' lambda**

$$\Lambda = \frac{|Q_e|}{|Q_h + Q_e|} = \prod \frac{1}{1+\lambda_i},$$

where λ_i are the solutions of the characteristic equation $|Q_h - \lambda Q_e| = 0$.

- **Pillai's trace**

$$V = trace\left(Q_h \left(Q_h + Q_e\right)^{-1}\right) = \sum \theta_i,$$

where θ_i values are the solutions of the characteristic equation $Q_h - \theta(Q_h + Q_e) = 0$.

- **Hotelling-Lawley trace**

$$U = trace\left(Q_h Q_e^{-1}\right) = \sum \lambda_i.$$

- **Roy's maximum root statistic**

$$\Theta = \max\left(eig\left(Q_h Q_e^{-1}\right)\right).$$

References

[1] Charles, S. D. *Statistical Methods for the Analysis of Repeated Measurements*. Springer Texts in Statistics. Springer-Verlag, New York, Inc., 2002.

See Also

`coeftest` | `manova`

9

Parametric Regression Analysis

Parametric Regression Analysis

In this section...

What Is Parametric Regression?

Regression is the process of fitting models to data. The models must have numerical responses. For models with categorical responses, see "Parametric Classification" on page 15-2 or "Supervised Learning Workflow and Algorithms" on page 16-2. The regression process depends on the model. If a model is parametric, regression estimates the parameters from the data. If a model is linear in the parameters, estimation is based on methods from linear algebra that minimize the norm of a residual vector. If a model is nonlinear in the parameters, estimation is based on search methods from optimization that minimize the norm of a residual vector.

Choose a Regression Function

You have:	You want:	Use this:
Continuous or categorical predictors, continuous response, linear model	Fitted model coefficients	`fitlm`. See "Linear Regression" on page 9-11.
Continuous or categorical predictors, continuous response, linear model of unknown complexity	Fitted model and fitted coefficients	`stepwiselm`. See "Stepwise Regression" on page 9-124.
Continuous or categorical predictors, response possibly with restrictions such as nonnegative or integer-valued, generalized linear model	Fitted generalized linear model coefficients	`fitglm` or `stepwiseglm`. See "Generalized Linear Models" on page 10-12.
Continuous predictors with a continuous nonlinear response, parametrized nonlinear model	Fitted nonlinear model coefficients	`fitnlm`. See "Nonlinear Regression" on page 11-2.

You have:	You want:	Use this:
Continuous predictors, continuous response, linear model	Set of models from ridge, lasso, or elastic net regression	`lasso` or `ridge` See "Lasso and Elastic Net" on page 9-134 or "Ridge Regression" on page 9-131.
Correlated continuous predictors, continuous response, linear model	Fitted model and fitted coefficients	`plsregress` See "Partial Least Squares" on page 9-147.
Continuous or categorical predictors, continuous response, unknown model	Nonparametric model	`fitrtree` or `fitensemble` See "Classification Trees and Regression Trees" on page 16-33 or "Ensemble Methods" on page 16-68.
Categorical predictors only	ANOVA	`anova`, `anova1`, `anova2`, `anovan`
Continuous predictors, multivariable response, linear model	Fitted multivariate regression model coefficients	`mvregress`
Continuous predictors, continuous response, mixed-effects model	Fitted mixed-effects model coefficients	`nlmefit` or `nlmefitsa` See "Mixed-Effects Models" on page 11-20.

Update Legacy Code with New Fitting Methods

There are several Statistics and Machine Learning Toolbox functions for performing regression. The following sections describe how to replace calls to older functions to new versions:

regress into fitlm

Previous Syntax

```
[b,bint,r,rint,stats] = regress(y,X)
```

where `X` contains a column of ones.

Current Syntax

```
mdl = fitlm(X,y)
```

where you do not add a column of ones to `X`.

Equivalent values of the previous outputs:

- `b` — `mdl.Coefficients.Estimate`
- `bint` — `coefCI(mdl)`
- `r` — `mdl.Residuals.Raw`
- `rint` — There is no exact equivalent. Try examining `mdl.Residuals.Studentized` to find outliers.
- `stats` — `mdl` contains various properties that replace components of `stats`.

regstats into fitlm

Previous Syntax

```
stats = regstats(y,X,model,whichstats)
```

Current Syntax

```
mdl = fitlm(X,y,model)
```

Obtain statistics from the properties and methods of `mdl`. For example, see the `mdl.Diagnostics` and `mdl.Residuals` properties.

robustfit into fitlm

Previous Syntax

```
[b,stats] = robustfit(X,y,wfun,tune,const)
```

Current Syntax

```
mdl = fitlm(X,y,'robust','on') % bisquare
```

Or to use the *wfun* weight and the *tune* tuning parameter:

```
opt.RobustWgtFun = 'wfun';
opt.Tune = tune; % optional
mdl = fitlm(X,y,'robust',opt)
```

Obtain statistics from the properties and methods of `mdl`. For example, see the `mdl.Diagnostics` and `mdl.Residuals` properties.

stepwisefit into stepwiselm

Previous Syntax

```
[b,se,pval,inmodel,stats,nextstep,history] = stepwisefit(X,y,Name,Value)
```

Current Syntax

```
mdl = stepwiselm(ds,modelspec,Name,Value)
```

or

```
mdl = stepwiselm(X,y,modelspec,Name,Value)
```

Obtain statistics from the properties and methods of `mdl`. For example, see the `mdl.Diagnostics` and `mdl.Residuals` properties.

glmfit into fitglm

Previous Syntax

```
[b,dev,stats] = glmfit(X,y,distr,param1,val1,...)
```

Current Syntax

```
mdl = fitglm(X,y,distr,...)
```

Obtain statistics from the properties and methods of `mdl`. For example, the deviance is `mdl.Deviance`, and to compare `mdl` against a constant model, use `devianceTest(mdl)`.

nlinfit into fitnlm

Previous Syntax

```
[beta,r,J,COVB,mse] = nlinfit(X,y,fun,beta0,options)
```

Current Syntax

```
mdl = fitnlm(X,y,fun,beta0,'Options',options)
```

Equivalent values of the previous outputs:

- `beta` — `mdl.Coefficients.Estimate`
- `r` — `mdl.Residuals.Raw`
- `covb` — `mdl.CoefficientCovariance`
- `mse` — `mdl.mse`

`mdl` does not provide the Jacobian (`J`) output. The primary purpose of `J` was to pass it into `nlparci` or `nlpredci` to obtain confidence intervals for the estimated coefficients (parameters) or predictions. Obtain those confidence intervals as:

```
parci = coefCI(mdl)
[pred,predci] = predict(mdl)
```

What Are Linear Regression Models?

Regression models describe the relationship between a *dependent variable*, y, and *independent variable* or variables, X. The dependent variable is also called the *response variable*. Independent variables are also called *explanatory* or *predictor variables*. Continuous predictor variables might be called *covariates*, whereas categorical predictor variables might be also referred to as *factors*. The matrix, X, of observations on predictor variables is usually called the *design matrix*.

A multiple linear regression model is

$$y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_p X_{ip} + \varepsilon_i, \quad i = 1, \cdots, n,$$

where

- y_i is the ith response.
- β_k is the kth coefficient, where β_0 is the constant term in the model. Sometimes, design matrices might include information about the constant term. However, `fitlm` or `stepwiselm` by default includes a constant term in the model, so you must not enter a column of 1s into your design matrix X.
- X_{ij} is the ith observation on the jth predictor variable, j = 1, ..., p.
- ε_i is the ith noise term, that is, random error.

In general, a linear regression model can be a model of the form

$$y_i = \beta_0 + \sum_{k=1}^{K} \beta_k f_k\left(X_{i1}, X_{i2}, \cdots, X_{ip}\right) + \varepsilon_i, \quad i = 1, \cdots, n,$$

where f (.) is a scalar-valued function of the independent variables, X_{ij}s. The functions, f (X), might be in any form including nonlinear functions or polynomials. The linearity, in the linear regression models, refers to the linearity of the coefficients β_k. That is, the response variable, y, is a linear function of the coefficients, β_k.

Some examples of linear models are:

$$y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \varepsilon_i$$
$$y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{1i}^3 + \beta_4 X_{2i}^2 + \varepsilon_i$$
$$y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{1i} X_{2i} + \beta_4 \log X_{3i} + \varepsilon_i$$

The following, however, are not linear models since they are not linear in the unknown coefficients, β_k.

$$\log y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \varepsilon_i$$
$$y_i = \beta_0 + \beta_1 X_{1i} + \frac{1}{\beta_2 X_{2i}} + e^{\beta_3 X_{1i} X_{2i}} + \varepsilon_i$$

The usual assumptions for linear regression models are:

- The noise terms, ε_i, are uncorrelated.
- The noise terms, ε_i, have independent and identical normal distributions with mean zero and constant variance, σ^2. Thus

$$\begin{aligned} E(y_i) &= E\left(\sum_{k=0}^{K} \beta_k f_k\left(X_{i1}, X_{i2}, \cdots, X_{ip}\right) + \varepsilon_i\right) \\ &= \sum_{k=0}^{K} \beta_k f_k\left(X_{i1}, X_{i2}, \cdots, X_{ip}\right) + E(\varepsilon_i) \\ &= \sum_{k=0}^{K} \beta_k f_k\left(X_{i1}, X_{i2}, \cdots, X_{ip}\right) \end{aligned}$$

  and

$$V(y_i) = V\left(\sum_{k=0}^{K} \beta_k f_k\left(X_{i1}, X_{i2}, \cdots, X_{ip}\right) + \varepsilon_i\right) = V(\varepsilon_i) = \sigma^2$$

  So the variance of y_i is the same for all levels of X_{ij}.
- The responses y_i are uncorrelated.

The fitted linear function is

$$\hat{y}_i = b_0 + \sum_{k=1}^{K} b_k f_k\left(X_{i1}, X_{i2}, \cdots, X_{ip}\right), \quad i = 1, \cdots, n,$$

where $\hat{y}_i$ is the estimated response and b_ks are the fitted coefficients. The coefficients are estimated so as to minimize the mean squared difference between the prediction vector *bf*(*X*) and the true response vector *y*, that is $\hat{y} - y$. This method is called the *method of least squares*. Under the assumptions on the noise terms, these coefficients also maximize the likelihood of the prediction vector.

In a linear regression model of the form $y = \beta_1 X_1 + \beta_2 X_2 + ... + \beta_p X_p$, the coefficient β_k expresses the impact of a one-unit change in predictor variable, X_j, on the mean of the response, E(*y*) provided that all other variables are held constant. The sign of the coefficient gives the direction of the effect. For example, if the linear model is $E(y) = 1.8 - 2.35X_1 + X_2$, then –2.35 indicates a 2.35 unit decrease in the mean response with a one-unit increase in X_1, given X_2 is held constant. If the model is $E(y) = 1.1 + 1.5X_1^2 + X_2$, the coefficient of X_1^2 indicates a 1.5 unit increase in the mean of *Y* with a one-unit increase in X_1^2 given all else held constant. However, in the case of $E(y) = 1.1 + 2.1X_1 + 1.5X_1^2$, it is difficult to interpret the coefficients similarly, since it is not possible to hold X_1 constant when X_1^2 changes or vice versa.

References

[1] Neter, J., M. H. Kutner, C. J. Nachtsheim, and W. Wasserman. *Applied Linear Statistical Models*. IRWIN, The McGraw-Hill Companies, Inc., 1996.

[2] Seber, G. A. F. *Linear Regression Analysis*. Wiley Series in Probability and Mathematical Statistics. John Wiley and Sons, Inc., 1977.

See Also

`fitlm` | `LinearModel` | `stepwiselm`

Related Examples

- “Interpret Linear Regression Results” on page 9-63
- “Regression Using Dataset Arrays” on page 9-48
- “Linear Regression with Interaction Effects” on page 9-54
- “Regression with Categorical Covariates” on page 2-58
- “Linear Regression Workflow” on page 9-41

Linear Regression

In this section...

Prepare Data

To begin fitting a regression, put your data into a form that fitting functions expect. All regression techniques begin with input data in an array `X` and response data in a separate vector `y`, or input data in a table or dataset array `tbl` and response data as a column in `tbl`. Each row of the input data represents one observation. Each column represents one predictor (variable).

For a table or dataset array `tbl`, indicate the response variable with the `'ResponseVar'` name-value pair:

```
mdl = fitlm(tbl,'ResponseVar','BloodPressure');
% or
mdl = fitglm(tbl,'ResponseVar','BloodPressure');
```

The response variable is the last column by default.

You can use numeric *categorical* predictors. A categorical predictor is one that takes values from a fixed set of possibilities.

- For a numeric array `X`, indicate the categorical predictors using the `'Categorical'` name-value pair. For example, to indicate that predictors `2` and `3` out of six are categorical:

  ```
  mdl = fitlm(X,y,'Categorical',[2,3]);
  % or
  mdl = fitglm(X,y,'Categorical',[2,3]);
  ```

```
% or equivalently
mdl = fitlm(X,y,'Categorical',logical([0 1 1 0 0 0]));
```

- For a table or dataset array `tbl`, fitting functions assume that these data types are categorical:

  - Logical
  - Categorical (nominal or ordinal)
  - String or character array

  If you want to indicate that a numeric predictor is categorical, use the `'Categorical'` name-value pair.

Represent missing numeric data as `NaN`. To represent missing data for other data types, see "Missing Group Values" on page 2-54.

Dataset Array for Input and Response Data

To create a dataset array from an Excel spreadsheet:

```
ds = dataset('XLSFile','hospital.xls',...
     'ReadObsNames',true);
```

To create a dataset array from workspace variables:

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
```

Table for Input and Response Data

To create a table from an Excel spreadsheet:

```
tbl = readtable('hospital.xls',...
     'ReadRowNames',true);
```

To create a table from workspace variables:

```
load carsmall
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
```

Numeric Matrix for Input Data, Numeric Vector for Response

For example, to create numeric arrays from workspace variables:

```
load carsmall
X = [Weight Horsepower Cylinders Model_Year];
y = MPG;
```

To create numeric arrays from an Excel spreadsheet:

```
[X Xnames] = xlsread('hospital.xls');
y = X(:,4); % response y is systolic pressure
X(:,4) = []; % remove y from the X matrix
```

Notice that the nonnumeric entries, such as `sex`, do not appear in `X`.

Choose a Fitting Method

There are three ways to fit a model to data:

- "Least-Squares Fit" on page 9-13
- "Robust Fit" on page 9-13
- "Stepwise Fit" on page 9-13

Least-Squares Fit

Use `fitlm` to construct a least-squares fit of a model to the data. This method is best when you are reasonably certain of the model's form, and mainly need to find its parameters. This method is also useful when you want to explore a few models. The method requires you to examine the data manually to discard outliers, though there are techniques to help (see "Residuals — Model Quality for Training Data" on page 9-23).

Robust Fit

Use `fitlm` with the `RobustOpts` name-value pair to create a model that is little affected by outliers. Robust fitting saves you the trouble of manually discarding outliers. However, `step` does not work with robust fitting. This means that when you use robust fitting, you cannot search stepwise for a good model.

Stepwise Fit

Use `stepwiselm` to find a model, and fit parameters to the model. `stepwiselm` starts from one model, such as a constant, and adds or subtracts terms one at a time, choosing an optimal term each time in a greedy fashion, until it cannot improve further. Use stepwise fitting to find a good model, which is one that has only relevant terms.

The result depends on the starting model. Usually, starting with a constant model leads to a small model. Starting with more terms can lead to a more complex model, but one that has lower mean squared error. See “Compare large and small stepwise models” on page 9-124.

You cannot use robust options along with stepwise fitting. So after a stepwise fit, examine your model for outliers (see “Residuals — Model Quality for Training Data” on page 9-23).

Choose a Model or Range of Models

There are several ways of specifying a model for linear regression. Use whichever you find most convenient.

For `fitlm`, the model specification you give is the model that is fit. If you do not give a model specification, the default is `'linear'`.

For `stepwiselm`, the model specification you give is the starting model, which the stepwise procedure tries to improve. If you do not give a model specification, the default starting model is `'constant'`, and the default upper bounding model is `'interactions'`. Change the upper bounding model using the `Upper` name-value pair.

Note: There are other ways of selecting models, such as using `lasso`, `lassoglm`, `sequentialfs`, or `plsregress`.

Brief String

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).

String	Model Type
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

For example, to specify an interaction model using `fitlm` with matrix predictors:

```
mdl = fitlm(X,y,'interactions');
```

To specify a model using `stepwiselm` and a table or dataset array `tbl` of predictors, suppose you want to start from a constant and have a linear model upper bound. Assume the response variable in `tbl` is in the third column.

```
mdl2 = stepwiselm(tbl,'constant',...
    'Upper','linear','ResponseVar',3);
```

Terms Matrix

A terms matrix is a t-by-(p + 1) matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

```
load hospital
ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
```

Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

```
T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     1     0     0     0
     0     0     1     0
     0     0     0     1
```

Redefine the dataset array.

```
ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
```

Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

```
T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]
```

```
T =

     0     0     0
     1     0     0
     0     1     0
     1     1     0
     0     2     0
```

Fit a linear model.

```
mdl = fitlm(X,MPG,T)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1*x2 + x2^2

Estimated Coefficients:
                   Estimate       SE            tStat      pValue
    (Intercept)          48.906        12.589     3.8847    0.00019665
    x1                 0.54418       0.57125    0.95261       0.34337
    x2                -0.012781     0.0060312    -2.1192      0.036857
    x1:x2           -0.00010892    0.00017925    -0.6076         0.545
    x2^2             9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)

1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for a model specification is a string of the form `'Y ~ terms'`,

- *Y* is the response name.
- *terms* contains
  - Variable names
  - `+` to include the next variable
  - `-` to exclude the next variable
  - `:` to define an interaction, a product of terms
  - `*` to define an interaction and all lower-order terms
  - `^` to raise the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
  - `()` to group terms

Tip Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

Examples:
`'Y ~ A + B + C'` is a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example, since `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example, since `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

For example, to specify an interaction model using `fitlm` with matrix predictors:

```
mdl = fitlm(X,y,'y ~ x1*x2*x3 - x1:x2:x3');
```

To specify a model using `stepwiselm` and a table or dataset array `tbl` of predictors, suppose you want to start from a constant and have a linear model upper bound. Assume the response variable in `tbl` is named `'y'`, and the predictor variables are named `'x1'`, `'x2'`, and `'x3'`.

```
mdl2 = stepwiselm(tbl,'y ~ 1','Upper','y ~ x1 + x2 + x3');
```

Fit Model to Data

The most common optional arguments for fitting:

- For robust regression in `fitlm`, set the `'RobustOpts'` name-value pair to `'on'`.
- Specify an appropriate upper bound model in `stepwiselm`, such as set `'Upper'` to `'linear'`.
- Indicate which variables are categorical using the `'CategoricalVars'` name-value pair. Provide a vector with column numbers, such as `[1 6]` to specify that predictors `1` and `6` are categorical. Alternatively, give a logical vector the same length as the data columns, with a `1` entry indicating that variable is categorical. If there are seven predictors, and predictors `1` and `6` are categorical, specify `logical([1,0,0,0,0,1,0])`.

- For a table or dataset array, specify the response variable using the `'ResponseVar'` name-value pair. The default is the last column in the array.

For example,

```
mdl = fitlm(X,y,'linear',...
    'RobustOpts','on','CategoricalVars',3);
mdl2 = stepwiselm(tbl,'constant',...
    'ResponseVar','MPG','Upper','quadratic');
```

Examine Quality and Adjust the Fitted Model

After fitting a model, examine the result.

Model Display

A linear regression model shows several diagnostics when you enter its name or enter `disp(mdl)`. This display gives some of the basic information to check whether the fitted model represents the data adequately.

For example, fit a linear model to data constructed with two out of five predictors not present and with no intercept term:

```
X = randn(100,5);
y = X*[1;0;3;0;-1]+randn(100,1);
mdl = fitlm(X,y)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4 + x5

Estimated Coefficients:
                   Estimate     SE          tStat       pValue
```

```
    (Intercept)     0.038164    0.099458     0.38372       0.70205
    x1               0.92794    0.087307      10.628    8.5494e-18
    x2             -0.075593     0.10044    -0.75264       0.45355
    x3                2.8965    0.099879          29    1.1117e-48
    x4              0.045311     0.10832     0.41831       0.67667
    x5              -0.99708     0.11799     -8.4504     3.593e-13

Number of observations: 100, Error degrees of freedom: 94
Root Mean Squared Error: 0.972
R-squared: 0.93,  Adjusted R-Squared 0.926
F-statistic vs. constant model: 248, p-value = 1.5e-52
```

Notice that:

- The display contains the estimated values of each coefficient in the `Estimate` column. These values are reasonably near the true values `[0;1;0;3;0;-1]`.
- There is a standard error column for the coefficient estimates.
- The reported `pValue` (which are derived from the t statistics under the assumption of normal errors) for predictors 1, 3, and 5 are extremely small. These are the three predictors that were used to create the response data `y`.
- The `pValue` for `(Intercept)`, `x2` and `x4` are much larger than 0.01. These three predictors were not used to create the response data `y`.
- The display contains R^2, adjusted R^2, and F statistics.

ANOVA

To examine the quality of the fitted model, consult an ANOVA table. For example, use `anova` on a linear model with five predictors:

```
X = randn(100,5);
y = X*[1;0;3;0;-1]+randn(100,1);
mdl = fitlm(X,y);
tbl = anova(mdl)
```

```
tbl =
              SumSq      DF    MeanSq     F          pValue
    x1         106.62     1     106.62     112.96    8.5494e-18
    x2        0.53464     1    0.53464    0.56646       0.45355
    x3         793.74     1     793.74     840.98    1.1117e-48
    x4        0.16515     1    0.16515    0.17498       0.67667
    x5         67.398     1     67.398      71.41     3.593e-13
    Error      88.719    94    0.94382
```

This table gives somewhat different results than the default display (see "Model Display" on page 9-20). The table clearly shows that the effects of `x2` and `x4` are not significant. Depending on your goals, consider removing `x2` and `x4` from the model.

Diagnostic Plots

Diagnostic plots help you identify outliers, and see other problems in your model or fit. For example, load the `carsmall` data, and make a model of `MPG` as a function of `Cylinders` (nominal) and `Weight`:

```
load carsmall
tbl = table(Weight,MPG,Cylinders);
tbl.Cylinders = ordinal(tbl.Cylinders);
mdl = fitlm(tbl,'MPG ~ Cylinders*Weight + Weight^2');#
```

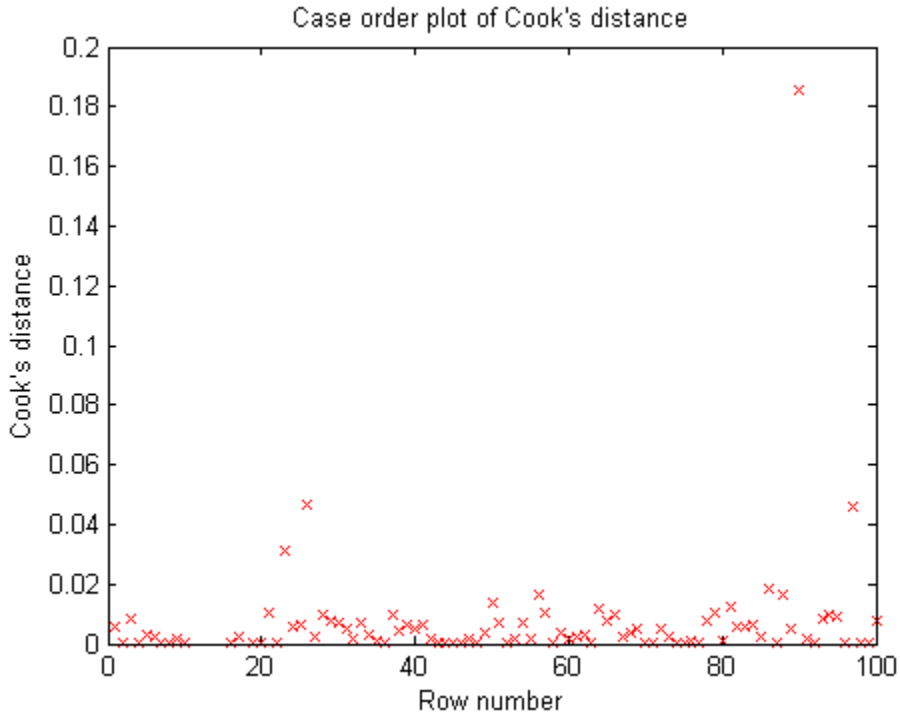
Make a leverage plot of the data and model.

```
plotDiagnostics(mdl)
```

There are a few points with high leverage. But this plot does not reveal whether the high-leverage points are outliers.

Look for points with large Cook's distance.

```
plotDiagnostics(mdl,'cookd')
```



There is one point with large Cook's distance. Identify it and remove it from the model. You can use the Data Cursor to click the outlier and identify it, or identify it programmatically:

```
[~,larg] = max(mdl.Diagnostics.CooksDistance);
mdl2 = fitlm(tbl,'MPG ~ Cylinders*Weight + Weight^2',...
    'Exclude',larg);
```

Residuals — Model Quality for Training Data

There are several residual plots to help you discover errors, outliers, or correlations in the model or data. The simplest residual plots are the default histogram plot, which

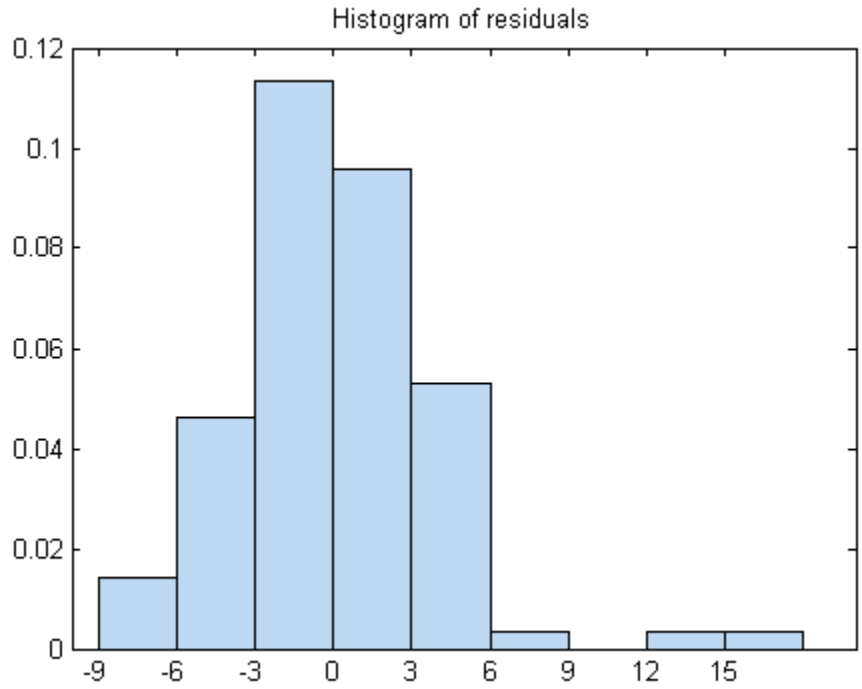
shows the range of the residuals and their frequencies, and the probability plot, which shows how the distribution of the residuals compares to a normal distribution with matched variance.

Load the `carsmall` data, and make a model of `MPG` as a function of `Cylinders` (nominal) and `Weight`:

```
load carsmall
tbl = table(Weight,MPG,Cylinders);
tbl.Cylinders = ordinal(tbl.Cylinders);
mdl = fitlm(tbl,'MPG ~ Cylinders*Weight + Weight^2');
```

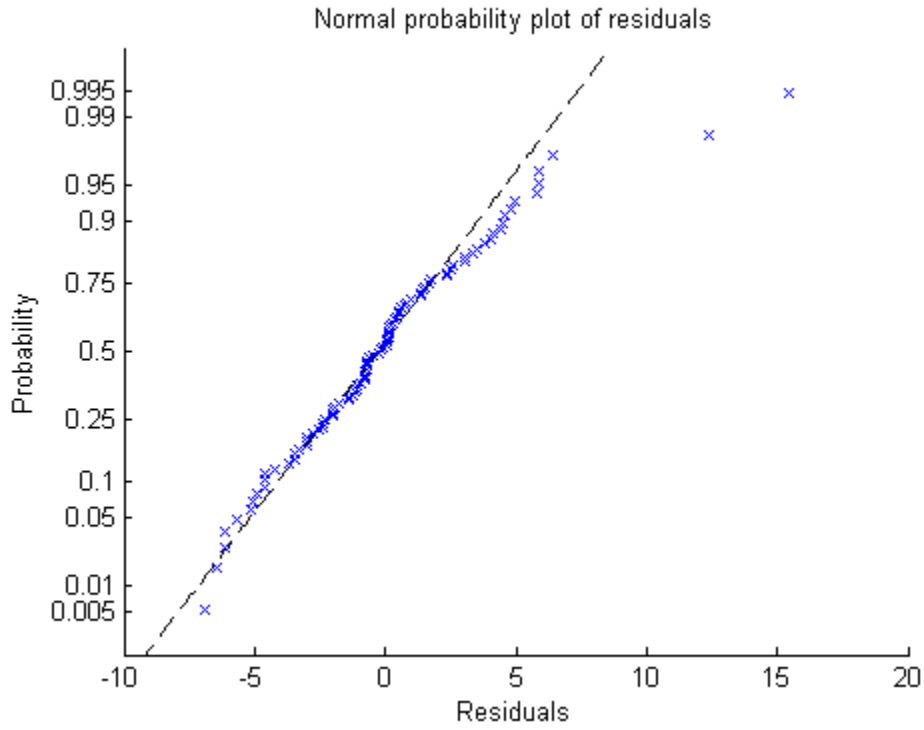
Examine the residuals:

```
plotResiduals(mdl)
```



The observations above 12 are potential outliers.

```
plotResiduals(mdl,'probability')
```



The two potential outliers appear on this plot as well. Otherwise, the probability plot seems reasonably straight, meaning a reasonable fit to normally distributed residuals.

You can identify the two outliers and remove them from the data:

```
outl = find(mdl.Residuals.Raw > 12)
```

```
outl =

    90
    97
```

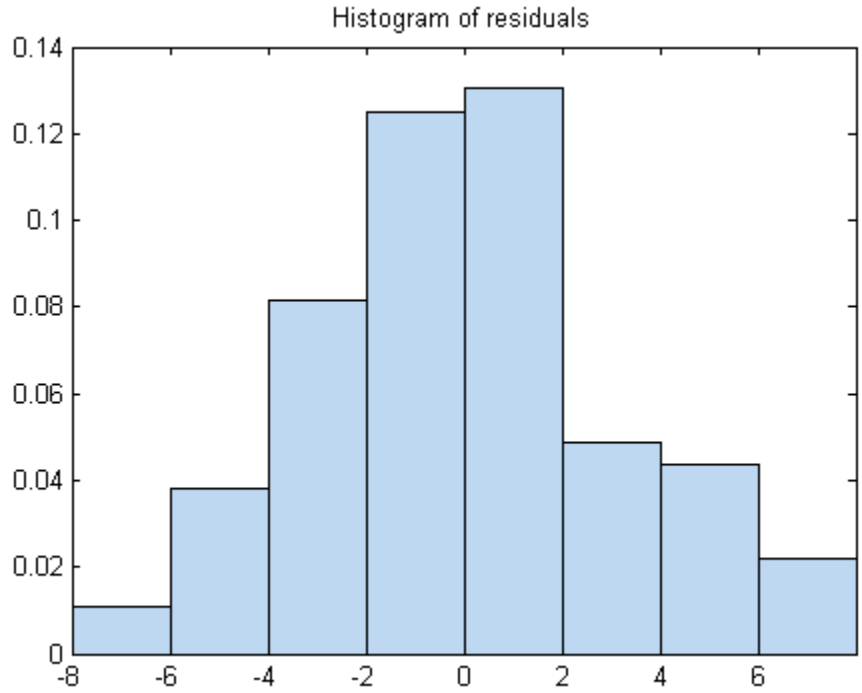
To remove the outliers, use the `Exclude` name-value pair:

```
mdl2 = fitlm(tbl,'MPG ~ Cylinders*Weight + Weight^2',...
```

```
    'Exclude',outl);
```

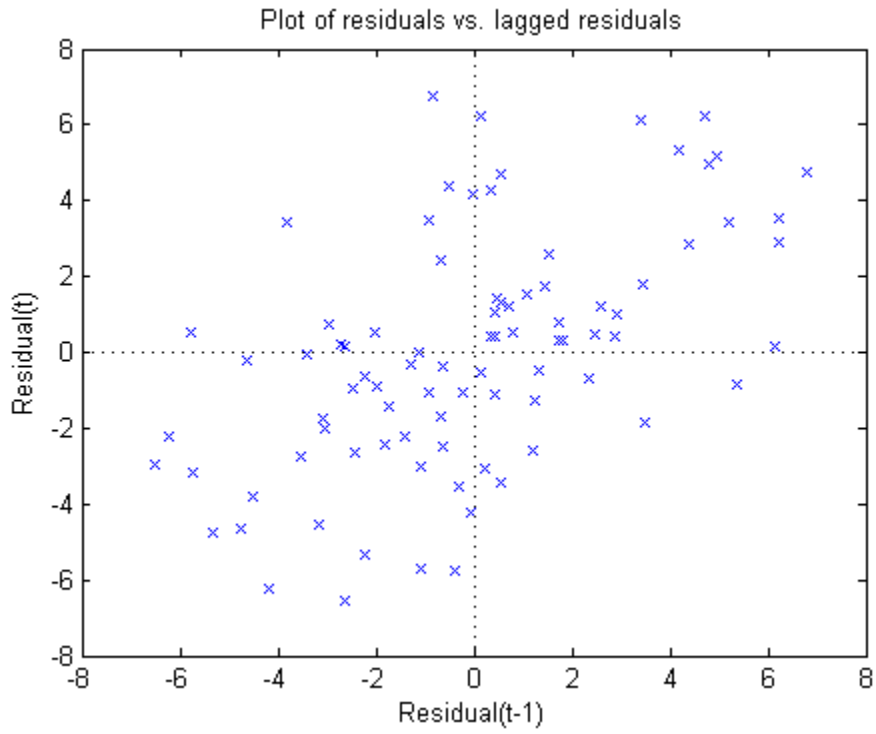
Examine a residuals plot of `mdl2`:

```
plotResiduals(mdl2)
```



The new residuals plot looks fairly symmetric, without obvious problems. However, there might be some serial correlation among the residuals. Create a new plot to see if such an effect exists.

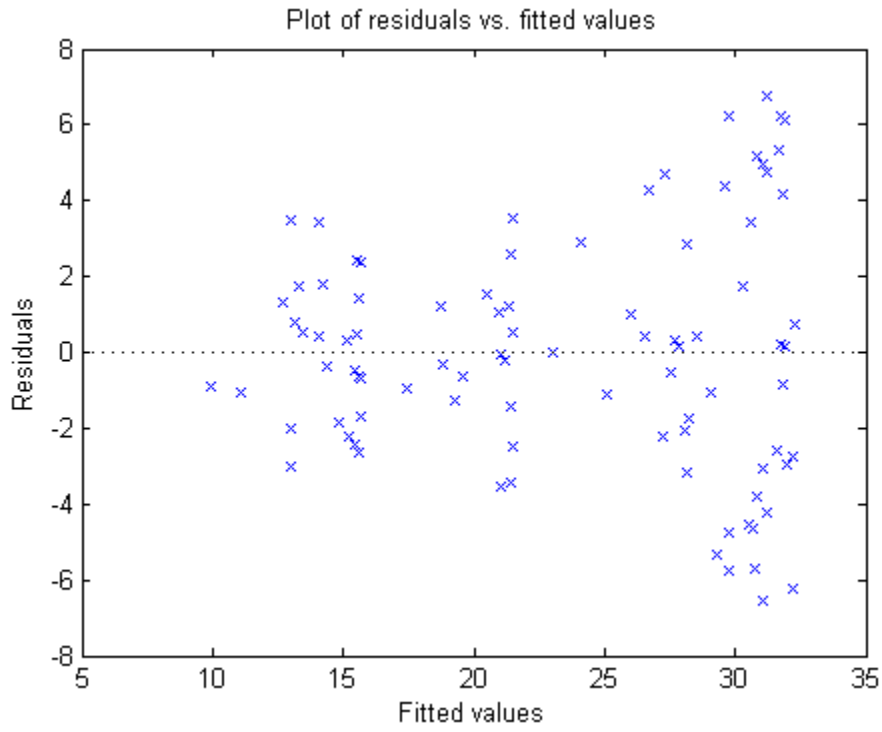
```
plotResiduals(mdl2,'lagged')
```



The scatter plot shows many more crosses in the upper-right and lower-left quadrants than in the other two quadrants, indicating positive serial correlation among the residuals.

Another potential issue is when residuals are large for large observations. See if the current model has this issue.

```
plotResiduals(mdl2,'fitted')
```



There is some tendency for larger fitted values to have larger residuals. Perhaps the model errors are proportional to the measured values.

Plots to Understand Predictor Effects

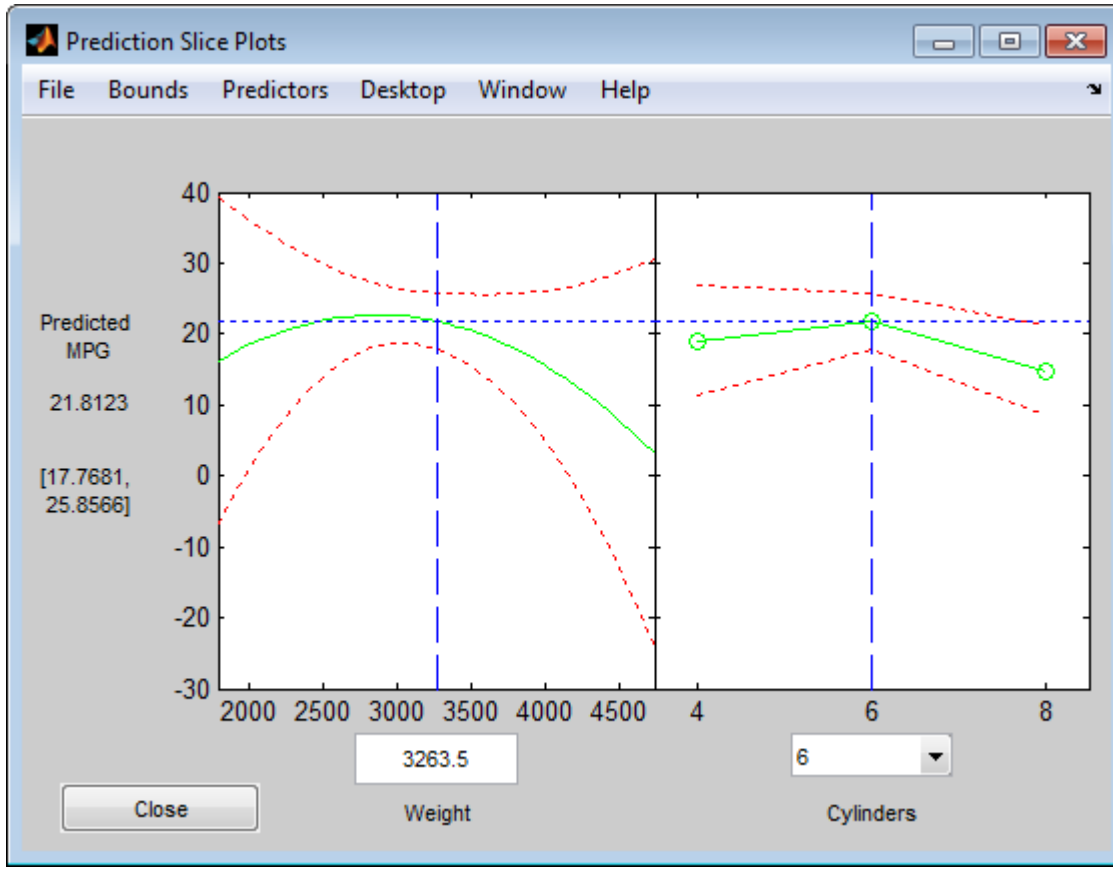
This example shows how to understand the effect each predictor has on a regression model using a variety of available plots.

1. Create a model of mileage from some predictors in the `carsmall` data.

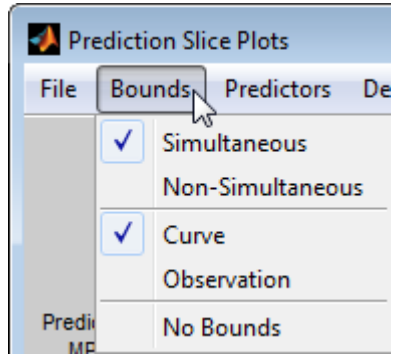
```
load carsmall
tbl = table(Weight,MPG,Cylinders);
tbl.Cylinders = ordinal(tbl.Cylinders);
mdl = fitlm(tbl,'MPG ~ Cylinders*Weight + Weight^2');
```

2. Examine a slice plot of the responses. This displays the effect of each predictor separately.

```
plotSlice(mdl)
```

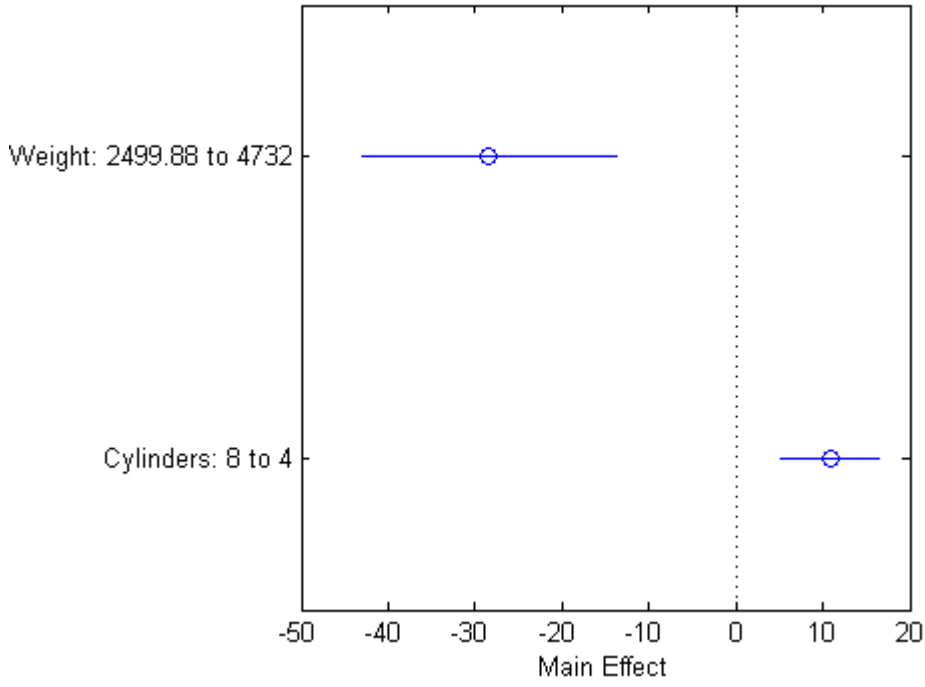


You can drag the individual predictor values, which are represented by dashed blue vertical lines. You can also choose between simultaneous and non-simultaneous confidence bounds, which are represented by dashed red curves.



3 Use an effects plot to show another view of the effect of predictors on the response.

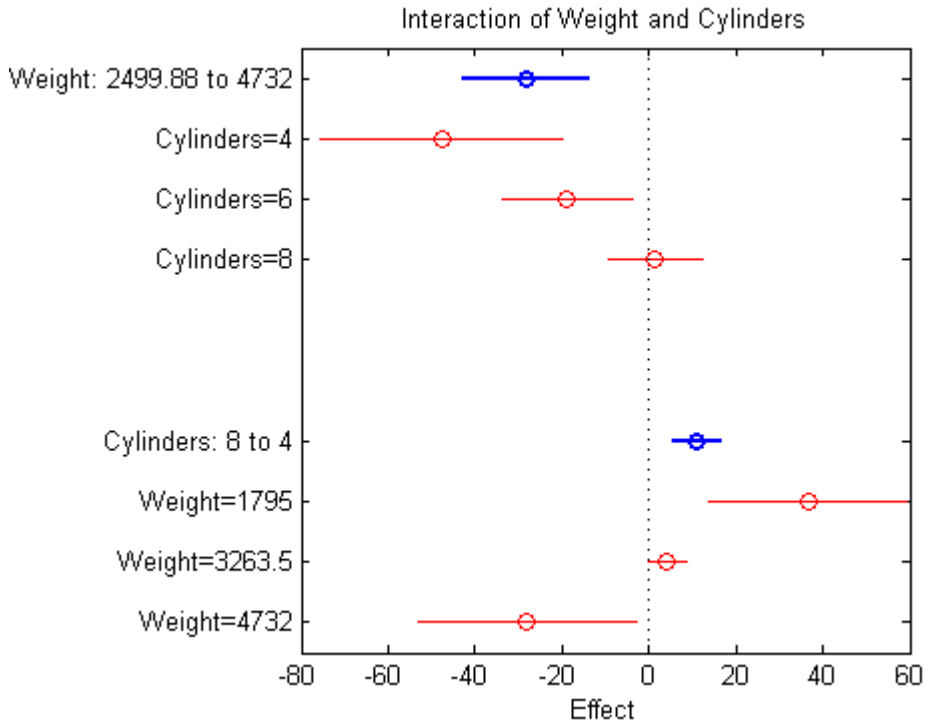
```
plotEffects(mdl)
```



This plot shows that changing `Weight` from about 2500 to 4732 lowers `MPG` by about 30 (the location of the upper blue circle). It also shows that changing the number of cylinders from 8 to 4 raises `MPG` by about 10 (the lower blue circle). The horizontal blue lines represent confidence intervals for these predictions. The predictions come from averaging over one predictor as the other is changed. In cases such as this, where the two predictors are correlated, be careful when interpreting the results.

4 Instead of viewing the effect of averaging over a predictor as the other is changed, examine the joint interaction in an interaction plot.

```
plotInteraction(mdl,'Weight','Cylinders')
```

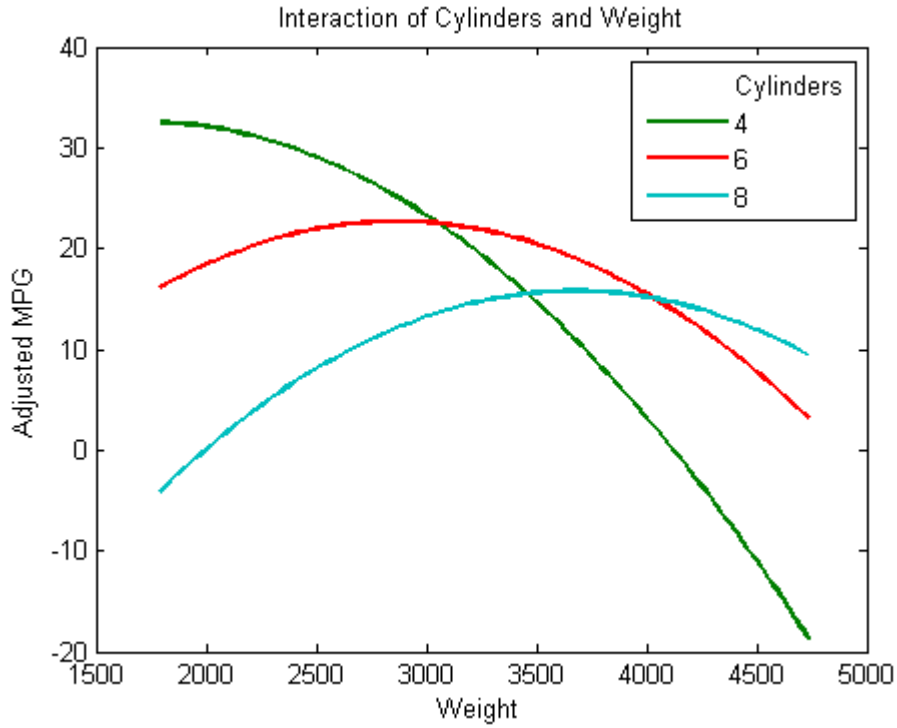


The interaction plot shows the effect of changing one predictor with the other held fixed. In this case, the plot is much more informative. It shows, for example, that lowering the number of cylinders in a relatively light car (`Weight` = 1795) leads to an

increase in mileage, but lowering the number of cylinders in a relatively heavy car (`Weight` = 4732) leads to a decrease in mileage.

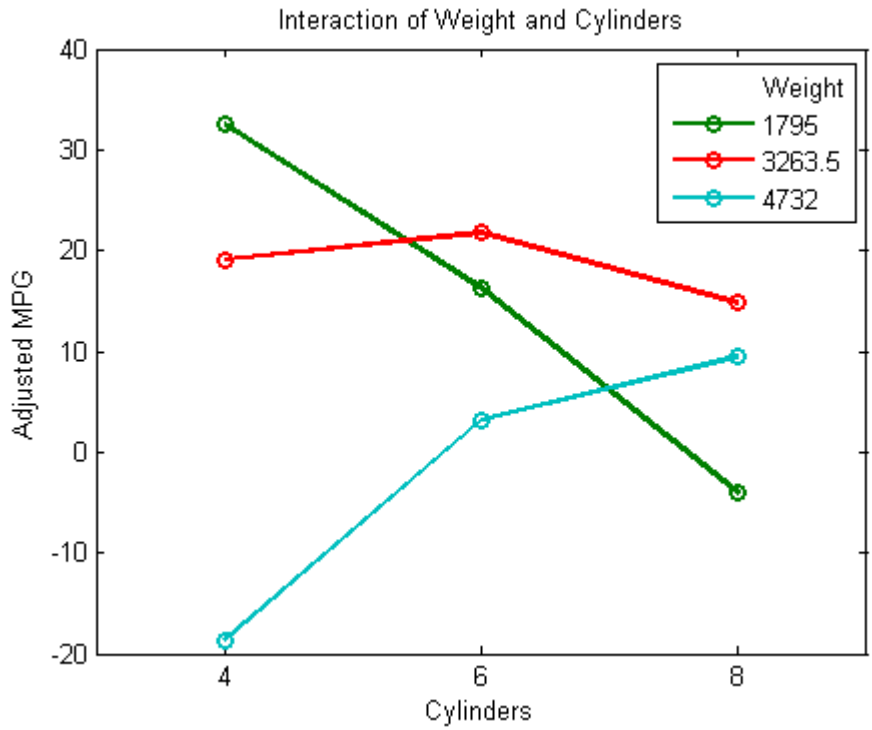
5 For an even more detailed look at the interactions, look at an interaction plot with predictions. This plot holds one predictor fixed while varying the other, and plots the effect as a curve. Look at the interactions for various fixed numbers of cylinders.

```
plotInteraction(mdl,'Cylinders','Weight','predictions')
```



Now look at the interactions with various fixed levels of weight.

```
plotInteraction(mdl,'Weight','Cylinders','predictions')
```



Plots to Understand Terms Effects

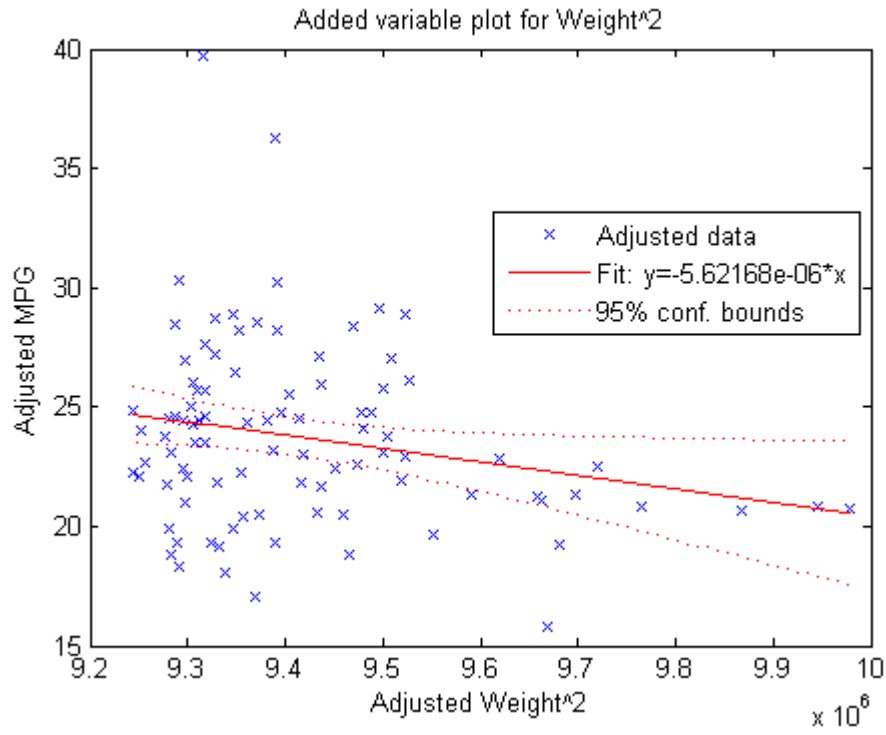
This example shows how to understand the effect of each term in a regression model using a variety of available plots.

1 Create a model of mileage from some predictors in the `carsmall` data.

```
load carsmall
tbl = table(Weight,MPG,Cylinders);
tbl.Cylinders = ordinal(tbl.Cylinders);
mdl = fitlm(tbl,'MPG ~ Cylinders*Weight + Weight^2');
```

2 Create an added variable plot with `Weight^2` as the added variable.

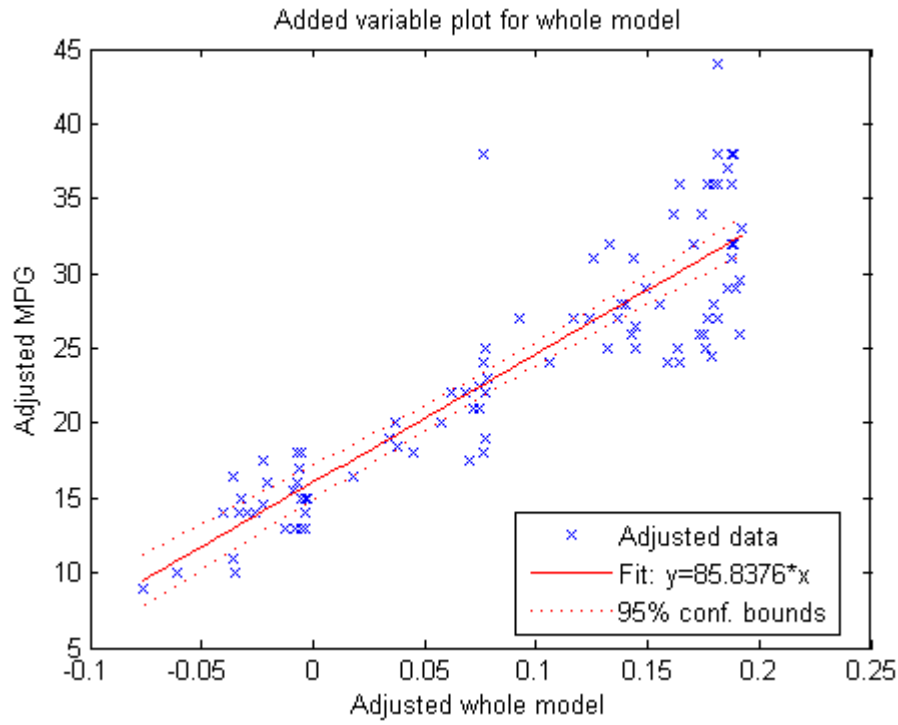
```
plotAdded(mdl,'Weight^2')
```



This plot shows the results of fitting both `Weight^2` and `MPG` to the terms other than `Weight^2`. The reason to use `plotAdded` is to understand what additional improvement in the model you get by adding `Weight^2`. The coefficient of a line fit to these points is the coefficient of `Weight^2` in the full model. The `Weight^2` predictor is just over the edge of significance (`pValue` < 0.05) as you can see in the coefficients table display. You can see that in the plot as well. The confidence bounds look like they could not contain a horizontal line (constant y), so a zero-slope model is not consistent with the data.

3 Create an added variable plot for the model as a whole.

```
plotAdded(mdl)
```



The model as a whole is very significant, so the bounds don't come close to containing a horizontal line. The slope of the line is the slope of a fit to the predictors projected onto their best-fitting direction, or in other words, the norm of the coefficient vector.

Change Models

There are two ways to change a model:

- `step` — Add or subtract terms one at a time, where `step` chooses the most important term to add or remove.
- `addTerms` and `removeTerms` — Add or remove specified terms. Give the terms in any of the forms described in "Choose a Model or Range of Models" on page 9-14.

If you created a model using `stepwiselm`, `step` can have an effect only if you give different upper or lower models. `step` does not work when you fit a model using `RobustOpts`.

For example, start with a linear model of mileage from the `carbig` data:

```
load carbig
tbl = table(Acceleration,Displacement,Horsepower,Weight,MPG);
mdl = fitlm(tbl,'linear','ResponseVar','MPG')
```

```
mdl =


Linear regression model:
    MPG ~ 1 + Acceleration + Displacement + Horsepower + Weight

Estimated Coefficients:
                    Estimate      SE            tStat       pValue
    (Intercept)         45.251         2.456      18.424    7.0721e-55
    Acceleration     -0.023148        0.1256     -0.1843       0.85388
    Displacement     -0.0060009     0.0067093     -0.89441       0.37166
    Horsepower        -0.043608      0.016573     -2.6312      0.008849
    Weight           -0.0052805    0.00081085     -6.5123    2.3025e-10


Number of observations: 392, Error degrees of freedom: 387
Root Mean Squared Error: 4.25
R-squared: 0.707,  Adjusted R-Squared 0.704
F-statistic vs. constant model: 233, p-value = 9.63e-102
```

Try to improve the model using `step` for up to 10 steps:

```
mdl1 = step(mdl,'NSteps',10)
```

```
1. Adding Displacement:Horsepower, FStat = 87.4802, pValue = 7.05273e-19

mdl1 =


Linear regression model:
    MPG ~ 1 + Acceleration + Weight + Displacement*Horsepower

Estimated Coefficients:
                            Estimate      SE            tStat      pValue
    (Intercept)                61.285        2.8052     21.847    1.8593e-69
    Acceleration              -0.34401       0.11862      -2.9     0.0039445
    Displacement             -0.081198      0.010071    -8.0623    9.5014e-15
    Horsepower                -0.24313      0.026068    -9.3265    8.6556e-19
    Weight                   -0.0014367    0.00084041    -1.7095      0.088166
    Displacement:Horsepower  0.00054236    5.7987e-05     9.3531    7.0527e-19


Number of observations: 392, Error degrees of freedom: 386
Root Mean Squared Error: 3.84
R-squared: 0.761,  Adjusted R-Squared 0.758
F-statistic vs. constant model: 246, p-value = 1.32e-117
```

`step` stopped after just one change.

To try to simplify the model, remove the `Acceleration` and `Weight` terms from `mdl1`:

```
mdl2 = removeTerms(mdl1,'Acceleration + Weight')
```

```
mdl2 =


Linear regression model:
    MPG ~ 1 + Displacement*Horsepower

Estimated Coefficients:
                            Estimate      SE           tStat      pValue
    (Intercept)                53.051       1.526     34.765    3.0201e-121
    Displacement              -0.098046    0.0066817   -14.674     4.3203e-39
    Horsepower                 -0.23434     0.019593    -11.96     2.8024e-28
    Displacement:Horsepower   0.00058278   5.193e-05     11.222     1.6816e-25


Number of observations: 392, Error degrees of freedom: 388
Root Mean Squared Error: 3.94
R-squared: 0.747,  Adjusted R-Squared 0.745
F-statistic vs. constant model: 381, p-value = 3e-115
```

`mdl2` uses just `Displacement` and `Horsepower`, and has nearly as good a fit to the data as `mdl1` in the `Adjusted R-Squared` metric.

Predict or Simulate Responses to New Data

There are three ways to use a linear model to predict or simulate the response to new data:

- “predict” on page 9-37
- “feval” on page 9-38
- “random” on page 9-39

predict

This example shows how to predict and obtain confidence intervals on the predictions using the `predict` method.

1. Load the `carbig` data and make a default linear model of the response `MPG` to the `Acceleration`, `Displacement`, `Horsepower`, and `Weight` predictors.

   ```
   load carbig
   X = [Acceleration,Displacement,Horsepower,Weight];
   mdl = fitlm(X,MPG);
   ```

2 Create a three-row array of predictors from the minimal, mean, and maximal values. There are some NaN values, so use functions that ignore NaN values.

```
Xnew = [nanmin(X);nanmean(X);nanmax(X)]; % new data
```

3 Find the predicted model responses and confidence intervals on the predictions.

```
[NewMPG NewMPGCI] = predict(mdl,Xnew)
```

```
NewMPG =
   34.1345
   23.4078
    4.7751

NewMPGCI =
   31.6115   36.6575
   22.9859   23.8298
    0.6134    8.9367
```

The confidence bound on the mean response is narrower than those for the minimum or maximum responses, which is quite sensible.

feval

When you construct a model from a table or dataset array, `feval` is often more convenient for predicting mean responses than `predict`. However, `feval` does not provide confidence bounds.

This example shows how to predict mean responses using the `feval` method.

1 Load the `carbig` data and make a default linear model of the response `MPG` to the `Acceleration`, `Displacement`, `Horsepower`, and `Weight` predictors.

```
load carbig
tbl = table(Acceleration,Displacement,Horsepower,Weight,MPG);
mdl = fitlm(tbl,'linear','ResponseVar','MPG');
```

2 Create a three-row array of predictors from the minimal, mean, and maximal values. There are some NaN values, so use functions that ignore NaN values.

```
X = [Acceleration,Displacement,Horsepower,Weight];
Xnew = [nanmin(X);nanmean(X);nanmax(X)]; % new data
```

The `Xnew` array has the correct number of columns for prediction, so `feval` can use it for predictions.

3 Find the predicted model responses.

```
NewMPG = feval(mdl,Xnew)
```

```
NewMPG =
   34.1345
   23.4078
    4.7751
```

random

The `random` method simulates new random response values, equal to the mean prediction plus a random disturbance with the same variance as the training data.

This example shows how to simulate responses using the `random` method.

1 Load the `carbig` data and make a default linear model of the response `MPG` to the `Acceleration`, `Displacement`, `Horsepower`, and `Weight` predictors.

```
load carbig
X = [Acceleration,Displacement,Horsepower,Weight];
mdl = fitlm(X,MPG);
```

2 Create a three-row array of predictors from the minimal, mean, and maximal values. There are some `NaN` values, so use functions that ignore `NaN` values.

```
Xnew = [nanmin(X);nanmean(X);nanmax(X)]; % new data
```

3 Generate new predicted model responses including some randomness.

```
rng('default') % for reproducibility
NewMPG = random(mdl,Xnew)
```

```
NewMPG =

   36.4178
   31.1958
   -4.8176
```

4 Because a negative value of `MPG` does not seem sensible, try predicting two more times.

```
NewMPG = random(mdl,Xnew)
```

```
NewMPG =
```

```
   37.7959
   24.7615
   -0.7783

NewMPG = random(mdl,Xnew)

NewMPG =

   32.2931
   24.8628
   19.9715
```

Clearly, the predictions for the third (maximal) row of `Xnew` are not reliable.

Share Fitted Models

Suppose you have a linear regression model, such as `mdl` from the following commands:

```
load carbig
tbl = table(Acceleration,Displacement,Horsepower,Weight,MPG);
mdl = fitlm(tbl,'linear','ResponseVar','MPG');
```

To share the model with other people, you can:

- Provide the model display.

```
mdl

mdl =


Linear regression model:
    MPG ~ 1 + Acceleration + Displacement + Horsepower + Weight

Estimated Coefficients:
                   Estimate      SE            tStat       pValue
    (Intercept)         45.251         2.456      18.424    7.0721e-55
    Acceleration     -0.023148        0.1256     -0.1843       0.85388
    Displacement    -0.0060009     0.0067093    -0.89441       0.37166
    Horsepower       -0.043608      0.016573     -2.6312      0.008849
    Weight          -0.0052805    0.00081085     -6.5123    2.3025e-10


Number of observations: 392, Error degrees of freedom: 387
```

```
Root Mean Squared Error: 4.25
R-squared: 0.707,  Adjusted R-Squared 0.704
F-statistic vs. constant model: 233, p-value = 9.63e-102
```

- Provide just the model definition and coefficients.

```
mdl.CoefficientNames

ans =

    '(Intercept)'    'Acceleration'    'Displacement'    'Horsepower'    'Weight'

mdl.Coefficients.Estimate

ans =

   45.2511
   -0.0231
   -0.0060
   -0.0436
   -0.0053

mdl.Formula

ans =

MPG ~ 1 + Acceleration + Displacement + Horsepower + Weight
```

Linear Regression Workflow

This example shows how to fit a linear regression model. A typical workflow involves the following: import data, fit a regression, test its quality, modify it to improve the quality, and share it.

Step 1. Import the data into a dataset array.

`hospital.xls` is an Excel® spreadsheet containing patient names, sex, age, weight, blood pressure, and dates of treatment in an experimental protocol. First read the data into a table.

```
patients = readtable('hospital.xls',...
    'ReadRowNames',true);
```

Examine the first row of data.

```
patients(1,:)

ans =

                name      sex    age    wgt    smoke    sys    dia    trial1    trial2
              ________    ___    ___    ___    _____    ___    ___    ______    ______

    YPL-320    'SMITH'    'm'    38     176    1        124    93     18        -99
```

The `sex` and `smoke` fields seem to have two choices each. So change these fields to nominal.

```
patients.smoke = nominal(patients.smoke,{'No','Yes'});
patients.sex = nominal(patients.sex);
```

Step 2. Create a fitted model.

Your goal is to model the systolic pressure as a function of a patient's age, weight, sex, and smoking status. Create a linear formula for `'sys'` as a function of `'age'`, `'wgt'`, `'sex'`, and `'smoke'` .

```
modelspec = 'sys ~ age + wgt + sex + smoke';
mdl = fitlm(patients,modelspec)

mdl =


Linear regression model:
    sys ~ 1 + sex + age + wgt + smoke

Estimated Coefficients:
                   Estimate        SE        tStat        pValue
                   ________    ________    ________    __________

    (Intercept)       118.28      7.6291      15.504    9.1557e-28
    sex_m            0.88162      2.9473     0.29913       0.76549
    age              0.08602     0.06731       1.278       0.20438
    wgt             -0.016685    0.055714    -0.29947       0.76524
    smoke_Yes           9.884      1.0406       9.498    1.9546e-15


Number of observations: 100, Error degrees of freedom: 95
```

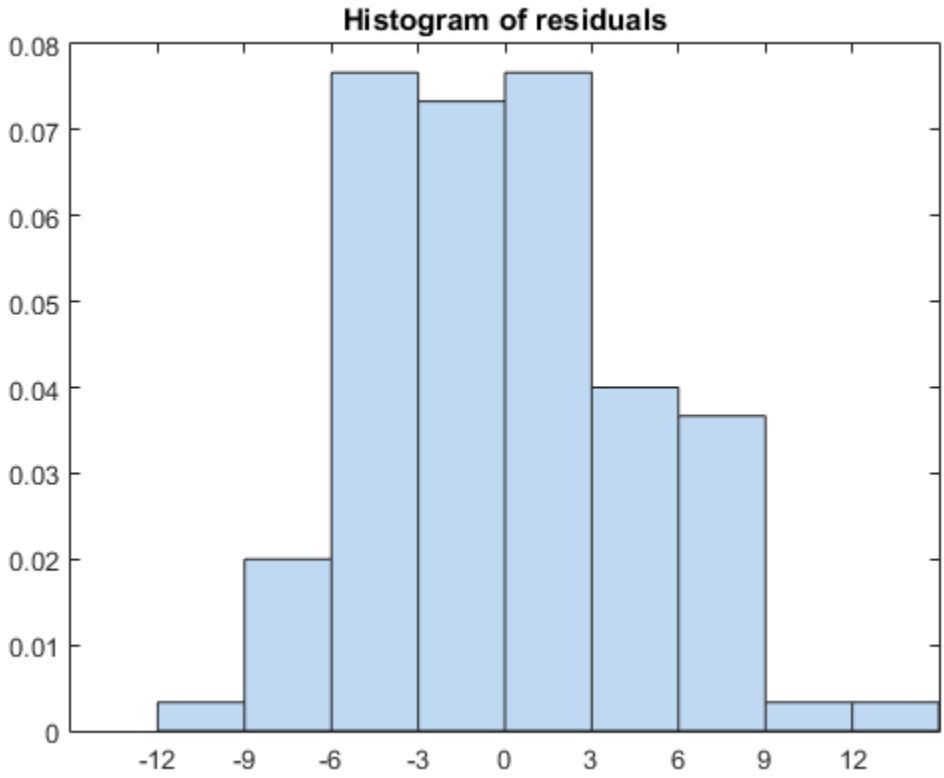
```
Root Mean Squared Error: 4.81
R-squared: 0.508,  Adjusted R-Squared 0.487
F-statistic vs. constant model: 24.5, p-value = 5.99e-14
```

The sex, age, and weight predictors have rather high p-values, indicating that some of these predictors might be unnecessary.

Step 3. Locate and remove outliers.

See if there are outliers in the data that should be excluded from the fit. Plot the residuals.

```
plotResiduals(mdl)
```



There is one possible outlier, with a value greater than 12. This is probably not truly an outlier. For demonstration, here is how to find and remove it.

Find the outlier.

```
outlier = mdl.Residuals.Raw > 12;
find(outlier)
```

```
ans =

    84
```

Remove the outlier.

```
mdl = fitlm(patients,modelspec,...
    'Exclude',84);

mdl.ObservationInfo(84,:)
```

```
ans =

               Weights    Excluded    Missing    Subset
               _______    ________    _______    ______

    WXM-486    1          true        false      false
```

Observation 84 is no longer in the model.

Step 4. Simplify the model.

Try to obtain a simpler model, one with fewer predictors but the same predictive accuracy. `step` looks for a better model by adding or removing one term at a time. Allow `step` take up to 10 steps.

```
mdl1 = step(mdl,'NSteps',10)
```

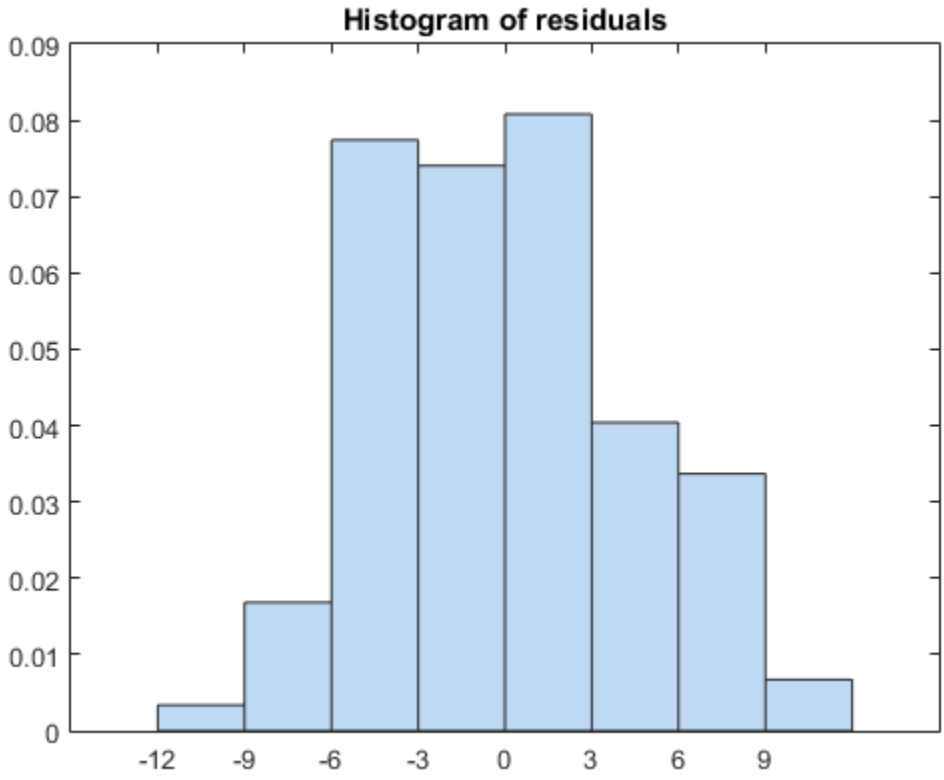
```
1. Removing wgt, FStat = 4.6001e-05, pValue = 0.9946
2. Removing sex, FStat = 0.063241, pValue = 0.80199

mdl1 =
```

```
Linear regression model:
    sys ~ 1 + age + smoke

Estimated Coefficients:
                   Estimate       SE       tStat       pValue
                   ________    ________    ______    __________

    (Intercept)     115.11       2.5364    45.383    1.1407e-66
    age            0.10782     0.064844    1.6628       0.09962
    smoke_Yes       10.054      0.97696    10.291    3.5276e-17


Number of observations: 99, Error degrees of freedom: 96
Root Mean Squared Error: 4.61
R-squared: 0.536,  Adjusted R-Squared 0.526
F-statistic vs. constant model: 55.4, p-value = 1.02e-16
```

`step` took two steps. This means it could not improve the model further by adding or subtracting a single term.

Plot the effectiveness of the simpler model on the training data.

```
plotResiduals(mdl1)
```



The residuals look about as small as those of the original model.

Step 5. Predict responses to new data.

Suppose you have four new people, aged 25, 30, 40, and 65, and the first and third smoke. Predict their systolic pressure using `mdl1`.

```
ages = [25;30;40;65];
smoker = {'Yes';'No';'Yes';'No'};
systolicnew = feval(mdl1,ages,smoker)
```

```
systolicnew =
```

```
  127.8561
  118.3412
  129.4734
  122.1149
```

To make predictions, you need only the variables that `mdl1` uses.

Step 6. Share the model.

You might want others to be able to use your model for prediction. Access the terms in the linear model.

```
coefnames = mdl1.CoefficientNames
```

```
coefnames =

    '(Intercept)'    'age'    'smoke_Yes'
```

View the model formula.

```
mdl1.Formula
```

```
ans =

sys ~ 1 + age + smoke
```

Access the coefficients of the terms.

```
coefvals = mdl1.Coefficients(:,1); % table
coefvals = table2array(coefvals)
```

```
coefvals =

  115.1066
    0.1078
   10.0540
```

The model is `sys = 115.1066 + 0.1078*age + 10.0540*smoke`, where `smoke` is `1` for a smoker, and `0` otherwise.

Regression Using Dataset Arrays

This example shows how to perform linear and stepwise regression analyses using dataset arrays.

Load sample data.

```
load imports-85
```

Store predictor and response variables in dataset array.

```
ds = dataset(X(:,7),X(:,8),X(:,9),X(:,15),'Varnames',...
{'curb_weight','engine_size','bore','price'});
```

Fit linear regression model.

Fit a linear regression model that explains the price of a car in terms of its curb weight, engine size, and bore.

```
fitlm(ds,'price~curb_weight+engine_size+bore')
```

```
ans =


Linear regression model:
    price ~ 1 + curb_weight + engine_size + bore

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        64.095        3.703     17.309    2.0481e-41
    curb_weight    -0.0086681    0.0011025    -7.8623      2.42e-13
    engine_size     -0.015806     0.013255    -1.1925       0.23452
    bore              -2.6998       1.3489    -2.0015      0.046711


Number of observations: 201, Error degrees of freedom: 197
Root Mean Squared Error: 3.95
R-squared: 0.674,  Adjusted R-Squared 0.669
F-statistic vs. constant model: 136, p-value = 1.14e-47
```

The command `fitlm(ds)` also returns the same result because `fitlm`, by default, assumes the predictor variable is in the last column of the dataset array `ds`.

Recreate dataset array and repeat analysis.

This time, put the response variable in the first column of the dataset array.

```
 ds = dataset(X(:,15),X(:,7),X(:,8),X(:,9),'Varnames',...
{'price','curb_weight','engine_size','bore'});
```

When the response variable is in the first column of `ds`, define its location. For example, `fitlm`, by default, assumes that `bore` is the response variable. You can define the response variable in the model using either:

```
fitlm(ds,'ResponseVar','price');
```

or

```
fitlm(ds,'ResponseVar',logical([1 0 0 0]));
```

Perform stepwise regression.

```
stepwiselm(ds,'quadratic','lower','price~1',...
'ResponseVar','price')
```

```
1. Removing bore^2, FStat = 0.01282, pValue = 0.90997
2. Removing engine_size^2, FStat = 0.078043, pValue = 0.78027
3. Removing curb_weight:bore, FStat = 0.70558, pValue = 0.40195

ans =


Linear regression model:
    price ~ 1 + curb_weight*engine_size + engine_size*bore + curb_weight^2

Estimated Coefficients:
                              Estimate       SE            tStat      pValue
    (Intercept)                  131.13        14.273     9.1873    6.2319e-17
    curb_weight                -0.043315     0.0085114    -5.0891    8.4682e-07
    engine_size                 -0.17102       0.13844    -1.2354       0.21819
    bore                         -12.244         4.999    -2.4493      0.015202
    curb_weight:engine_size    -6.3411e-05    2.6577e-05     -2.386      0.017996
    engine_size:bore             0.092554      0.037263     2.4838      0.013847
    curb_weight^2               8.0836e-06    1.9983e-06     4.0451    7.5432e-05


Number of observations: 201, Error degrees of freedom: 194
Root Mean Squared Error: 3.59
```

```
R-squared: 0.735,  Adjusted R-Squared 0.726
F-statistic vs. constant model: 89.5, p-value = 3.58e-53
```

The initial model is a quadratic formula, and the lowest model considered is the constant. Here, `stepwiselm` performs a backward elimination technique to determine the terms in the model. The final model is `price ~ 1 + curb_weight*engine_size + engine_size*bore + curb_weight^2`, which corresponds to

$$P = \beta_0 + \beta_C C + \beta_E E + \beta_B B + \beta_{CE} CE + \beta_{EB} EB + \beta_{C^2} C^2 + \varepsilon$$

where P is price, C is curb weight, E is engine size, B is bore, β_i is the coefficient for the corresponding term in the model, and ε is the error term. The final model includes all three main effects, the interaction effects for curb weight and engine size and engine size and bore, and the second-order term for curb weight.

See Also

`fitlm` | `LinearModel` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

Regression Using Tables

This example shows how to perform linear and stepwise regression analyses using tables.

Load sample data.

```
load imports-85
```

Store predictor and response variables in a table.

```
tbl = table(X(:,7),X(:,8),X(:,9),X(:,15),'VariableNames',...
{'curb_weight','engine_size','bore','price'});
```

Fit linear regression model.

Fit a linear regression model that explains the price of a car in terms of its curb weight, engine size, and bore.

```
fitlm(tbl,'price~curb_weight+engine_size+bore')
```

```
ans =


Linear regression model:
    price ~ 1 + curb_weight + engine_size + bore

Estimated Coefficients:
                    Estimate        SE         tStat
                   __________    _________    _______

    (Intercept)        64.095        3.703     17.309
    curb_weight    -0.0086681    0.0011025    -7.8623
    engine_size     -0.015806     0.013255    -1.1925
    bore              -2.6998       1.3489    -2.0015


                     pValue
                   __________

    (Intercept)    2.0481e-41
    curb_weight      2.42e-13
    engine_size       0.23452
    bore             0.046711
```

```
Number of observations: 201, Error degrees of freedom: 197
Root Mean Squared Error: 3.95
R-squared: 0.674,  Adjusted R-Squared 0.669
F-statistic vs. constant model: 136, p-value = 1.14e-47
```

The command `fitlm(tbl)` also returns the same result because `fitlm`, by default, assumes the predictor variable is in the last column of the table `tbl`.

Recreate table and repeat analysis.

This time, put the response variable in the first column of the table.

```
 tbl = table(X(:,15),X(:,7),X(:,8),X(:,9),'VariableNames',...
{'price','curb_weight','engine_size','bore'});
```

When the response variable is in the first column of `tbl`, define its location. For example, `fitlm`, by default, assumes that `bore` is the response variable. You can define the response variable in the model using either:

```
fitlm(tbl,'ResponseVar','price');
```

or

```
fitlm(tbl,'ResponseVar',logical([1 0 0 0]));
```

Perform stepwise regression.

```
stepwiselm(tbl,'quadratic','lower','price~1',...
'ResponseVar','price')

ans =


Linear regression model:
    price ~ [Linear formula with 7 terms in 3 predictors]

Estimated Coefficients:
                                Estimate          SE
                               ___________    __________

    (Intercept)                    131.13        14.273
    curb_weight                  -0.043315     0.0085114
    engine_size                   -0.17102       0.13844
    bore                           -12.244         4.999
    curb_weight:engine_size    -6.3411e-05    2.6577e-05
```

```
    engine_size:bore              0.092554      0.037263
    curb_weight^2                8.0836e-06    1.9983e-06


                                   tStat       pValue
                                  _______    __________

    (Intercept)                    9.1873    6.2319e-17
    curb_weight                   -5.0891    8.4682e-07
    engine_size                   -1.2354       0.21819
    bore                          -2.4493      0.015202
    curb_weight:engine_size        -2.386      0.017996
    engine_size:bore               2.4838      0.013847
    curb_weight^2                  4.0451    7.5432e-05


Number of observations: 201, Error degrees of freedom: 194
Root Mean Squared Error: 3.59
R-squared: 0.735,  Adjusted R-Squared 0.726
F-statistic vs. constant model: 89.5, p-value = 3.58e-53
```

The initial model is a quadratic formula, and the lowest model considered is the constant. Here, `stepwiselm` performs a backward elimination technique to determine the terms in the model. The final model is `price ~ 1 + curb_weight*engine_size + engine_size*bore + curb_weight^2`, which corresponds to

$$P = \beta_0 + \beta_C C + \beta_E E + \beta_B B + \beta_{CE} CE + \beta_{EB} EB + \beta_{C^2} C^2 + \varepsilon$$

where P is price, C is curb weight, E is engine size, B is bore, β_i is the coefficient for the corresponding term in the model, and ε is the error term. The final model includes all three main effects, the interaction effects for curb weight and engine size and engine size and bore, and the second-order term for curb weight.

See Also

`fitlm` | `LinearModel` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

Linear Regression with Interaction Effects

This example shows how to construct and analyze a linear regression model with interaction effects and interpret the results.

Load sample data.

```
load hospital
```

To retain only the first column of blood pressure, store data in a new dataset array.

```
ds = dataset(hospital.Sex,hospital.Age,hospital.Weight,hospital.Smoker,...
hospital.BloodPressure(:,1),'Varnames',{'Sex','Age','Weight','Smoker',...
'BloodPressure'});
```

Perform stepwise linear regression.

For the initial model, use the full model with all terms and their pairwise interactions.

```
mdl = stepwiselm(ds,'interactions')
```

```
1. Removing Sex:Smoker, FStat = 0.050738, pValue = 0.8223
2. Removing Weight:Smoker, FStat = 0.07758, pValue = 0.78124
3. Removing Age:Weight, FStat = 1.9717, pValue = 0.16367
4. Removing Sex:Age, FStat = 0.32389, pValue = 0.57067
5. Removing Age:Smoker, FStat = 2.4939, pValue = 0.11768

mdl =


Linear regression model:
    BloodPressure ~ 1 + Age + Smoker + Sex*Weight

Estimated Coefficients:
                       Estimate    SE          tStat      pValue
    (Intercept)         133.17       10.337     12.883      1.76e-22
    Sex_Male           -35.269       17.524    -2.0126      0.047015
    Age                0.11584     0.067664      1.712      0.090198
    Weight             -0.1393     0.080211    -1.7367      0.085722
    Smoker_1            9.8307       1.0229     9.6102    1.2391e-15
    Sex_Male:Weight     0.2341      0.11192     2.0917      0.039162


Number of observations: 100, Error degrees of freedom: 94
Root Mean Squared Error: 4.72
```

```
R-squared: 0.53,  Adjusted R-Squared 0.505
F-statistic vs. constant model: 21.2, p-value = 4e-14
```

The final model in formula form is `BloodPressure ~ 1 + Age + Smoker + Sex*Weight`. This model includes all four main effects (Age, Smoker, Sex, Weight) and the two-way interaction between `Sex` and `Weight`. This model corresponds to

$$BP = \beta_0 + \beta_A X_A + \beta_{Sm} I_{Sm} + \beta_S I_S + \beta_W X_W + \beta_{SW} X_W I_S + \varepsilon,$$

where

- BP is the blood pressure
- β_i are the coefficients
- I_{Sm} is the indicator variable for smoking; $I_{Sm} = 1$ indicates a smoking patient whereas $I_{Sm} = 0$ indicates a nonsmoking patient
- I_S is the indicator variable for sex; $I_S = 1$ indicates a male patient whereas $I_S = 0$ indicates a female patient
- X_A is the `Age` variable
- X_W is the `Weight` variable
- ε is the error term

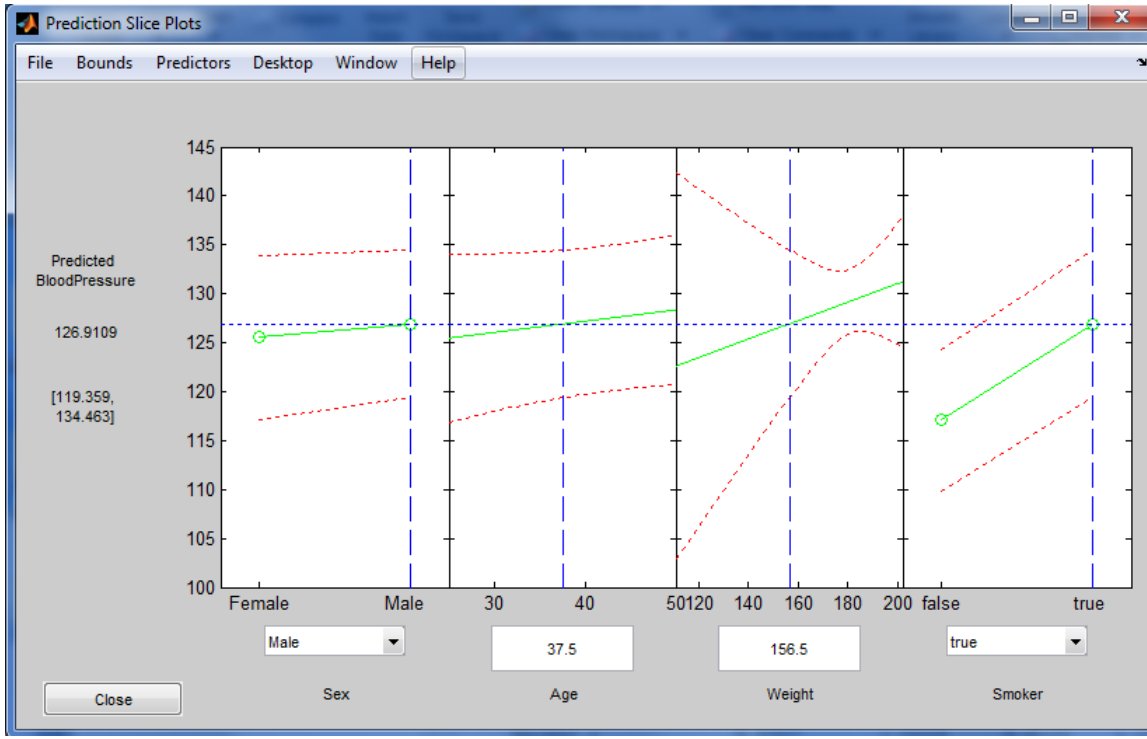
The following table shows the fitted linear model for each gender and smoking combination.

I_{Sm}	I_S	Linear Model
1 (Male)	1 (Smoker)	$BP = (\beta_0 + \beta_{Sm} + \beta_S) + \beta_A X_A + (\beta_W + \beta_{SW}) X_W$ $\widehat{BP} = 107.5617 + 0.11584 X_A + 0.11826 X_W$
1 (Male)	0 (Nonsmoker)	$BP = (\beta_0 + \beta_{Sm}) + \beta_A X_A + \beta_W X_W$ $\widehat{BP} = 143.0007 + 0.11584 X_A - 0.1393 X_W$
0 (Female)	1 (Smoker)	$BP = (\beta_0 + \beta_S) + \beta_A X_A + (\beta_W + \beta_{SW}) X_W$ $\widehat{BP} = 97.901 + 0.11584 X_A + 0.11826 X_W$
0 (Female)	0 (Nonsmoker)	$BP = \beta_0 + \beta_A X_A + \beta_W X_W$ $\widehat{BP} = 133.17 + 0.11584 X_A - 0.1393 X_W$

As seen from these models, β_{Sm} and β_S show how much the intercept of the response function changes when the indicator variable takes the value 1 compared to when it takes the value 0. β_{SW}, however, shows the effect of the Weight variable on the response variable when the indicator variable for sex takes the value 1 compared to when it takes the value 0. You can explore the main and interaction effects in the final model using the methods of the `LinearModel` class as follows.

Plot prediction slice plots.

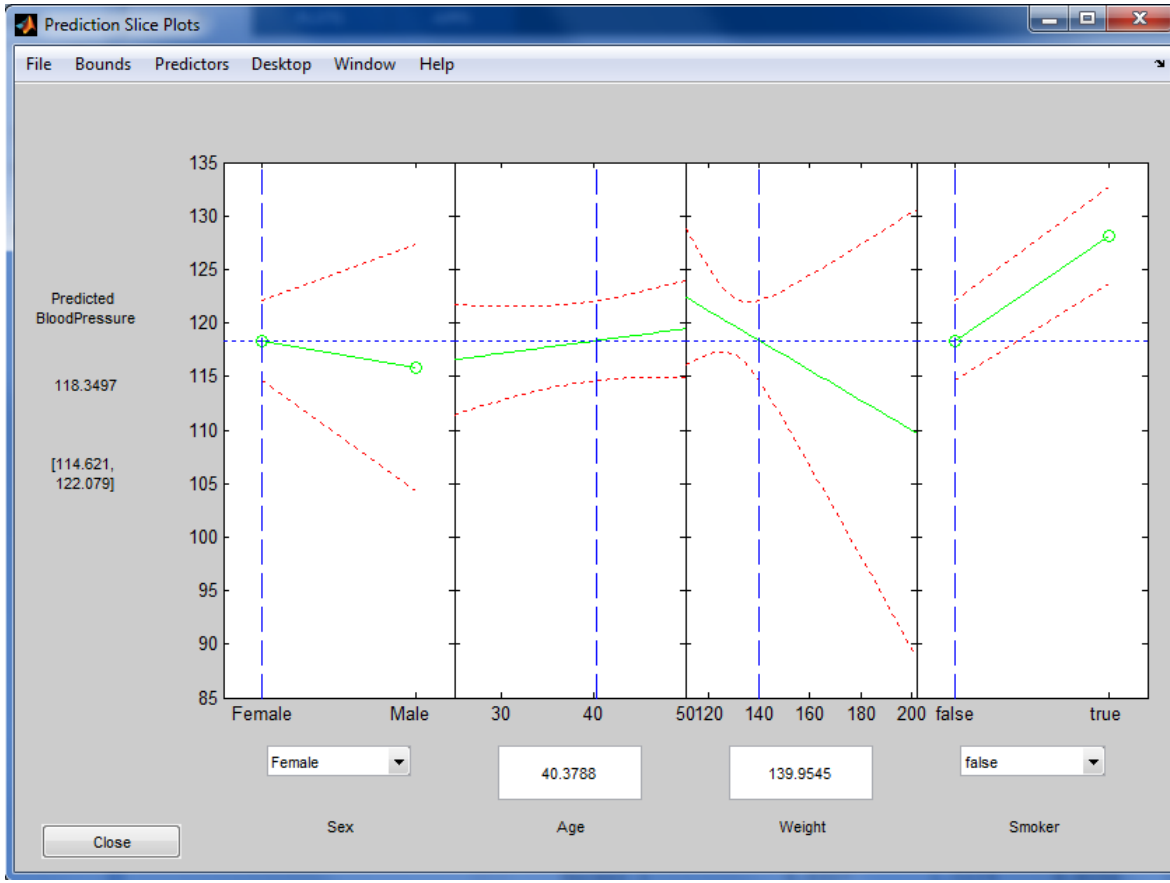
```
figure()
plotSlice(mdl)
```



This plot shows the main effects for all predictor variables. The green line in each panel shows the change in the response variable as a function of the predictor variable when all other predictor variables are held constant. For example, for a smoking male patient aged 37.5, the expected blood pressure increases as the weight of the patient increases, given all else the same.

The dashed red curves in each panel show the 95% confidence bounds for the predicted response values.

The horizontal dashed blue line in each panel shows the predicted response for the specific value of the predictor variable corresponding to the vertical dashed blue line. You can drag these lines to get the predicted response values at other predictor values, as shown next.

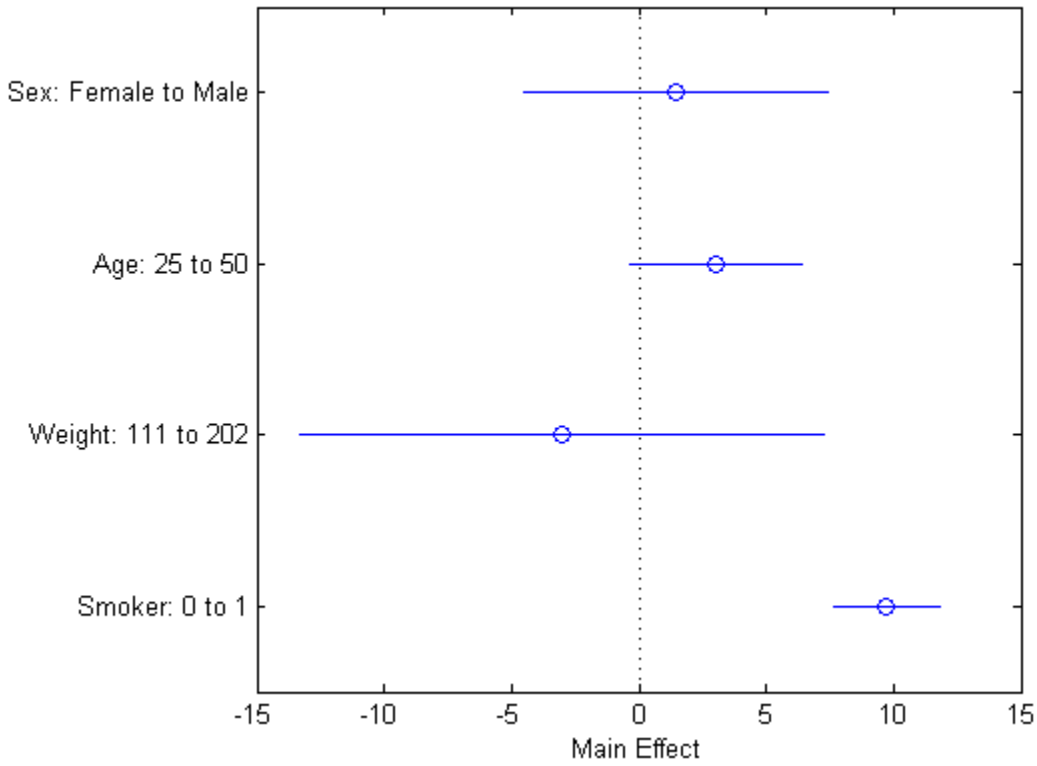


For example, the predicted value of the response variable is 118.3497 when a patient is female, nonsmoking, age 40.3788, and weighs 139.9545 pounds. The values in the square brackets, [114.621, 122.079], show the lower and upper limits of a 95% confidence

interval for the estimated response. Note that, for a nonsmoking female patient, the expected blood pressure decreases as the weight increases, given all else is held constant.

Plot main effects.

```
figure()
plotEffects(mdl)
```

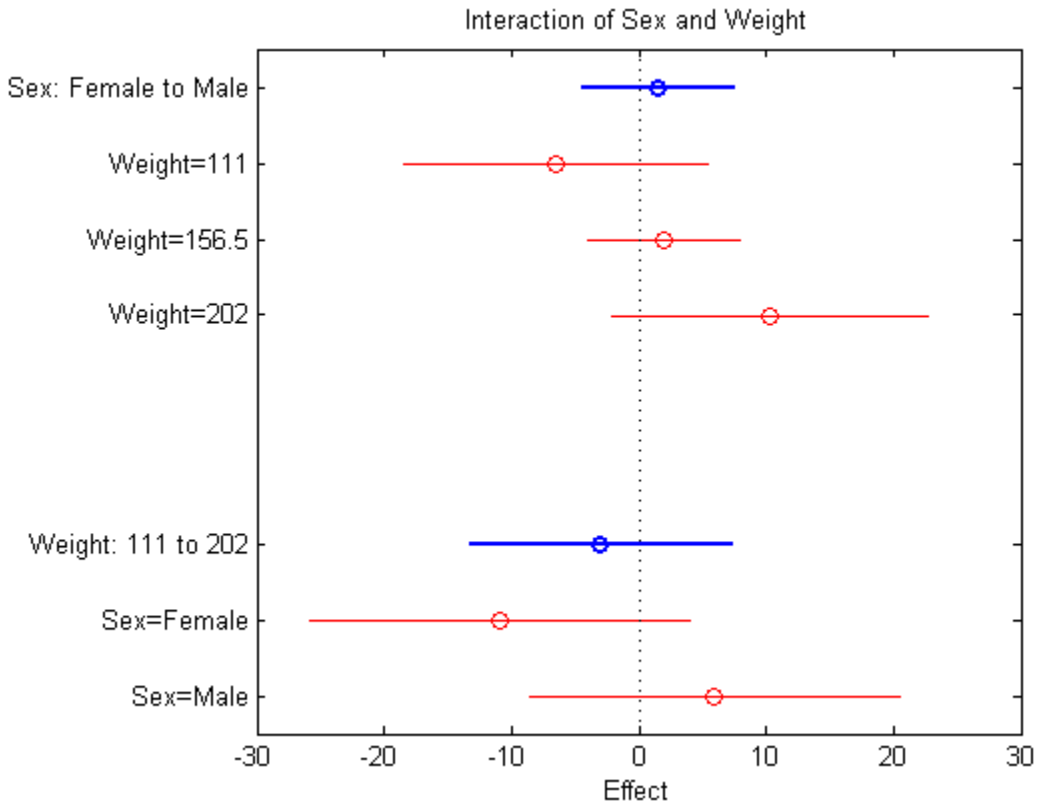


This plot displays the main effects. The circles show the magnitude of the effect and the blue lines show the upper and lower confidence limits for the main effect. For example, being a smoker increases the expected blood pressure by 10 units, compared to being a nonsmoker, given all else is held constant. Expected blood pressure increases about two units for males compared to females, again, given other predictors held constant. An

increase in age from 25 to 50 causes an expected increase of 4 units, whereas a change in weight from 111 to 202 causes about a 4-unit decrease in the expected blood pressure, given all else held constant.

Plot interaction effects.

```
figure()
plotInteraction(mdl,'Sex','Weight')
```



This plot displays the impact of a change in one factor given the other factor is fixed at a value.

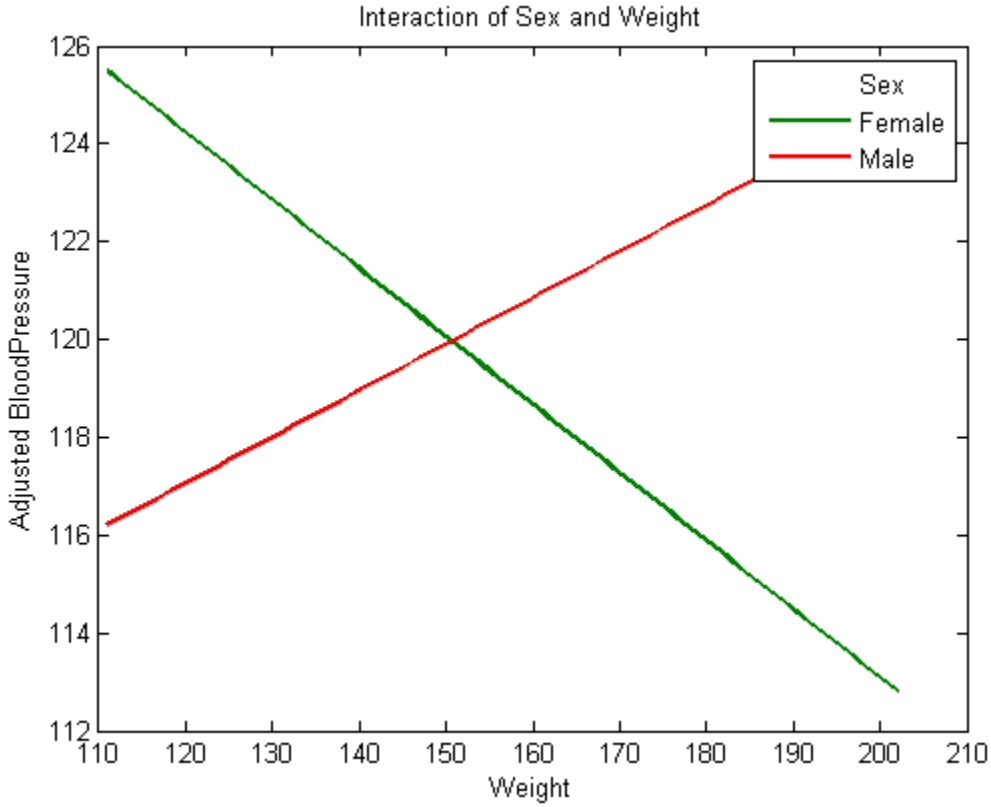
Be cautious while interpreting the interaction effects. When there is not enough data on all factor combinations or the data is highly correlated, it might be difficult to determine

the interaction effect of changing one factor while keeping the other fixed. In such cases, the estimated interaction effect is an extrapolation from the data.

The blue circles show the main effect of a specific term, as in the main effects plot. The red circles show the impact of a change in one term for fixed values of the other term. For example, in the bottom half of this plot, the red circles show the impact of a weight change in female and male patients, separately. You can see that an increase in a female's weight from 111 to 202 pounds causes about a 14-unit decrease in the expected blood pressure, while an increase of the same amount in the weight of a male patient causes about a 5-unit increase in the expected blood pressure, again given other predictors are held constant.

Plot prediction effects.

```
figure()
plotInteraction(mdl,'Sex','Weight','predictions')
```



This plot shows the effect of changing one variable as the other predictor variable is held constant. In this example, the last figure shows the response variable, blood pressure, as a function of weight, when the variable sex is fixed at males and females. The lines for males and females are crossing which indicates a strong interaction between weight and sex. You can see that the expected blood pressure increases as the weight of a male patient increases, but decreases as the weight of a female patient increases.

See Also

`LinearModel.fit` | `LinearModel.stepwise` | `LinearModel` | `plotEffects` | `plotInteraction` | `plotSlice`

Related Examples

- "Plots to Understand Predictor Effects" on page 9-28

Interpret Linear Regression Results

This example shows how to display and interpret linear regression output statistics.

Load sample data and define predictor variables.

```
load carsmall
X = [Weight,Horsepower,Acceleration];
```

Fit linear regression model.

```
lm = fitlm(X,MPG,'linear')
```

```
lm =


Linear regression model:
    y ~ 1 + x1 + x2 + x3

Estimated Coefficients:
                   Estimate      SE           tStat        pValue
    (Intercept)        47.977       3.8785        12.37    4.8957e-21
    x1             -0.0065416    0.0011274      -5.8023    9.8742e-08
    x2              -0.042943     0.024313      -1.7663       0.08078
    x3              -0.011583      0.19333    -0.059913       0.95236


Number of observations: 93, Error degrees of freedom: 89
Root Mean Squared Error: 4.09
R-squared: 0.752,  Adjusted R-Squared 0.744
F-statistic vs. constant model: 90, p-value = 7.38e-27
```

This linear regression outputs display shows the following.

`y ~ 1 + x1 + x2 + x3`	Linear regression model in the formula form using Wilkinson notation. Here it corresponds to: $$y = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \varepsilon.$$
First column (under `Estimated Coefficients`)	Terms included in the model.

`Estimate`	Coefficient estimates for each corresponding term in the model. For example, the estimate for the constant term (`intercept`) is 47.977.
`SE`	Standard error of the coefficients.
`tStat`	*t*-statistic for each coefficient to test the null hypothesis that the corresponding coefficient is zero against the alternative that it is different from zero, given the other predictors in the model. Note that `tStat = Estimate/SE`. For example, the *t*-statistic for the intercept is 47.977/3.8785 = 12.37.
`pValue`	*p*-value for the F statistic of the hypotheses test that the corresponding coefficient is equal to zero or not. For example, the *p*-value of the F-statistic for `x2` is greater than 0.05, so this term is not significant at the 5% significance level given the other terms in the model.
`Number of observations`	Number of rows without any `NaN` values. For example, `Number of observations` is 93 because the `MPG` data vector has 6 `NaN` values and one of the data vectors, `Horsepower`, has one `NaN` value for a different observation.
`Error degrees of freedom`	$n - p$, where n is the number of observations, and p is the number of coefficients in the model, including the intercept. For example, the model has four predictors, so the `Error degrees of freedom` is $93 - 4 = 89$.
`Root mean squared error`	Square root of the mean squared error, which estimates the standard deviation of the error distribution.
`R-squared` and `Adjusted R-squared`	Coefficient of determination and adjusted coefficient of determination, respectively. For example, the `R-squared` value suggests that the model explains approximately 75% of the variability in the response variable `MPG`.
`F-statistic vs. constant model`	Test statistic for the F-test on the regression model. It tests for a significant linear regression relationship between the response variable and the predictor variables.
`p-value`	*p*-value for the F-test on the model. For example, the model is significant with a *p*-value of 7.3816e-27.

You can request this display by using `disp`. For example, if you name your model `lm`, then you can display the outputs using `disp(lm)`.

Perform analysis of variance (ANOVA) for the model.

```
anova(lm,'summary')
```

```
ans =

              SumSq     DF    MeanSq     F         pValue
    Total     6004.8    92    65.269
    Model       4516     3    1505.3     89.987    7.3816e-27
    Residual  1488.8    89    16.728
```

This ANOVA display shows the following.

`SumSq`	Sum of squares for the regression model, `Model`, the error term, `Residual`, and the total, `Total`.
`DF`	Degrees of freedom for each term. Degrees of freedom is $n - 1$ for the total, $p - 1$ for the model, and $n - p$ for the error term, where n is the number of observations, and p is the number of coefficients in the model, including the intercept. For example, `MPG` data vector has six `NaN` values and one of the data vectors, `Horsepower`, has one `NaN` value for a different observation, so the total degrees of freedom is $93 - 1 = 92$. There are four coefficients in the model, so the model `DF` is $4 - 1 = 3$, and the `DF` for error term is $93 - 4 = 89$.
`MeanSq`	Mean squared error for each term. Note that `MeanSq = SumSq/DF`. For example, the mean squared error for the error term is 1488.8/89 = 16.728. The square root of this value is the `root mean squared error` in the linear regression display, or 4.09.
`F`	F-statistic value, which is the same as `F-statistic vs. constant model` in the linear regression display. In this example, it is 89.987, and in the linear regression display this F-statistic value is rounded up to 90.
`pValue`	p-value for the F-test on the model. In this example, it is 7.3816e-27.

If there are higher-order terms in the regression model, `anova` partitions the model `SumSq` into the part explained by the higher-order terms and the rest. The corresponding F-statistics are for testing the significance of the linear terms and higher-order terms as separate groups.

If the data includes replicates, or multiple measurements at the same predictor values, then the `anova` partitions the error `SumSq` into the part for the replicates and the rest. The corresponding F-statistic is for testing the lack-of-fit by comparing the model residuals with the model-free variance estimate computed on the replicates.

See the anova method for details.

Decompose ANOVA table for model terms.

```
anova(lm)

ans =

              SumSq       DF    MeanSq       F             pValue
    x1          563.18     1      563.18       33.667    9.8742e-08
    x2          52.187     1      52.187       3.1197       0.08078
    x3        0.060046     1    0.060046    0.0035895       0.95236
    Error       1488.8    89      16.728
```

This anova display shows the following:

First column	Terms included in the model.
SumSq	Sum of squared error for each term except for the constant.
DF	Degrees of freedom. In this example, DF is 1 for each term in the model and $n - p$ for the error term, where n is the number of observations, and p is the number of coefficients in the model, including the intercept. For example, the DF for the error term in this model is $93 - 4 = 89$. If any of the variables in the model is a categorical variable, the DF for that variable is the number of indicator variables created for its categories (number of categories – 1).
MeanSq	Mean squared error for each term. Note that MeanSq = SumSq/DF. For example, the mean squared error for the error term is 1488.8/89 = 16.728.
F	F-values for each coefficient. The F-value is the ratio of the mean squared of each term and mean squared error, that is, F = MeanSq(x_i)/MeanSq(Error). Each F-statistic has an F distribution, with the numerator degrees of freedom, DF value for the corresponding term, and the denominator degrees of freedom, $n - p$. n is the number of observations, and p is the number of coefficients in the model. In this example, each F-statistic has an $F_{(1, 89)}$ distribution.
pValue	p-value for each hypothesis test on the coefficient of the corresponding term in the linear model. For example, the p-value for the F-statistic coefficient of x2 is 0.08078, and is not significant at the 5% significance level given the other terms in the model.

Display coefficient confidence intervals.

```
coefCI(lm)
```

```
ans =

   40.2702   55.6833
   -0.0088   -0.0043
   -0.0913    0.0054
   -0.3957    0.3726
```

The values in each row are the lower and upper confidence limits, respectively, for the default 95% confidence intervals for the coefficients. For example, the first row shows the lower and upper limits, 40.2702 and 55.6833, for the intercept, β_0. Likewise, the second row shows the limits for β_1 and so on. Confidence intervals provide a measure of precision for linear regression coefficient estimates. A 100(1–α)% confidence interval gives the range the corresponding regression coefficient will be in with 100(1–α)% confidence.

You can also change the confidence level. Find the 99% confidence intervals for the coefficients.

```
coefCI(lm,0.01)
```

```
ans =

   37.7677   58.1858
   -0.0095   -0.0036
   -0.1069    0.0211
   -0.5205    0.4973
```

Perform hypothesis test on coefficients.

Test the null hypothesis that all predictor variable coefficients are equal to zero versus the alternate hypothesis that at least one of them is different from zero.

```
[p,F,d] = coefTest(lm)
```

```
p =

   7.3816e-27


F =
```

```
   89.9874


d =

     3
```

Here, `coefTest` performs an F-test for the hypothesis that all regression coefficients (except for the intercept) are zero versus at least one differs from zero, which essentially is the hypothesis on the model. It returns `p`, the *p*-value, `F`, the F-statistic, and `d`, the numerator degrees of freedom. The F-statistic and *p*-value are the same as the ones in the linear regression display and ANOVA for the model. The degrees of freedom is $4 - 1 = 3$ because there are four predictors (including the intercept) in the model.

Now, perform a hypothesis test on the coefficients of the first and second predictor variables.

```
H = [0 1 0 0; 0 0 1 0];
[p,F,d] = coefTest(lm,H)
```

```
p =

   5.1702e-23


F =

   96.4873


d =

     2
```

The numerator degrees of freedom is the number of coefficients tested, which is 2 in this example. The results indicate that at least one of β_2 and β_3 differs from zero.

See Also

`anova` | `fitlm` | `LinearModel` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20

More About

- "Coefficient Standard Errors and Confidence Intervals" on page 9-74
- "Coefficient of Determination (R-Squared)" on page 9-78
- "F-statistic and t-statistic" on page 9-93
- "Summary of Output and Diagnostic Statistics" on page 9-112

Cook's Distance

Purpose

Cook's distance is useful for identifying outliers in the X values (observations for predictor variables). It also shows the influence of each observation on the fitted response values. An observation with Cook's distance larger than three times the mean Cook's distance might be an outlier.

Definition

Cook's distance is the scaled change in fitted values. Each element in `CooksDistance` is the normalized change in the vector of coefficients due to the deletion of an observation. The Cook's distance, D_i, of observation i is

$$D_i = \frac{\sum_{j=1}^{n} \left(\hat{y}_j - \hat{y}_{j(i)} \right)^2}{p\,MSE},$$

where

- $\hat{y}_j$ is the jth fitted response value.
- $\hat{y}_{j(i)}$ is the jth fitted response value, where the fit does not include observation i.
- MSE is the mean squared error.
- p is the number of coefficients in the regression model.

Cook's distance is algebraically equivalent to the following expression:

$$D_i = \frac{r_i^2}{p\,MSE}\left(\frac{h_{ii}}{\left(1 - h_{ii}\right)^2} \right),$$

where r_i is the ith residual, and h_{ii} is the ith leverage value.

`CooksDistance` is an n-by-1 column vector in the `Diagnostics` table of the `LinearModel` object.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Display the Cook's distance values by indexing into the property using dot notation,

  ```
  mdl.Diagnostics.CooksDistance
  ```

- Plot the Cook's distance values using

  ```
  plotDiagnostics(mdl,'cookd')
  ```

  For details, see the `plotDiagnostics` method of the `LinearModel` class.

Determine Outliers Using Cook's Distance

This example shows how to use Cook's Distance to determine the outliers in the data.

Load the sample data and define the independent and response variables.

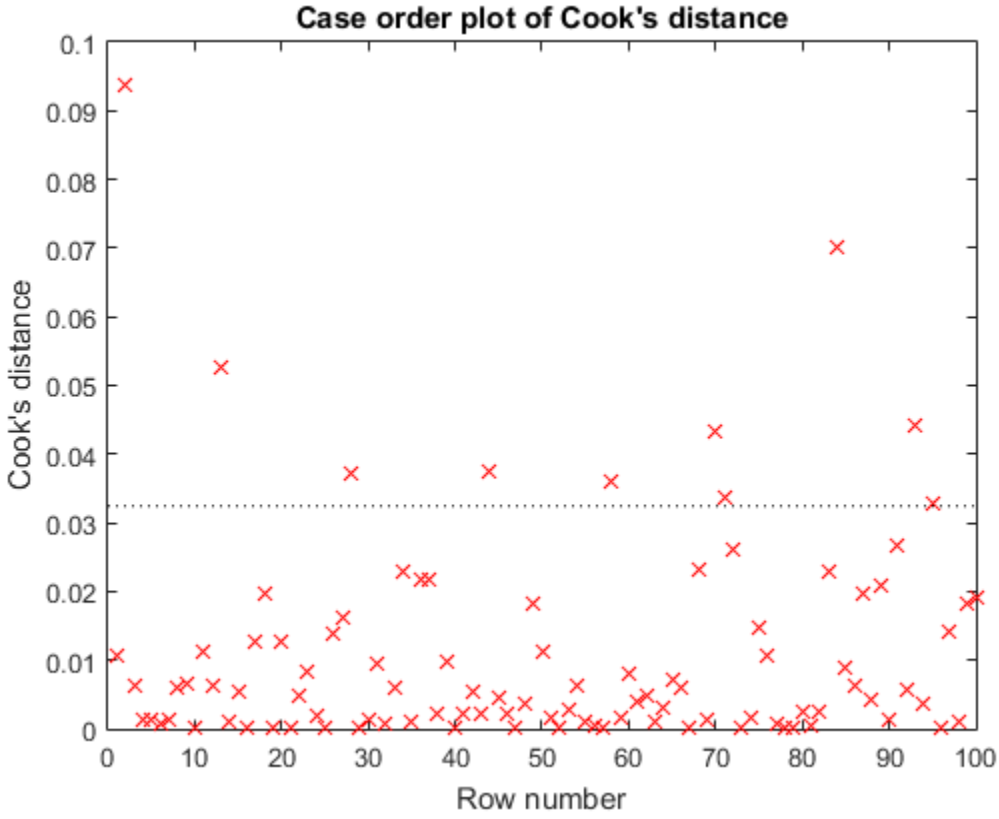
```
load hospital
X = double(hospital(:,2:5));
y = hospital.BloodPressure(:,1);
```

Fit the linear regression model.

```
mdl = fitlm(X,y);
```

Plot the Cook's distance values.

```
plotDiagnostics(mdl,'cookd')
```



The dashed line in the figure corresponds to the recommended threshold value, `3*mean(mdl.Diagnostics.CooksDistance)`. The plot has some observations with Cook's distance values greater than the threshold value, which for this example is 3*(0.0108) = 0.0324. In particular, there are two Cook's distance values that are relatively higher than the others, which exceed the threshold value. You might want to find and omit these from your data and rebuild your model.

Find the observations with Cook's distance values that exceed the threshold value.

```
find((mdl.Diagnostics.CooksDistance)>3*mean(mdl.Diagnostics.CooksDistance))
```

```
ans =
```

```
     2
    13
    28
    44
    58
    70
    71
    84
    93
    95
```

Find the observations with Cook's distance values that are relatively larger than the other observations with Cook's distances exceeding the threshold value.

```
find((mdl.Diagnostics.CooksDistance)>5*mean(mdl.Diagnostics.CooksDistance))
```

```
ans =

     2
    84
```

See Also

`fitlm` | `LinearModel` | `plotDiagnostics` | `stepwiselm`

Related Examples

- "Examine Quality and Adjust the Fitted Model" on page 9-20
- "Interpret Linear Regression Results" on page 9-63

Coefficient Standard Errors and Confidence Intervals

In this section...

Coefficient Covariance and Standard Errors

Purpose

Estimated coefficient variances and covariances capture the precision of regression coefficient estimates. The coefficient variances and their square root, the standard errors, are useful in testing hypotheses for coefficients.

Definition

The estimated covariance matrix is

$$\Sigma = MSE(X'X)^{-1},$$

where MSE is the mean squared error, and X is the matrix of observations on the predictor variables. `CoefficientCovariance`, a property of the fitted model, is a p-by-p covariance matrix of regression coefficient estimates. p is the number of coefficients in the regression model. The diagonal elements are the variances of the individual coefficients.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can display the coefficient covariances using

```
mdl.CoefficientCovariance
```

Compute Coefficient Covariance and Standard Errors

This example shows how to compute the covariance matrix and standard errors of the coefficients.

Load the sample data and define the predictor and response variables.

```
load hospital
y = hospital.BloodPressure(:,1);
X = double(hospital(:,2:5));
```

Fit a linear regression model.

```
mdl = fitlm(X,y);
```

Display the coefficient covariance matrix.

```
CM = mdl.CoefficientCovariance
```

```
CM =

   27.5113   11.0027   -0.1542   -0.2444    0.2702
   11.0027    8.6864    0.0021   -0.1547   -0.0838
   -0.1542    0.0021    0.0045   -0.0001   -0.0029
   -0.2444   -0.1547   -0.0001    0.0031   -0.0026
    0.2702   -0.0838   -0.0029   -0.0026    1.0829
```

Compute the coefficient standard errors.

```
SE = diag(sqrt(CM))
```

```
SE =

    5.2451
    2.9473
    0.0673
    0.0557
    1.0406
```

Coefficient Confidence Intervals

Purpose

The coefficient confidence intervals provide a measure of precision for linear regression coefficient estimates. A 100(1–α)% confidence interval gives the range that the corresponding regression coefficient will be in with 100(1–α)% confidence.

Definition

The 100*(1–α)% confidence intervals for linear regression coefficients are

$$b_i \pm t_{(1-\alpha/2,n-p)} SE(b_i),$$

where b_i is the coefficient estimate, $SE(b_i)$ is the standard error of the coefficient estimate, and $t_{(1-\alpha/2,n-p)}$ is the 100(1–α/2) percentile of t-distribution with $n - p$ degrees of freedom. n is the number of observations and p is the number of regression coefficients.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can obtain the default 95% confidence intervals for coefficients using

```
coefCI(mdl)
```

You can also change the confidence level using

```
coefCI(mdl,alpha)
```

For details, see the `coefCI` and `coefTest` methods of `LinearModel` class.

Compute Coefficient Confidence Intervals

This example shows how to compute coefficient confidence intervals.

Load the sample data and fit a linear regression model.

```
load hald
mdl = fitlm(ingredients,heat);
```

Display the 95% coefficient confidence intervals.

```
coefCI(mdl)
```

```
ans =

  -99.1786  223.9893
   -0.1663    3.2685
   -1.1589    2.1792
```

```
   -1.6385    1.8423
   -1.7791    1.4910
```

The values in each row are the lower and upper confidence limits, respectively, for the default 95% confidence intervals for the coefficients. For example, the first row shows the lower and upper limits, -99.1786 and 223.9893, for the intercept, β_0. Likewise, the second row shows the limits for β_1 and so on.

Display the 90% confidence intervals for the coefficients (α = 0.1).

```
coefCI(mdl,0.1)
```

```
ans =

  -67.8949  192.7057
    0.1662    2.9360
   -0.8358    1.8561
   -1.3015    1.5053
   -1.4626    1.1745
```

The confidence interval limits become narrower as the confidence level decreases.

See Also

`anova` | `coefCI` | `coefTest` | `fitlm` | `LinearModel` | `plotDiagnostics` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

Coefficient of Determination (R-Squared)

Purpose

Coefficient of determination (R-squared) indicates the proportionate amount of variation in the response variable y explained by the independent variables X in the linear regression model. The larger the R-squared is, the more variability is explained by the linear regression model.

Definition

R-squared is the proportion of the total sum of squares explained by the model. `Rsquared`, a property of the fitted model, is a structure with two fields:

- `Ordinary` — Ordinary (unadjusted) R-squared

$$R^2 = \frac{SSR}{SST} = 1 - \frac{SSE}{SST}.$$

- `Adjusted` — R-squared adjusted for the number of coefficients

$$R^2_{adj} = 1 - \left(\frac{n-1}{n-p}\right)\frac{SSE}{SST}.$$

SSE is the sum of squared error, SSR is the sum of squared regression, SST is the sum of squared total, n is the number of observations, and p is the number of regression coefficients (including the intercept). Because R-squared increases with added predictor variables in the regression model, the adjusted R-squared adjusts for the number of predictor variables in the model. This makes it more useful for comparing models with a different number of predictors.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can obtain either R-squared value as a scalar by indexing into the property using dot notation, for example,

```
mdl.Rsquared.Ordinary
mdl.Rsquared.Adjusted
```

You can also obtain the SSE, SSR, and SST using the properties with the same name.

```
mdl.SSE
mdl.SSR
mdl.SST
```

Display Coefficient of Determination

This example shows how to display R-squared (coefficient of determination) and adjusted R-squared. Load the sample data and define the response and independent variables.

```
load hospital
y = hospital.BloodPressure(:,1);
X = double(hospital(:,2:5));
```

Fit a linear regression model.

```
mdl = fitlm(X,y)
```

```
mdl =


Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4

Estimated Coefficients:
                   Estimate        SE        tStat        pValue
                   ________    ________    ________    __________

    (Intercept)        117.4      5.2451      22.383    1.1667e-39
    x1               0.88162      2.9473     0.29913       0.76549
    x2               0.08602     0.06731       1.278       0.20438
    x3              -0.016685    0.055714    -0.29947       0.76524
    x4                 9.884      1.0406       9.498    1.9546e-15


Number of observations: 100, Error degrees of freedom: 95
Root Mean Squared Error: 4.81
R-squared: 0.508,  Adjusted R-Squared 0.487
F-statistic vs. constant model: 24.5, p-value = 5.99e-14
```

The R-squared and adjusted R-squared values are 0.508 and 0.487, respectively. Model explains about 50% of the variability in the response variable.

Access the R-squared and adjusted R-squared values using the property of the fitted `LinearModel` object.

```
mdl.Rsquared.Ordinary
```

```
ans =

    0.5078
```

```
mdl.Rsquared.Adjusted
```

```
ans =

    0.4871
```

The adjusted R-squared value is smaller than the ordinary R-squared value.

See Also

`anova` | `fitlm` | `LinearModel` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

Delete-1 Statistics

In this section...

Delete-1 Change in Covariance (covratio)

Purpose

Delete-1 change in covariance (covratio) identifies the observations that are influential in the regression fit. An influential observation is one where its exclusion from the model might significantly alter the regression function. Values of covratio larger than $1 + 3*p/n$ or smaller than $1 - 3*p/n$ indicate influential points, where p is the number of regression coefficients, and n is the number of observations.

Definition

The covratio statistic is the ratio of the determinant of the coefficient covariance matrix with observation i deleted to the determinant of the covariance matrix for the full model:

$$\text{cov}\,ratio = \frac{\det\left\{MSE(i)\left[X'(i)X(i)\right]^{-1}\right\}}{\det\left[MSE(X'X)^{-1}\right]}.$$

`CovRatio` is an n-by-1 vector in the `Diagnostics` table of the fitted `LinearModel` object. Each element is the ratio of the generalized variance of the estimated coefficients when the corresponding element is deleted to the generalized variance of the coefficients using all the data.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Display the `CovRatio` by indexing into the property using dot notation

  ```
  mdl.Diagnostics.CovRatio
  ```

- Plot the delete-1 change in covariance using

  ```
  plotDiagnostics(mdl,'CovRatio')
  ```

  For details, see the `plotDiagnostics` method of the `LinearModel` class.

Determine Influential Observations Using CovRatio

This example shows how to use the `CovRatio` statistics to determine the influential points in data. Load the sample data and define the response and predictor variables.

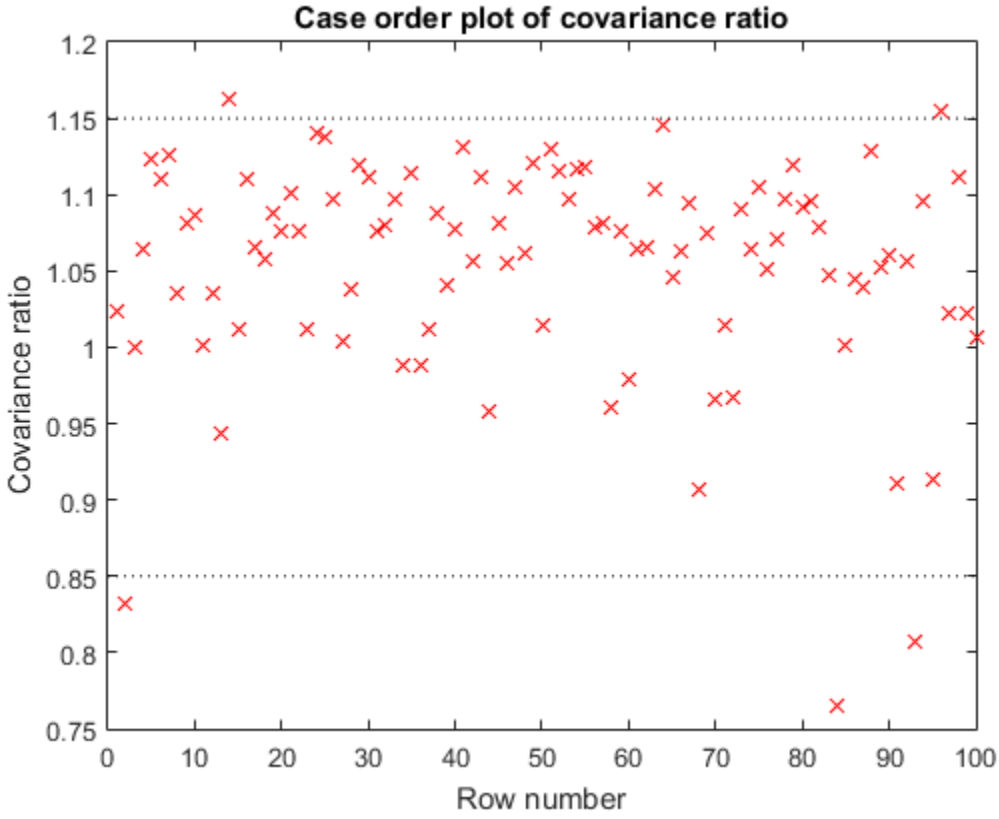
```
load hospital
y = hospital.BloodPressure(:,1);
X = double(hospital(:,2:5));
```

Fit a linear regression model.

```
mdl = fitlm(X,y);
```

Plot the `CovRatio` statistics.

```
plotDiagnostics(mdl,'CovRatio')
```



For this example, the threshold limits are 1 + 3*5/100 = 1.15 and 1 - 3*5/100 = 0.85. There are a few points beyond the limits, which might be influential points.

Find the observations that are beyond the limits.

```
find((mdl.Diagnostics.CovRatio)>1.15|(mdl.Diagnostics.CovRatio)<0.85)
```

```
ans =

     2
    14
    84
    93
```

96

Delete-1 Scaled Difference in Coefficient Estimates (Dfbetas)

Purpose

The sign of a delete-1 scaled difference in coefficient estimate (Dfbetas) for coefficient j and observation i indicates whether that observation causes an increase or decrease in the estimate of the regression coefficient. The absolute value of a Dfbetas indicates the magnitude of the difference relative to the estimated standard deviation of the regression coefficient. A Dfbetas value larger than 3/sqrt(n) in absolute value indicates that the observation has a large influence on the corresponding coefficient.

Definition

Dfbetas for coefficient j and observation i is the ratio of the difference in the estimate of coefficient j using all observations and the one obtained by removing observation i, and the standard error of the coefficient estimate obtained by removing observation i. The Dfbetas for coefficient j and observation i is

$$Dfbetas_{ij} = \frac{b_j - b_{j(i)}}{\sqrt{MSE_{(i)}\left(1 - h_{ii}\right)}},$$

where b_j is the estimate for coefficient j, $b_{j(i)}$ is the estimate for coefficient j by removing observation i, $MSE_{(i)}$ is the mean squared error of the regression fit by removing observation i, and h_{ii} is the leverage value for observation i. `Dfbetas` is an n-by-p matrix in the `Diagnostics` table of the fitted `LinearModel` object. Each cell of `Dfbetas` corresponds to the Dfbetas value for the corresponding coefficient obtained by removing the corresponding observation.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can obtain the Dfbetas values as an n-by-p matrix by indexing into the property using dot notation,

```
mdl.Diagnostics.Dfbetas
```

Determine Observations Influential on Coefficients Using Dfbetas

This example shows how to determine the observations that have large influence on coefficients using `Dfbetas`. Load the sample data and define the response and independent variables.

```
load hospital
y = hospital.BloodPressure(:,1);
X = double(hospital(:,2:5));
```

Fit a linear regression model.

```
mdl = fitlm(X,y);
```

Find the `Dfbetas` values that are high in absolute value.

```
[row,col] = find(abs(mdl.Diagnostics.Dfbetas)>3/sqrt(100));
disp([row col])
```

```
     2     1
    28     1
    84     1
    93     1
     2     2
    13     3
    84     3
     2     4
    84     4
```

Delete-1 Scaled Change in Fitted Values (Dffits)

Purpose

The delete-1 scaled change in fitted values (Dffits) show the influence of each observation on the fitted response values. Dffits values with an absolute value larger than 2*sqrt(p/n) might be influential.

Definition

Dffits for observation i is

$$Dffits_i = sr_i \sqrt{\frac{h_{ii}}{1-h_{ii}}},$$

where sr_i is the studentized residual, and h_{ii} is the leverage value of the fitted `LinearModel` object. `Dffits` is an n-by-1 column vector in the `Diagnostics` table of the fitted `LinearModel` object. Each element in `Dffits` is the change in the fitted value caused by deleting the corresponding observation and scaling by the standard error.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Display the `Dffits` values by indexing into the property using dot notation

  ```
  mdl.Diagnostics.Dffits
  ```

- Plot the delete-1 scaled change in fitted values using

  ```
  plotDiagnostics(mdl,'Dffits')
  ```

  For details, see the `plotDiagnostics` method of the `LinearModel` class for details.

Determine Observations Influential on Fitted Response Using Dffits

This example shows how to determine the observations that are influential on the fitted response values using `Dffits` values. Load the sample data and define the response and independent variables.

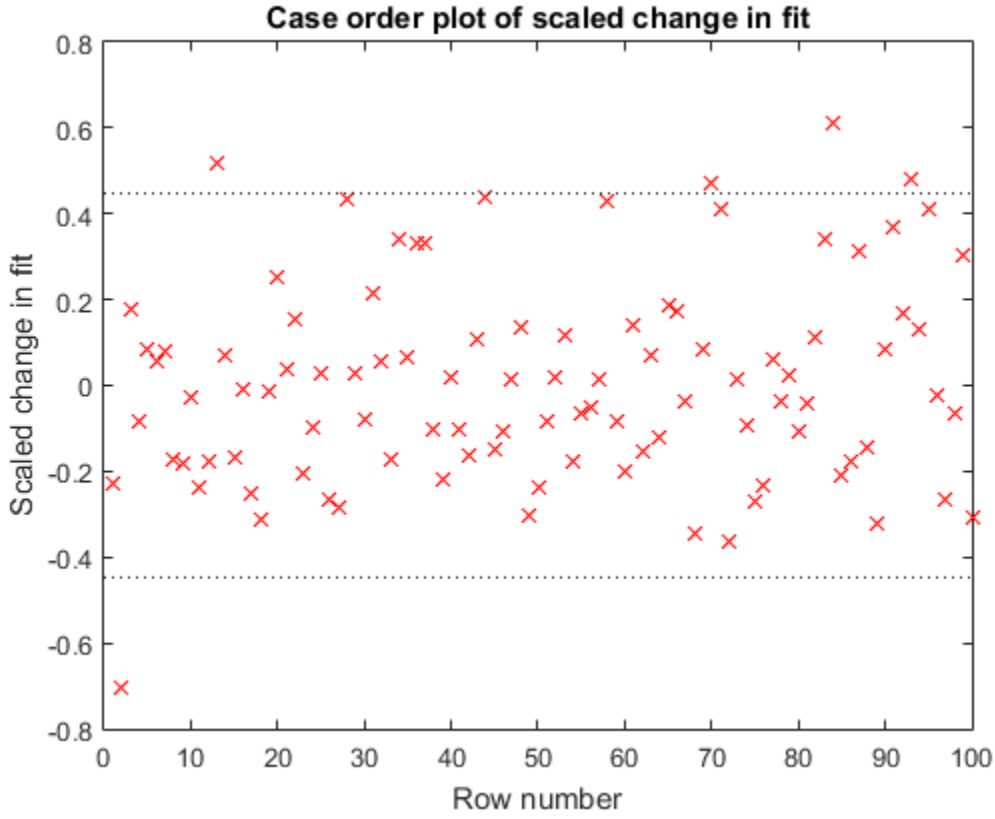
```
load hospital
y = hospital.BloodPressure(:,1);
X = double(hospital(:,2:5));
```

Fit a linear regression model.

```
mdl = fitlm(X,y);
```

Plot the Dffits values.

```
plotDiagnostics(mdl,'Dffits')
```



The influential threshold limit for the absolute value of Dffits in this example is 2*sqrt(5/100) = 0.45. Again, there are some observations with Dffits values beyond the recommended limits.

Find the Dffits values that are large in absolute value.

```
find(abs(mdl.Diagnostics.Dffits)>2*sqrt(4/100))
```

```
ans =

     2
    13
    28
```

```
44
58
70
71
84
93
95
```

Delete-1 Variance (S2_i)

Purpose

The delete-1 variance (S2_i) shows how the mean squared error changes when an observation is removed from the data set. You can compare the S2_i values with the value of the mean squared error.

Definition

S2_i is a set of residual variance estimates obtained by deleting each observation in turn. The S2_i value for observation i is

$$S2\_i = MSE_{(i)} = \frac{\sum_{j \neq i}^{n} \left[y_j - y_{j(i)} \right]^2}{n - p - 1},$$

where y_j is the jth observed response value. `S2_i` is an n-by-1 vector in the `Diagnostics` table of the fitted `LinearModel` object. Each element in `S2_i` is the mean squared error of the regression obtained by deleting that observation.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Display the `S2_i` vector by indexing into the property using dot notation

  ```
  mdl.Diagnostics.S2_i
  ```

- Plot the delete-1 variance values using

```
plotDiagnostics(mdl,'S2_i')
```

For details, see the `plotDiagnostics` method of the `LinearModel` class.

Compute and Examine Delete-1 Variance Values

This example shows how to compute and plot S2_i values to examine the change in the mean squared error when an observation is removed from the data. Load the sample data and define the response and independent variables.

```
load hospital
y = hospital.BloodPressure(:,1);
X = double(hospital(:,2:5));
```

Fit a linear regression model.

```
mdl = fitlm(X,y);
```

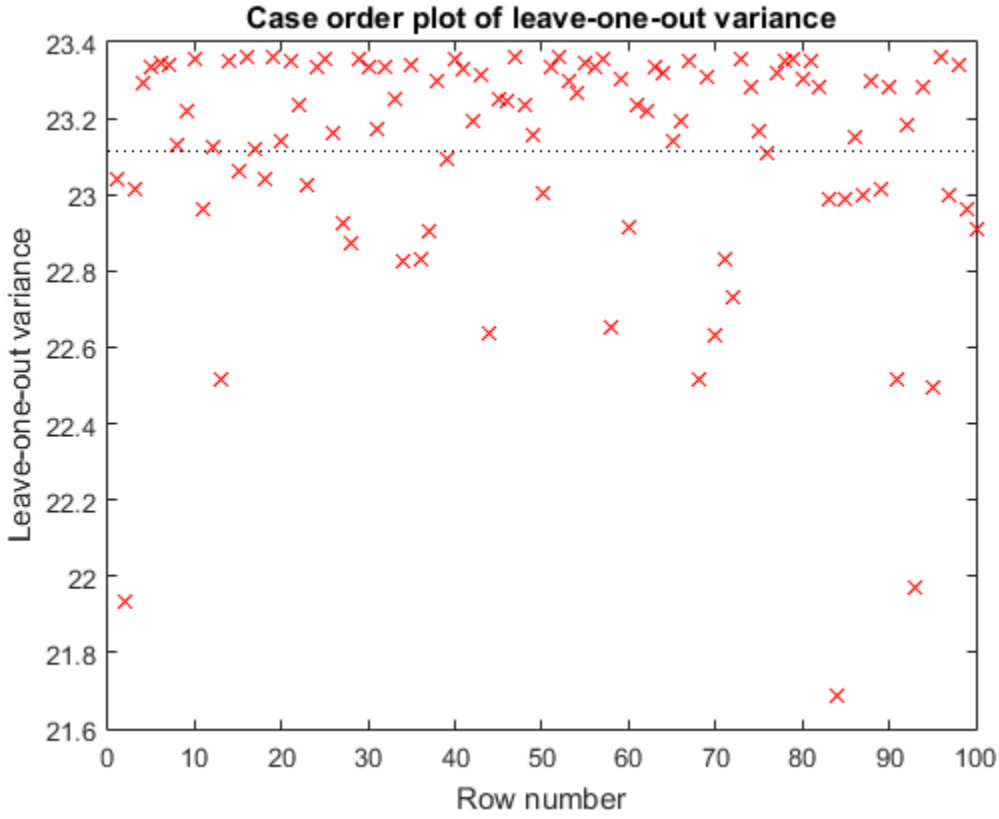
Display the MSE value for the model.

```
mdl.MSE
```

```
ans =

   23.1140
```

Plot the S2_i values.

```
plotDiagnostics(mdl,'S2_i')
```



This plot makes it easy to compare the S2_i values to the MSE value of 23.114, indicated by the horizontal dashed lines. You can see how deleting one observation changes the error variance.

See Also

`fitlm` | `LinearModel` | `plotDiagnostics` | `plotResiduals` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

Durbin-Watson Test

Purpose

The Durbin-Watson test assesses whether there is autocorrelation among the residuals or not.

Definition

The Durbin-Watson test statistic, `DW`, is

$$DW = \frac{\sum_{i=1}^{n-1} (r_{i+1} - r_i)^2}{\sum_{i=1}^{n} r_i^2}.$$

Here, r_i is the ith raw residual, and n is the number of observations.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can perform the Durbin-Watson test using

```
dwtest(mdl)
```

For details, see the `dwtest` method of the `LinearModel` class.

Test for Autocorrelation Among Residuals

This example shows how to test for autocorrelation among the residuals of a linear regression model.

Load the sample data and fit a linear regression model.

```
load hald
mdl = fitlm(ingredients,heat);
```

Perform a two-sided Durbin-Watson test to determine if there is any autocorrelation among the residuals of the linear model, `mdl`.

```
[p,DW] = dwtest(mdl,'exact','both')

p =

    0.6285

DW =

    2.0526
```

The value of the Durbin-Watson test statistic is 2.0526. The p-value of 0.6285 suggest that the residuals are not autocorrelated.

See Also

`dwtest` | `fitlm` | `LinearModel` | `plotResiduals` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

F-statistic and t-statistic

In this section...

F-statistic

Purpose

In linear regression, the F-statistic is the test statistic for the analysis of variance (ANOVA) approach to test the significance of the model or the components in the model.

Definition

The F-statistic in the linear model output display is the test statistic for testing the statistical significance of the model. The F-statistic values in the `anova` display are for assessing the significance of the terms or components in the model.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Find the `F-statistic vs. constant model` in the output display or by using

  ```
  disp(mdl)
  ```
- Display the ANOVA for the model using

  ```
  anova(mdl,'summary')
  ```
- Obtain the F-statistic values for the components, except for the constant term using

  ```
  anova(mdl)
  ```
  For details, see the `anova` method of the `LinearModel` class.

Assess Fit of Model Using F-statistic

This example shows how to use assess the fit of the model and the significance of the regression coefficients using F-statistic.

Load the sample data.

```
load carbig
tbl = table(Acceleration,Cylinders,Weight,MPG);
tbl.Cylinders = ordinal(Cylinders);
```

Fit a linear regression model.

```
mdl = fitlm(tbl,'MPG~Acceleration*Weight+Cylinders+Weight^2')
```

```
mdl =


Linear regression model:
    MPG ~ 1 + Cylinders + Acceleration*Weight + Weight^2

Estimated Coefficients:
                           Estimate         SE         tStat        pValue
                          __________    __________    ________    __________

    (Intercept)              50.816        7.5669      6.7156     6.661e-11
    Acceleration           0.023343       0.33931    0.068796       0.94519
    Cylinders_4               7.167        2.0596      3.4798     0.0005587
    Cylinders_5              10.963        3.1299      3.5028    0.00051396
    Cylinders_6              4.7415        2.1257      2.2306      0.026279
    Cylinders_8               5.057        2.2981      2.2005      0.028356
    Weight                -0.017497     0.0034674     -5.0461    6.9371e-07
    Acceleration:Weight   7.0745e-05    0.00011171      0.6333       0.52691
    Weight^2              1.5767e-06    3.6909e-07      4.2719    2.4396e-05


Number of observations: 398, Error degrees of freedom: 389
Root Mean Squared Error: 4.02
R-squared: 0.741,  Adjusted R-Squared 0.736
F-statistic vs. constant model: 139, p-value = 2.94e-109
```

The F-statistic of the linear fit versus the constant model is 139, with a p-value of 2.94e-109. The model is significant at the 5% significance level. The R-squared value of 0.741 means the model explains about 74% of the variability in the response.

Display the ANOVA table for the fitted model.

```
anova(mdl,'summary')
```

```
ans =

                    SumSq      DF     MeanSq       F          pValue
                    _____    ____    ______    ______    ___________

    Total           24253     397     61.09
    Model           17981       8    2247.6    139.41    2.9432e-109
    . Linear        17667       6    2944.4    182.63    7.5446e-110
    . Nonlinear    314.36       2    157.18    9.7492     7.3906e-05
    Residual       6271.6     389    16.122
    . Lack of fit  6267.1     387    16.194    7.1973        0.12968
    . Pure error      4.5       2      2.25
```

This display separates the variability in the model into linear and nonlinear terms. Since there are two non-linear terms (`Weight^2` and the interaction between `Weight` and `Acceleration`), the nonlinear degrees of freedom in the `DF` column is 2. There are six linear terms in the model (four `Cylinders` indicator variables, `Weight`, and `Acceleration`). The corresponding F-statistics in the `F` column are for testing the significance of the linear and nonlinear terms as separate groups.

The residual term is also separated into two parts; first is the error due to the lack of fit, and second is the pure error independent from the model, obtained from the replicated observations. The corresponding F-statistics in the `F` column are for testing the lack of fit, that is, whether the proposed model is an adequate fit or not.

Display the ANOVA table for the model terms.

```
anova(mdl)
```

```
ans =

                        SumSq      DF     MeanSq       F          pValue
                        _____    ____    ______    _______    ___________

    Acceleration        104.99       1    104.99     6.5122       0.011095
    Cylinders           408.94       4    102.23     6.3412     5.9573e-05
    Weight              2187.5       1    2187.5     135.68     4.1974e-27
    Acceleration:Weight 6.4662       1    6.4662    0.40107        0.52691
    Weight^2            294.22       1    294.22     18.249     2.4396e-05
    Error               6271.6     389    16.122
```

This display decomposes the ANOVA table into the model terms. The corresponding F-statistics in the `F` column are for assessing the statistical significance of each term. The F-test for `Cylinders` test whether at least one of the coefficients of indicator variables for cylinders categories is different from zero or not. That is, whether different numbers of cylinders have a significant effect on `MPG` or not. The degrees of freedom for each model term is the numerator degrees of freedom for the corresponding F-test. Most of the terms have 1 degree of freedom, but the degrees of freedom for `Cylinders` is 4. Because there are four indicator variables for this term.

t-statistic

Purpose

In linear regression, the t-statistic is useful for making inferences about the regression coefficients. The hypothesis test on coefficient i tests the null hypothesis that it is equal to zero – meaning the corresponding term is not significant – versus the alternate hypothesis that the coefficient is different from zero.

Definition

For a hypotheses test on coefficient i, with

$H_0 : \beta_i = 0$

$H_1 : \beta_i \neq 0$,

the t-statistic is:

$$t = \frac{b_i}{SE(b_i)},$$

where $SE(b_i)$ is the standard error of the estimated coefficient b_i.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Find the coefficient estimates, the standard errors of the estimates (`SE`), and the t-statistic values of hypothesis tests for the corresponding coefficients (`tStat`) in the output display.

- Call for the display using

  ```
  display(mdl)
  ```

Assess Significance of Regression Coefficients Using t-statistic

This example shows how to test for the significance of the regression coefficients using t-statistic.

Load the sample data and fit the linear regression model.

```
load hald
mdl = fitlm(ingredients,heat)
```

```
mdl =


Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4

Estimated Coefficients:
                   Estimate      SE        tStat       pValue
                   ________    _______    ________    ________

    (Intercept)      62.405     70.071      0.8906     0.39913
    x1               1.5511    0.74477      2.0827    0.070822
    x2              0.51017    0.72379     0.70486      0.5009
    x3              0.10191    0.75471     0.13503     0.89592
    x4             -0.14406    0.70905    -0.20317     0.84407


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 2.45
R-squared: 0.982,  Adjusted R-Squared 0.974
F-statistic vs. constant model: 111, p-value = 4.76e-07
```

You can see that for each coefficient, `tStat = Estimate/SE`. The p-values for the hypotheses tests are in the `pValue` column. Each t-statistic tests for the significance of each term given other terms in the model. According to these results, none of the coefficients seem significant at the 5% significance level, although the R-squared value for the model is really high at 0.97. This often indicates possible multicollinearity among the predictor variables.

Use stepwise regression to decide which variables to include in the model.

```
load hald
mdl = stepwiselm(ingredients,heat)

1. Adding x4, FStat = 22.7985, pValue = 0.000576232
2. Adding x1, FStat = 108.2239, pValue = 1.105281e-06

mdl =


Linear regression model:
    y ~ 1 + x1 + x4

Estimated Coefficients:
                   Estimate       SE        tStat       pValue
                   ________    ________    _______    __________

    (Intercept)       103.1       2.124      48.54    3.3243e-13
    x1                 1.44     0.13842     10.403    1.1053e-06
    x4              -0.61395    0.048645    -12.621    1.8149e-07


Number of observations: 13, Error degrees of freedom: 10
Root Mean Squared Error: 2.73
R-squared: 0.972,  Adjusted R-Squared 0.967
F-statistic vs. constant model: 177, p-value = 1.58e-08
```

In this example, `stepwiselm` starts with the constant model (default) and uses forward selection to incrementally add `x4` and `x1`. Each predictor variable in the final model is significant given the other one is in the model. The algorithm stops when adding none of the other predictor variables significantly improves in the model. For details on stepwise regression, see `stepwiselm`.

See Also

`anova` | `coefCI` | `coefTest` | `fitlm` | `LinearModel` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

Hat Matrix and Leverage

In this section...

Hat Matrix

Purpose

The hat matrix provides a measure of leverage. It is useful for investigating whether one or more observations are outlying with regard to their X values, and therefore might be excessively influencing the regression results.

Definition

The hat matrix is also known as the *projection matrix* because it projects the vector of observations, y, onto the vector of predictions, $\hat{y}$, thus putting the "hat" on y. The hat matrix H is defined in terms of the data matrix X:

$H = X(X^TX)^{-1}X^T$

and determines the fitted or predicted values since

$$\hat{y} = Hy = Xb.$$

The diagonal elements of H, h_{ii}, are called leverages and satisfy

$$0 \le h_{ii} \le 1$$

$$\sum_{i=1}^{n} h_{ii} = p,$$

where p is the number of coefficients, and n is the number of observations (rows of X) in the regression model. `HatMatrix` is an n-by-n matrix in the `Diagnostics` table.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Display the `HatMatrix` by indexing into the property using dot notation

  ```
  mdl.Diagnostics.HatMatrix
  ```

  When n is large, `HatMatrix` might be computationally expensive. In those cases, you can obtain the diagonal values directly, using

  ```
  mdl.Diagnostics.Leverage
  ```

Leverage

Purpose

Leverage is a measure of the effect of a particular observation on the regression predictions due to the position of that observation in the space of the inputs. In general, the farther a point is from the center of the input space, the more leverage it has. Because the sum of the leverage values is p, an observation i can be considered as an outlier if its leverage substantially exceeds the mean leverage value, p/n, for example, a value larger than $2*p/n$.

Definition

The leverage of observation i is the value of the ith diagonal term, h_{ii}, of the hat matrix, H, where
$H = X(X^TX)^{-1}X^T$.
The diagonal terms satisfy

$$0 \le h_{ii} \le 1$$

$$\sum_{i=1}^{n} h_{ii} = p,$$

where p is the number of coefficients in the regression model, and n is the number of observations. The minimum value of h_{ii} is $1/n$ for a model with a constant term. If the fitted model goes through the origin, then the minimum leverage value is 0 for an observation at $x = 0$.

It is possible to express the fitted values, $\hat{y}$, by the observed values, y, since

$$\hat{y} = Hy = Xb.$$

Hence, h_{ii} expresses how much the observation y_i has impact on $\hat{y}_i$. A large value of h_{ii} indicates that the ith case is distant from the center of all X values for all n cases and has more leverage. `Leverage` is an n-by-1 column vector in the `Diagnostics` table.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Display the `Leverage` vector by indexing into the property using dot notation

  ```
  mdl.Diagnostics.Leverage
  ```

- Plot the leverage for the values fitted by your model using

  ```
  plotDiagnostics(mdl)
  ```

  See the `plotDiagnostics` method of the `LinearModel` class for details.

Determine High Leverage Observations

This example shows how to compute `Leverage` values and assess high leverage observations. Load the sample data and define the response and independent variables.

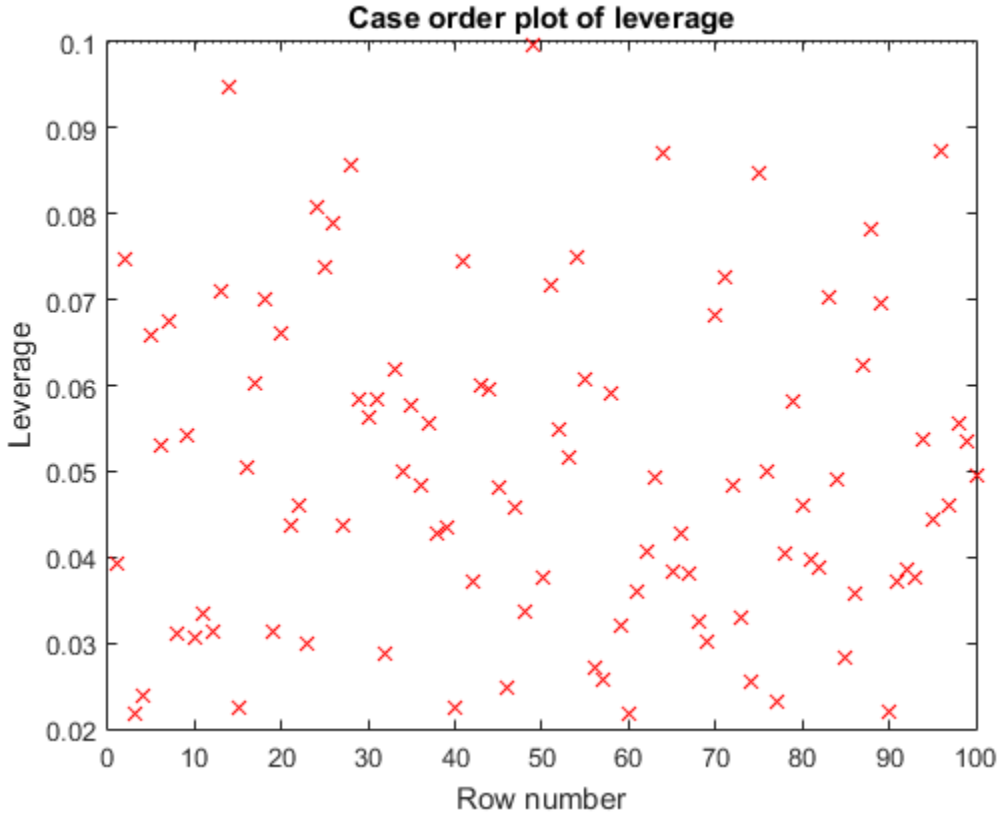
```
load hospital
y = hospital.BloodPressure(:,1);
X = double(hospital(:,2:5));
```

Fit a linear regression model.

```
mdl = fitlm(X,y);
```

Plot the leverage values.

```
plotDiagnostics(mdl)
```



For this example, the recommended threshold value is 2*5/100 = 0.1. There is no indication of high leverage observations.

See Also

`fitlm` | `LinearModel` | `plotDiagnostics` | `stepwiselm`

Related Examples

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Interpret Linear Regression Results” on page 9-63

Residuals

Purpose

Residuals are useful for detecting outlying y values and checking the linear regression assumptions with respect to the error term in the regression model. High-leverage observations have smaller residuals because they often shift the regression line or surface closer to them. You can also use residuals to detect some forms of heteroscedasticity and autocorrelation.

Definition

The `Residuals` matrix is an n-by-4 table containing four types of residuals, with one row for each observation.

Raw Residuals

Observed minus fitted values, that is,

$$r_i = y_i - \hat{y}_i.$$

Pearson Residuals

Raw residuals divided by the root mean squared error, that is,

$$pr_i = \frac{r_i}{\sqrt{MSE}},$$

where r_i is the raw residual and MSE is the mean squared error.

Standardized Residuals

Standardized residuals are raw residuals divided by their estimated standard deviation. The standardized residual for observation i is

$$st_i = \frac{r_i}{\sqrt{MSE(1-h_{ii})}},$$

where MSE is the mean squared error and h_{ii} is the leverage value for observation i.

Studentized Residuals

Studentized residuals are the raw residuals divided by an independent estimate of the residual standard deviation. The residual for observation i is divided by an estimate of the error standard deviation based on all observations except for observation i.

$$sr_i = \frac{r_i}{\sqrt{MSE_{(i)}(1-h_{ii})}},$$

where $MSE_{(i)}$ is the mean squared error of the regression fit calculated by removing observation i, and h_{ii} is the leverage value for observation i. The studentized residual sr_i has a t-distribution with $n-p-1$ degrees of freedom.

How To

After obtaining a fitted model, say, `mdl`, using `fitlm` or `stepwiselm`, you can:

- Find the `Residuals` table under `mdl` object.
- Obtain any of these columns as a vector by indexing into the property using dot notation, for example,

  ```
  mdl.Residuals.Raw
  ```

- Plot any of the residuals for the values fitted by your model using

  ```
  plotResiduals(mdl)
  ```

  For details, see the `plotResiduals` method of the `LinearModel` class.

Assess Model Assumptions Using Residuals

This example shows how to assess the model assumptions by examining the residuals of a fitted linear regression model.

Load the sample data and store the independent and response variables in a table.

```
load imports-85
```

```
 tbl = table(X(:,7),X(:,8),X(:,9),X(:,15),'VariableNames',...
{'curb_weight','engine_size','bore','price'});
```

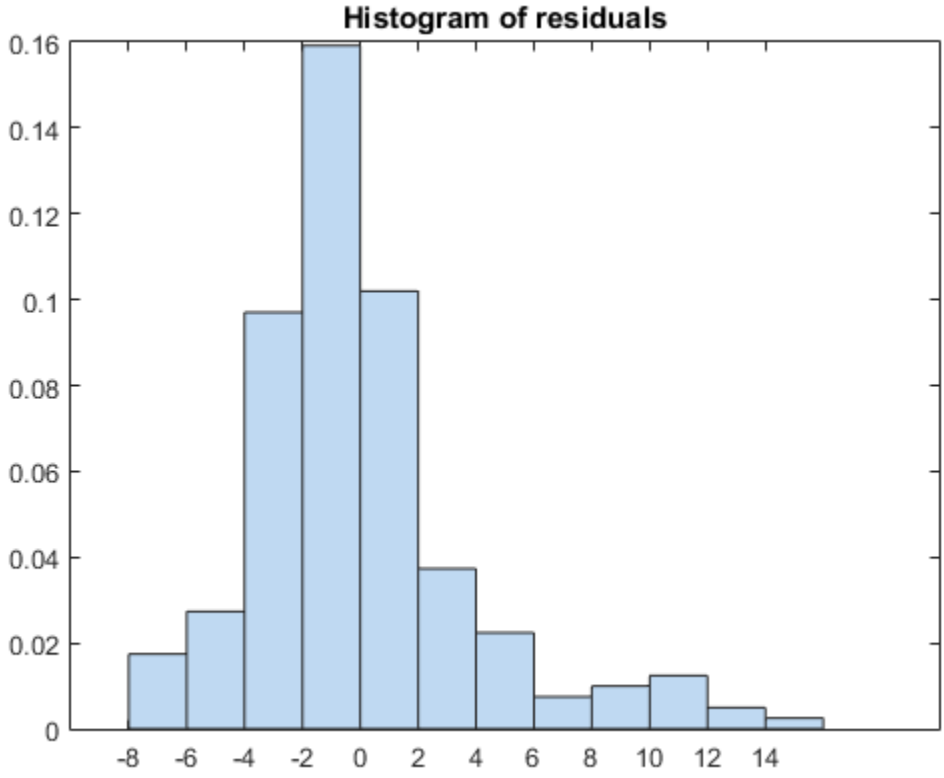
Fit a linear regression model.

```
mdl = fitlm(tbl)
```

```
mdl =


Linear regression model:
    price ~ 1 + curb_weight + engine_size + bore

Estimated Coefficients:
                    Estimate        SE         tStat       pValue
                   __________    _________    _______    __________

    (Intercept)        64.095        3.703     17.309    2.0481e-41
    curb_weight    -0.0086681    0.0011025    -7.8623      2.42e-13
    engine_size     -0.015806     0.013255    -1.1925       0.23452
    bore              -2.6998       1.3489    -2.0015      0.046711


Number of observations: 201, Error degrees of freedom: 197
Root Mean Squared Error: 3.95
R-squared: 0.674,  Adjusted R-Squared 0.669
F-statistic vs. constant model: 136, p-value = 1.14e-47
```

Plot the histogram of raw residuals.

```
plotResiduals(mdl)
```



The histogram shows that the residuals are slightly right skewed.

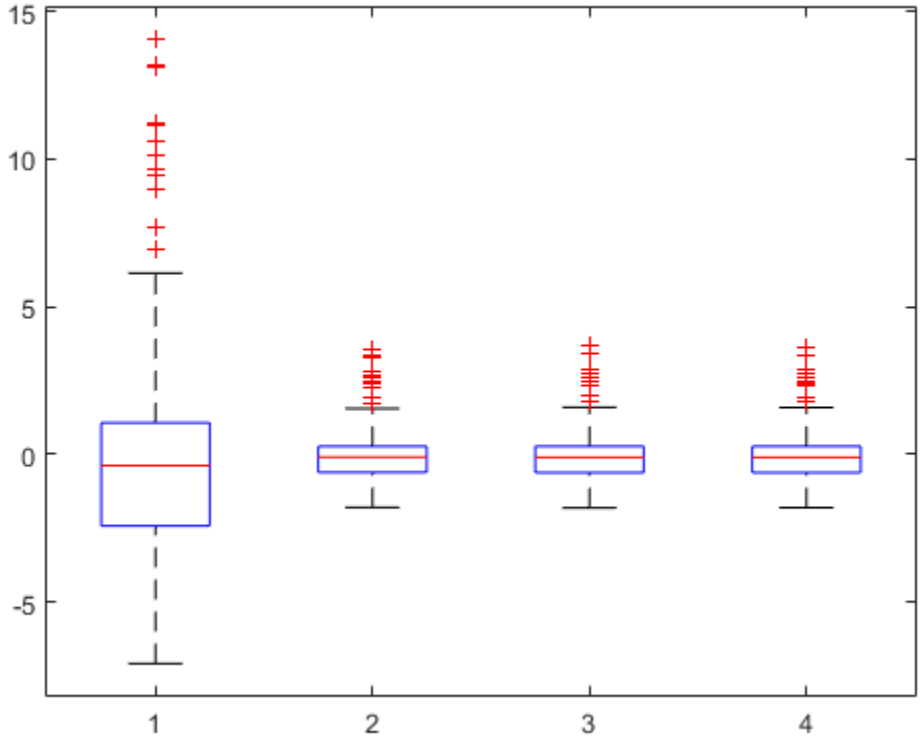
Plot the box plot of all four types of residuals.

```
Res = table2array(mdl.Residuals);
```

You can see the right-skewed structure of the residuals in the box plot as well.

Plot the normal probability plot of the raw residuals.

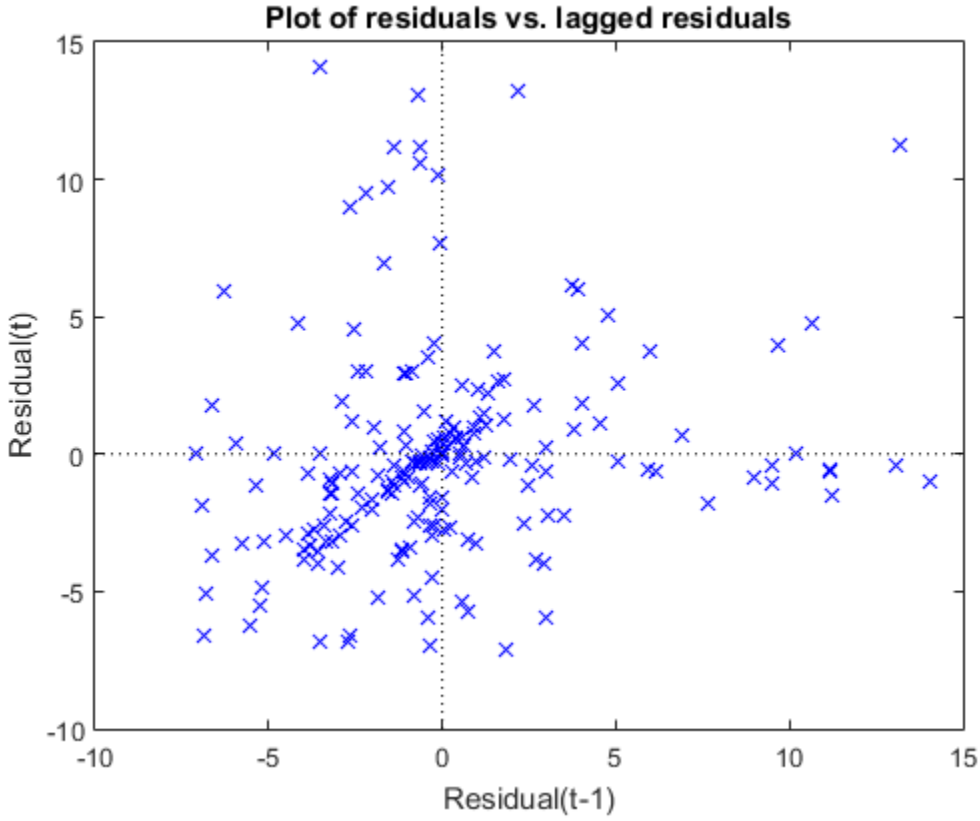
```
plotResiduals(mdl,'probability')
boxplot(Res)
```



This normal probability plot also shows the deviation from normality and the skewness on the right tail of the distribution of residuals.

Plot the residuals versus lagged residuals.

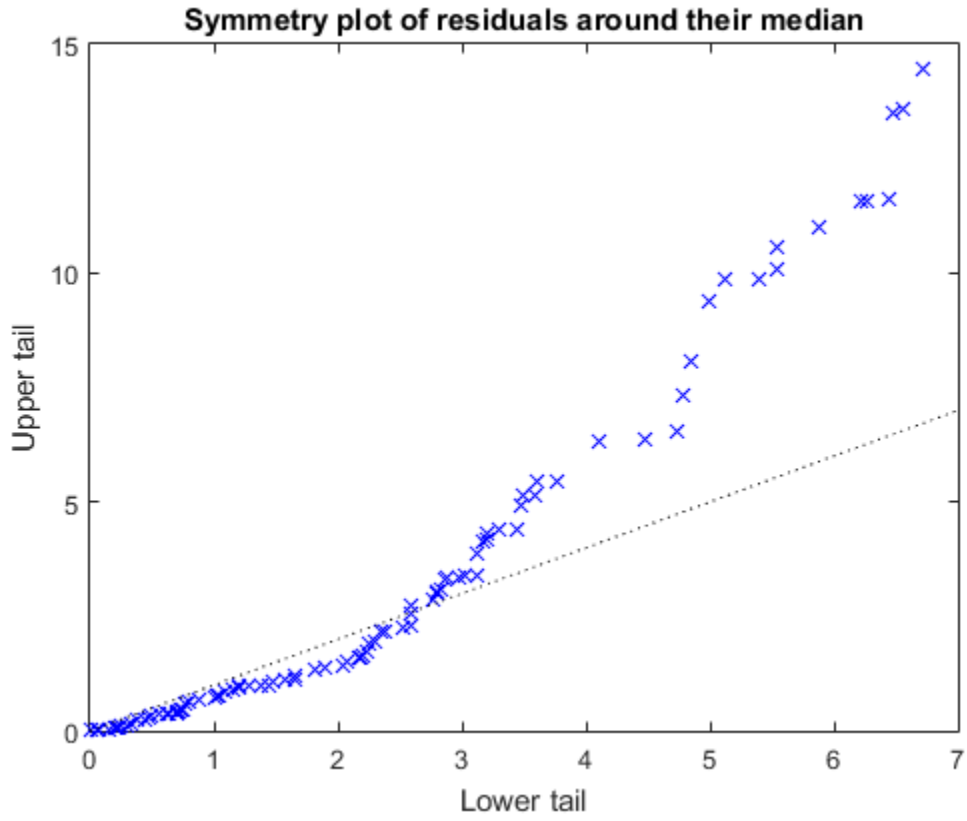
```
plotResiduals(mdl,'lagged')
```



This graph shows a trend, which indicates a possible correlation among the residuals. You can further check this using `dwtest(mdl)`. Serial correlation among residuals usually means that the model can be improved.

Plot the symmetry plot of residuals.

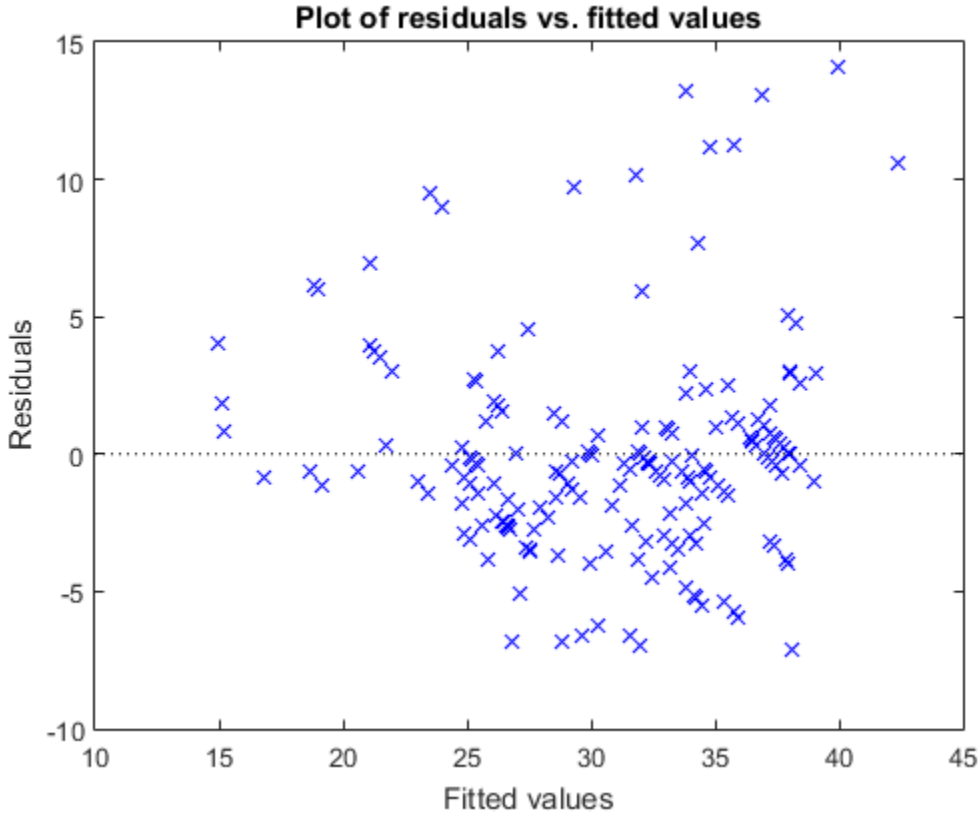
```
plotResiduals(mdl,'symmetry')
```



This plot also suggests that the residuals are not distributed equally around their median, as would be expected for normal distribution.

Plot the residuals versus the fitted values.

```
plotResiduals(mdl,'fitted')
```



The increase in the variance as the fitted values increase suggests possible heteroscedasticity.

References

[1] Atkinson, A. T. *Plots, Transformations, and Regression. An Introduction to Graphical Methods of Diagnostic Regression Analysis.* New York: Oxford Statistical Science Series, Oxford University Press, 1987.

[2] Neter, J., M. H. Kutner, C. J. Nachtsheim, and W. Wasserman. *Applied Linear Statistical Models*. IRWIN, The McGraw-Hill Companies, Inc., 1996.

[3] Belsley, D. A., E. Kuh, and R. E. Welsch. *Regression Diagnostics, Identifying Influential Data and Sources of Collinearity*. Wiley Series in Probability and Mathematical Statistics, John Wiley and Sons, Inc., 1980.

See Also

`dwtest` | `fitlm` | `LinearModel` | `plotDiagnostics` | `plotResiduals` | `stepwiselm`

Related Examples

- "Examine Quality and Adjust the Fitted Model" on page 9-20
- "Interpret Linear Regression Results" on page 9-63

Summary of Output and Diagnostic Statistics

Name	LinearModel	regstats
"Cook's Distance" on page 9-70	`CooksDistance` and `cookd`	`cookd`
"Coefficient Confidence Intervals" on page 9-75	`coefCI`	N/A
"Coefficient Covariance and Standard Errors" on page 9-74	`CoefficientCovariance`	`covb`
"Coefficient of Determination (R-Squared)" on page 9-78	`Rsquared`: `Ordinary`, `Adjusted`	`rsquare`, `adjrsquare`
"Delete-1 Change in Covariance (covratio)" on page 9-81	`CovRatio`	`covratio`
"Delete-1 Scaled Difference in Coefficient Estimates (Dfbetas)" on page 9-84	`Dfbetas`	`dfbetas`
"Delete-1 Scaled Change in Fitted Values (Dffits)" on page 9-85	`Dffits`	`dffits`
"Delete-1 Variance (S2_i)" on page 9-88	`S2_i`	`s2_i`
"Durbin-Watson Test" on page 9-91	`dwtest`	`dwstat`
"F-statistic" on page 9-93	`Fstat`	`fstat`
"Hat Matrix" on page 9-99	`HatMatrix`	`hatmat`
"Leverage" on page 9-100	`Leverage`	`leverage`
"Residuals" on page 9-103	`Residuals`: `Raw`, `Pearson`, `Studentized`, `Standardized`	`r`, `studres`, `standres`
"t-statistic" on page 9-96	`tstats`	`tstat`

See Also

`dwtest` | `fitlm` | `LinearModel` | `plotDiagnostics` | `plotResiduals` | `stepwiselm`

Related Examples

- "Examine Quality and Adjust the Fitted Model" on page 9-20
- "Interpret Linear Regression Results" on page 9-63

Wilkinson Notation

In this section...

Overview

Wilkinson notation provides a way to describe regression and repeated measures models without specifying coefficient values. This specialized notation identifies the response variable and which predictor variables to include or exclude from the model. You can also include squared and higher-order terms, interaction terms, and grouping variables in the model formula.

Specifying a model using Wilkinson notation provides several advantages:

- You can include or exclude individual predictors and interaction terms from the model. For example, using the `'Interactions'` name-value pair available in each model fitting functions includes interaction terms for all pairs of variables. Using Wilkinson notation instead allows you to include only the interaction terms of interest.
- You can change the model formula without changing the design matrix, if your input data uses the `table` data type. For example, if you fit an initial model using all the available predictor variables, but decide to remove a variable that is not statistically significant, then you can re-write the model formula to include only the variables of interest. You do not need to make any changes to the input data itself.

Statistics and Machine Learning Toolbox offers several model fitting functions that use Wilkinson notation, including:

- Linear models (using `fitlm` and `stepwiselm`)
- Generalized linear models (using `fitglm`)

- Linear mixed-effects models (using `fitlme` and `fitlmematrix`)
- Generalized linear mixed-effects models (using `fitglme`)
- Repeated measures models (using `fitrm`)

Formula Specification

A formula for model specification is a string of the form `y ~ terms`, where `y` is the name of the response variable, and `terms` defines the model using the predictor variable names and the following operators.

Predictor Variables

Predictor Terms in Model	Wilkinson Notation
intercept	`1`
no intercept	`–1`
x_1	`x1`
x_1, x_2	`x1 + x2`
x_1, x_2, x_1x_2	`x1*x2` or `x1 + x2 + x1:x2`
x_1x_2	`x1:x2`
x_1, x_1^2	`x1^2`
x_1^2	`x1^2 – x1`

Wilkinson notation includes an intercept term in the model by default, even if you do not add 1 to the model formula. To exclude the intercept from the model, use -1 in the formula.

The `*` operator (for interactions) and the `^` operator (for power and exponents) automatically include all lower-order terms. For example, if you specify `x^3`, the model will automatically include x^3, $x2$, and x. If you want to exclude certain variables from the model, use the – operator to remove the unwanted terms.

Random-Effects and Mixed-Effects Models

For random-effects and mixed-effects models, the formula specification includes the names of the predictor variables and the grouping variables. For example, if the predictor

variable x_1 is a random effect grouped by the variable g, then represent this in Wilkinson notation as follows:

```
(x1 | g)
```

Repeated Measures Models

For repeated measures models, the formula specification includes all of the repeated measures as responses, and the factors as predictor variables. Specify the response variables for repeated measures models as described in the following table.

Response Terms in Model	Wilkinson Notation
y_1	`y1`
y_1, y_2, y_3	`y1,y2,y3`
y_1, y_2, y_3, y_4, y_5,	`y1–y5`

For example, if you have three repeated measures as responses and the factors x_1, x_2, and x_3 as the predictor variables, then you can define the repeated measures model using Wilkinson notation as follows:

```
y1,y2,y3 ~ x1 + x2 + x3
```

or

```
y1-y3 ~ x1 + x2 + x3
```

Variable Names

If the input data (response and predictor variables) is stored in a table or dataset array, you can specify the formula using the variable names. For example, load the `carsmall` sample data. Create a table containing `Weight`, `Acceleration`, and `MPG`. Name each variable using the `'VariableNames'` name-value pair argument of the fitting function `fitlm`. Then fit the following model to the data:

$$MPG = \beta_0 + \beta_1 Weight + \beta_2 Acceleration$$

```
load carsmall
tbl = table(Weight,Acceleration,MPG,'VariableNames',{'Weight','Acceleration','MPG'});
mdl = fitlm(tbl,'MPG ~ Weight + Acceleration')

mdl =
```

```
Linear regression model:
    MPG ~ 1 + Weight + Acceleration

Estimated Coefficients:
                    Estimate         SE         tStat       pValue
                   __________    __________    _______    __________

    (Intercept)         45.155        3.4659     13.028    1.6266e-22
    Weight          -0.0082475    0.00059836    -13.783    5.3165e-24
    Acceleration       0.19694       0.14743     1.3359       0.18493


Number of observations: 94, Error degrees of freedom: 91
Root Mean Squared Error: 4.12
R-squared: 0.743,  Adjusted R-Squared 0.738
F-statistic vs. constant model: 132, p-value = 1.38e-27
```

The model object display uses the variable names provided in the input table.

If the input data is stored as a matrix, you can specify the formula using default variable names such as `y`, `x1`, and `x2`. For example, load the `carsmall` sample data. Create a matrix containing the predictor variables `Weight` and `Acceleration`. Then fit the following model to the data:

$$MPG = \beta_0 + \beta_1 Weight + \beta_2 Acceleration$$

```
load carsmall
X = [Weight,Acceleration];
y = MPG;
mdl = fitlm(X,y,'y ~ x1 + x2')

mdl =


Linear regression model:
    y ~ 1 + x1 + x2

Estimated Coefficients:
                    Estimate         SE         tStat       pValue
                   __________    __________    _______    __________

    (Intercept)         45.155        3.4659     13.028    1.6266e-22
```

```
    x1             -0.0082475    0.00059836    -13.783    5.3165e-24
    x2               0.19694       0.14743     1.3359       0.18493


Number of observations: 94, Error degrees of freedom: 91
Root Mean Squared Error: 4.12
R-squared: 0.743,  Adjusted R-Squared 0.738
F-statistic vs. constant model: 132, p-value = 1.38e-27
```

The term `x1` in the model specification formula corresponds to the first column of the predictor variable matrix `X`. The term `x2` corresponds to the second column of the input matrix. The term `y` corresponds to the response variable.

Linear Model Examples

Use `fitlm` and `stepwiselm` to fit linear models.

Intercept and Two Predictors

For a linear regression model with an intercept and two fixed-effects predictors, such as

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \varepsilon_i,$$

specify the model formula using Wilkinson notation as follows:

```
'y ~ x1 + x2'
```

No Intercept and Two Predictors

For a linear regression model with no intercept and two fixed-effects predictors, such as

$$y_i = \beta_1 x_{i1} + \beta_2 x_{i2} + \varepsilon_i,$$

specify the model formula using Wilkinson notation as follows:

```
'y ~ -1 + x1 + x2'
```

Intercept, Two Predictors, and an Interaction Term

For a linear regression model with an intercept, two fixed-effects predictors, and an interaction term, such as

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i1} x_{i2} + \varepsilon_i ,$$

specify the model formula using Wilkinson notation as follows:

```
'y ~ x1*x2'
```

or

```
'y ~ x1 + x2 + x1:x2'
```

Intercept, Three Predictors, and All Interaction Effects

For a linear regression model with an intercept, three fixed-effects predictors, and interaction effects between all three predictors plus all lower-order terms, such as

$$y_i = \beta_0 + \beta_1 xi_1 + \beta_2 x_{i2} + \beta_3 x_{i3} + \beta_4 x_1 x_{i2} + \beta_5 x_1 x_{i3} + \beta_6 x_2 x_{i3} + \beta_7 x_{i1} x_{i2} x_{i3} + \varepsilon_i ,$$

specify the model formula using Wilkinson notation as follows:

```
'y ~ x1*x2*x3'
```

Intercept, Three Predictors, and Selected Interaction Effects

For a linear regression model with an intercept, three fixed-effects predictors, and interaction effects between two of the predictors, such as

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3} + \beta_4 x_1 x_{i2} + \varepsilon_i ,$$

specify the model formula using Wilkinson notation as follows:

```
'y ~ x1*x2 + x3'
```

or

```
'y ~ x1 + x2 + x3 + x1:x2'
```

Intercept, Three Predictors, and Lower-Order Interaction Effects Only

For a linear regression model with an intercept, three fixed-effects predictors, and pairwise interaction effects between all three predictors, but excluding an interaction effect between all three predictors simultaneously, such as

$$y_i = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3} + \beta_4 x_1 x_{i2} + \beta_5 x_{i1} x_{i3} + \beta_6 x_{i2} x_{i3} + \varepsilon_i ,$$

specify the model formula using Wilkinson notation as follows:

```
'y ~ x1*x2*x3 - x1:x2:x3'
```

Linear Mixed-Effects Model Examples

Use `fitlme` and `fitlmematrix` to fit linear mixed-effects models.

Random Effect Intercept, No Predictors

For a linear mixed-effects model that contains a random intercept but no predictor terms, such as

$$y_{im} = \beta_{0m},$$

where

$$\beta_{0m} = \beta_{00} + b_{0m},\ b_{0m} \sim N\left(0, \sigma_0^2\right)$$

and g is the grouping variable with m levels, specify the model formula using Wilkinson notation as follows:

```
'y ~ (1 | g)'
```

Random Intercept and Fixed Slope for One Predictor

For a linear mixed-effects model that contains a fixed intercept, random intercept, and fixed slope for the continuous predictor variable, such as

$$y_{im} = \beta_{0m} + \beta_1 x_{im},$$

where

$$\beta_{0m} = \beta_{00} + b_{0m},\ b_{0m} \sim N\left(0, \sigma_0^2\right)$$

and g is the grouping variable with m levels, specify the model formula using Wilkinson notation as follows:

```
'y ~ x1 + (1 | g)'
```

Random Intercept and Random Slope for One Predictor

For a linear mixed-effects model that contains a fixed intercept, plus a random intercept and a random slope that have a possible correlation between them, such as

$$y_{im} = \beta_{0m} + \beta_{1m} x_{im},$$

where

$$\beta_{0m} = \beta_{00} + b_{0m}$$

$$\beta_{1m} = \beta_{10} + b_{1m}$$

$$\begin{bmatrix} b_{0m} \\ b_{1m} \end{bmatrix} \sim N\left\{0, \sigma^2 D(\theta)\right\}$$

and D is a 2-by-2 symmetric and positive semidefinite covariance matrix, parameterized by a variance component vector θ, specify the model formula using Wilkinson notation as follows:

```
'y ~ x1 + (x1 | g)'
```

The pattern of the random effects covariance matrix is determined by the model fitting function. To specify the covariance matrix pattern, use the name-value pairs available through `fitlme` when fitting the model. For example, you can specify the assumption that the random intercept and random slope are independent of one another using the `'CovariancePattern'` name-value pair argument in `fitlme`.

Generalized Linear Model Examples

Use `fitglm` and `stepwiseglm` to fit generalized linear models.

In a generalized linear model, the y response variable has a distribution other than normal, but you can represent the model as an equation that is linear in the regression coefficients. Specifying a generalized linear model requires three parts:

- Distribution of the response variable
- Link function
- Linear predictor

The distribution of the response variable and the link function are specified using name-value pair arguments in the fit function `fitglm` or `stepwiseglm`.

The linear predictor portion of the equation, which appears on the right side of the ~ symbol in the model specification formula, uses Wilkinson notation in the same way as for the linear model examples.

A generalized linear model models the link function, rather than the actual response, as y. This is reflected in the output display for the model object.

Intercept and Two Predictors

For a generalized linear regression model with an intercept and two predictors, such as

$$\log(y_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2},$$

specify the model formula using Wilkinson notation as follows:

```
'y ~ x1 + x2'
```

Generalized Linear Mixed-Effects Model Examples

Use `fitglme` to fit generalized linear mixed-effects models.

In a generalized linear mixed-effects model, the y response variable has a distribution other than normal, but you can represent the model as an equation that is linear in the regression coefficients. Specifying a generalized linear model requires three parts:

- Distribution of the response variable
- Link function
- Linear predictor

The distribution of the response variable and the link function are specified using name-value pair arguments in the fit function `fitglme`.

The linear predictor portion of the equation, which appears on the right side of the ~ symbol in the model specification formula, uses Wilkinson notation in the same way as for the linear mixed-effects model examples.

A generalized linear model models the link function as y, not the response itself. This is reflected in the output display for the model object.

The pattern of the random effects covariance matrix is determined by the model fitting function. To specify the covariance matrix pattern, use the name-value pairs available through `fitglme` when fitting the model. For example, you can specify the assumption that the random intercept and random slope are independent of one another using the `'CovariancePattern'` name-value pair argument in `fitglme`.

Random Intercept and Fixed Slope for One Predictor

For a generalized linear mixed-effects model that contains a fixed intercept, random intercept, and fixed slope for the continuous predictor variable, where the response can be modeled using a Poisson distribution, such as

$$\log(y_{im}) = \beta_0 + \beta_1 x_{im} + b_i,$$

where

$$b_i \sim N\left(0, \sigma_b^2\right)$$

and g is the grouping variable with m levels, specify the model formula using Wilkinson notation as follows:

```
'y ~ x1 + (1 | g)'
```

Repeated Measures Model Examples

Use `fitrm` to fit repeated measures models.

One Predictor

For a repeated measures model with five response measurements and one predictor variable, specify the model formula using Wilkinson notation as follows:

```
'y1-y5 ~ x1'
```

Three Predictors and an Interaction Term

For a repeated measures model with five response measurements and three predictor variables, plus an interaction between two of the predictor variables, specify the model formula using Wilkinson notation as follows:

```
'y1-y5 ~ x1*x2 + x3'
```

Stepwise Regression

In this section...

Stepwise Regression to Select Appropriate Models

`stepwiselm` creates a linear model and automatically adds to or trims the model. To create a small model, start from a constant model. To create a large model, start with a model containing many terms. A large model usually has lower error as measured by the fit to the original data, but might not have any advantage in predicting new data.

`stepwiselm` can use all the name-value options from `fitlm`, with additional options relating to the starting and bounding models. In particular:

- For a small model, start with the default lower bounding model: `'constant'` (a model that has no predictor terms).
- The default upper bounding model has linear terms and interaction terms (products of pairs of predictors). For an upper bounding model that also includes squared terms, set the `Upper` name-value pair to `'quadratic'`.

Compare large and small stepwise models

This example shows how to compare models that `stepwiselm` returns starting from a constant model and starting from a full interaction model.

Load the `carbig` data and create a table from some of the data.

```
load carbig
tbl = table(Acceleration,Displacement,Horsepower,Weight,MPG);
```

Create a mileage model stepwise starting from the constant model.

```
mdl1 = stepwiselm(tbl,'constant','ResponseVar','MPG')
```

```
1. Adding Weight, FStat = 888.8507, pValue = 2.9728e-103
2. Adding Horsepower, FStat = 3.8217, pValue = 0.00049608
3. Adding Horsepower:Weight, FStat = 64.8709, pValue = 9.93362e-15

mdl1 =
```

```
Linear regression model:
    MPG ~ 1 + Horsepower*Weight

Estimated Coefficients:
                       Estimate      SE            tStat      pValue
    (Intercept)           63.558       2.3429      27.127    1.2343e-91
    Horsepower          -0.25084     0.027279     -9.1952    2.3226e-18
    Weight              -0.010772    0.00077381    -13.921    5.1372e-36
    Horsepower:Weight   5.3554e-05   6.6491e-06     8.0542    9.9336e-15


Number of observations: 392, Error degrees of freedom: 388
Root Mean Squared Error: 3.93
R-squared: 0.748,  Adjusted R-Squared 0.746
F-statistic vs. constant model: 385, p-value = 7.26e-116
```

Create a mileage model stepwise starting from the full interaction model.

```
mdl2 = stepwiselm(tbl,'interactions','ResponseVar','MPG')
```

```
1. Removing Acceleration:Displacement, FStat = 0.024186, pValue = 0.8765
2. Removing Displacement:Weight, FStat = 0.33103, pValue = 0.56539
3. Removing Acceleration:Horsepower, FStat = 1.7334, pValue = 0.18876
4. Removing Acceleration:Weight, FStat = 0.93269, pValue = 0.33477
5. Removing Horsepower:Weight, FStat = 0.64486, pValue = 0.42245

mdl2 =


Linear regression model:
    MPG ~ 1 + Acceleration + Weight + Displacement*Horsepower

Estimated Coefficients:
                            Estimate      SE            tStat      pValue
    (Intercept)                61.285       2.8052      21.847    1.8593e-69
    Acceleration              -0.34401      0.11862       -2.9     0.0039445
    Displacement             -0.081198     0.010071     -8.0623    9.5014e-15
    Horsepower                -0.24313     0.026068     -9.3265    8.6556e-19
    Weight                  -0.0014367    0.00084041     -1.7095      0.088166
    Displacement:Horsepower  0.00054236   5.7987e-05      9.3531    7.0527e-19


Number of observations: 392, Error degrees of freedom: 386
Root Mean Squared Error: 3.84
R-squared: 0.761,  Adjusted R-Squared 0.758
F-statistic vs. constant model: 246, p-value = 1.32e-117
```

Notice that:

- `mdl1` has four coefficients (the `Estimate` column), and `mdl2` has six coefficients.
- The adjusted R-squared of `mdl1` is `0.746`, which is slightly less (worse) than that of `mdl2`, `0.758`.

Create a mileage model stepwise with a full quadratic model as the upper bound, starting from the full quadratic model:

```
mdl3 = stepwiselm(tbl,'quadratic',...
    'ResponseVar','MPG','Upper','quadratic');
```

Compare the three model complexities by examining their formulas.

```
mdl1.Formula
```

```
ans =
MPG ~ 1 + Horsepower*Weight
```

```
mdl2.Formula
```

```
ans =
MPG ~ 1 + Acceleration + Weight + Displacement*Horsepower
```

```
mdl3.Formula
```

```
ans =
MPG ~ 1 + Weight + Acceleration*Displacement
        + Displacement*Horsepower + Acceleration^2
```

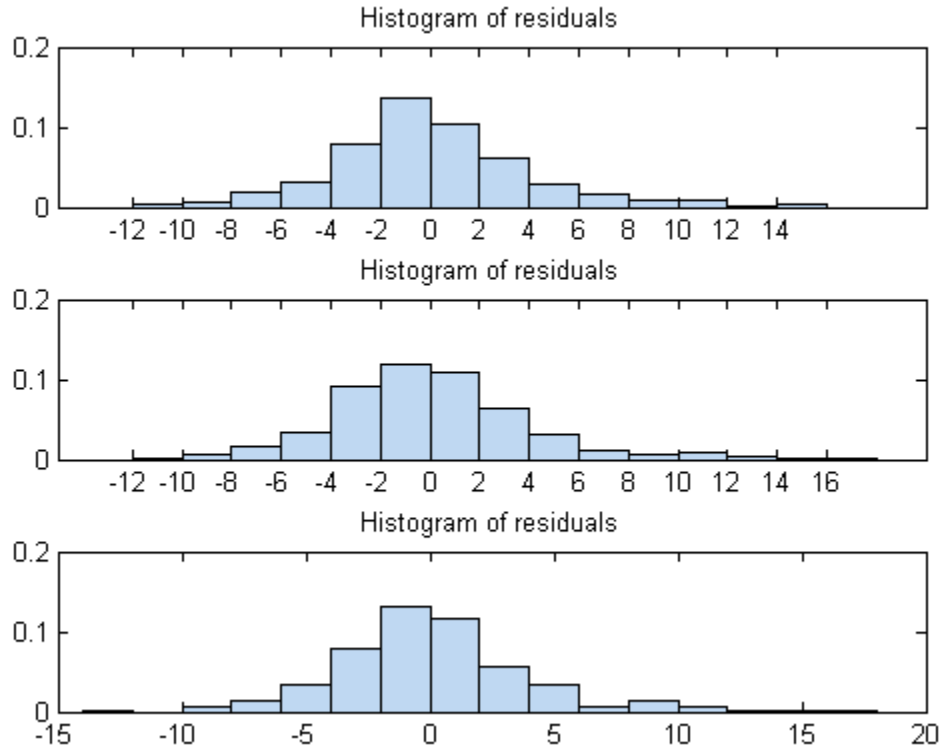
The adjusted R^2 values improve slightly as the models become more complex:

```
RSquared = [mdl1.Rsquared.Adjusted, ...
    mdl2.Rsquared.Adjusted, mdl3.Rsquared.Adjusted]
```

```
RSquared =
    0.7465    0.7580    0.7599
```

Compare residual plots of the three models.

```
subplot(3,1,1)
plotResiduals(mdl1)
subplot(3,1,2)
plotResiduals(mdl2)
subplot(3,1,3)
plotResiduals(mdl3)
```



The models have similar residuals. It is not clear which fits the data better.

Interestingly, the more complex models have larger maximum deviations of the residuals:

```
Rrange1 = [min(mdl1.Residuals.Raw),max(mdl1.Residuals.Raw)];
Rrange2 = [min(mdl2.Residuals.Raw),max(mdl2.Residuals.Raw)];
Rrange3 = [min(mdl3.Residuals.Raw),max(mdl3.Residuals.Raw)];
Rranges = [Rrange1;Rrange2;Rrange3]
```

```
Rranges =
  -10.7725   14.7314
  -11.4407   16.7562
  -12.2723   16.7927
```

Robust Regression — Reduce Outlier Effects

In this section...

What Is Robust Regression?

The models described in "What Are Linear Regression Models?" on page 9-8 are based on certain assumptions, such as a normal distribution of errors in the observed responses. If the distribution of errors is asymmetric or prone to outliers, model assumptions are invalidated, and parameter estimates, confidence intervals, and other computed statistics become unreliable. Use `fitlm` with the `RobustOpts` name-value pair to create a model that is not much affected by outliers. The robust fitting method is less sensitive than ordinary least squares to large changes in small parts of the data.

Robust regression works by assigning a weight to each data point. Weighting is done automatically and iteratively using a process called *iteratively reweighted least squares*. In the first iteration, each point is assigned equal weight and model coefficients are estimated using ordinary least squares. At subsequent iterations, weights are recomputed so that points farther from model predictions in the previous iteration are given lower weight. Model coefficients are then recomputed using weighted least squares. The process continues until the values of the coefficient estimates converge within a specified tolerance.

Robust Regression versus Standard Least-Squares Fit

This example shows how to use robust regression. It compares the results of a robust fit to a standard least-squares fit.

Step 1. Prepare data.

Load the `moore` data. The data is in the first five columns, and the response in the sixth.

```
load moore
X = [moore(:,1:5)];
y = moore(:,6);
```

Step 2. Fit robust and nonrobust models.

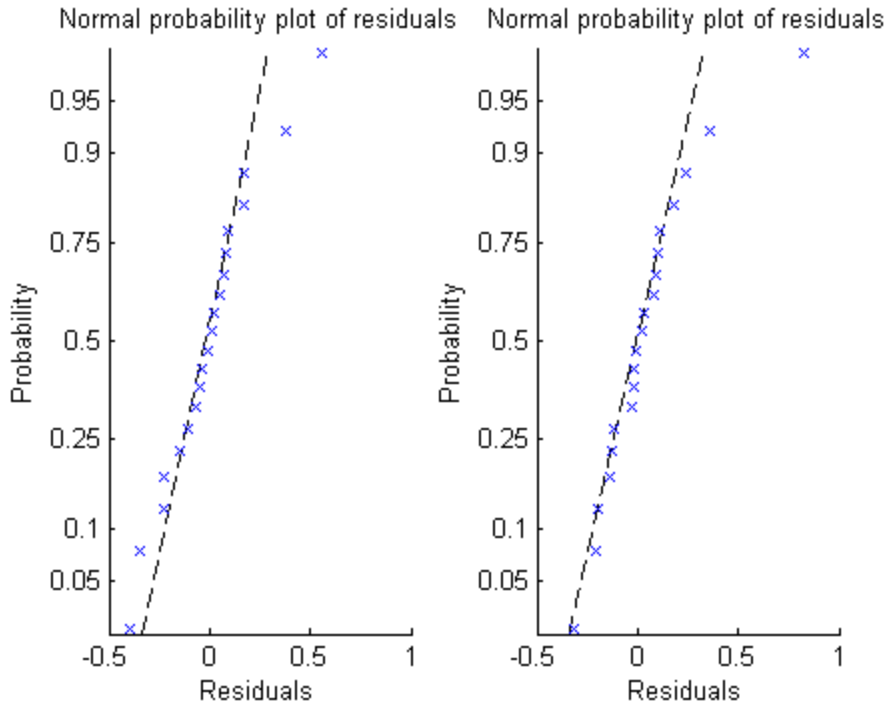
Fit two linear models to the data, one using robust fitting, one not.

```
mdl = fitlm(X,y); % not robust
mdlr = fitlm(X,y,'RobustOpts','on');
```

Step 3. Examine model residuals.

Examine the residuals of the two models.

```
subplot(1,2,1);plotResiduals(mdl,'probability')
subplot(1,2,2);plotResiduals(mdlr,'probability')
```



The residuals from the robust fit (right half of the plot) are nearly all closer to the straight line, except for the one obvious outlier.

4. Remove the outlier from the standard model

Find the index of the outlier. Examine the weight of the outlier in the robust fit.

```
[~,outlier] = max(mdlr.Residuals.Raw);
mdlr.Robust.Weights(outlier)
```

```
ans =

    0.0246
```

Check the median weight.

```
median(mdlr.Robust.Weights)
```

```
ans =

    0.9718
```

This weight of the outlier in the robust fit is much less than a typical weight of an observation.

Ridge Regression

In this section...

Introduction to Ridge Regression

Coefficient estimates for the models described in "Linear Regression" on page 9-11 rely on the independence of the model terms. When terms are correlated and the columns of the design matrix X have an approximate linear dependence, the matrix $(X^TX)^{-1}$ becomes close to singular. As a result, the least-squares estimate

$$\hat{\beta} = (X^T X)^{-1} X^T y$$

becomes highly sensitive to random errors in the observed response y, producing a large variance. This situation of *multicollinearity* can arise, for example, when data are collected without an experimental design.

Ridge regression addresses the problem by estimating regression coefficients using

$$\hat{\beta} = (X^T X + kI)^{-1} X^T y$$

where k is the *ridge parameter* and I is the identity matrix. Small positive values of k improve the conditioning of the problem and reduce the variance of the estimates. While biased, the reduced variance of ridge estimates often result in a smaller mean square error when compared to least-squares estimates.

The Statistics and Machine Learning Toolbox function `ridge` carries out ridge regression.

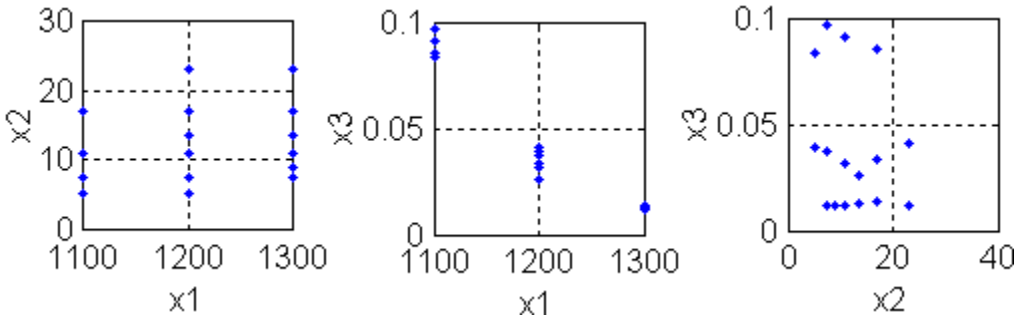
Ridge Regression

For example, load the data in `acetylene.mat`, with observations of the predictor variables `x1`, `x2`, `x3`, and the response variable `y`:

```
load acetylene
```

Plot the predictor variables against each other:

```
subplot(1,3,1)
plot(x1,x2,'.')
xlabel('x1'); ylabel('x2'); grid on; axis square

subplot(1,3,2)
plot(x1,x3,'.')
xlabel('x1'); ylabel('x3'); grid on; axis square

subplot(1,3,3)
plot(x2,x3,'.')
xlabel('x2'); ylabel('x3'); grid on; axis square
```



Note the correlation between `x1` and the other two predictor variables.

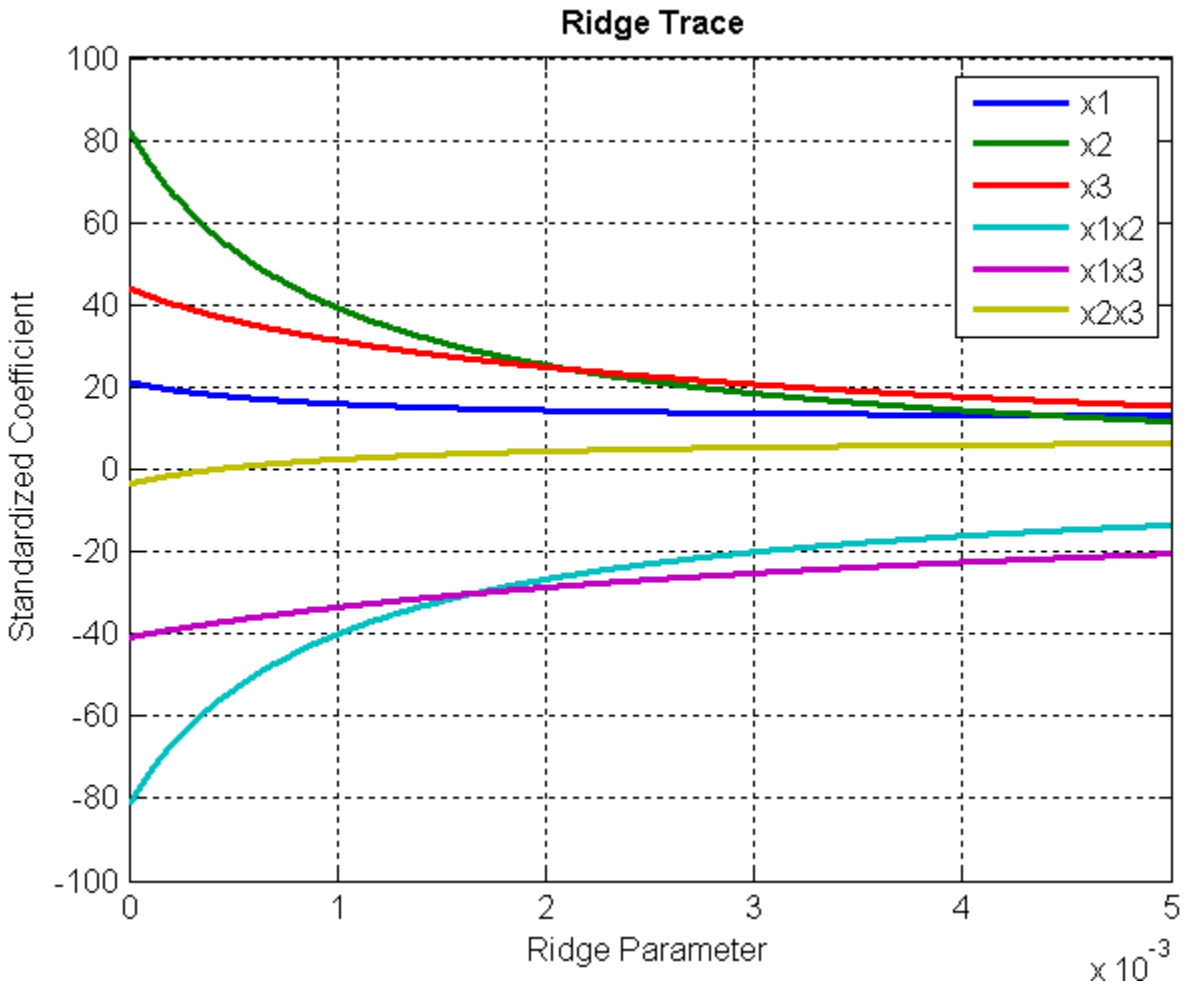
Use `ridge` and `x2fx` to compute coefficient estimates for a multilinear model with interaction terms, for a range of ridge parameters:

```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
k = 0:1e-5:5e-3;
betahat = ridge(y,D,k);
```

Plot the ridge trace:

```
figure
plot(k,betahat,'LineWidth',2)
ylim([-100 100])
grid on
xlabel('Ridge Parameter')
ylabel('Standardized Coefficient')
```

```
title('{\bf Ridge Trace}')
legend('x1','x2','x3','x1x2','x1x3','x2x3')
```



The estimates stabilize to the right of the plot. Note that the coefficient of the `x2x3` interaction term changes sign at a value of the ridge parameter $\approx 5 \times 10^{-4}$.

Lasso and Elastic Net

In this section...

What Are Lasso and Elastic Net?

Lasso is a regularization technique. Use `lasso` to:

- Reduce the number of predictors in a regression model.
- Identify important predictors.
- Select among redundant predictors.
- Produce shrinkage estimates with potentially lower predictive errors than ordinary least squares.

Elastic net is a related technique. Use elastic net when you have several highly correlated variables. `lasso` provides elastic net regularization when you set the `Alpha` name-value pair to a number strictly between `0` and `1`.

See "Lasso and Elastic Net Details" on page 9-144.

For lasso regularization of regression ensembles, see `regularize`.

Lasso Regularization

To see how `lasso` identifies and discards unnecessary predictors:

1. Generate `200` samples of five-dimensional artificial data `X` from exponential distributions with various means:

```
rng(3,'twister') % for reproducibility
X = zeros(200,5);
```

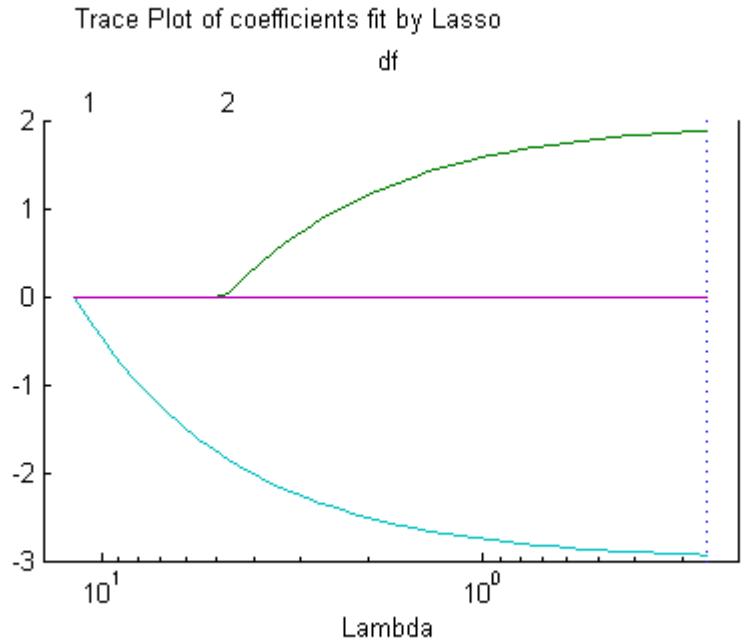
```
for ii = 1:5
    X(:,ii) = exprnd(ii,200,1);
end
```

2 Generate response data `Y = X*r + eps` where `r` has just two nonzero components, and the noise `eps` is normal with standard deviation `0.1`:

```
r = [0;2;0;-3;0];
Y = X*r + randn(200,1)*.1;
```

3 Fit a cross-validated sequence of models with `lasso`, and plot the result:

```
[b fitinfo] = lasso(X,Y,'CV',10);
lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
```



The plot shows the nonzero coefficients in the regression for various values of the `Lambda` regularization parameter. Larger values of `Lambda` appear on the left side of the graph, meaning more regularization, resulting in fewer nonzero regression coefficients.

The dashed vertical lines represent the `Lambda` value with minimal mean squared error (on the right), and the `Lambda` value with minimal mean squared error plus one standard deviation. This latter value is a recommended setting for `Lambda`. These lines appear only when you perform cross validation. Cross validate by setting the `'CV'` name-value pair. This example uses 10-fold cross validation.

The upper part of the plot shows the degrees of freedom (df), meaning the number of nonzero coefficients in the regression, as a function of Lambda. On the left, the large value of Lambda causes all but one coefficient to be 0. On the right all five coefficients are nonzero, though the plot shows only two clearly. The other three coefficients are so small that you cannot visually distinguish them from 0.

For small values of `Lambda` (toward the right in the plot), the coefficient values are close to the least-squares estimate. See step 5.

4 Find the `Lambda` value of the minimal cross-validated mean squared error plus one standard deviation. Examine the MSE and coefficients of the fit at that `Lambda`:

```
lam = fitinfo.Index1SE;
fitinfo.MSE(lam)

ans =
    0.1398

b(:,lam)

ans =
         0
    1.8855
         0
   -2.9367
         0
```

`lasso` did a good job finding the coefficient vector `r`.

5 For comparison, find the least-squares estimate of `r`:

```
rhat = X\Y

rhat =

   -0.0038
    1.9952
```

```
    0.0014
   -2.9993
    0.0031
```

The estimate `b(:,lam)` has slightly more mean squared error than the mean squared error of `rhat`:

```
res = X*rhat - Y; % calculate residuals
MSEmin = res'*res/200 % b(:,lam) value is 0.1398

MSEmin =
    0.0088
```

But `b(:,lam)` has only two nonzero components, and therefore can provide better predictive estimates on new data.

Lasso and Elastic Net with Cross Validation

Consider predicting the mileage (`MPG`) of a car based on its weight, displacement, horsepower, and acceleration. The `carbig` data contains these measurements. The data seem likely to be correlated, making elastic net an attractive choice.

1. Load the data:

   ```
   load carbig
   ```

2. Extract the continuous (noncategorical) predictors (`lasso` does not handle categorical predictors):

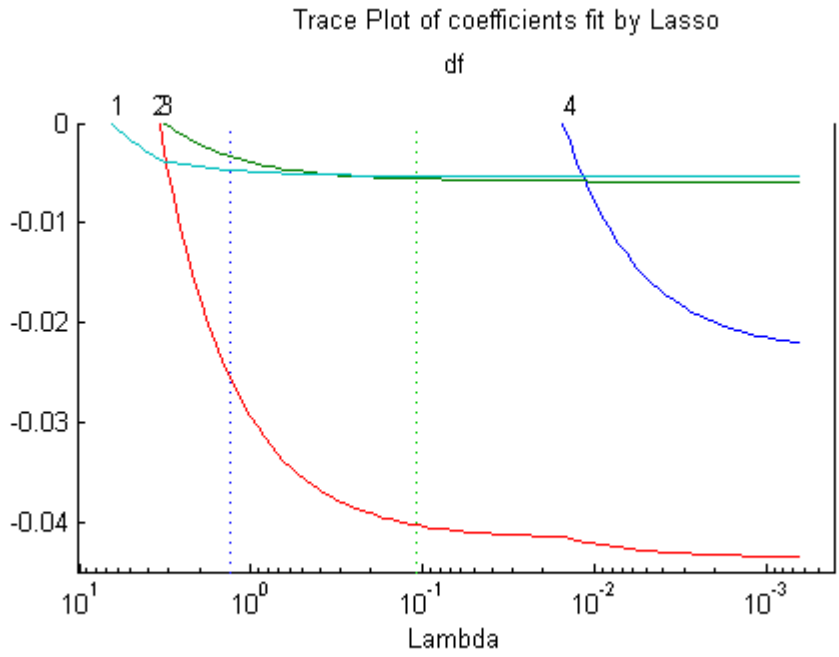
   ```
   X = [Acceleration Displacement Horsepower Weight];
   ```

3. Perform a lasso fit with 10-fold cross validation:

   ```
   [b fitinfo] = lasso(X,MPG,'CV',10);
   ```

4. Plot the result:

   ```
   lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
   ```



5 Calculate the correlation of the predictors:

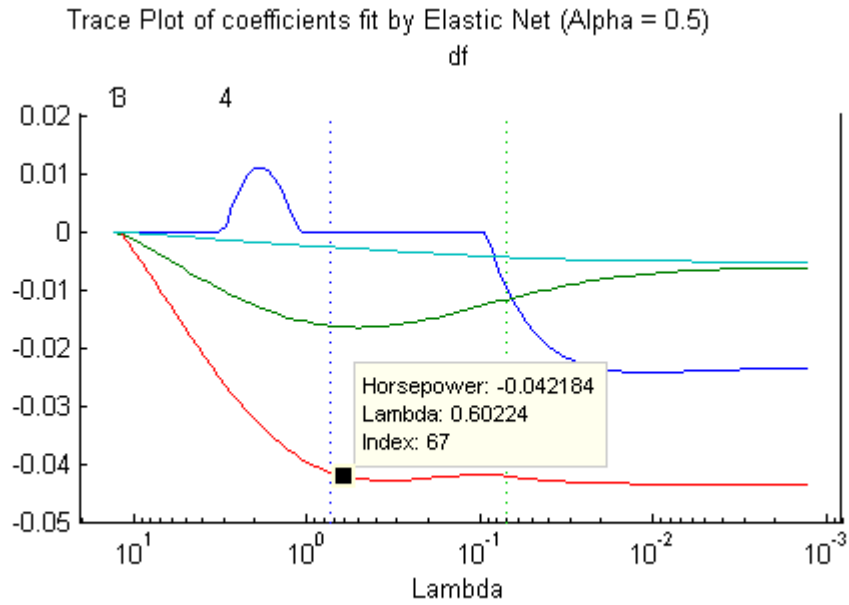
```
% Eliminate NaNs so corr runs
nonan = ~any(isnan([X MPG]),2);
Xnonan = X(nonan,:);
MPGnonan = MPG(nonan,:);
corr(Xnonan)

ans =
    1.0000   -0.5438   -0.6892   -0.4168
   -0.5438    1.0000    0.8973    0.9330
   -0.6892    0.8973    1.0000    0.8645
   -0.4168    0.9330    0.8645    1.0000
```

6 Because some predictors are highly correlated, perform elastic net fitting. Use `Alpha = 0.5`:

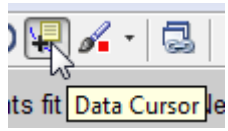
```
[ba fitinfoa] = lasso(X,MPG,'CV',10,'Alpha',.5);
```

7 Plot the result. Name each predictor so you can tell which curve is which:

```
pnames = {'Acceleration','Displacement',...
    'Horsepower','Weight'};
lassoPlot(ba,fitinfoa,'PlotType','Lambda',...
    'XScale','log','PredictorNames',pnames);
```



When you activate the data cursor



and click the plot, you see the name of the predictor, the coefficient, the value of `Lambda`, and the index of that point, meaning the column in `b` associated with that fit.

Here, the elastic net and lasso results are not very similar. Also, the elastic net plot reflects a notable qualitative property of the elastic net technique. The elastic net retains three nonzero coefficients as `Lambda` increases (toward the left of the plot), and these three coefficients reach `0` at about the same `Lambda` value. In contrast, the lasso plot shows two of the three coefficients becoming `0` at the same value of `Lambda`, while another coefficient remains nonzero for higher values of `Lambda`.

This behavior exemplifies a general pattern. In general, elastic net tends to retain or drop groups of highly correlated predictors as `Lambda` increases. In contrast, lasso tends to drop smaller groups, or even individual predictors.

Wide Data via Lasso and Parallel Computing

Lasso and elastic net are especially well suited to *wide* data, meaning data with more predictors than observations. Obviously, there are redundant predictors in this type of data. Use `lasso` along with cross validation to identify important predictors.

Cross validation can be slow. If you have a Parallel Computing Toolbox license, speed the computation using parallel computing.

1. Load the `spectra` data:

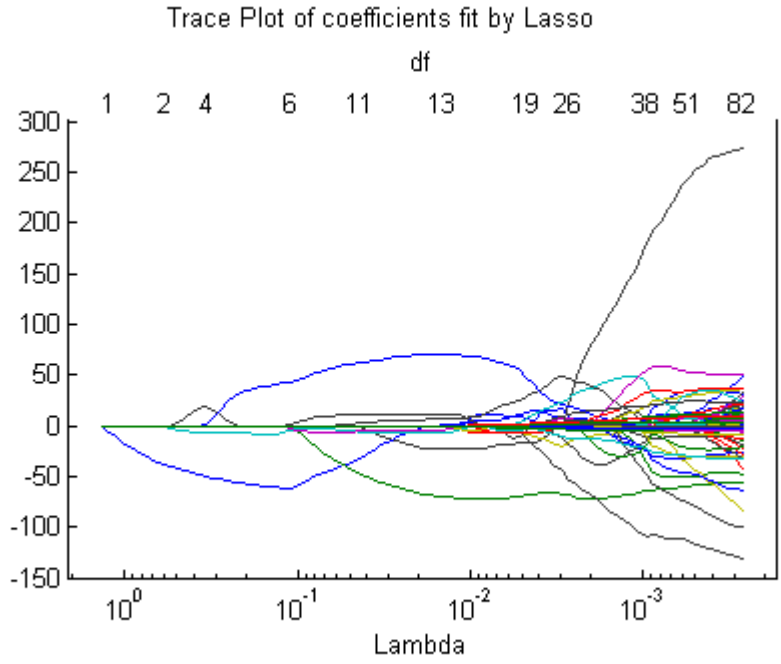
```
load spectra
Description

Description =

== Spectral and octane data of gasoline ==

NIR spectra and octane numbers of 60 gasoline samples

NIR:     NIR spectra, measured in 2 nm intervals from 900 nm to 1700 nm
octane:  octane numbers
spectra: a dataset array containing variables for NIR and octane

Reference:
Kalivas, John H., "Two Data Sets of Near Infrared Spectra," Chemometrics
and Intelligent Laboratory Systems, v.37 (1997) pp.255–259
```

2. Compute the default `lasso` fit:

```
[b fitinfo] = lasso(NIR,octane);
```

3. Plot the number of predictors in the fitted lasso regularization as a function of `Lambda`, using a logarithmic *x*-axis:

```
lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
```

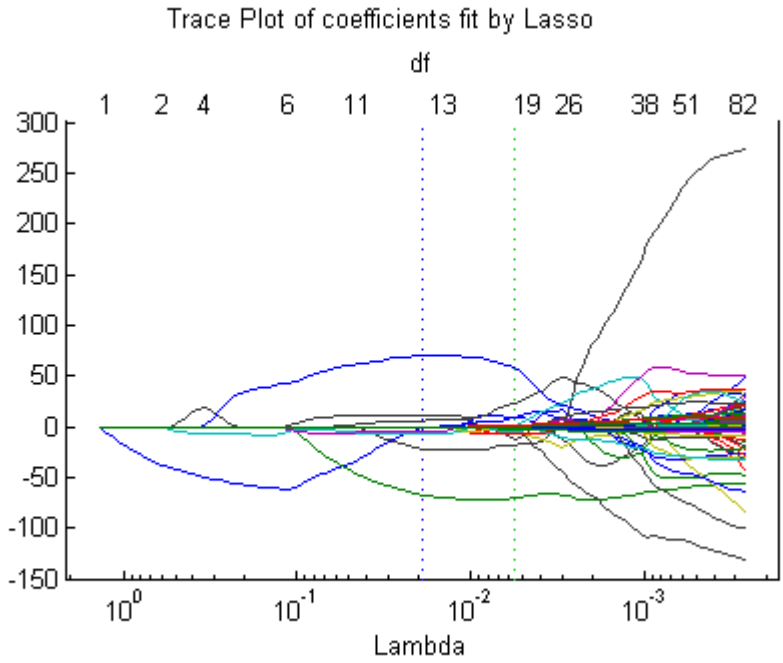


4 It is difficult to tell which value of `Lambda` is appropriate. To determine a good value, try fitting with cross validation:

```
tic
[b fitinfo] = lasso(NIR,octane,'CV',10);
% A time-consuming operation
toc

Elapsed time is 226.876926 seconds.
```

5 Plot the result:

```
lassoPlot(b,fitinfo,'PlotType','Lambda','XScale','log');
```



You can see the suggested value of `Lambda` is over `1e-2`, and the `Lambda` with minimal MSE is under `1e-2`. These values are in the `fitinfo` structure:

```
fitinfo.LambdaMinMSE
ans =
    0.0057

fitinfo.Lambda1SE
ans =
    0.0190
```

6 Examine the quality of the fit for the suggested value of `Lambda`:

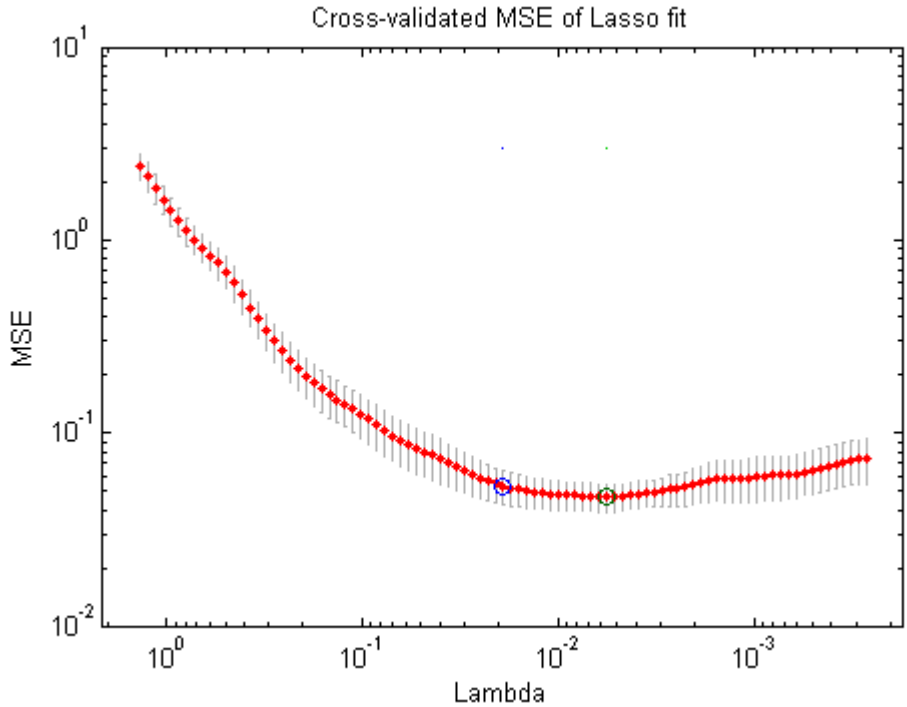
```
lambdaindex = fitinfo.Index1SE;
fitinfo.MSE(lambdaindex)

ans =
```

```
    0.0532

fitinfo.DF(lambdaindex)

ans =
    11
```

The fit uses just 11 of the 401 predictors, and achieves a cross-validated MSE of `0.0532`.

7 Examine the plot of cross-validated MSE:

```
lassoPlot(b,fitinfo,'PlotType','CV');
% Use a log scale for MSE to see small MSE values better
set(gca,'YScale','log');
```



As `Lambda` increases (toward the left), MSE increases rapidly. The coefficients are reduced too much and they do not adequately fit the responses.

As `Lambda` decreases, the models are larger (have more nonzero coefficients). The increasing MSE suggests that the models are overfitted.

The default set of `Lambda` values does not include values small enough to include all predictors. In this case, there does not appear to be a reason to look at smaller values. However, if you want smaller values than the default, use the `LambdaRatio` parameter, or supply a sequence of `Lambda` values using the `Lambda` parameter. For details, see the `lasso` reference page.

8 To compute the cross-validated lasso estimate faster, use parallel computing (available with a Parallel Computing Toolbox license):

```
parpool()
Starting parpool using the 'local' profile ... connected to 2 workers.

ans =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
      IdleTimeout: 30
          Cluster: [1x1 parallel.cluster.Local]
     RequestQueue: [1x1 parallel.RequestQueue]
      SpmdEnabled: 1

opts = statset('UseParallel',true);
tic;
[b fitinfo] = lasso(NIR,octane,'CV',10,'Options',opts);
toc
Elapsed time is 114.712260 seconds.
```

Computing in parallel using two workers is faster on this problem.

Lasso and Elastic Net Details

Overview of Lasso and Elastic Net

Lasso is a regularization technique for performing linear regression. Lasso includes a penalty term that constrains the size of the estimated coefficients. Therefore, it resembles ridge regression. Lasso is a *shrinkage estimator*: it generates coefficient estimates that are biased to be small. Nevertheless, a lasso estimator can have smaller

mean squared error than an ordinary least-squares estimator when you apply it to new data.

Unlike ridge regression, as the penalty term increases, lasso sets more coefficients to zero. This means that the lasso estimator is a smaller model, with fewer predictors. As such, lasso is an alternative to stepwise regression and other model selection and dimensionality reduction techniques.

Elastic net is a related technique. Elastic net is a hybrid of ridge regression and lasso regularization. Like lasso, elastic net can generate reduced models by generating zero-valued coefficients. Empirical studies have suggested that the elastic net technique can outperform lasso on data with highly correlated predictors.

Definition of Lasso

The *lasso* technique solves this regularization problem. For a given value of λ, a nonnegative parameter, `lasso` solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)^2+\lambda\sum_{j=1}^{p}|\beta_j|\right),$$

where

- N is the number of observations.
- y_i is the response at observation i.
- x_i is data, a vector of p values at observation i.
- λ is a positive regularization parameter corresponding to one value of Lambda.
- The parameters β_0 and β are scalar and p-vector respectively.

As λ increases, the number of nonzero components of β decreases.

The lasso problem involves the L^1 norm of β, as contrasted with the elastic net algorithm.

Definition of Elastic Net

The *elastic net* technique solves this regularization problem. For an α strictly between 0 and 1, and a nonnegative λ, elastic net solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)^2+\lambda P_\alpha(\beta)\right),$$

where

$$P_\alpha(\beta)=\frac{(1-\alpha)}{2}\|\beta\|_2^2+\alpha\|\beta\|_1=\sum_{j=1}^{p}\left(\frac{(1-\alpha)}{2}\beta_j^2+\alpha|\beta_j|\right).$$

Elastic net is the same as lasso when $\alpha = 1$. As α shrinks toward 0, elastic net approaches `ridge` regression. For other values of α, the penalty term $P_\alpha(\beta)$ interpolates between the L^1 norm of β and the squared L^2 norm of β.

References

[1] Tibshirani, R. *Regression shrinkage and selection via the lasso.* Journal of the Royal Statistical Society, Series B, Vol 58, No. 1, pp. 267–288, 1996.

[2] Zou, H. and T. Hastie. *Regularization and variable selection via the elastic net.* Journal of the Royal Statistical Society, Series B, Vol. 67, No. 2, pp. 301–320, 2005.

[3] Friedman, J., R. Tibshirani, and T. Hastie. *Regularization paths for generalized linear models via coordinate descent.* Journal of Statistical Software, Vol 33, No. 1, 2010. http://www.jstatsoft.org/v33/i01

[4] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning,* 2nd edition. Springer, New York, 2008.

Partial Least Squares

In this section...

Introduction to Partial Least Squares

Partial least-squares (*PLS*) regression is a technique used with data that contain correlated predictor variables. This technique constructs new predictor variables, known as *components*, as linear combinations of the original predictor variables. PLS constructs these components while considering the observed response values, leading to a parsimonious model with reliable predictive power.

The technique is something of a cross between multiple linear regression and principal component analysis:

- Multiple linear regression finds a combination of the predictors that best fit a response.
- Principal component analysis finds combinations of the predictors with large variance, reducing correlations. The technique makes no use of response values.
- PLS finds combinations of the predictors that have a large covariance with the response values.

PLS therefore combines information about the variances of both the predictors and the responses, while also considering the correlations among them.

PLS shares characteristics with other regression and feature transformation techniques. It is similar to ridge regression in that it is used in situations with correlated predictors. It is similar to stepwise regression (or more general feature selection techniques) in that it can be used to select a smaller set of model terms. PLS differs from these methods, however, by transforming the original predictor space into the new component space.

The Statistics and Machine Learning Toolbox function `plsregress` carries out PLS regression.

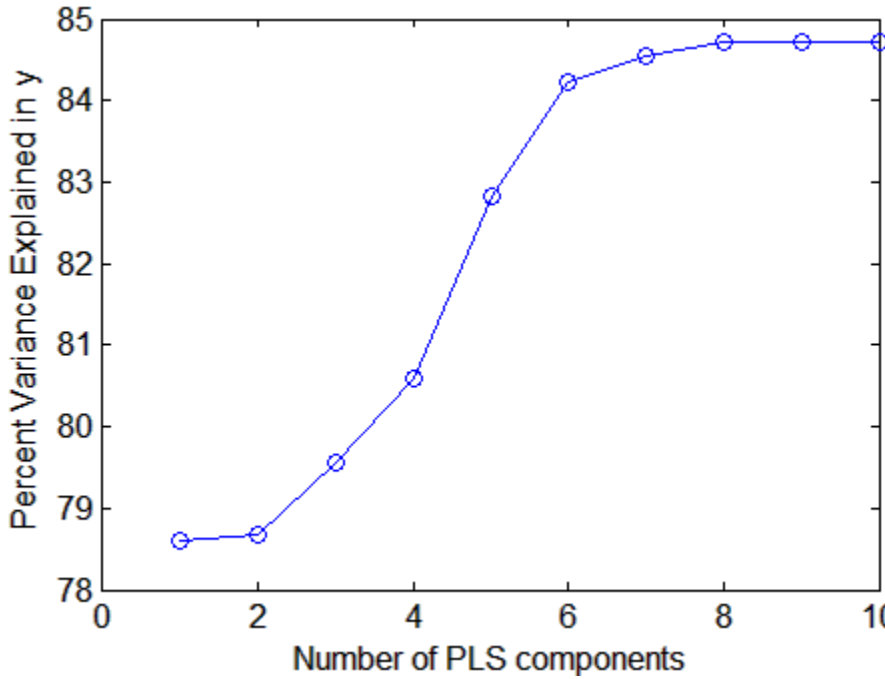
Partial Least Squares

For example, consider the data on biochemical oxygen demand in `moore.mat`, padded with noisy versions of the predictors to introduce correlations:

```
load moore
y = moore(:,6);              % Response
X0 = moore(:,1:5);           % Original predictors
X1 = X0+10*randn(size(X0));  % Correlated predictors
X = [X0,X1];
```

Use `plsregress` to perform PLS regression with the same number of components as predictors, then plot the percentage variance explained in the response as a function of the number of components:

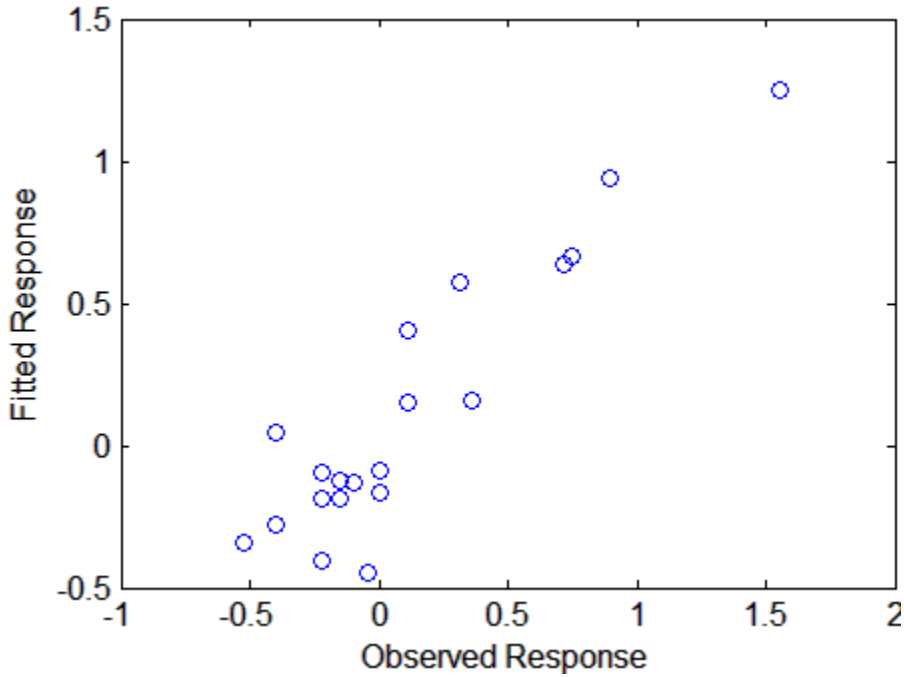
```
[XL,yl,XS,YS,beta,PCTVAR] = plsregress(X,y,10);

plot(1:10,cumsum(100*PCTVAR(2,:)),'-bo');
xlabel('Number of PLS components');
ylabel('Percent Variance Explained in y');
```



Choosing the number of components in a PLS model is a critical step. The plot gives a rough indication, showing nearly 80% of the variance in `y` explained by the first component, with as many as five additional components making significant contributions.

The following computes the six-component model:

```
[XL,yl,XS,YS,beta,PCTVAR,MSE,stats] = plsregress(X,y,6);
yfit = [ones(size(X,1),1) X]*beta;

plot(y,yfit,'o')
```



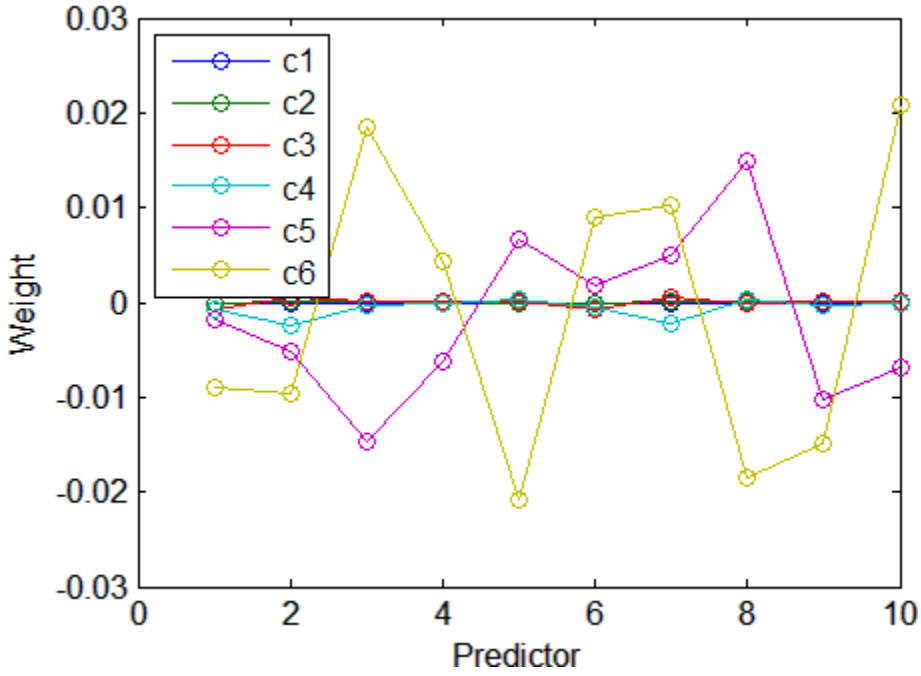
The scatter shows a reasonable correlation between fitted and observed responses, and this is confirmed by the R^2 statistic:

```
TSS = sum((y-mean(y)).^2);
RSS = sum((y-yfit).^2);
Rsquared = 1 - RSS/TSS
Rsquared =
    0.8421
```

A plot of the weights of the ten predictors in each of the six components shows that two of the components (the last two computed) explain the majority of the variance in X:

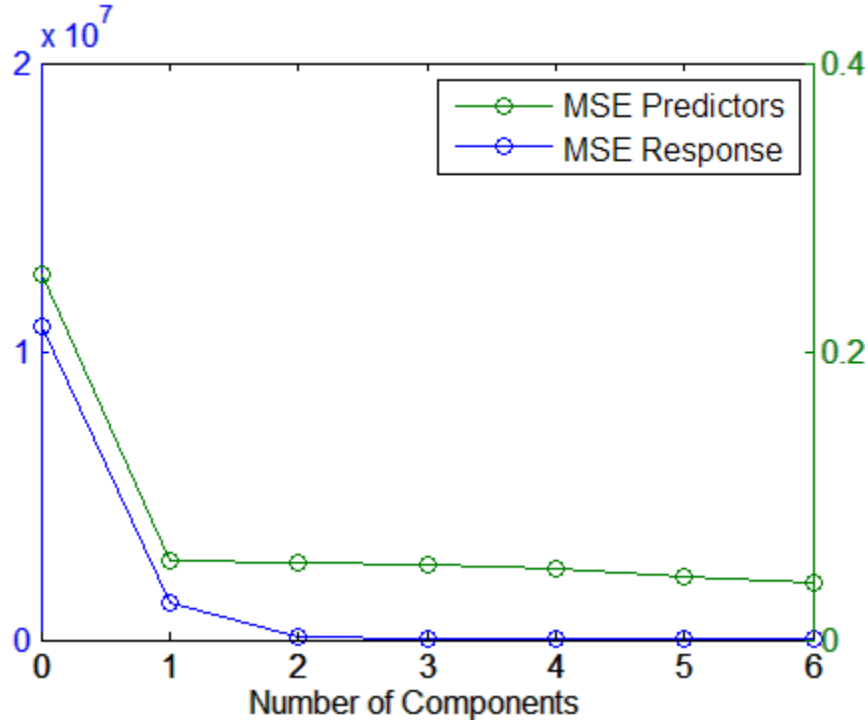
```
plot(1:10,stats.W,'o-');
```

```
legend({'c1','c2','c3','c4','c5','c6'},'Location','NW')
xlabel('Predictor');
ylabel('Weight');
```



A plot of the mean-squared errors suggests that as few as two components may provide an adequate model:

```
[axes,h1,h2] = plotyy(0:6,MSE(1,:),0:6,MSE(2,:));
set(h1,'Marker','o')
set(h2,'Marker','o')
legend('MSE Predictors','MSE Response')
xlabel('Number of Components')
```



The calculation of mean-squared errors by `plsregress` is controlled by optional parameter name/value pairs specifying cross-validation type and the number of Monte Carlo repetitions.

Linear Mixed-Effects Models

Linear mixed-effects models are extensions of linear regression models for data that are collected and summarized in groups. These models describe the relationship between a response variable and independent variables, with coefficients that can vary with respect to one or more grouping variables. A mixed-effects model consists of two parts, fixed effects and random effects. Fixed-effects terms are usually the conventional linear regression part, and the random effects are associated with individual experimental units drawn at random from a population. The random effects have prior distributions whereas fixed effects do not. Mixed-effects models can represent the covariance structure related to the grouping of data by associating the common random effects to observations that have the same level of a grouping variable. The standard form of a linear mixed-effects model is

$$y = \underbrace{X\beta}_{fixed} + \underbrace{Zb}_{random} + \underbrace{\varepsilon}_{error},$$

where

- y is the n-by-1 response vector, and n is the number of observations.
- X is an n-by-p fixed-effects design matrix.
- β is a p-by-1 fixed-effects vector.
- Z is an n-by-q random-effects design matrix.
- b is a q-by-1 random-effects vector.
- ε is the n-by-1 observation error vector.

The assumptions for the linear mixed-effects model are:

- Random-effects vector, b, and the error vector, ε, have the following prior distributions:

  $$b \sim N\left(0, \sigma^2 D(\theta)\right),$$
  $$\varepsilon \sim N\left(0, \sigma^2 I\right),$$

  where D is a symmetric and positive semidefinite matrix, parameterized by a variance component vector θ, I is an n-by-n identity matrix, and σ^2 is the error variance.

- Random-effects vector, b, and the error vector, ε, are independent from each other.

Mixed-effects models are also called *multilevel models* or *hierarchical models* depending on the context. Mixed-effects models is a more general term than the latter two. Mixed-effects models might include factors that are not necessarily multilevel or hierarchical, for example crossed factors. That is why mixed-effects is the terminology preferred here. Sometimes mixed-effects models are expressed as multilevel regression models (first level and grouping level models) that are fit simultaneously. For example, a varying or random intercept model, with one continuous predictor variable x and one grouping variable with M levels, can be expressed as

$$y_{im} = \beta_{0m} + \beta_1 x_{im} + \varepsilon_{im}, \quad i = 1,2,..,n, \quad m = 1,2,...,M, \quad \varepsilon_{im} \sim N\left(0,\sigma^2\right),$$
$$\beta_{0m} = \beta_{00} + b_{0m}, \quad b_{0m} \sim N\left(0,\sigma_0^2\right),$$

where y_{im} corresponds to data for observation i and group m, n is the total number of observations, and b_{0m} and ε_{im} are independent of each other. After substituting the group-level parameters in the first-level model, the model for the response vector becomes

$$y_{im} = \underbrace{\beta_{00} + \beta_1 x_{im}}_{\text{fixed effects}} + \underbrace{b_{0m}}_{\text{random effects}} + \varepsilon_{im}.$$

A random intercept and slope model with one continuous predictor variable x, where both the intercept and slope vary independently by a grouping variable with M levels is

$$y_{im} = \beta_{0m} + \beta_{1m} x_{im} + \varepsilon_{im}, \quad i = 1,2,...,n, \quad m = 1,2,...,M, \quad \varepsilon_{im} \sim N\left(0,\sigma^2\right),$$
$$\beta_{0m} = \beta_{00} + b_{0m}, \quad b_{0m} \sim N\left(0,\sigma_0^2\right),$$
$$\beta_{1m} = \beta_{10} + b_{1m}, \quad b_{1m} \sim N\left(0,\sigma_1^2\right),$$

or

$$b_m = \begin{pmatrix} b_{0m} \\ b_{1m} \end{pmatrix} \sim N\left(0, \begin{pmatrix} \sigma_0^2 & 0 \\ 0 & \sigma_1^2 \end{pmatrix}\right).$$

You might also have correlated random effects. In general, for a model with a random intercept and slope, the distribution of the random effects is

$$b_m = \begin{pmatrix} b_{0m} \\ b_{1m} \end{pmatrix} \sim N\left(0, \sigma^2 D(\theta)\right),$$

where D is a 2-by-2 symmetric and positive semidefinite matrix, parameterized by a variance component vector θ.

After substituting the group-level parameters in the first-level model, the model for the response vector is

$$y_{im} = \underbrace{\beta_{00} + \beta_{10} x_{im}}_{fixed\ effects} + \underbrace{b_{0m} + b_{1m} x_{im}}_{random\ effects} + \varepsilon_{im}, \quad i = 1,2,\ldots,n, \quad m = 1,2,\ldots,M.$$

If you express the group-level variable, x_{im}, in the random-effects term by z_{im}, this model is

$$y_{im} = \underbrace{\beta_{00} + \beta_{10} x_{im}}_{fixed\ effects} + \underbrace{b_{0m} + b_{1m} z_{im}}_{random\ effects} + \varepsilon_{im}, \quad i = 1,2,\ldots,n, \quad m = 1,2,\ldots,M.$$

In this case, the same terms appear in both the fixed-effects design matrix and random-effects design matrix. Each z_{im} and x_{im} correspond to the level m of the grouping variable.

It is also possible to explain more of the group-level variations by adding more group-level predictor variables. A random-intercept and random-slope model with one continuous predictor variable x, where both the intercept and slope vary independently by a grouping variable with M levels, and one group-level predictor variable v_m is

$$\begin{aligned} y_{im} &= \beta_{0im} + \beta_{1im} x_{im} + \varepsilon_{im}, \quad i = 1,2,\ldots,n, \quad m = 1,2,\ldots,M, \quad \varepsilon_{im} \sim N\left(0, \sigma^2\right), \\ \beta_{0im} &= \beta_{00} + \beta_{01} v_{im} + b_{0m}, \quad b_{0m} \sim N\left(0, \sigma_0^2\right), \\ \beta_{1im} &= \beta_{10} + \beta_{11} v_{im} + b_{1m}, \quad b_{1m} \sim N\left(0, \sigma_1^2\right). \end{aligned}$$

This model results in main effects of the group-level predictor and an interaction term between the first-level and group-level predictor variables in the model for the response variable as

$$\begin{aligned} y_{im} &= \beta_{00} + \beta_{01} v_{im} + b_{0m} + (\beta_{10} + \beta_{11} v_{im} + b_{1m}) x_{im} + \varepsilon_{im}, \quad i = 1,2,\ldots,n, \quad m = 1,2,\ldots,M, \\ &= \underbrace{\beta_{00} + \beta_{10} x_{im} + \beta_{01} v_{im} + \beta_{11} v_{im} x_{im}}_{\textit{fixed effects}} + \underbrace{b_{0m} + b_{1m} x_{im}}_{\textit{random effects}} + \varepsilon_{im}. \end{aligned}$$

The term $\beta_{11} v_m x_{im}$ is often called a cross-level interaction in many textbooks on multilevel models. The model for the response variable y can be expressed as

$$y_{im} = \begin{bmatrix} 1 & x_{1im} & v_{im} & v_{im} x_{1im} \end{bmatrix} \begin{bmatrix} \beta_{00} \\ \beta_{10} \\ \beta_{01} \\ \beta_{11} \end{bmatrix} + \begin{bmatrix} 1 & x_{1im} \end{bmatrix} \begin{bmatrix} b_{0m} \\ b_{1m} \end{bmatrix} + \varepsilon_{im}, \quad i = 1,2,\ldots,n, \quad m = 1,2,\ldots,M,$$

which corresponds to the standard form given earlier,

$$y = X\beta + Zb + \varepsilon.$$

In general, if there are R grouping variables, and $m(r,i)$ shows the level of grouping variable r, for observation i, then the model for the response variable for observation i is

$$y_i = x_i^T \beta + \sum_{r=1}^{R} z_{ir} b_{m(r,i)}^{(r)} + \varepsilon_i, \quad i = 1,2,\ldots,n,$$

where β is a p-by-1 fixed-effects vector, $b^{(r)}{}_{m(r,i)}$ is a $q(r)$-by-1 random-effects vector for the rth grouping variable and level $m(r,i)$, and ε_i is a 1-by-1 error term for observation i.

References

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[5] Gelman, A. and J. Hill. *Data Analysis Using Regression and Multilevel/Hierarchical Models*. New York, NY: Cambridge University Press, 2007.

See Also

`fitlme` | `fitlmematrix` | `LinearMixedModel`

More About

- "Prepare Data for Linear Mixed-Effects Models" on page 9-157

Prepare Data for Linear Mixed-Effects Models

In this section...

Tables and Dataset Arrays

To fit a linear-mixed effects model, you must store your data in a table or dataset array. In your table or dataset array, you must have a column for each variable including the response variable. More specifically, the table or dataset array, say `tbl`, must contain the following:

- A response variable y
- Predictive variables X_j which can be continuous or grouping variables
- Grouping variables g_1, g_2, ..., g_R,

where the grouping variables in X_j and g_r can be categorical, logical, character arrays, or a cell arrays of strings, $r = 1, 2, ..., R$.

You must organize your data so that each row represents an observation. And each row should contain the value of variables and the levels of grouping variables corresponding to that observation. For example, if you have data from an experiment with four treatment options, on five different types of individuals chosen randomly from a population of individuals (blocks), the table or dataset array must look like this.

Block	Treatment	Response
1	1	y11
1	2	y12
1	3	y13
1	4	y14
...	...	...
5	1	y51
5	2	y52

Block	Treatment	Response
5	3	y53
5	4	y54

Now, consider a split-plot experiment, where the effect of four different types of fertilizers on the yield of tomato plants is studied. The soil where the tomato plants are planted is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five types of tomato plants, (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. Then, the tomato plants in the plots are divided into subplots, where each subplot is treated by one of the four fertilizers. The data from this experiment looks like:

Soil	Tomato	Fertilizer	Yield
'Sandy'	'Plum'	1	104
'Sandy'	'Plum'	2	136
'Sandy'	'Plum'	3	158
'Sandy'	'Plum'	4	174
'Sandy'	'Cherry'	1	57
'Sandy'	'Cherry'	2	86
...	...	...	...
'Sandy'	'Vine'	3	99
'Sandy'	'Vine'	4	117
'Silty'	'Plum'	1	120
'Silty'	'Plum'	2	115
...	...	...	...
'Loamy'	'Vine'	3	111
'Loamy'	'Vine'	4	105

You must specify the model you want to fit using the `formula` input argument to `fitlme`.

In general, a formula for model specification is a string of the term `'y ~ terms'`. For linear mixed-effects models, this formula is in the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` contains the fixed-

effects terms and `random1, ..., randomR` contain the random-effects terms. For example, for the previous fertilizer experiment, consider the following mixed-effects model

$$y_{imjk} = \beta_0 + \sum_{m=2}^{4} \beta_{1m} I[F]_{im} + \sum_{j=2}^{5} \beta_{2j} I[T]_{ij} + b_{0k} S_k + b_{0jk} (S * T)_{jk} + \varepsilon_{imjk},$$

where i = 1, 2, ..., 60, the index m corresponds to the fertilizer types, j corresponds to the tomato types, and k = 1, 2, 3 corresponds to the blocks (soil). S_k represents the kth soil type, and $I[F]_{im}$ is the dummy variable representing level m of the fertilizer. Similarly, $I[T]_{ij}$ is the dummy variable representing the level j of the tomato type.

You can fit this model using the formula `'Yield ~ 1 + Fertilizer + Tomato + (1|Soil)+(1|Soil:Tomato)'`.

For detailed information on how to specify your model using formula, see "Relationship Between Formula and Design Matrices" on page 9-163.

Design Matrices

If you cannot easily describe your model using a formula, you can create design matrices to define the fixed and random effects, and fit the model using `fitlmematrix(X,y,Z,G)`. You must create your design matrices as follows.

Fixed-effects and random-effects design matrices `X` and `Z`:

- Enter a column of 1s for the intercept using `ones(n,1)`, where n is the total number of observations.
- If `X1` is a continuous variable, then enter `X1` as it is in a separate column.
- If `X1` is a categorical variable with m levels, then there must be $m - 1$ dummy variables for $m - 1$ levels of `X1` in `X`.

  For example, consider an experiment where you want to study the impact of quality of raw materials from four different providers on the productivity of a production line. If you fit a linear mixed-effects model with intercept and provider as the fixed-effects terms, intercept is the random-effects term, and you use reference contrasts coding, then you must construct your fixed- and random-effects design matrices as follows.

  ```
  D = dummyvar(provider); % Create dummy variables
  ```

```
X = [ones(n,1) D(:,2) D(:,3) D(:,4)];
Z = [ones(n,1)];
```

Because reference contrast coding uses the first provider as the reference, and the model has an intercept, you must use the dummy variables for only the last three providers.

- If there is an interaction term of predictor variables `X1` and `X2`, then you must enter a column that you form by elementwise product of the vectors `X1` and `X2`.

  For example, if you want to fit a model, where there is an intercept, a continuous treatment factor, a continuous time factor, and their interaction as the fixed-effects in a longitudinal study, and time is the random-effects term, then your fixed- and random-effects design matrices should look like

  ```
  X = [ones(n,1),treatment,time,treatment.*time];
  y = response;
  Z = [time];
  ```

Grouping variables `G`:

There is one column for each grouping variable and a column of elementwise product of the grouping variables in case of a nesting.

For example, if you want to group plots (`plot`) within blocks (`block`), then you must add a column of elementwise product of `plot` by `block`. More specifically, if you want to fit a model where there is intercept and a continuous treatment factor as the fixed-effects in a split-block experiment, and the intercept and treatment are grouped by the plots nested within blocks, then the design matrices should look like this.

```
X = [ones(n,1),treatment];
y = response;
Z = [ones(n,1),treatment];
G = [block.*plot];
```

Suppose in the earlier quality of raw materials example, the raw materials arrive in bulks, and the bulks are nested within providers. If you want to fit a linear mixed-effects model, where intercept is grouped by the bulks within providers, then your design matrices should look like this.

```
D = dummyvar(provider);
X = [ones(n,1) D(:,2) D(:,3) D(:,4)];
y = response;
Z = ones(n,1);
```

```
G = [provider.*bulks];
```

In the earlier longitudinal study example, if you want to add random effects for intercept and time grouped by subjects that participated in the study, then your design matrices should look like

```
X = [ones(n,1),treatment,time, treatment.*time];
y = response;
Z = [ones(n,1),time];
G = subject;
```

Relation of Matrix Form to Tables and Dataset Arrays

`fitlme(tbl,formula)` and `fitlmematrix(X,y,Z,G)` are equivalent in functionality, such that

- `y` is the n-by-1 response vector.
- `X` is an n-by-p fixed-effects design matrix. `fitlme` constructs this from the expression `fixed` in `formula`.
- `Z` is an R-by-1 cell array with `Z{r}` being an n-by-$q(r)$ random-effects design matrix constructed from the rth expression in `random` in `formula`, $r = 1, 2, ..., R$.
- `G` is an R-by-1 cell array with `G{r}` being an n-by-1 grouping variable, g_r, in `formula` with $M(r)$ levels or groups.

For example, if `tbl` is a table or dataset array containing the response variable `y`, the continuous variables `X1` and `X2`, and the grouping variable `g`, then to fit a linear mixed-effects model that corresponds to the formula expression `'y ~ X1+ X2+ (X1*X2|g)'` using `fitlmematrix(X,y,Z,G)` the input arguments must correspond to the following:

```
y = tbl.y
X = [ones(n,1), tbl.X1, tbl.X2]
Z = [ones(n,1), tbl.X1, tbl.X2, tbl.X1.*tbl.X2]
G = ds.g
```

See Also

`fitlme` | `fitlmematrix` | `LinearMixedModel`

More About

- “Linear Mixed-Effects Models” on page 9-152

- “Relationship Between Formula and Design Matrices” on page 9-163

Relationship Between Formula and Design Matrices

In this section...

Formula

In general, a formula for model specification is a string of the form `'y ~ terms'`. For the linear mixed-effects models, this formula is in the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` and `random` contain the fixed-effects and the random-effects terms.

Suppose a table `tbl` contains the following:

- A response variable, `y`
- Predictor variables, X_j, which can be continuous or grouping variables
- Grouping variables, g_1, g_2, ..., g_R,

where the grouping variables in X_j and g_r can be categorical, logical, character arrays, or cell arrays of strings.

Then, in a formula of the form, `'y ~ fixed + (random`$_1$`|`g_1`) + ... + (random`$_R$`|`g_R`)'`, the term `fixed` corresponds to a specification of the fixed-effects design matrix `X`, `random`$_1$ is a specification of the random-effects design matrix Z_1 corresponding to grouping variable g_1, and similarly `random`$_R$ is a specification of the random-effects design matrix Z_R corresponding to grouping variable g_R. You can express the `fixed` and `random` terms using Wilkinson notation.

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
1	Constant (intercept) term

Wilkinson Notation	Factors in Standard Notation
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1.*X2 (elementwise multiplication of X1 and X2)`
`X1:X2`	`X1.*X2` only
`- X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`. Here are some examples for linear mixed-effects model specification.

Examples:

Formula	Description
`'y ~ X1 + X2'`	Fixed effects for the intercept, `X1` and `X2`. This is equivalent to `'y ~ 1 + X1 + X2'`.
`'y ~ -1 + X1 + X2'`	No intercept and fixed effects for `X1` and `X2`. The implicit intercept term is suppressed by including `-1`.
`'y ~ 1 + (1 | g1)'`	Fixed effects for the intercept plus random effect for the intercept for each level of the grouping variable `g1`.
`'y ~ X1 + (1 | g1)'`	Random intercept model with a fixed slope.
`'y ~ X1 + (X1 | g1)'`	Random intercept and slope, with possible correlation between them. This is equivalent to `'y ~ 1 + X1 + (1 + X1| g1)'`.
`'y ~ X1 + (1 | g1) + (-1 + X1 | g1)'`	Independent random effects terms for intercept and slope.

Formula	Description
`'y ~ 1 + (1 | g1) + (1 | g2) + (1 | g1:g2)'`	Random intercept model with independent main effects for `g1` and `g2`, plus an independent interaction effect.

Design Matrices for Fixed and Random Effects

`fitlme` converts the expressions in the `fixed` and `random` parts (not grouping variables) of a formula into design matrices as follows:

- Each term in a formula adds one or more columns to the corresponding design matrix.
- A term containing a single continuous variable adds one column to the design matrix.
- A fixed term containing a categorical variable `X` with k levels adds $(k - 1)$ dummy variables to the design matrix.

  For example, if the variable `Supplier` represents three different suppliers a manufacturer receives parts from, i.e. a categorical variable with three levels, and out of six batches of parts, the first two batches come from supplier 1 (level 1), the second two batches come from supplier 2 (level 2), and the last two batches come from supplier 3 (level 3), such as

  ```
  Supplier =

       1
       1
       2
       2
       3
       3
  ```

  Then, adding `Supplier` to the formula as a fixed-effects or random-effects term adds the following two dummy variables to the corresponding design matrix, using the `'reference'` contrast:

  ```
   0     0
   0     0
   1     0
   1     0
   0     1
   0     1
  ```

For more details on dummy variables, see "Dummy Indicator Variables" on page 2-55. For other contrast options, see the `'DummyVarCoding'` name-value pair argument of `fitlme`.

- If `X1` and `X2` are continuous variables, the product term `X1:X2` adds one column obtained by elementwise multiplication of `X1` and `X2` to the design matrix.
- If `X1` is continuous and `X2` is categorical with k levels, the product term `X1:X2` multiplies elementwise `X1` with the $(k-1)$ dummy variables representing `X2`, and adds these $(k-1)$ columns to the design matrix.

  For example, if `Drug` is the amount of a drug given to patients, a continuous treatment, and `Time` is three distinct points in time when the health measures are taken, a categorical variable with three levels, and out of nine observations, the first three are observed at time point 1, the second three are observed at time point 2, and the last three are observed at time point 3 so that

```
[Drug Time] =

    0.1000    1.0000
    0.2000    1.0000
    0.5000    2.0000
    0.6000    2.0000
    0.3000    3.0000
    0.8000    3.0000
```

  Then, the product term `Drug:Time` adds the following two variables to the design matrix:

```
     0          0
     0          0
0.5000          0
0.6000          0
     0     0.3000
     0     0.8000
```

- If `X1` and `X2` are categorical variables with k and m levels respectively, the product term `X1:X2` adds $(k-1)*(m-1)$ dummy variables to the design matrix formed by taking the elementwise product of each dummy variable representing `X1` with each dummy variable representing `X2`.

  For example, in an experiment to determine the impact of the type of corn and the popping method on the yield, suppose there are three types of `Corn` and two types of `Method` as follows:

```
1    oil
1    oil
1    air
1    air
2    oil
2    oil
2    air
2    air
3    oil
3    oil
3    air
3    air
```

Then, the interaction term `Corn:Method` adds the following to the design matrix:

```
 0     0
 0     0
 0     0
 0     0
 1     0
 1     0
 0     0
 0     0
 0     1
 0     1
 0     0
 0     0
```

- The term `X1*X2` adds the necessary number of columns for `X1`, `X2`, and `X1:X2` to the design matrix.
- The term `X1^2` adds the necessary number of columns for `X1` and `X1:X1` to the design matrix.
- The symbol `1` (one) in the formula stands for a column of all 1s. By default a column of 1s is included in the design matrix. To exclude a column of ones from the design matrix, you must explicitly specify `−1` as a term in the expression.

Grouping Variables

`fitlme` handles the grouping variables in the `(.|group)` part of a formula as follows:

- If a grouping variable has k levels, then k dummy variables represent this grouping.

For example, suppose `District` is a categorical grouping variable with three levels, showing the three types of districts, and out of six schools, the first two are in district 1, the second two are in district 2, and the last two are in district 3, so that

```
District =

     1
     1
     2
     2
     3
     3
```

Then, the dummy variables that represent this grouping are:

```
  1     0     0
  1     0     0
  0     1     0
  0     1     0
  0     0     1
  0     0     1
```

- If `X1` is a continuous random-effects variable and `X2` is a grouping variable with k levels, then the random term `(X1 – 1|X2)` multiplies elementwise `X1` with the k dummy variables representing `X2` and adds these k columns to the random-effects design matrix.

  For example, suppose `Score` is a continuous variable showing the scores of students from a math exam in a school, and `Class` is a categorical variable with three levels, showing the three different classes in a school. Also, suppose out of nine observations first three correspond to the scores of students in the first class, the second three correspond to scores of students in the second class, and the last three correspond to the scores of students in the third class, such as

  ```
  [Score Class] =

      78.0000    1.0000
      68.0000    1.0000
      81.0000    2.0000
      53.0000    2.0000
      85.0000    3.0000
      72.0000    3.0000
  ```

  Then, the random term `(Score – 1|Class)` adds the following three columns to the random-effects design matrix:

```
   78.0000         0         0
   68.0000         0         0
         0   81.0000         0
         0   53.0000         0
         0         0   85.0000
         0         0   72.0000
```

- If `X1` is a continuous predictor variable and `X2` and `X3` are grouping variables with k and m levels respectively, the term `(X1|X2:X3)` represents this grouping of `X1` with $k*m$ dummy variables formed by taking the elementwise product of each dummy variable representing `X2` with each dummy variable representing `X3`.

  For example, suppose `Treatment` is a continuous predictor variable, and there are three levels of `Block` and two levels of `Plot` nested within the block as follows:

```
   0.1000    1    a
   0.2000    1    b
   0.5000    2    a
   0.6000    2    b
   0.3000    3    a
   0.8000    3    b
```

  Then, the random term `(Treatment – 1|Block:Plot)` adds the following to the random-effects design matrix:

```
   0.1000         0         0         0         0         0
         0   0.2000         0         0         0         0
         0         0   0.5000         0         0         0
         0         0         0   0.6000         0         0
         0         0         0         0   0.3000         0
         0         0         0         0         0   0.8000
```

See Also

`fitlme` | `fitlmematrix` | `LinearMixedModel`

More About

- “Prepare Data for Linear Mixed-Effects Models” on page 9-157

Estimating Parameters in Linear Mixed-Effects Models

In this section...

A linear mixed-effects model is of the form

$$y = \underbrace{X\beta}_{fixed} + \underbrace{Zb}_{random} + \underbrace{\varepsilon}_{error},$$

where

- y is the n-by-1 response vector, and n is the number of observations.
- X is an n-by-p fixed-effects design matrix.
- β is a p-by-1 fixed-effects vector.
- Z is an n-by-q random-effects design matrix.
- b is a q-by-1 random-effects vector.
- ε is the n-by-1 observation error vector.

The random-effects vector, b, and the error vector, ε, are assumed to have the following independent prior distributions:

$$b \sim N\left(0, \sigma^2 D(\theta)\right),$$
$$\varepsilon \sim N\left(0, \sigma^2 I\right),$$

where D is a symmetric and positive semidefinite matrix, parameterized by a variance component vector θ, I is an n-by-n identity matrix, and σ^2 is the error variance.

In this model, the parameters to estimate are the fixed-effects coefficients β, and the variance components θ and ε. The two most commonly used approaches to parameter estimation in linear mixed-effects models are maximum likelihood and restricted maximum likelihood methods.

Maximum Likelihood (ML)

The maximum likelihood estimation includes both regression coefficients and the variance components, that is, both fixed-effects and random-effects terms in the likelihood function.

For a linear mixed-effects model defined above, the conditional response of the response variable y given β, b, θ, and σ^2 is

$$y \mid b,\beta,\theta,\sigma^2 \sim N\left(X\beta + Zb, \sigma^2 I_n\right).$$

The likelihood of y given β, θ, and σ^2 is

$$P\left(y \mid \beta,\theta,\sigma^2\right) = \int P\left(y \mid b,\beta,\theta,\sigma^2\right) P\left(b \mid \theta,\sigma^2\right) db,$$

where

$$P\left(b \mid \theta,\sigma^2\right) = \frac{1}{\left(2\pi\sigma^2\right)^{q/2}} \frac{1}{\left|D(\theta)\right|^{1/2}} \exp\left\{-\frac{1}{2\sigma^2} b^T D^{-1} b\right\} \quad \text{and}$$

$$P\left(y \mid b,\beta,\theta,\sigma^2\right) = \frac{1}{\left(2\pi\sigma^2\right)^{n/2}} \exp\left\{-\frac{1}{2\sigma^2}(y - X\beta - Zb)^T (y - X\beta - Zb)\right\}.$$

Suppose $\Lambda(\theta)$ is the lower triangular Cholesky factor of $D(\theta)$ and $\Delta(\theta)$ is the inverse of $\Lambda(\theta)$. Then,

$$D(\theta)^{-1} = \Delta(\theta)^T \Delta(\theta).$$

Define

$$r^2(\beta,b,\theta) = b^T \Delta(\theta)^T \Delta(\theta) b + (y - X\beta - Zb)^T (y - X\beta - Zb),$$

and suppose b^* is the value of b that satisfies

$$\left.\frac{\partial r^2(\beta,b,\theta)}{\partial b}\right|_{b^*} = 0$$

for given β and θ. Then, the likelihood function is

$$P\left(y \mid \beta,\theta,\sigma^2\right) = \left(2\pi\sigma^2\right)^{-n/2}\left|D(\theta)\right|^{-1/2}\exp\left\{-\frac{1}{2\sigma^2}r^2\left(\beta,b^*(\beta),\theta\right)\right\}\frac{1}{\left|\Delta^T\Delta + Z^TZ\right|^{1/2}}.$$

$P(y \mid \beta,\theta,\sigma^2)$ is first maximized with respect to β and σ^2 for a given θ. Thus the optimized solutions $\hat{\beta}(\theta)$ and $\hat{\sigma}^2(\theta)$ are obtained as functions of θ. Substituting these solutions into the likelihood function produces $P\left(y \mid \beta(\theta),\theta,\sigma^2(\theta)\right)$. This expression is called a profiled likelihood where β and σ^2 have been profiled out. $P\left(y \mid \beta(\theta),\theta,\sigma^2(\theta)\right)$ is a function of θ, and the algorithm then optimizes it with respect to θ. Once it finds the optimal estimate of θ, the estimates of β and σ^2 are given by $\hat{\beta}(\theta)$.

The ML method treats β as fixed but unknown quantities when the variance components are estimated, but does not take into account the degrees of freedom lost by estimating the fixed effects. This causes ML estimates to be biased with smaller variances. However, one advantage of ML over REML is that it is possible to compare two models in terms of their fixed- and random-effects terms. On the other hand, if you use REML to estimate the parameters, you can only compare two models, that are nested in their random-effects terms, with the same fixed-effects design.

Restricted Maximum Likelihood (REML)

Restricted maximum likelihood estimation includes only the variance components, that is, the parameters that parameterize the random-effects terms in the linear mixed-effects model. β is estimated in a second step. Assuming a uniform improper prior distribution for β and integrating the likelihood $P(y \mid \beta,\theta,\sigma^2)$ with respect to β results in the restricted likelihood $P(y \mid \theta,\sigma^2)$. That is,

$$P\left(y \mid \theta,\sigma^2\right) = \int P\left(y \mid \beta,\theta,\sigma^2\right)P(\beta)d\beta = \int P\left(y \mid \beta,\theta,\sigma^2\right)d\beta.$$

The algorithm first profiles out $\hat{\sigma}_R^2$ and maximizes remaining objective function with respect to θ to find $\hat{\theta}_R$. The restricted likelihood is then maximized with respect to σ^2 to find $\hat{\sigma}_R^2$. Then, it estimates β by finding its expected value with respect to the posterior distribution

$$P\left(\beta \mid y, \theta_R, \sigma_R^2\right).$$

REML accounts for the degrees of freedom lost by estimating the fixed effects, and makes a less biased estimation of random effects variances. The estimates of θ and σ^2 are invariant to the value of β and less sensitive to outliers in the data compared to ML estimates. However, if you use REML to estimate the parameters, you can only compare two models that have the identical fixed-effects design matrices and are nested in their random-effects terms.

References

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[3] Raudenbush, S. W. and A. S. Bryk. *Hierarchical Linear Models: Applications and Data Analysis Methods*, 2nd ed. Thousand Oaks, CA: Sage Publications, 2002.

[4] Hox, J. *Multilevel Analysis, Techniques and Applications*. Lawrence Erlbaum Associates, Inc, 2002.

[5] Snidjers, T. and R. Bosker. *Multilevel Analysis*. Thousand Oaks, CA: Sage Publications, 1999.

[6] McCulloch, C.E., R. S. Shayle, and J. M. Neuhaus. *Generalized, Linear, and Mixed Models*. Wiley, 2008.

See Also

`fitlme` | `fitlmematrix` | `LinearMixedModel`

More About

- “Linear Mixed-Effects Models” on page 9-152

Linear Mixed-Effects Model Workflow

This example shows how to fit and analyze a linear mixed-effects model (LME).

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables containing estimated influenza rates (in 9 different regions, estimated from Google® searches, plus a nationwide estimate from the CDC).

Reorganize and plot the data.

To fit a linear-mixed effects model, your data must be in a properly formatted dataset array. To fit a linear mixed-effects model with the influenza rates as the responses, combine the nine columns corresponding to the regions into a tall array. The new dataset array, `flu2`, must have the response variable `FluRate`, the nominal variable `Region` that shows which region each estimate is from, the nationwide estimate `WtdILI`, and the grouping variable `Date`.

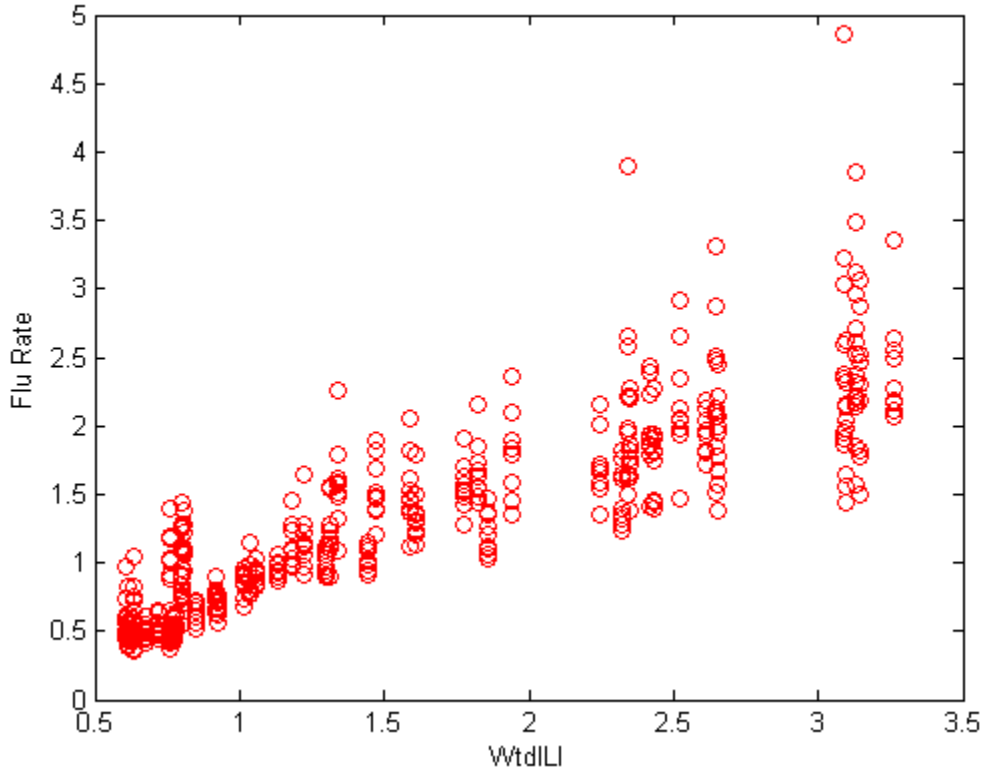
```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Define `flu2` as a `table`.

```
flu2 = dataset2table(flu2);
```

Plot flu rates versus the nationwide estimate.

```
plot(flu2.WtdILI,flu2.FluRate,'ro')
xlabel('WtdILI')
ylabel('Flu Rate')
```



You can see that the flu rates in regions have a direct relationship with the nationwide estimate.

Fit an LME model and interpret the results.

Fit a linear mixed-effects model with the nationwide estimate as the predictor variable and a random intercept that varies by `Date`.

```
lme = fitlme(flu2,'FluRate ~ 1 + WtdILI + (1|Date)')
```

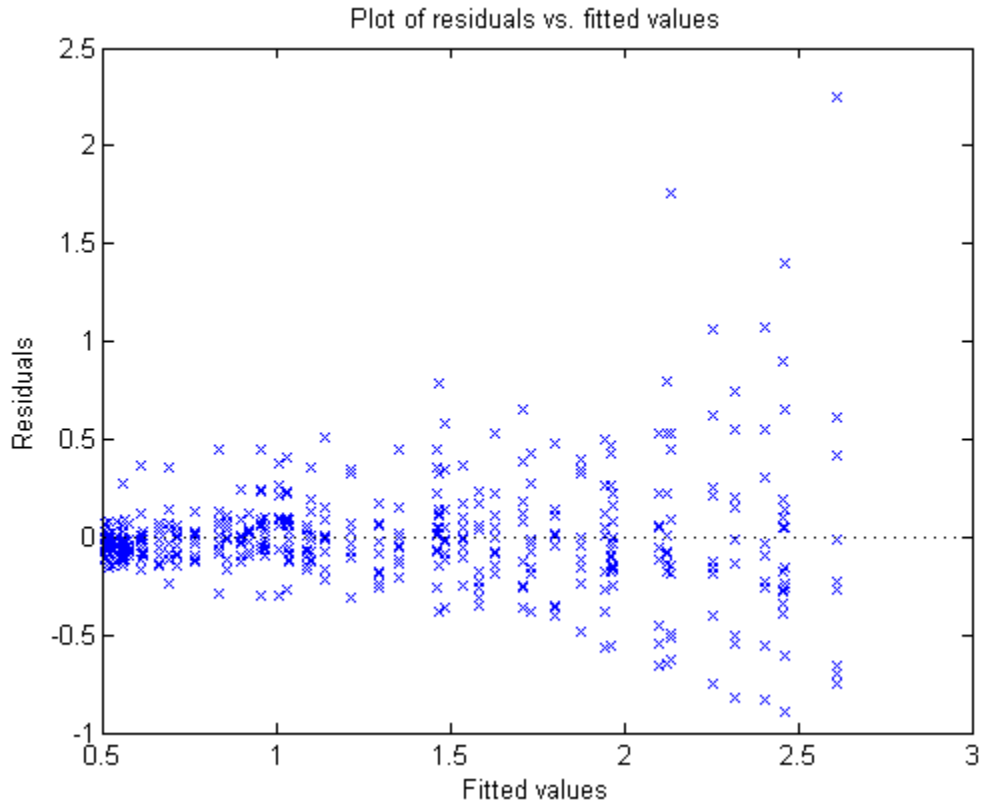
```
lme =


Linear mixed-effects model fit by ML
```

```
Model information:
    Number of observations             468
    Fixed effects coefficients           2
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    FluRate ~ 1 + WtdILI + (1 | Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    286.24    302.83    -139.12          278.24

Fixed effects coefficients (95% CIs):
    Name                 Estimate    SE          tStat     DF     pValue        Lower
    '(Intercept)'        0.16385     0.057525    2.8484    466     0.0045885    0.0508
    'WtdILI'              0.7236     0.032219    22.459    466    3.0502e-76     0.660

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1                Name2                Type         Estimate    Lower      Upper
    '(Intercept)'        '(Intercept)'        'std'        0.17146     0.13227    0.222

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.30201     0.28217    0.32324
```

The small p-values of 0.0045885 and 3.0502e-76 indicate that both the intercept and nationwide estimate are significant. Also, the confidence limits for the standard deviation of the random-effects term, σ_b, do not include 0 (0.13227, 0.22226), which indicates that the random-effects term is significant.

Plot the raw residuals versus the fitted values.

```
figure();
plotResiduals(lme,'fitted')
```



The variance of residuals increases with increasing fitted response values, which is known as heteroscedasticity.

Find the two observations on the top right that appear like outliers.

```
find(residuals(lme) > 1.5)
```

```
ans =

    98
   107
```

Refit the model by removing these observations.

```
lme = fitlme(flu2,'FluRate ~ 1 + WtdILI + (1|Date)','Exclude',[98,107]);
```

Improve the model.

Determine if including an independent random term for the nationwide estimate grouped by `Date` improves the model.

```
altlme = fitlme(flu2,'FluRate ~ 1 + WtdILI + (1|Date) + (WtdILI-1|Date)',...
'Exclude',[98,107])
```

```
altlme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             466
    Fixed effects coefficients           2
    Random effects coefficients        104
    Covariance parameters                3

Formula:
    FluRate ~ 1 + WtdILI + (1 | Date) + (WtdILI | Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    179.39    200.11    -84.694          169.39

Fixed effects coefficients (95% CIs):
    Name                Estimate    SE          tStat     DF     pValue       Lower
    '(Intercept)'       0.17837     0.054585    3.2676    464     0.001165     0.0711
    'WtdILI'            0.70836     0.030594    23.153    464    2.123e-79    0.64824

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1               Name2               Type         Estimate    Lower      Upper
    '(Intercept)'       '(Intercept)'       'std'        0.16631     0.12977    0.213

Group: Date (52 Levels)
    Name1           Name2           Type         Estimate      Lower    Upper
    'WtdILI'        'WtdILI'        'std'        4.7264e-08    NaN      NaN

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.26691     0.24934    0.28572
```

The estimated standard deviation of `WtdILI` term is nearly 0 and its confidence interval cannot be computed. This is an indication that the model is overparameterized and the `(WtdILI-1|Date)` term is not significant. You can formally test this using the `compare` method as follows: `compare(lme,altlme,'CheckNesting',true)`.

Add a random effects-term for intercept grouped by Region to the initial model `lme`.

```
lme2 = fitlme(flu2,'FluRate ~ 1 + WtdILI + (1|Date) + (1|Region)',...
'Exclude',[98,107]);
```

Compare the models `lme` and `lme2`.

```
compare(lme,lme2,'CheckNesting',true)
```

```
ans =


    Theoretical Likelihood Ratio Test

    Model    DF    AIC       BIC       LogLik     LRStat    deltaDF    pValue
    lme      4     177.39    193.97    -84.694
    lme2     5     62.265    82.986    -26.133    117.12    1          0
```

The *p*-value of 0 indicates that `lme2` is a better fit than `lme`.

Now, check if adding a potentially correlated random-effects term for the intercept and national average improves the model `lme2`.

```
lme3 = fitlme(flu2,'FluRate ~ 1 + WtdILI + (1|Date) + (1 + WtdILI|Region)',...
'Exclude',[98,107])
```

```
lme3 =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             466
    Fixed effects coefficients           2
    Random effects coefficients         70
    Covariance parameters                5

Formula:
    FluRate ~ 1 + WtdILI + (1 | Date) + (1 + WtdILI | Region)
```

```
Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    13.338    42.348    0.33076          -0.66153

Fixed effects coefficients (95% CIs):
    Name                Estimate    SE          tStat     DF     pValue         Lower
    '(Intercept)'        0.1795     0.054953    3.2665    464     0.0011697     0.0715
    'WtdILI'            0.70719      0.04252    16.632    464    4.6451e-49      0.623

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1               Name2               Type         Estimate    Lower      Upper
    '(Intercept)'       '(Intercept)'       'std'        0.17634     0.14093    0.220

Group: Region (9 Levels)
    Name1               Name2               Type          Estimate     Lower
    '(Intercept)'       '(Intercept)'       'std'         0.0077037    3.2273e-16
    'WtdILI'            '(Intercept)'       'corr'        -0.059604      -0.99996
    'WtdILI'            'WtdILI'            'std'          0.088069      0.051693

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.20976     0.19568    0.22486
```

The estimate for the standard deviation of the random-effects term for intercept grouped by Region is 0.0077037, its confidence interval is very large and includes zero. This indicates that the random-effects for intercept grouped by Region is insignificant. The correlation between the random-effects for intercept and `WtdILI` is –0.059604. Its confidence interval is also very large and includes zero. This is an indication that the correlation is not significant.

Refit the model by eliminating the intercept from the `(1 + WtdILI | Region)` random-effects term.

```
lme3 = fitlme(flu2,'FluRate ~ 1 + WtdILI + (1|Date) + (WtdILI - 1|Region)',...
'Exclude',[98,107])
```

```
lme3 =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             466
```

```
    Fixed effects coefficients           2
    Random effects coefficients         61
    Covariance parameters                3

Formula:
    FluRate ~ 1 + WtdILI + (1 | Date) + (WtdILI | Region)

Model fit statistics:
    AIC       BIC      LogLikelihood    Deviance
    9.3395    30.06    0.33023          -0.66046

Fixed effects coefficients (95% CIs):
    Name                 Estimate    SE          tStat     DF     pValue         Lower
    '(Intercept)'         0.1795     0.054892    3.2702    464     0.0011549     0.0716
    'WtdILI'             0.70718     0.042486    16.645    464    4.0496e-49     0.623

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1                Name2                Type         Estimate    Lower      Upper
    '(Intercept)'        '(Intercept)'        'std'        0.17633     0.14092    0.22

Group: Region (9 Levels)
    Name1           Name2           Type         Estimate    Lower       Upper
    'WtdILI'        'WtdILI'        'std'        0.087925    0.054474    0.14192

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.20979     0.19585    0.22473
```

All terms in the new model `lme3` are significant.

Compare `lme2` and `lme3`.

```
compare(lme2,lme3,'CheckNesting',true,'NSim',100)
```

```
ans =


    Simulated Likelihood Ratio Test: Nsim = 100, Alpha = 0.05

    Model    DF    AIC       BIC       LogLik     LRStat    pValue      Lower          U
    lme2     5     62.265    82.986    -26.133
    lme3     5     9.3395     30.06    0.33023    52.926    0.009901    0.00025064     0
```

The p-value of 0.009901 indicates that `lme3` is a better fit than `lme2`.

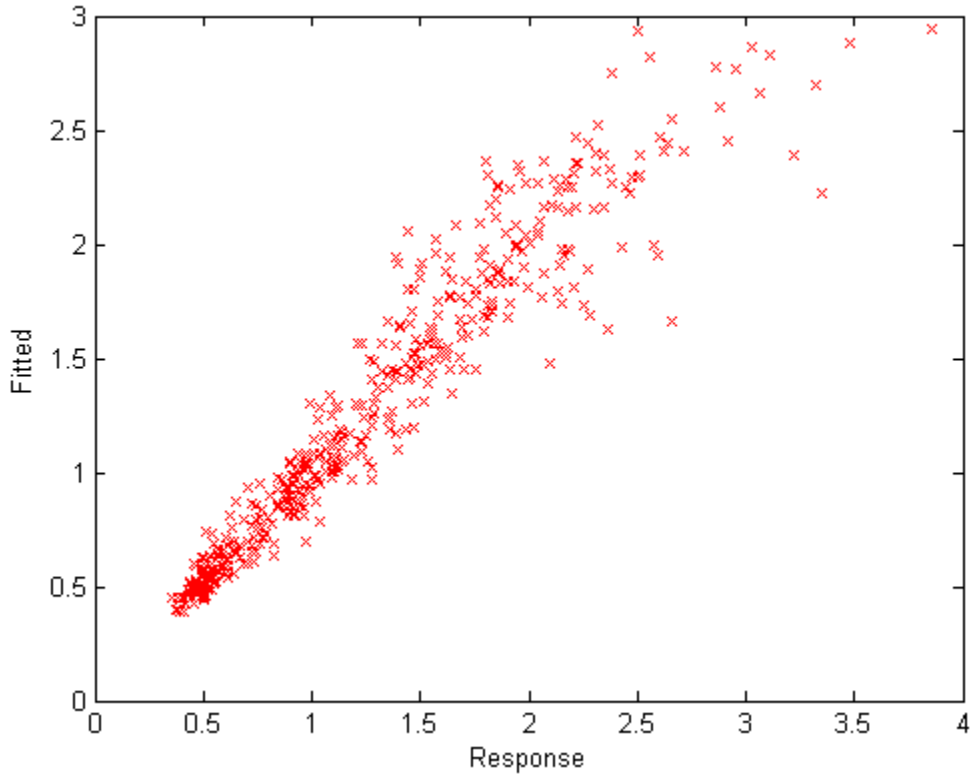
Add a quadratic fixed-effects term to the model `lme3`.

```
lme4 = fitlme(flu2,'FluRate ~ 1 + WtdILI^2 + (1|Date) + (WtdILI - 1|Region)',...
'Exclude',[98,107])

lme4 =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             466
    Fixed effects coefficients           3
    Random effects coefficients         61
    Covariance parameters                3

Formula:
    FluRate ~ 1 + WtdILI + WtdILI^2 + (1 | Date) + (WtdILI | Region)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    6.7234    31.588    2.6383           -5.2766

Fixed effects coefficients (95% CIs):
    Name                 Estimate     SE         tStat       DF     pValue        Lower
    '(Intercept)'        -0.063406    0.12236    -0.51821    463       0.60456    -0.30
    'WtdILI'                1.0594    0.16554      6.3996    463    3.8232e-10     0.73
    'WtdILI^2'           -0.096919     0.0441     -2.1977    463      0.028463    -0.18

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1                Name2                Type         Estimate    Lower      Upper
    '(Intercept)'        '(Intercept)'        'std'        0.16732     0.13326    0.210

Group: Region (9 Levels)
    Name1           Name2           Type         Estimate    Lower       Upper
    'WtdILI'        'WtdILI'        'std'        0.087865    0.054443    0.1418

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.20979     0.19585    0.22473
```

The p-value of 0.028463 indicates that the coefficient of the quadratic term `WtdILI^2` is significant.

Plot the fitted response versus the observed response and residuals.

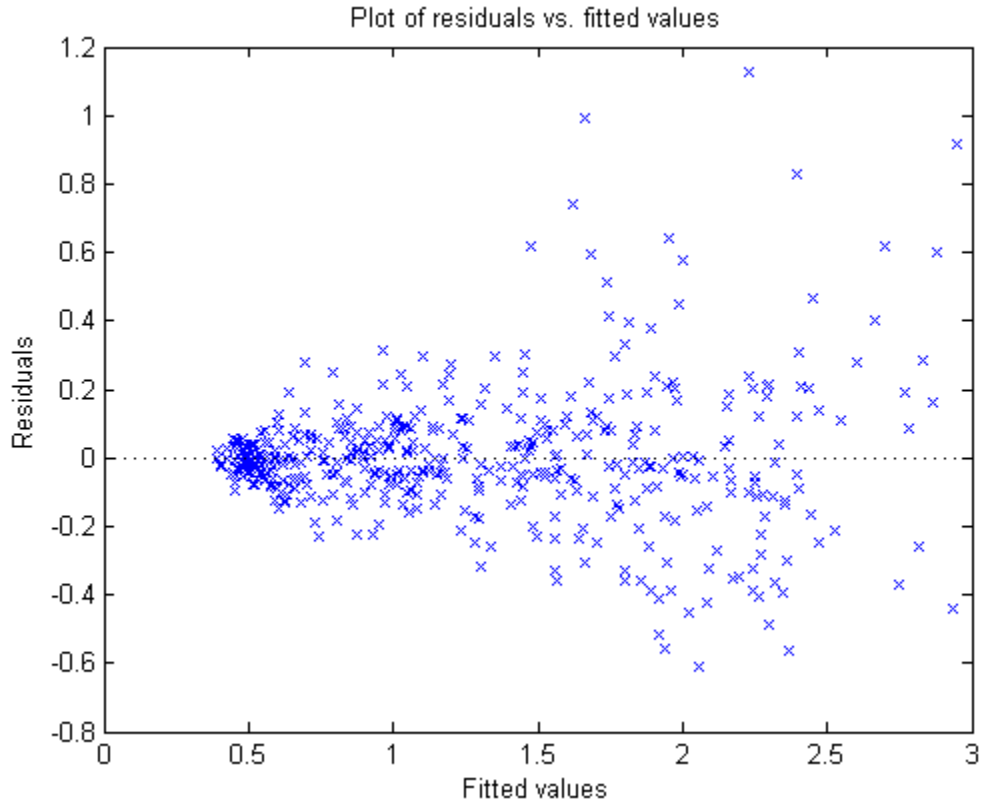
```
F = fitted(lme4);
R = response(lme4);
figure();
plot(R,F,'rx')
xlabel('Response')
ylabel('Fitted')
```



The fitted versus observed response values form almost 45-degree angle indicating a good fit.

Plot the residuals versus the fitted values.

```
figure();
plotResiduals(lme4,'fitted')
```



Although it has improved, you can still see some heteroscedasticity in the model. This might be due to another predictor that does not exist in the data set, hence not in the model.

Find the fitted flu rate value for region ENCentral, date 11/6/2005.

```
F(flu2.Region == 'ENCentral' & flu2.Date == '11/6/2005')
```

```
ans =

    1.4860
```

Randomly generate response values.

Randomly generate response values for a national estimate of 1.625, region MidAtl, and date 4/23/2006. First, define the new table. Because Date and Region are nominal in the original table, you must define them similarly in the new table.

```
tblnew.Date = nominal('4/23/2006');
tblnew.WtdILI = 1.625;
tblnew.Region = nominal('MidAtl');
tblnew = struct2table(tblnew);
```

Now, generate the response value.

```
random(lme4,tblnew)
```

```
ans =

    1.5048
```

Fit Mixed-Effects Spline Regression

This example shows how to fit a mixed-effects linear spline model.

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

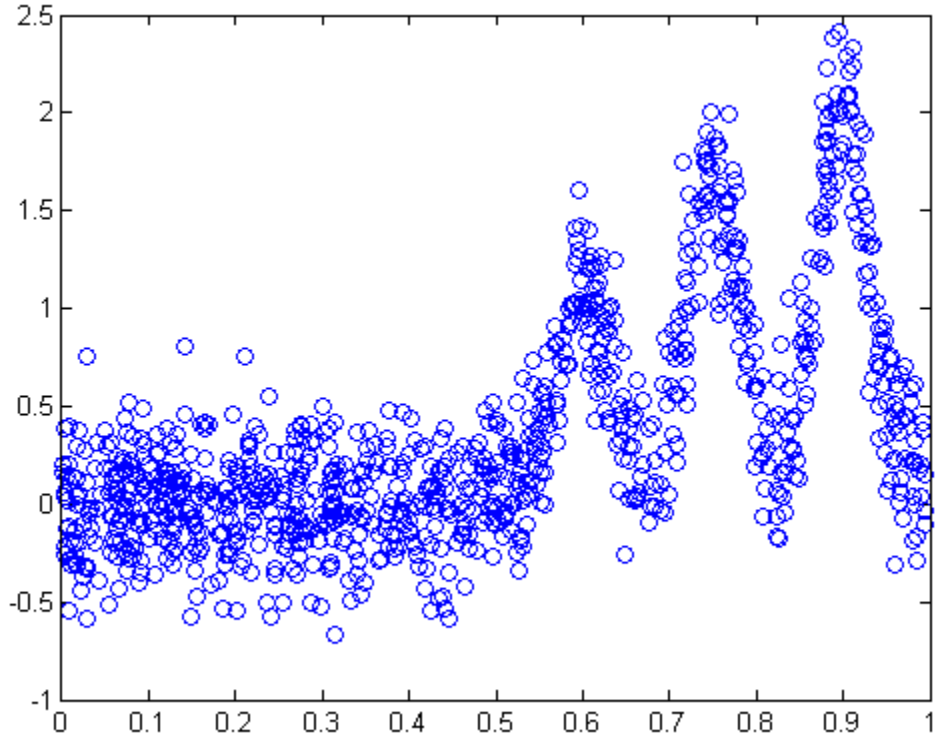
Load the sample data.

```
load mespline
```

This is simulated data.

Plot y versus sorted x.

```
[x_sorted,I] = sort(x,'ascend');
plot(x_sorted,y(I),'o')
```



Fit the following mixed-effects linear spline regression model

$$y_i = \beta_1 + \beta_2 x_i + \sum_{j=1}^{K} b_j \left(x_i - k_j\right)_+ + \varepsilon_i,$$

where k_j is the j th knot, and K is the total number of knots. Assume that $b_j \sim N(0,\sigma^2_b)$ and $\varepsilon \sim N(0,\sigma^2)$.

Define the knots.

```
k = linspace(0.05,0.95,100);
```

Define the design matrices.

```
X = [ones(1000,1),x];
Z = zeros(length(x),length(k));
for j = 1:length(k)
      Z(:,j) = max(X(:,2) - k(j),0);
end
```

Fit the model with an isotropic covariance structure for the random effects.

```
lme = fitlmematrix(X,y,Z,[],'CovariancePattern','Isotropic');
```

Fit a fixed-effects only model.

```
X = [X Z];
lme_fixed = fitlmematrix(X,y,[],[]);
```

Compare `lme_fixed` and `lme` via a simulated likelihood ratio test.

```
compare(lme,lme_fixed,'NSim',500,'CheckNesting',true)
```

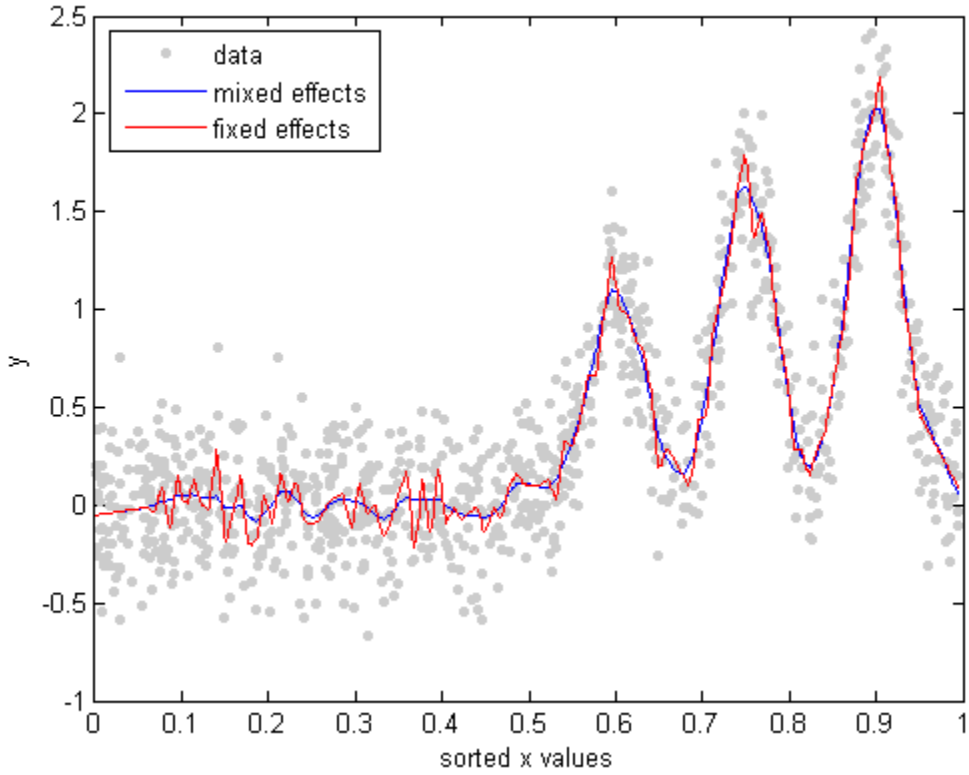
```
ans =


    Simulated Likelihood Ratio Test: Nsim = 500, Alpha = 0.05

    Model        DF     AIC       BIC       LogLik     LRStat    pValue     Lower
    lme            4    170.62    190.25    -81.309
    lme_fixed    103    113.38    618.88     46.309    255.24    0.64471    0.60105
```

The *p*-value of 0.64471 indicates that the fixed-effects only model is not a better fit than the mixed-effects spline regression model.

Plot the fitted values from both models on top of the original response data.

```
R = response(lme);
figure();
plot(x_sorted,R(I),'o', 'MarkerFaceColor',[0.8,0.8,0.8],...
    'MarkerEdgeColor',[0.8,0.8,0.8],'MarkerSize',4);
hold on
F = fitted(lme);
F_fixed = fitted(lme_fixed);
plot(x_sorted,F(I),'b');
plot(x_sorted,F_fixed(I),'r');
legend('data','mixed effects','fixed effects','Location','NorthWest')
```

```
xlabel('sorted x values');
ylabel('y');
hold off
```



You can also see from the figure that the mixed-effects model provides a better fit to data than the fixed-effects only model.

Generalized Linear Models

Multinomial Models for Nominal Responses

The outcome of a response variable might be one of a restricted set of possible values. If there are only two possible outcomes, such as a yes or no answer to a question, these responses are called binary responses. If there are multiple outcomes, then they are called polytomous responses. Some examples include the degree of a disease (mild, medium, severe), preferred districts to live in a city, and so on. When the response variable is *nominal*, there is no natural order among the response variable categories. Nominal response models explain and predict the probability that an observation is in each category of a categorical response variable.

A nominal response model is one of several natural extensions of the binary logit model and is also called a *multinomial logit* model. The multinomial logit model explains the relative risk of being in one category versus being in the reference category, k, using a linear combination of predictor variables. Consequently, the probability of each outcome is expressed as a nonlinear function of p predictor variables. The `'interactions','on'` name-value pair argument in `mnrfit` corresponds to this multinomial model with separate intercept and slopes among categories. `mnrfit` uses the default logit link function for multinomial models. You cannot specify a different link function for multinomial responses.

The multinomial logit model is

$$\ln\left(\frac{\pi_1}{\pi_k}\right) = \alpha_1 + \beta_{11}X_1 + \beta_{12}X_2 + \cdots + \beta_{1p}X_p,$$
$$\ln\left(\frac{\pi_2}{\pi_k}\right) = \alpha_2 + \beta_{21}X_1 + \beta_{22}X_2 + \cdots + \beta_{2p}X_p,$$
$$\vdots$$
$$\ln\left(\frac{\pi_{k-1}}{\pi_k}\right) = \alpha_{(k-1)} + \beta_{(k-1)1}X_1 + \beta_{(k-1)2}X_2 + \cdots + \beta_{(k-1)p}X_p,$$

where $\pi_j = \mathrm{P}(y = j)$ is the probability of an outcome being in category j, k is the number of response categories, and p is the number of predictor variables. Theoretically, any category can be the reference category, but `mnrfit` chooses the last one, k, as the reference category. Thus, `mnrfit` assumes the coefficients of the kth category are zero. The total of $j - 1$ equations are solved simultaneously to estimate the coefficients. `mnrfit` uses the iteratively weighted least squares algorithm to find the maximum likelihood estimates.

The coefficients in the model express the effects of the predictor variables on the relative risk or the log odds of being in category j versus the reference category, here k. For example, the coefficient β_{23} indicates that the probability of the response variable being in category 2 compared to the probability of being in category k increases $\exp(\beta_{23})$ times for each unit increase in X_3, given all else is held constant. Or it indicates that the relative log odds of the response variable being category 2 versus in category k increases β_{23} times with a one-unit increase in X_3, given all else equal.

Based on the nominal response model, and the assumption that the coefficients for the last category are zero, the probability of being in each category is

$$\pi_j = P(y = j) = \frac{e^{\alpha_j + \sum_{l=1}^{p} \beta_{jl} x_l}}{1 + \sum_{j=1}^{k-1} e^{\alpha_j + \sum_{l=1}^{p} \beta_{jl} x_l}}, \quad j = 1, \cdots, k-1.$$

The probability of the kth category becomes

$$\pi_k = P(y = k) = \frac{1}{1 + \sum_{j=1}^{k-1} e^{\alpha_j + \sum_{l=1}^{p} \beta_{jl} x_l}},$$

which is simply equal to $1 - \pi_1 - \pi_2 - \ldots - \pi_{k-1}$.

After estimating the model coefficients using `mnrfit`, you can estimate the category probabilities or the number in each category using `mnrval` (the default name-value pair is `'type','category'`). This function accepts the coefficient estimates and the model statistics `mnrfit` returns and estimates the categorical probabilities or the number in each category and their confidence bounds. You can also specify the cumulative or conditional probabilities or numbers to estimate using the `'type'` name-value pair argument in `mnrval`.

References

[1] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

[2] Long, J. S. *Regression Models for Categorical and Limited Dependent Variables*. Sage Publications, 1997.

[3] Dobson, A. J., and A. G. Barnett. *An Introduction to Generalized Linear Models*. Chapman and Hall/CRC. Taylor & Francis Group, 2008.

See Also

`fitglm` | `glmfit` | `glmval` | `mnrfit` | `mnrval`

More About

- "Multinomial Models for Ordinal Responses" on page 10-5
- "Hierarchical Multinomial Models" on page 10-9

Multinomial Models for Ordinal Responses

The outcome of a response variable might be one of a restricted set of possible values. If there are only two possible outcomes, such as male and female for gender, these responses are called binary responses. If there are multiple outcomes, then they are called polytomous responses. Some examples of polytomous responses include levels of a disease (mild, medium, severe), preferred districts to live in a city, the species for a certain flower type, and so on. Sometimes there might be a natural order among the response categories. These responses are called *ordinal responses*.

The ordering might be inherent in the category choices, such as an individual being not satisfied, satisfied, or very satisfied with an online customer service. The ordering might also be introduced by categorization of a latent (continuous) variable, such as in the case of an individual being in the low risk, medium risk, or high risk group for developing a certain disease, based on a quantitative medical measure such as blood pressure.

You can specify a multinomial regression model that uses the natural ordering among the response categories. This ordinal model describes the relationship between the cumulative probabilities of the categories and predictor variables.

Different link functions can describe this relationship with logit and probit being the most used.

- **Logit:** The default link function `mnrfit` uses for ordinal categories is the *logit* link function. This models the *log cumulative odds*. The `'link','logit'` name-value pair specifies this in `mnrfit`. Log cumulative odds is the logarithm of the ratio of the probability that a response belongs to a category with a value less than or equal to category j, $P(y \le c_j)$, and the probability that a response belongs to a category with a value greater than category j, $P(y > c_j)$.

  Ordinal models are usually based on the assumption that the effects of predictor variables are the same for all categories on the logarithmic scale. That is, the model has different intercepts but common slopes (coefficients) among categories. This model is called *parallel regression* or the *proportional odds* model. It is the default for ordinal responses, and the `'interactions','off'` name-value pair specifies this model in `mnrfit`.

  The proportional odds model is

$$\ln\left(\frac{P(y \le c_1)}{P(y > c_1)}\right) = \ln\left(\frac{\pi_1}{\pi_2 + \cdots + \pi_k}\right) = \alpha_1 + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p,$$
$$\ln\left(\frac{P(y \le c_2)}{P(y > c_2)}\right) = \ln\left(\frac{\pi_1 + \pi_2}{\pi_3 + \cdots + \pi_k}\right) = \alpha_2 + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p,$$
$$\vdots$$
$$\ln\left(\frac{P(y \le c_{k-1})}{P(y > c_{k-1})}\right) = \ln\left(\frac{\pi_1 + \pi_2 + \cdots + \pi_{k-1}}{\pi_k}\right) = \alpha_{k-1} + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p,$$

where π_j, $j = 1, 2, ..., k$, are the category probabilities.

For example, for a response variable with three categories, there are $3 - 1 = 2$ equations as follows:

$$\ln\left(\frac{\pi_1}{\pi_2 + \pi_3}\right) = \alpha_1 + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p,$$
$$\ln\left(\frac{\pi_1 + \pi_2}{\pi_3}\right) = \alpha_2 + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p.$$

Under the proportional odds assumption, the partial effect of a predictor variable X is invariant to the choice of the response variable category, j. For example, if there are three categories, then the coefficients express the impact of a predictor variable on the relative risk or log odds of the response value being in category 1 versus categories 2 or 3, or in category 1 or 2 versus category 3.

Thus, a unit change in variable X_2 would mean a change in the cumulative odds of the response value being in category 1 versus categories 2 or 3, or category 1 or 2 versus category 3 by a factor of $\exp(\beta_2)$, given all else equal.

You can alternatively fit a model with different intercept and slopes among the categories by using the `'interactions','on'` name-value pair argument. However, using this option for ordinal models when the equal slopes model is true causes a loss of efficiency (you lose the advantage of estimating fewer parameters).

- **Probit:** The `'link','probit'` name-value pair argument uses the *probit* link function which is based on a normally distributed latent variable assumption. For ordinal response variables this is also called an *ordered probit* model. Consider the

regression model that describes the relationship of a latent variable y^* of an ordinal process and a vector of predictor variables, X,

$$y = \beta X + \varepsilon,$$

where the error term ε has a standard normal distribution. Suppose there is the following relationship between the latent variable y^* and the observed variable y:

$$\begin{aligned} y &= c_1 \quad if \quad \alpha_0 < y^* \le \alpha_1, \\ y &= c_2 \quad if \quad \alpha_1 < y^* \le \alpha_2, \\ &\vdots \qquad\qquad \vdots \\ y &= c_k \quad if \quad \alpha_{k-1} < y^* \le \alpha_k, \end{aligned}$$

where $a_0 = -\infty$ and $a_k = \infty$. Then, the cumulative probability of y being in category j or one of earlier categories, $P(y \le c_j)$, is equal to

$$P\left(y \le c_j\right) = P\left(y^* < \alpha_j\right) = P\left(\beta X + \varepsilon < \alpha_j\right) = P\left(\varepsilon < \alpha_j - \beta X\right) = \Phi\left(\alpha_j - \beta X\right),$$

where Φ is standard normal cumulative distribution function. Thus,

$$\Phi^{-1}\left(P\left(y \le c_j\right)\right) = \alpha_j - \beta X,$$

where a_j corresponds to the cut points of the latent variable and the intercept in the regression model. This only holds under the assumptions of a normal latent variable and parallel regression. More generally, for a response variable with k categories and multiple predictors, the ordered probit model is

$$\begin{aligned} \Phi^{-1}\left(P\left(y \le c_1\right)\right) &= \alpha_1 + \beta_1 X_1 + \cdots + \beta_p X_p, \\ \Phi^{-1}\left(P\left(y \le c_2\right)\right) &= \alpha_2 + \beta_1 X_1 + \cdots + \beta_p X_p, \\ &\vdots \qquad\qquad\qquad \vdots \\ \Phi^{-1}\left(P\left(y \le c_{k-1}\right)\right) &= \alpha_{k-1} + \beta_1 X_1 + \cdots + \beta_p X_p, \end{aligned}$$

where $P(y \le c_j) = \pi_1 + \pi_2 + \ldots + \pi_j$.

The coefficients indicate the impact of a unit change in the predictor variable on the likelihood of a state. A positive coefficient, β_1, for example, indicates an increase in the underlying latent variable with an increase in the corresponding predictor variable, X_1. Hence, it causes a decrease in $P(y \le c_1)$ and an increase in $P(y \le c_k)$.

After estimating the model coefficients using `mnrfit`, you can estimate the cumulative probabilities or the cumulative number in each category using `mnrval` with the `'type','cumulative'` name-value pair option. `mnrval` accepts the coefficient estimates and the model statistics `mnrfit` returns, and estimates the categorical probabilities or the number in each category and their confidence intervals. You can specify which category or conditional probabilities or numbers to estimate by changing the value of the `'type'` name-value pair argument.

References

[1] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

[2] Long, J. S. *Regression Models for Categorical and Limited Dependent Variables*. Sage Publications, 1997.

[3] Dobson, A. J., and A. G. Barnett. *An Introduction to Generalized Linear Models*. Chapman and Hall/CRC. Taylor & Francis Group, 2008.

See Also

`fitglm` | `glmfit` | `glmval` | `mnrfit` | `mnrval`

More About

- "Multinomial Models for Nominal Responses" on page 10-2
- "Hierarchical Multinomial Models" on page 10-9

Hierarchical Multinomial Models

The outcome of a response variable might sometimes be one of a restricted set of possible values. If there are only two possible outcomes, such as male and female for gender, these responses are called binary responses. If there are multiple outcomes, then they are called polytomous responses. These responses are usually qualitative rather than quantitative, such as preferred districts to live in a city, the severity level of a disease, the species for a certain flower type, and so on. Polytomous responses might also have categories which are not independent of each other. Instead the response happens in a sequential manner, or one category is nested in the previous one. These types of responses are called *hierarchical*, *or sequential*, or *nested multinomial responses*.

For example, if the response is the number of cigarettes a person smokes in a given day, the first level is whether the person is a smoker or not. Given that he or she is a smoker, the number of cigarettes he or she smokes can be from one to five or more than five a day. Given that it is more than 5, this person might be smoking from 6 to 10 or more than 10 cigarettes a day, and so on. The risk group at each level changes accordingly. At level one, the risk group is all of the individuals of interest (smoker or not), say m. If out of m individuals, y_1 of them are not smokers, then at level two, the risk group is the number of all smoking individuals, $m - y_1$. If y_2 of these $m - y_1$ individuals smoke from one to five cigarettes a day, then at level three, the risk group is $m - y_1 - y_2$. So, at each level, the number of people in that category becomes a conditional binomial observation.

The hierarchical multinomial regression models are extensions of binary regression models based on conditional binary observations. The default is a model with different intercept and slopes (coefficients) among categories, in which case `mnrfit` fits a sequence of conditional binomial models. The `'interactions','on'` name-value pair specifies this in `mnrfit`. The default link function is logit and the `'link','logit'` name-value pair specifies this model in `mnrfit`.

Suppose the probability that an individual is in category j given that he or she is not in the previous categories is π_j, and the cumulative probability that a response belongs to a category j or a previous category is $P(y \le c_j)$. Then the hierarchical model with a logit link function and different slopes assumption is

$$\ln\left(\frac{\pi_1}{1-P(y\le c_1)}\right)=\ln\left(\frac{\pi_1}{1-\pi_1}\right)=\alpha_1+\beta_{11}X_1+\beta_{12}X_2+\cdots+\beta_{1p}X_p,$$
$$\ln\left(\frac{\pi_2}{1-P(y\le c_2)}\right)=\ln\left(\frac{\pi_2}{1-(\pi_1+\pi_2)}\right)=\alpha_2+\beta_{21}X_2+\beta_{22}X_2+\cdots+\beta_{2p}X_p,$$
$$\vdots$$
$$\ln\left(\frac{\pi_{k-1}}{1-P(y\le c_{k-1})}\right)=\ln\left(\frac{\pi_{k-1}}{1-(\pi_1+\cdots+\pi_{k-1})}\right)=\alpha_{k-1}+\beta_{(k-1)1}X_1+\beta_{(k-1)2}X_2+\cdots+\beta_{(k-1)p}X_p.$$

For example, for a response variable with four sequential categories, there are $4 - 1 = 3$ equations as follows:

$$\ln\left(\frac{\pi_1}{\pi_2+\pi_3+\pi_4}\right)=\alpha_1+\beta_{11}X_1+\beta_{12}X_2+\cdots+\beta_{1p}X_p,$$
$$\ln\left(\frac{\pi_2}{\pi_3+\pi_4}\right)=\alpha_2+\beta_{21}X_1+\beta_{22}X_2+\cdots+\beta_{2p}X_p,$$
$$\ln\left(\frac{\pi_3}{\pi_4}\right)=\alpha_3+\beta_{31}X_1+\beta_{32}X_2+\cdots+\beta_{3p}X_p.$$

The coefficients β_{ij} are interpreted within each level. For example, for the previous smoking example, β_{12} shows the impact of X_2 on the log odds of a person being a smoker versus a nonsmoker, provided that everything else is held constant. Alternatively, β_{22} shows the impact of X_2 on the log odds of a person smoking one to five cigarettes versus more than five cigarettes a day, given that he or she is a smoker, provided that everything else is held constant. Similarly, β_{23}, shows the effect of X_2 on the log odds of a person smoking 6 to 10 cigarettes versus more than 10 cigarettes a day, given that he or she smokes more than 5 cigarettes a day, provided that everything else is held constant.

You can specify other link functions for hierarchical models. The `'link','probit'` name-value pair argument uses the probit link function. With the separate slopes assumption, the model becomes

$$\begin{aligned}
\Phi^{-1}(\pi_1) &= \alpha_1 + \beta_{11}X_1 + \cdots + \beta_{1p}X_p, \\
\Phi^{-1}(\pi_2) &= \alpha_2 + \beta_{21}X_1 + \cdots + \beta_{2p}X_p, \\
&\vdots \qquad\qquad\qquad \vdots \\
\Phi^{-1}(\pi_k) &= \alpha_k + \beta_{k1}X_1 + \cdots + \beta_{kp}X_p,
\end{aligned}$$

where π_j is the conditional probability of being in category j, given that it is not in categories previous to category j. And $\Phi^{-1}(.)$ is the inverse of the standard normal cumulative distribution function.

After estimating the model coefficients using `mnrfit`, you can estimate the cumulative probabilities or the cumulative number in each category using `mnrval` with the `'type','conditional'` name-value pair argument. The function `mnrval` accepts the coefficient estimates and the model statistics `mnrfit` returns, and estimates the categorical probabilities or the number in each category and their confidence bounds. You can specify which category or cumulative probabilities or numbers to estimate by changing the value of the `'type'` name-value pair argument in `mnrval`.

References

[1] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

[2] Liao, T. F. *Interpreting Probability Models: Logit, Probit, and Other Generalized Linear Models* Series: Quantitative Applications in the Social Sciences. Sage Publications, 1994.

See Also

`fitglm` | `glmfit` | `glmval` | `mnrfit` | `mnrval`

More About

- "Multinomial Models for Nominal Responses" on page 10-2
- "Multinomial Models for Ordinal Responses" on page 10-5

Generalized Linear Models

In this section...

What Are Generalized Linear Models?

Linear regression models describe a linear relationship between a response and one or more predictive terms. Many times, however, a nonlinear relationship exists. "Nonlinear Regression" on page 11-2 describes general nonlinear models. A special class of nonlinear models, called *generalized linear models*, uses linear methods.

Recall that linear models have these characteristics:

- At each set of values for the predictors, the response has a normal distribution with mean μ.
- A coefficient vector b defines a linear combination Xb of the predictors X.
- The model is $\mu = Xb$.

In generalized linear models, these characteristics are generalized as follows:

- At each set of values for the predictors, the response has a distribution that can be normal, binomial, Poisson, gamma, or inverse Gaussian, with parameters including a mean μ.
- A coefficient vector b defines a linear combination Xb of the predictors X.
- A *link function* f defines the model as $f(\mu) = Xb$.

Prepare Data

To begin fitting a regression, put your data into a form that fitting functions expect. All regression techniques begin with input data in an array `X` and response data in a separate vector `y`, or input data in a table or dataset array `tbl` and response data as a column in `tbl`. Each row of the input data represents one observation. Each column represents one predictor (variable).

For a table or dataset array `tbl`, indicate the response variable with the `'ResponseVar'` name-value pair:

```
mdl = fitlm(tbl,'ResponseVar','BloodPressure');
% or
mdl = fitglm(tbl,'ResponseVar','BloodPressure');
```

The response variable is the last column by default.

You can use numeric *categorical* predictors. A categorical predictor is one that takes values from a fixed set of possibilities.

- For a numeric array `X`, indicate the categorical predictors using the `'Categorical'` name-value pair. For example, to indicate that predictors `2` and `3` out of six are categorical:

  ```
  mdl = fitlm(X,y,'Categorical',[2,3]);
  % or
  mdl = fitglm(X,y,'Categorical',[2,3]);
  % or equivalently
  mdl = fitlm(X,y,'Categorical',logical([0 1 1 0 0 0]));
  ```

- For a table or dataset array `tbl`, fitting functions assume that these data types are categorical:

  - Logical
  - Categorical (nominal or ordinal)
  - String or character array

  If you want to indicate that a numeric predictor is categorical, use the `'Categorical'` name-value pair.

Represent missing numeric data as `NaN`. To represent missing data for other data types, see “Missing Group Values” on page 2-54.

- For a `'binomial'` model with data matrix `X`, the response `y` can be:
  - Binary column vector — Each entry represents success (`1`) or failure (`0`).
  - Two-column matrix of integers — The first column is the number of successes in each observation, the second column is the number of trials in that observation.
- For a `'binomial'` model with table or dataset `tbl`:
  - Use the `ResponseVar` name-value pair to specify the column of `tbl` that gives the number of successes in each observation.
  - Use the `BinomialSize` name-value pair to specify the column of `tbl` that gives the number of trials in each observation.

Dataset Array for Input and Response Data

For example, to create a dataset array from an Excel spreadsheet:

```
ds = dataset('XLSFile','hospital.xls',...
     'ReadObsNames',true);
```

To create a dataset array from workspace variables:

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
```

Table for Input and Response Data

To create a table from workspace variables:

```
load carsmall
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
```

Numeric Matrix for Input Data, Numeric Vector for Response

For example, to create numeric arrays from workspace variables:

```
load carsmall
X = [Weight Horsepower Cylinders Model_Year];
y = MPG;
```

To create numeric arrays from an Excel spreadsheet:

```
[X Xnames] = xlsread('hospital.xls');
y = X(:,4); % response y is systolic pressure
X(:,4) = []; % remove y from the X matrix
```

Notice that the nonnumeric entries, such as `sex`, do not appear in `X`.

Choose Generalized Linear Model and Link Function

Often, your data suggests the distribution type of the generalized linear model.

Response Data Type	Suggested Model Distribution Type
Any real number	`'normal'`
Any positive number	`'gamma'` or `'inverse gaussian'`
Any nonnegative integer	`'poisson'`
Integer from 0 to `n`, where `n` is a fixed positive value	`'binomial'`

Set the model distribution type with the `Distribution` name-value pair. After selecting your model type, choose a link function to map between the mean μ and the linear predictor Xb.

Value	Description
`'comploglog'`	$\log(-\log((1-\mu))) = Xb$
`'identity'`, default for the distribution `'normal'`	$\mu = Xb$
`'log'`, default for the distribution `'poisson'`	$\log(\mu) = Xb$
`'logit'`, default for the distribution `'binomial'`	$\log(\mu/(1-\mu)) = Xb$
`'loglog'`	$\log(-\log(\mu)) = Xb$
`'probit'`	$\Phi^{-1}(\mu) = Xb$, where Φ is the normal (Gaussian) CDF function
`'reciprocal'`, default for the distribution `'gamma'`	$\mu^{-1} = Xb$

Value	Description
`p` (a number), default for the distribution `'inverse gaussian'` (with $p = -2$)	$\mu^p = Xb$
Cell array of the form `{FL FD FI}`, containing three function handles, created using `@`, that define the link (`FL`), the derivative of the link (`FD`), and the inverse link (`FI`). Equivalently, can be a structure of function handles with field `Link` containing `FL`, field `Derivative` containing `FD`, and field `Inverse` containing `FI`.	User-specified link function (see "Custom Link Function" on page 10-16)

The nondefault link functions are mainly useful for binomial models. These nondefault link functions are `'comploglog'`, `'loglog'`, and `'probit'`.

Custom Link Function

The link function defines the relationship $f(\mu) = Xb$ between the mean response μ and the linear combination $Xb = X*b$ of the predictors. You can choose one of the built-in link functions or define your own by specifying the link function `FL`, its derivative `FD`, and its inverse `FI`:

- The link function `FL` calculates $f(\mu)$.
- The derivative of the link function `FD` calculates $df(\mu)/d\mu$.
- The inverse function `FI` calculates $g(Xb) = \mu$.

You can specify a custom link function in either of two equivalent ways. Each way contains function handles that accept a single array of values representing μ or Xb, and returns an array the same size. The function handles are either in a cell array or a structure:

- Cell array of the form `{FL FD FI}`, containing three function handles, created using `@`, that define the link (`FL`), the derivative of the link (`FD`), and the inverse link (`FI`).
- Structure `s` with three fields, each containing a function handle created using `@`:
  - `s.Link` — Link function

- `s.Derivative` — Derivative of the link function
- `s.Inverse` — Inverse of the link function

For example, to fit a model using the `'probit'` link function:

```
x = [2100 2300 2500 2700 2900 ...
     3100 3300 3500 3700 3900 4100 4300]';
n = [48 42 31 34 31 21 23 23 21 16 17 21]';
y = [1 2 0 3 8 8 14 17 19 15 17 21]';
g = fitglm(x,[y n],...
    'linear','distr','binomial','link','probit')

g =

Generalized Linear regression model:
    probit(y) ~ 1 + x1
    Distribution = Binomial

Estimated Coefficients:
                   Estimate     SE            tStat     pValue
    (Intercept)      -7.3628       0.66815    -11.02    3.0701e-28
    x1             0.0023039    0.00021352     10.79    3.8274e-27

12 observations, 10 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 241, p-value = 2.25e-54
```

You can perform the same fit using a custom link function that performs identically to the `'probit'` link function:

```
s = {@norminv,@(x)1./normpdf(norminv(x)),@normcdf};
g = fitglm(x,[y n],...
    'linear','distr','binomial','link',s)

g =

Generalized Linear regression model:
    link(y) ~ 1 + x1
    Distribution = Binomial

Estimated Coefficients:
                   Estimate     SE            tStat     pValue
    (Intercept)      -7.3628       0.66815    -11.02    3.0701e-28
    x1             0.0023039    0.00021352     10.79    3.8274e-27
```

```
12 observations, 10 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 241, p-value = 2.25e-54
```

The two models are the same.

Equivalently, you can write `s` as a structure instead of a cell array of function handles:

```
s.Link = @norminv;
s.Derivative = @(x) 1./normpdf(norminv(x));
s.Inverse = @normcdf;
g = fitglm(x,[y n],...
    'linear','distr','binomial','link',s)

g =

Generalized Linear regression model:
    link(y) ~ 1 + x1
    Distribution = Binomial

Estimated Coefficients:
                   Estimate     SE            tStat     pValue
    (Intercept)      -7.3628       0.66815    -11.02    3.0701e-28
    x1             0.0023039    0.00021352     10.79    3.8274e-27

12 observations, 10 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 241, p-value = 2.25e-54
```

Choose Fitting Method and Model

There are two ways to create a fitted model.

- Use `fitglm` when you have a good idea of your generalized linear model, or when you want to adjust your model later to include or exclude certain terms.
- Use `stepwiseglm` when you want to fit your model using stepwise regression. `stepwiseglm` starts from one model, such as a constant, and adds or subtracts terms one at a time, choosing an optimal term each time in a greedy fashion, until it cannot improve further. Use stepwise fitting to find a good model, one that has only relevant terms.

  The result depends on the starting model. Usually, starting with a constant model leads to a small model. Starting with more terms can lead to a more complex model, but one that has lower mean squared error.

In either case, provide a model to the fitting function (which is the starting model for `stepwiseglm`).

Specify a model using one of these methods.

- "Brief String" on page 10-19
- "Terms Matrix" on page 10-19
- "Formula" on page 10-22

Brief String

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

Terms Matrix

A terms matrix is a t-by-$(p + 1)$ matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
```

```
[0 1 2 0] % B*(C^2)
```

The 0 at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then 0 must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

  ```
  load hospital
  ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
  hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
  ```

  Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

  ```
  T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]

  T =

       0     0     0     0
       1     0     0     0
       0     0     1     0
       0     0     0     1
  ```

  Redefine the dataset array.

  ```
  ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
  hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
  ```

  Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

  ```
  T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]

  T =

       0     0     0     0
       0     1     0     0
       0     0     1     0
       0     0     0     1
  ```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

  Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

  ```
  T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]

  T =

       0     0     0
       1     0     0
       0     1     0
       1     1     0
       0     2     0
  ```

  Fit a linear model.

  ```
  mdl = fitlm(X,MPG,T)

  mdl =

  Linear regression model:
      y ~ 1 + x1*x2 + x2^2

  Estimated Coefficients:
                      Estimate       SE            tStat      pValue
      (Intercept)         48.906        12.589     3.8847    0.00019665
      x1                 0.54418       0.57125    0.95261       0.34337
      x2                -0.012781     0.0060312    -2.1192      0.036857
      x1:x2           -0.00010892    0.00017925    -0.6076         0.545
      x2^2             9.7518e-07    7.5389e-07     1.2935       0.19917

  Number of observations: 94, Error degrees of freedom: 89
  Root Mean Squared Error: 4.1
  R-squared: 0.751,  Adjusted R-Squared 0.739
  ```

```
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)

1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for a model specification is a string of the form `'Y ~ terms'`,

- *Y* is the response name.
- *terms* contains
  - Variable names
  - `+` to include the next variable
  - `-` to exclude the next variable

- `:` to define an interaction, a product of terms
- `*` to define an interaction and all lower-order terms
- `^` to raise the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
- `()` to group terms

Tip Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

Examples:
`'Y ~ A + B + C'` is a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example, since `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example, since `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Fit Model to Data

Create a fitted model using `fitglm` or `stepwiseglm`. Choose between them as in "Choose Fitting Method and Model" on page 10-18. For generalized linear models other than those with a normal distribution, give a `Distribution` name-value pair as in "Choose Generalized Linear Model and Link Function" on page 10-15. For example,

```
mdl = fitglm(X,y,'linear','Distribution','poisson')
% or
mdl = fitglm(X,y,'quadratic',...
         'Distribution','binomial')
```

Examine Quality and Adjust the Fitted Model

After fitting a model, examine the result.

Model Display

A linear regression model shows several diagnostics when you enter its name or enter `disp(mdl)`. This display gives some of the basic information to check whether the fitted model represents the data adequately.

For example, fit a Poisson model to data constructed with two out of five predictors not affecting the response, and with no intercept term:

```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[.4;.2;.3]);
y = poissrnd(mu);
mdl = fitglm(X,y,...
    'linear','Distribution','poisson')

mdl =


Generalized Linear regression model:
    log(y) ~ 1 + x1 + x2 + x3 + x4 + x5
    Distribution = Poisson

Estimated Coefficients:
                   Estimate      SE          tStat       pValue
    (Intercept)     0.039829     0.10793     0.36901       0.71212
    x1               0.38551    0.076116      5.0647    4.0895e-07
    x2             -0.034905    0.086685    -0.40266        0.6872
    x3              -0.17826    0.093552     -1.9054      0.056722
    x4               0.21929     0.09357      2.3436      0.019097
    x5               0.28918      0.1094      2.6432     0.0082126


100 observations, 94 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 44.9, p-value = 1.55e-08
```

Notice that:

- The display contains the estimated values of each coefficient in the `Estimate` column. These values are reasonably near the true values `[0;.4;0;0;.2;.3]`, except possibly the coefficient of `x3` is not terribly near `0`.
- There is a standard error column for the coefficient estimates.
- The reported `pValue` (which are derived from the t statistics under the assumption of normal errors) for predictors 1, 4, and 5 are small. These are the three predictors that were used to create the response data `y`.
- The `pValue` for `(Intercept)`, `x2` and `x3` are larger than 0.01. These three predictors were not used to create the response data `y`. The `pValue` for `x3` is just over `.05`, so might be regarded as possibly significant.
- The display contains the Chi-square statistic.

Diagnostic Plots

Diagnostic plots help you identify outliers, and see other problems in your model or fit. To illustrate these plots, consider binomial regression with a logistic link function.

The *logistic model* is useful for proportion data. It defines the relationship between the proportion p and the weight w by:
$\log[p/(1-p)] = b_1 + b_2 w$

This example fits a binomial model to data. The data are derived from `carbig.mat`, which contains measurements of large cars of various weights. Each weight in `w` has a corresponding number of cars in `total` and a corresponding number of poor-mileage cars in `poor`.

It is reasonable to assume that the values of `poor` follow binomial distributions, with the number of trials given by `total` and the percentage of successes depending on `w`. This distribution can be accounted for in the context of a logistic model by using a generalized linear model with link function $\log(\mu/(1-\mu)) = Xb$. This link function is called `'logit'`.

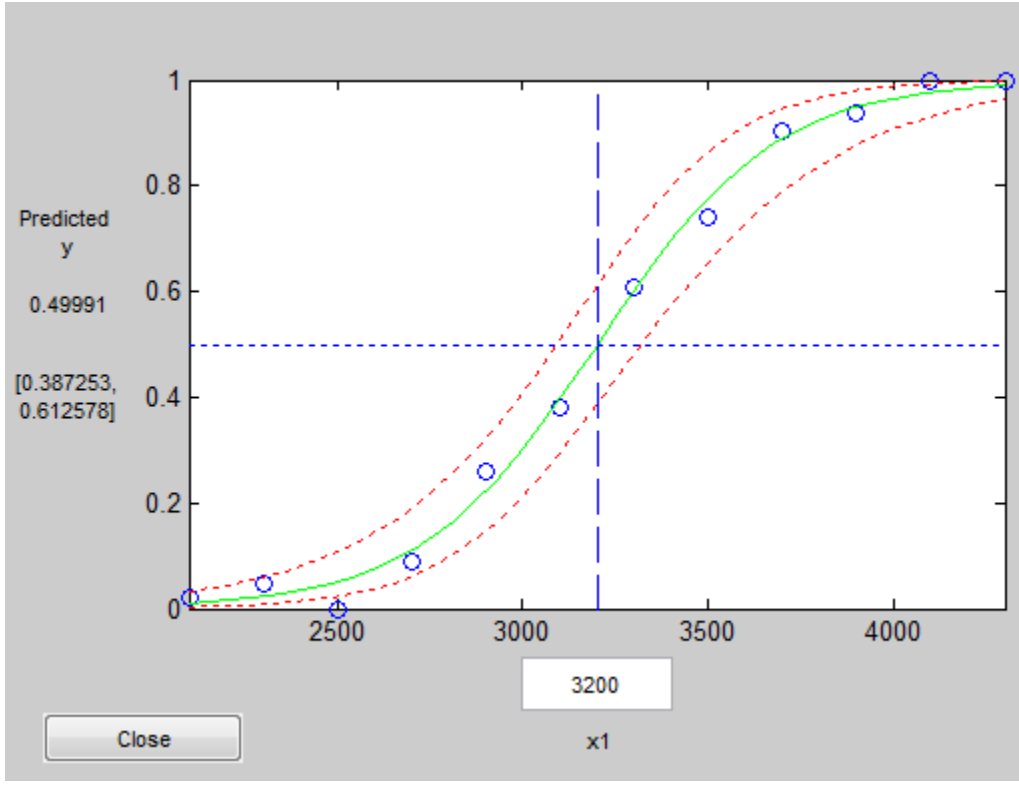
```
w = [2100 2300 2500 2700 2900 3100 ...
     3300 3500 3700 3900 4100 4300]';
total = [48 42 31 34 31 21 23 23 21 16 17 21]';
poor = [1 2 0 3 8 8 14 17 19 15 17 21]';
mdl = fitglm(w,[poor total],...
    'linear','Distribution','binomial','link','logit')
```

```
mdl =

Generalized Linear regression model:
```

```
    logit(y) ~ 1 + x1
    Distribution = Binomial

Estimated Coefficients:
                   Estimate      SE            tStat      pValue
    (Intercept)       -13.38         1.394     -9.5986    8.1019e-22
    x1             0.0041812    0.00044258      9.4474    3.4739e-21

12 observations, 10 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 242, p-value = 1.3e-54
```

See how well the model fits the data.

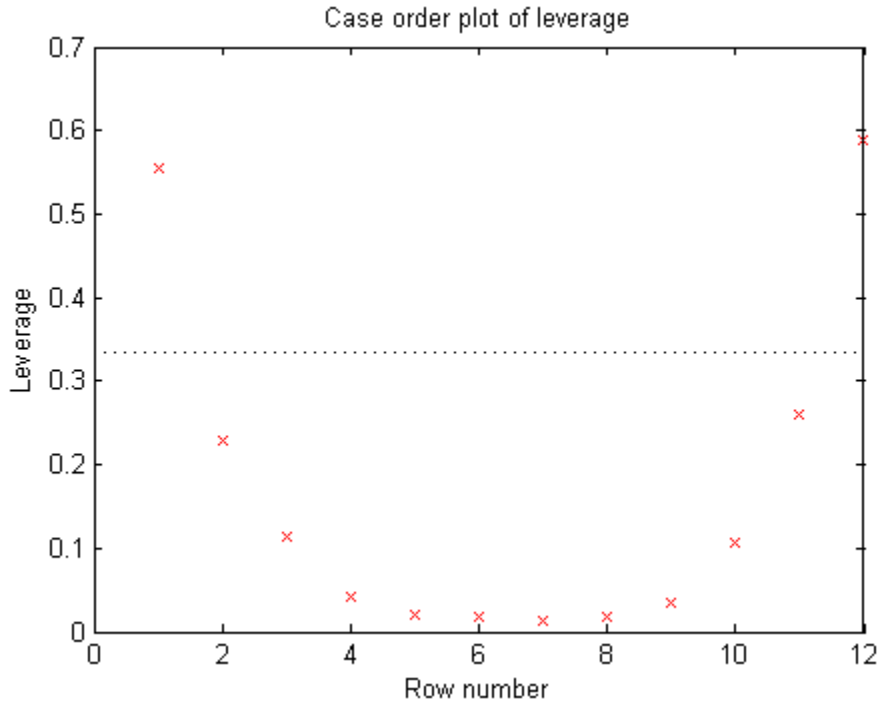
```
plotSlice(mdl)
```



The fit looks reasonably good, with fairly wide confidence bounds.

To examine further details, create a leverage plot.

```
plotDiagnostics(mdl)
```



This is typical of a regression with points ordered by the predictor variable. The leverage of each point on the fit is higher for points with relatively extreme predictor values (in either direction) and low for points with average predictor values. In examples with multiple predictors and with points not ordered by predictor value, this plot can help you identify which observations have high leverage because they are outliers as measured by their predictor values.

Residuals — Model Quality for Training Data

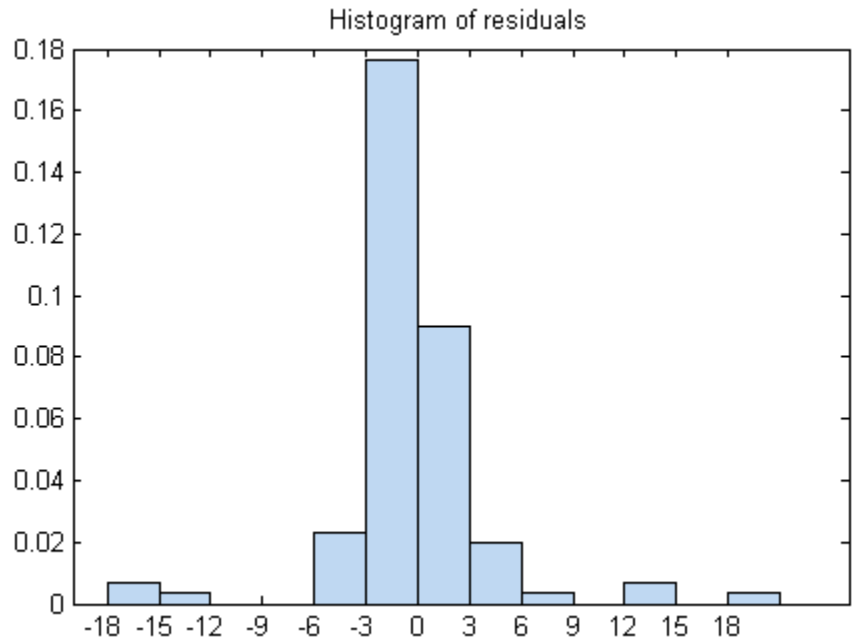
There are several residual plots to help you discover errors, outliers, or correlations in the model or data. The simplest residual plots are the default histogram plot, which shows the range of the residuals and their frequencies, and the probability plot, which shows how the distribution of the residuals compares to a normal distribution with matched variance.

This example shows residual plots for a fitted Poisson model. The data construction has two out of five predictors not affecting the response, and no intercept term:

```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[2;1;.5]);
y = poissrnd(mu);
mdl = fitglm(X,y,...
    'linear','Distribution','poisson');
```

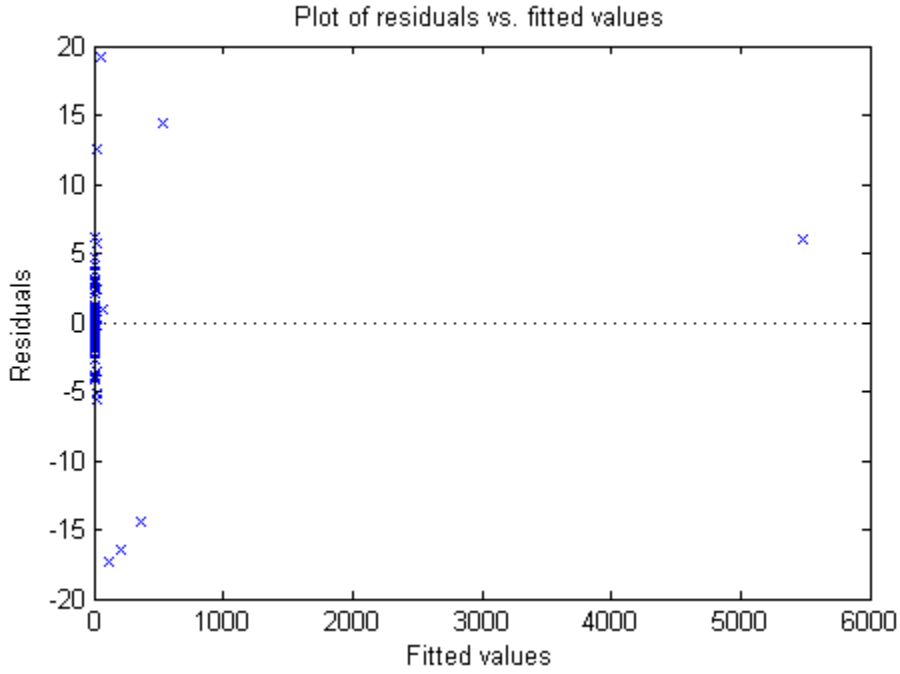
Examine the residuals:

```
plotResiduals(mdl)
```



While most residuals cluster near 0, there are several near ±18. So examine a different residuals plot.

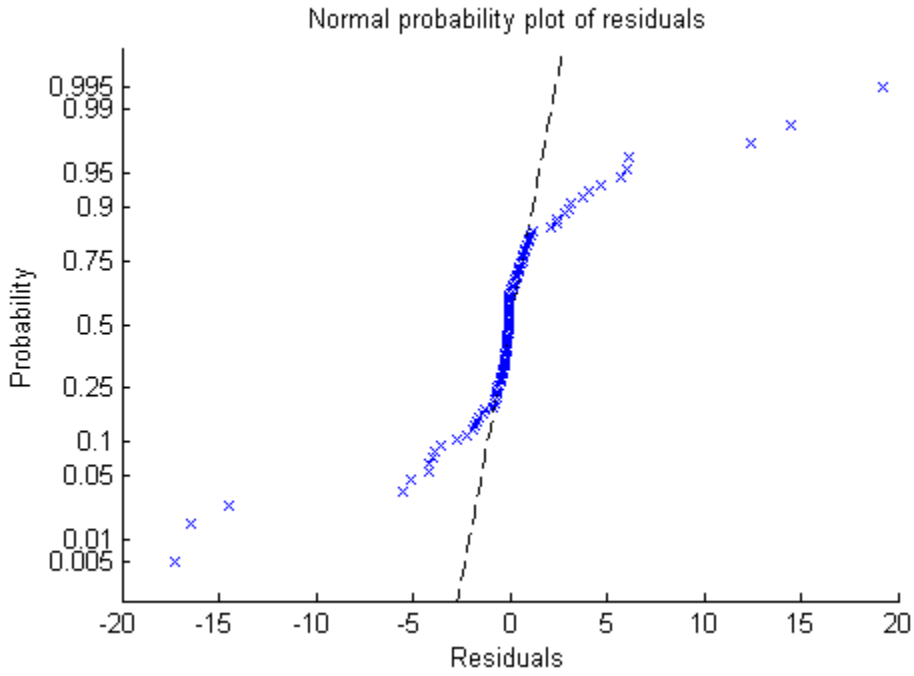
```
plotResiduals(mdl,'fitted')
```



The large residuals don't seem to have much to do with the sizes of the fitted values.

Perhaps a probability plot is more informative.

```
plotResiduals(mdl,'probability')
```



Now it is clear. The residuals do not follow a normal distribution. Instead, they have fatter tails, much as an underlying Poisson distribution.

Plots to Understand Predictor Effects and How to Modify a Model

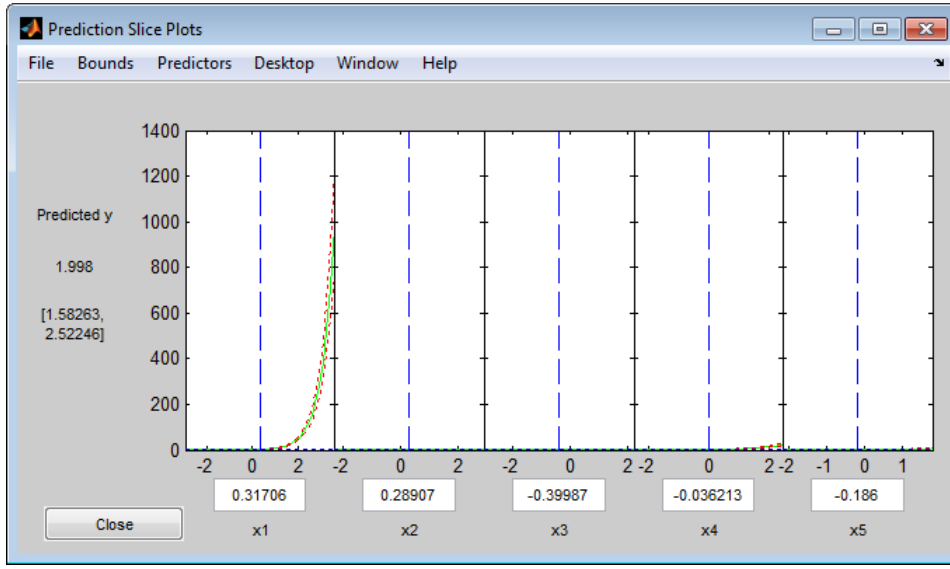
This example shows how to understand the effect each predictor has on a regression model, and how to modify the model to remove unnecessary terms.

1 Create a model from some predictors in artificial data. The data do not use the second and third columns in `X`. So you expect the model not to show much dependence on those predictors.

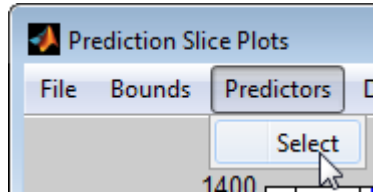
```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[2;1;.5]);
y = poissrnd(mu);
mdl = fitglm(X,y,...
    'linear','Distribution','poisson');
```

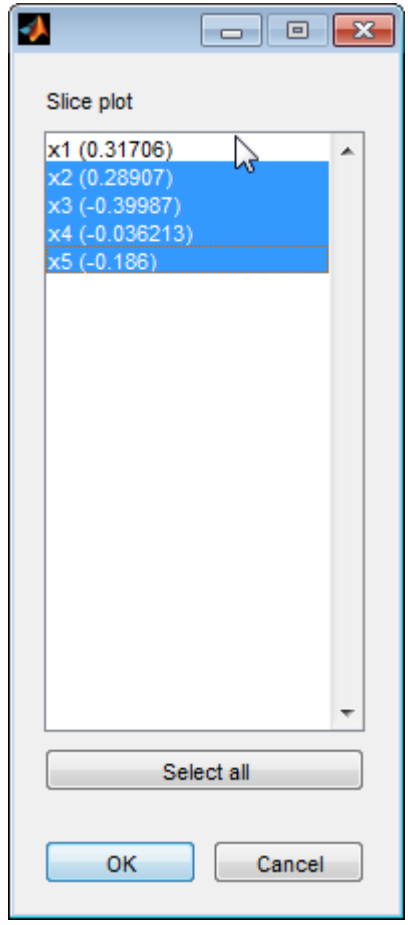
2 Examine a slice plot of the responses. This displays the effect of each predictor separately.

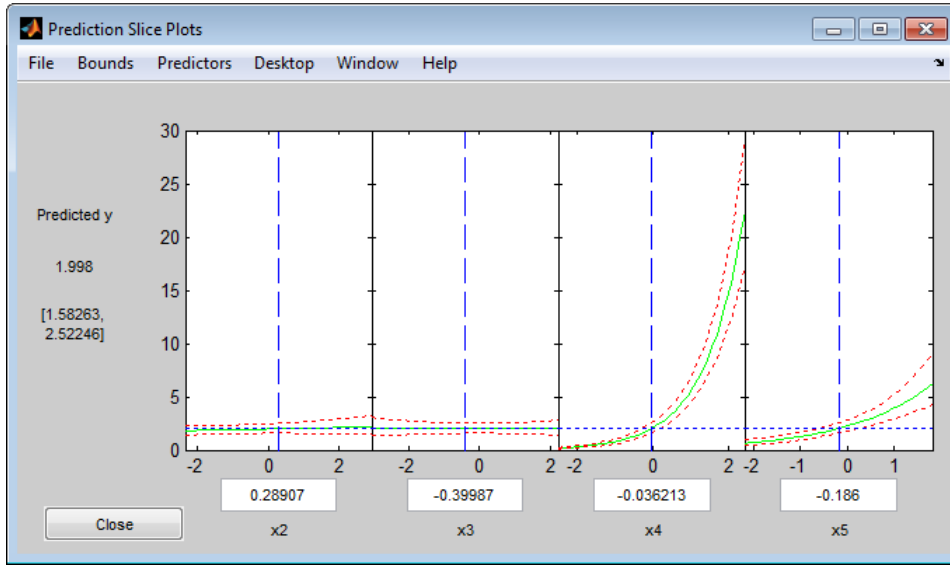
```
plotSlice(mdl)
```



The scale of the first predictor is overwhelming the plot. Disable it using the **Predictors** menu.




Slice plot
x1 (0.31706)
x2 (0.28907)
x3 (-0.39987)
x4 (-0.036213)
x5 (-0.186)
Select all
OK
Cancel



Now it is clear that predictors 2 and 3 have little to no effect.

You can drag the individual predictor values, which are represented by dashed blue vertical lines. You can also choose between simultaneous and non-simultaneous confidence bounds, which are represented by dashed red curves. Dragging the predictor lines confirms that predictors 2 and 3 have little to no effect.

3 Remove the unnecessary predictors using either `removeTerms` or `step`. Using `step` can be safer, in case there is an unexpected importance to a term that becomes apparent after removing another term. However, sometimes `removeTerms` can be effective when `step` does not proceed. In this case, the two give identical results.

```
mdl1 = removeTerms(mdl,'x2 + x3')
```

```
mdl1 =


Generalized Linear regression model:
    log(y) ~ 1 + x1 + x4 + x5
    Distribution = Poisson

Estimated Coefficients:
```

```
                   Estimate    SE          tStat     pValue
    (Intercept)    0.17604     0.062215    2.8295       0.004662
    x1              1.9122     0.024638    77.614             0
    x4             0.98521     0.026393    37.328    5.6696e-305
    x5             0.61321     0.038435    15.955     2.6473e-57


100 observations, 96 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 4.97e+04, p-value = 0
```

```
mdl1 = step(mdl,'NSteps',5,'Upper','linear')
```

```
1. Removing x3, Deviance = 93.856, Chi2Stat = 0.00075551, PValue = 0.97807
2. Removing x2, Deviance = 96.333, Chi2Stat = 2.4769, PValue = 0.11553

mdl1 =


Generalized Linear regression model:
    log(y) ~ 1 + x1 + x4 + x5
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)    0.17604     0.062215    2.8295       0.004662
    x1              1.9122     0.024638    77.614             0
    x4             0.98521     0.026393    37.328    5.6696e-305
    x5             0.61321     0.038435    15.955     2.6473e-57


100 observations, 96 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 4.97e+04, p-value = 0
```

Predict or Simulate Responses to New Data

There are three ways to use a linear model to predict the response to new data:

- “predict” on page 10-34
- “feval” on page 10-35
- “random” on page 10-37

predict

The `predict` method gives a prediction of the mean responses and, if requested, confidence bounds.

This example shows how to predict and obtain confidence intervals on the predictions using the `predict` method.

1. Create a model from some predictors in artificial data. The data do not use the second and third columns in `X`. So you expect the model not to show much dependence on these predictors. Construct the model stepwise to include the relevant predictors automatically.

```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[2;1;.5]);
y = poissrnd(mu);
mdl = stepwiseglm(X,y,...
    'constant','upper','linear','Distribution','poisson');
```

```
1. Adding x1, Deviance = 2515.02869, Chi2Stat = 47242.9622, PValue = 0
2. Adding x4, Deviance = 328.39679, Chi2Stat = 2186.6319, PValue = 0
3. Adding x5, Deviance = 96.3326, Chi2Stat = 232.0642, PValue = 2.114384e-52
```

2. Generate some new data, and evaluate the predictions from the data.

```
Xnew = randn(3,5) + repmat([1 2 3 4 5],[3,1]); % new data
[ynew,ynewci] = predict(mdl,Xnew)
```

```
ynew =

   1.0e+04 *

    0.1130
    1.7375
    3.7471


ynewci =

   1.0e+04 *

    0.0821    0.1555
    1.2167    2.4811
    2.8419    4.9407
```

feval

When you construct a model from a table or dataset array, `feval` is often more convenient for predicting mean responses than `predict`. However, `feval` does not provide confidence bounds.

This example shows how to predict mean responses using the `feval` method.

1. Create a model from some predictors in artificial data. The data do not use the second and third columns in X. So you expect the model not to show much dependence on these predictors. Construct the model stepwise to include the relevant predictors automatically.

```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[2;1;.5]);
y = poissrnd(mu);

X = array2table(X); % create data table
y = array2table(y);
tbl = [X y];

mdl = stepwiseglm(tbl,...
    'constant','upper','linear','Distribution','poisson');
```

```
1. Adding x1, Deviance = 2515.02869, Chi2Stat = 47242.9622, PValue = 0
2. Adding x4, Deviance = 328.39679, Chi2Stat = 2186.6319, PValue = 0
3. Adding x5, Deviance = 96.3326, Chi2Stat = 232.0642, PValue = 2.114384e-52
```

2. Generate some new data, and evaluate the predictions from the data.

```
Xnew = randn(3,5) + repmat([1 2 3 4 5],[3,1]); % new data
ynew = feval(mdl,Xnew(:,1),Xnew(:,4),Xnew(:,5)) % only need predictors 1,4,5
```

```
ynew =

   1.0e+04 *

    0.1130
    1.7375
    3.7471
```

Equivalently,

```
ynew = feval(mdl,Xnew(:,[1 4 5])) % only need predictors 1,4,5
```

```
ynew =

   1.0e+04 *

    0.1130
    1.7375
    3.7471
```

random

The `random` method generates new random response values for specified predictor values. The distribution of the response values is the distribution used in the model. `random` calculates the mean of the distribution from the predictors, estimated coefficients, and link function. For distributions such as normal, the model also provides an estimate of the variance of the response. For the binomial and Poisson distributions, the variance of the response is determined by the mean; `random` does not use a separate "dispersion" estimate.

This example shows how to simulate responses using the `random` method.

1. Create a model from some predictors in artificial data. The data do not use the second and third columns in `X`. So you expect the model not to show much dependence on these predictors. Construct the model stepwise to include the relevant predictors automatically.

```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[2;1;.5]);
y = poissrnd(mu);
mdl = stepwiseglm(X,y,...
    'constant','upper','linear','Distribution','poisson');
```

```
1. Adding x1, Deviance = 2515.02869, Chi2Stat = 47242.9622, PValue = 0
2. Adding x4, Deviance = 328.39679, Chi2Stat = 2186.6319, PValue = 0
3. Adding x5, Deviance = 96.3326, Chi2Stat = 232.0642, PValue = 2.114384e-52
```

2. Generate some new data, and evaluate the predictions from the data.

```
Xnew = randn(3,5) + repmat([1 2 3 4 5],[3,1]); % new data
ysim = random(mdl,Xnew)
```

```
ysim =

         1111
        17121
        37457
```

The predictions from `random` are Poisson samples, so are integers.

3. Evaluate the `random` method again, the result changes.

```
ysim = random(mdl,Xnew)
```

```
ysim =
```

```
        1175
       17320
       37126
```

Share Fitted Models

The model display contains enough information to enable someone else to recreate the model in a theoretical sense. For example,

```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[2;1;.5]);
y = poissrnd(mu);
mdl = stepwiseglm(X,y,...
    'constant','upper','linear','Distribution','poisson')
```

```
1. Adding x1, Deviance = 2515.02869, Chi2Stat = 47242.9622, PValue = 0
2. Adding x4, Deviance = 328.39679, Chi2Stat = 2186.6319, PValue = 0
3. Adding x5, Deviance = 96.3326, Chi2Stat = 232.0642, PValue = 2.114384e-52

mdl =


Generalized Linear regression model:
    log(y) ~ 1 + x1 + x4 + x5
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)    0.17604     0.062215    2.8295       0.004662
    x1              1.9122     0.024638    77.614             0
    x4             0.98521     0.026393    37.328    5.6696e-305
    x5             0.61321     0.038435    15.955     2.6473e-57


100 observations, 96 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 4.97e+04, p-value = 0
```

You can access the model description programmatically, too. For example,

```
mdl.Coefficients.Estimate
```

```
ans =

    0.1760
    1.9122
    0.9852
    0.6132
```

```
mdl.Formula
```

```
ans =

log(y) ~ 1 + x1 + x4 + x5
```

Generalized Linear Model Workflow

This example shows how to fit a generalized linear model and analyze the results. A typical workflow involves the following: import data, fit a generalized linear model, test its quality, modify it to improve the quality, and make predictions based on the model. It computes the probability that a flower is in one of two classes, based on the Fisher iris data.

Step 1. Load the data.

Load the Fisher iris data. Extract the rows that have classification versicolor or virginica. These are rows 51 to 150. Create logical response variables that are `true` for versicolor flowers.

```
load fisheriris
X = meas(51:end,:); % versicolor and virginica
y = strcmp('versicolor',species(51:end));
```

Step 2. Fit a generalized linear model.

Fit a binomial generalized linear model to the data.

```
mdl = fitglm(X,y,'linear',...
    'distr','binomial')


mdl =


Generalized Linear regression model:
    logit(y) ~ 1 + x1 + x2 + x3 + x4
    Distribution = Binomial

Estimated Coefficients:
                   Estimate      SE       tStat      pValue
                   ________    ______    _______    ________

    (Intercept)     42.638     25.708     1.6586    0.097204
    x1              2.4652     2.3943     1.0296     0.30319
    x2              6.6809     4.4796     1.4914     0.13585
```

```
    x3             -9.4294     4.7372    -1.9905    0.046537
    x4             -18.286     9.7426    -1.8769    0.060529


100 observations, 95 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 127, p-value = 1.95e-26
```

Step 3. Examine the result, consider alternative models.

Some p-values in the `pValue` column are not very small. Perhaps the model can be simplified.

See if some 95% confidence intervals for the coefficients include 0. If so, perhaps these model terms could be removed.

```
confint = coefCI(mdl)


confint =

   -8.3984   93.6740
   -2.2881    7.2185
   -2.2122   15.5739
  -18.8339   -0.0248
  -37.6277    1.0554
```

Only two of the predictors have coefficients whose confidence intervals do not include 0.

The coefficients of `'x1'` and `'x2'` have the largest p-values. Test whether both coefficients could be zero.

```
M = [0 1 0 0 0     % picks out coefficient for column 1
     0 0 1 0 0];   % picks out coefficient for column 2
p = coefTest(mdl,M)


p =

    0.1442
```

The p-value of about 0.14 is not very small. Drop those terms from the model.

```
mdl1 = removeTerms(mdl,'x1 + x2')
```

```
mdl1 =


Generalized Linear regression model:
    logit(y) ~ 1 + x3 + x4
    Distribution = Binomial

Estimated Coefficients:
                   Estimate      SE       tStat       pValue
                   ________    ______    _______    __________

    (Intercept)     45.272     13.612      3.326    0.00088103
    x3             -5.7545     2.3059    -2.4956      0.012576
    x4             -10.447     3.7557    -2.7816     0.0054092


100 observations, 97 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 118, p-value = 2.3e-26
```

Perhaps it would have been better to have `stepwiseglm` identify the model initially.

```
mdl2 = stepwiseglm(X,y,...
    'constant','Distribution','binomial','upper','linear')

1. Adding x4, Deviance = 33.4208, Chi2Stat = 105.2086, PValue = 1.099298e-24
2. Adding x3, Deviance = 20.5635, Chi2Stat = 12.8573, PValue = 0.000336166
3. Adding x2, Deviance = 13.2658, Chi2Stat = 7.29767, PValue = 0.00690441

mdl2 =


Generalized Linear regression model:
    logit(y) ~ 1 + x2 + x3 + x4
    Distribution = Binomial

Estimated Coefficients:
                   Estimate      SE       tStat      pValue
                   ________    ______    _______    ________

    (Intercept)     50.527     23.995     2.1057    0.035227
    x2              8.3761     4.7612     1.7592    0.078536
    x3             -7.8745     3.8407    -2.0503    0.040334
    x4              -21.43     10.707    -2.0014     0.04535
```

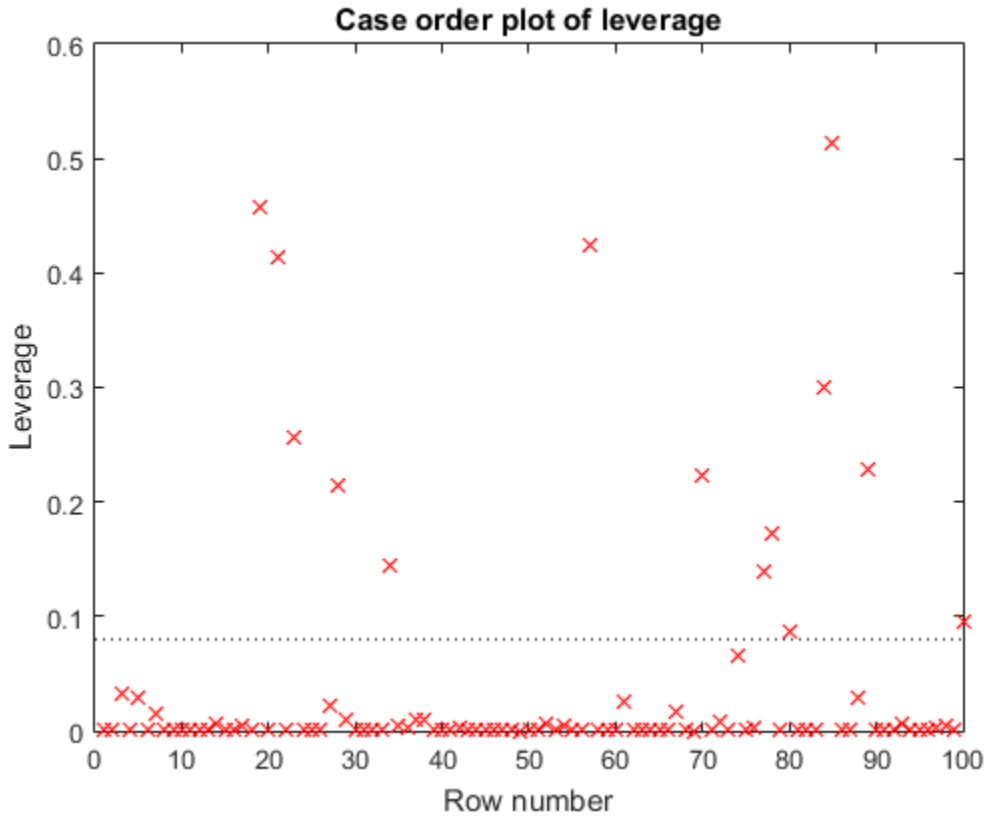
```
100 observations, 96 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 125, p-value = 5.4e-27
```

`stepwiseglm` included `'x2'` in the model, because it neither adds nor removes terms with p-values between 0.05 and 0.10.

Step 4. Look for outliers and exclude them.

Examine a leverage plot to look for influential outliers.

```
plotDiagnostics(mdl2,'leverage')
```



There is one observation with a leverage close to one. Using the Data Cursor, click the point, and find it has index 69.

See if the model coefficients change when you fit a model excluding this point.

```
oldCoeffs = mdl2.Coefficients.Estimate;
mdl3 = fitglm(X,y,'linear',...
    'distr','binomial','pred',2:4,'exclude',69);
newCoeffs = mdl3.Coefficients.Estimate;
disp([oldCoeffs newCoeffs])
```

```
   50.5268   50.5268
    8.3761    8.3761
   -7.8745   -7.8745
  -21.4296  -21.4296
```

The model coefficients do not change, suggesting that the response at the high-leverage point is consistent with the predicted value from the reduced model.

Step 5. Predict the probability that a new flower is versicolor.

Use `mdl2` to predict the probability that a flower with average measurements is versicolor. Generate confidence intervals for your prediction.

```
[newf newc] = predict(mdl2,mean(X))
```

```
newf =

    0.5086


newc =

    0.1863    0.8239
```

The model gives almost a 50% probability that the average flower is versicolor, with a wide confidence interval about this estimate.

References

[1] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

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Lasso Regularization of Generalized Linear Models

In this section...

What is Generalized Linear Model Lasso Regularization?

Lasso is a regularization technique. Use `lassoglm` to:

- Reduce the number of predictors in a generalized linear model.
- Identify important predictors.
- Select among redundant predictors.
- Produce shrinkage estimates with potentially lower predictive errors than ordinary least squares.

Elastic net is a related technique. Use it when you have several highly correlated variables. `lassoglm` provides elastic net regularization when you set the `Alpha` name-value pair to a number strictly between `0` and `1`.

For details about lasso and elastic net computations and algorithms, see "Generalized Linear Model Lasso and Elastic Net" on page 10-61. For a discussion of generalized linear models, see "What Are Generalized Linear Models?" on page 10-12.

Regularize Poisson Regression

This example shows how to identify and remove redundant predictors from a generalized linear model.

Create data with 20 predictors, and Poisson responses using just three of the predictors, plus a constant.

```
rng('default') % for reproducibility
X = randn(100,20);
```

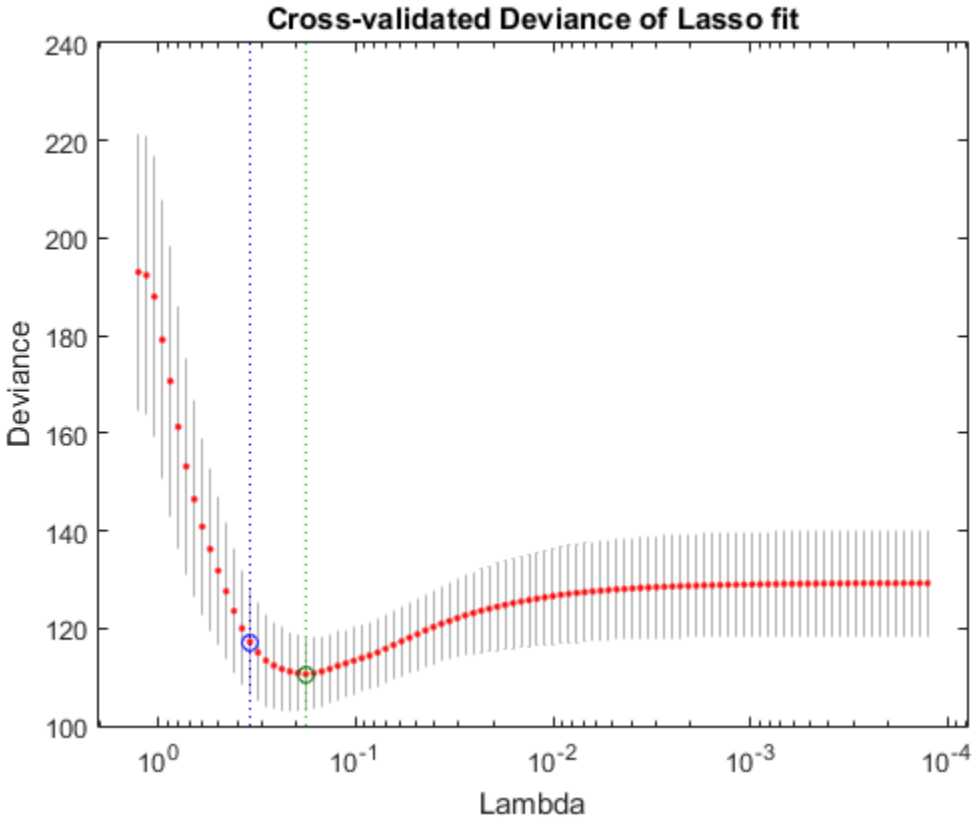
```
mu = exp(X(:,[5 10 15])*[.4;.2;.3] + 1);
y = poissrnd(mu);
```

Construct a cross-validated lasso regularization of a Poisson regression model of the data.

```
[B FitInfo] = lassoglm(X,y,'poisson','CV',10);
```

Examine the cross-validation plot to see the effect of the `Lambda` regularization parameter.

```
lassoPlot(B,FitInfo,'plottype','CV');
```



The green circle and dashed line locate the `Lambda` with minimal cross-validation error. The blue circle and dashed line locate the point with minimal cross-validation error plus one standard deviation.

Find the nonzero model coefficients corresponding to the two identified points.

```
minpts = find(B(:,FitInfo.IndexMinDeviance))
```

```
minpts =

     3
     5
     6
    10
    11
    15
    16
```

```
min1pts = find(B(:,FitInfo.Index1SE))
```

```
min1pts =

     5
    10
    15
```

The coefficients from the minimal plus one standard error point are exactly those coefficients used to create the data.

Find the values of the model coefficients at the minimal plus one standard error point.

```
B(min1pts,FitInfo.Index1SE)
```

```
ans =

    0.2903
    0.0789
    0.2081
```

The values of the coefficients are, as expected, smaller than the original `[0.4,0.2,0.3]`. Lasso works by "shrinkage," which biases predictor coefficients toward zero.

The constant term is in the `FitInfo.Intercept` vector.

```
FitInfo.Intercept(FitInfo.Index1SE)
```

```
ans =

    1.0879
```

The constant term is near 1, which is the value used to generate the data.

Regularize Logistic Regression

This example shows how to regularize binomial regression. The default (canonical) link function for binomial regression is the logistic function.

Step 1. Prepare the data.

Load the `ionosphere` data. The response `Y` is a cell array of `'g'` or `'b'` strings. Convert the cells to logical values, with `true` representing `'g'`. Remove the first two columns of `X` because they have some awkward statistical properties, which are beyond the scope of this discussion.

```
load ionosphere
Ybool = strcmp(Y,'g');
X = X(:,3:end);
```

Step 2. Create a cross-validated fit.

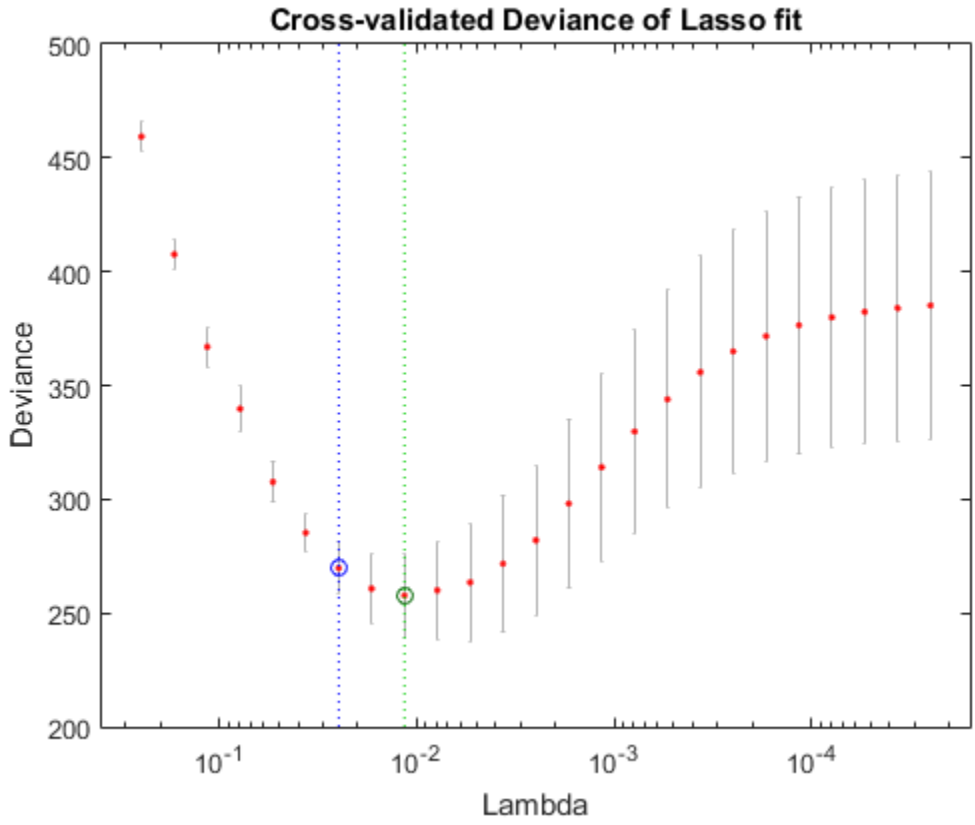
Construct a regularized binomial regression using 25 `Lambda` values and 10-fold cross validation. This process can take a few minutes.

```
rng('default') % for reproducibility
[B,FitInfo] = lassoglm(X,Ybool,'binomial',...
    'NumLambda',25,'CV',10);
```

Step 3. Examine plots to find appropriate regularization.

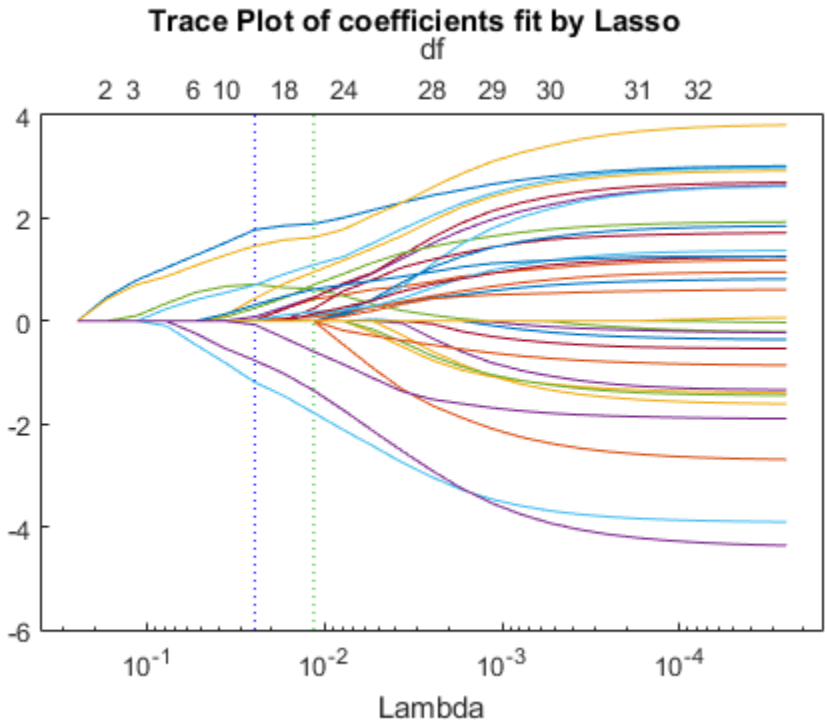
`lassoPlot` can give both a standard trace plot and a cross-validated deviance plot. Examine both plots.

```
lassoPlot(B,FitInfo,'PlotType','CV');
```



The plot identifies the minimum-deviance point with a green circle and dashed line as a function of the regularization parameter `Lambda`. The blue circled point has minimum deviance plus no more than one standard deviation.

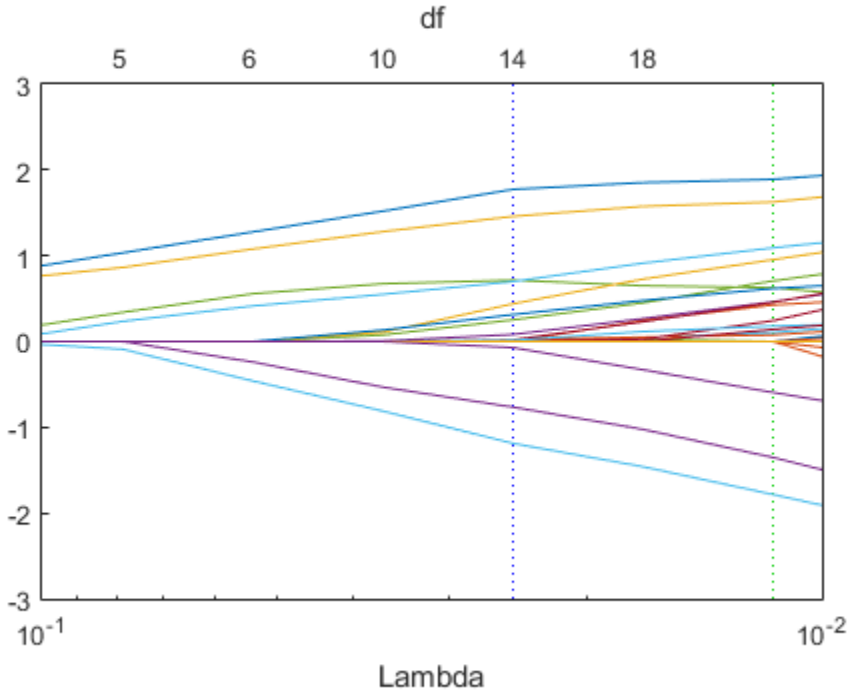
```
lassoPlot(B,FitInfo,'PlotType','Lambda','XScale','log');
```



The trace plot shows nonzero model coefficients as a function of the regularization parameter `Lambda`. Because there are 32 predictors and a linear model, there are 32 curves. As `Lambda` increases to the left, `lassoglm` sets various coefficients to zero, removing them from the model.

The trace plot is somewhat compressed. Zoom in to see more detail.

```
xlim([.01 .1])
ylim([-3 3])
```



As `Lambda` increases toward the left side of the plot, fewer nonzero coefficients remain.

Find the number of nonzero model coefficients at the `Lambda` value with minimum deviance plus one standard deviation point. The regularized model coefficients are in column `FitInfo.Index1SE` of the `B` matrix.

```
indx = FitInfo.Index1SE;
B0 = B(:,indx);
nonzeros = sum(B0 ~= 0)
```

```
nonzeros =

    14
```

When you set `Lambda` to `FitInfo.Index1SE`, `lassoglm` removes over half of the 32 original predictors.

Step 4. Create a regularized model.

The constant term is in the `FitInfo.Index1SE` entry of the `FitInfo.Intercept` vector. Call that value `cnst`.

The model is logit(mu) = log(mu/(1 - mu)) `X*B0 + cnst` . Therefore, for predictions, mu = `exp(X*B0 + cnst)/(1+exp(x*B0 + cnst))`.

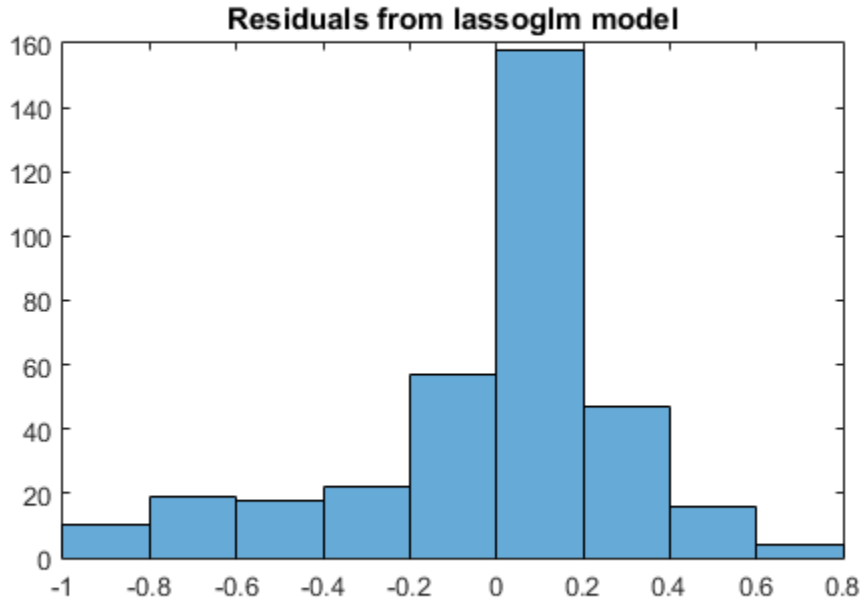
The `glmval` function evaluates model predictions. It assumes that the first model coefficient relates to the constant term. Therefore, create a coefficient vector with the constant term first.

```
cnst = FitInfo.Intercept(indx);
B1 = [cnst;B0];
```

Step 5. Examine residuals.

Plot the training data against the model predictions for the regularized `lassoglm` model.

```
preds = glmval(B1,X,'logit');
histogram(Ybool - preds) % plot residuals
title('Residuals from lassoglm model')
```



Step 6. Alternative: Use identified predictors in a least-squares generalized linear model.

Instead of using the biased predictions from the model, you can make an unbiased model using just the identified predictors.

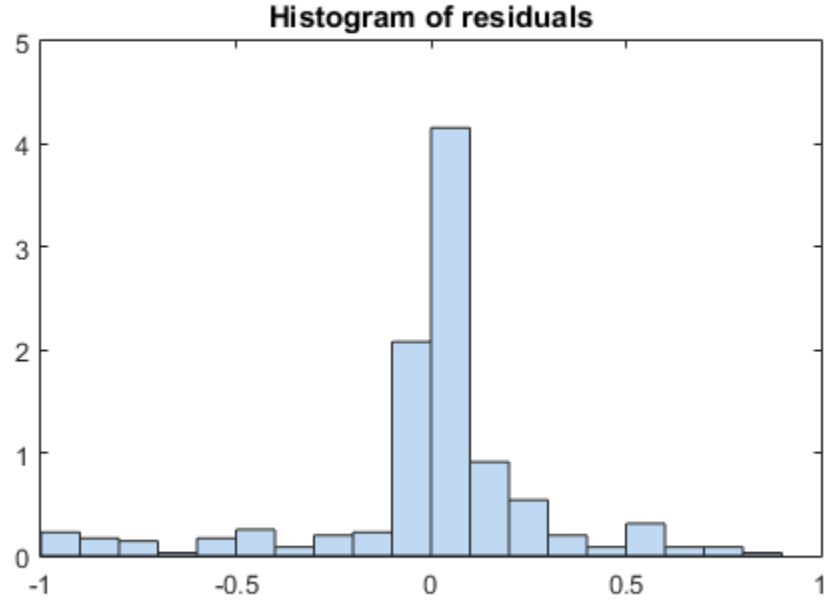
```
predictors = find(B0); % indices of nonzero predictors
mdl = fitglm(X,Ybool,'linear',...
    'Distribution','binomial','PredictorVars',predictors)
```

```
mdl =
```

```
Generalized Linear regression model:
    y ~ [Linear formula with 15 terms in 14 predictors]
    Distribution = Binomial

Estimated Coefficients:
                   Estimate       SE        tStat        pValue
                   ________    _______    ________    __________

    (Intercept)      -2.9367    0.50926     -5.7666    8.0893e-09
    x1                 2.492    0.60795       4.099    4.1502e-05
    x3                2.5501    0.63304      4.0284     5.616e-05
    x4               0.48816    0.50336      0.9698       0.33215
    x5                0.6158    0.62192     0.99015        0.3221
    x6                 2.294     0.5421      4.2317    2.3198e-05
    x7               0.77842    0.57765      1.3476        0.1778
    x12               1.7808    0.54316      3.2786     0.0010432
    x16            -0.070993    0.50515    -0.14054       0.88823
    x20              -2.7767    0.55131     -5.0365    4.7402e-07
    x24               2.0212    0.57639      3.5067    0.00045372
    x25              -2.3796    0.58274     -4.0835    4.4363e-05
    x27              0.79564    0.55904      1.4232       0.15467
    x29               1.2689    0.55468      2.2876      0.022162
    x32              -1.5681    0.54336     -2.8859     0.0039035


351 observations, 336 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 262, p-value = 1e-47
```

Plot the residuals of the model.

```
plotResiduals(mdl)
```



As expected, residuals from the least-squares model are slightly smaller than those of the regularized model. However, this does not mean that `mdl` is a better predictor for new data.

Regularize Wide Data in Parallel

This example shows how to regularize a model with many more predictors than observations. *Wide data* is data with more predictors than observations. Typically, with wide data you want to identify important predictors. Use `lassoglm` as an exploratory or screening tool to select a smaller set of variables to prioritize your modeling and research. Use parallel computing to speed up cross validation.

Load the `ovariancancer` data. This data has 216 observations and 4000 predictors in the `obs` workspace variable. The responses are binary, either `'Cancer'` or `'Normal'`, in the `grp` workspace variable. Convert the responses to binary for use in `lassoglm`.

```
load ovariancancer
y = strcmp(grp,'Cancer');
```

Set options to use parallel computing. Prepare to compute in parallel using `parpool`.

```
opt = statset('UseParallel',true);
parpool()
```

```
Starting parpool using the 'local' profile ... connected to 2 workers.

ans =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
      IdleTimeout: 30
          Cluster: [1x1 parallel.cluster.Local]
     RequestQueue: [1x1 parallel.RequestQueue]
      SpmdEnabled: 1
```

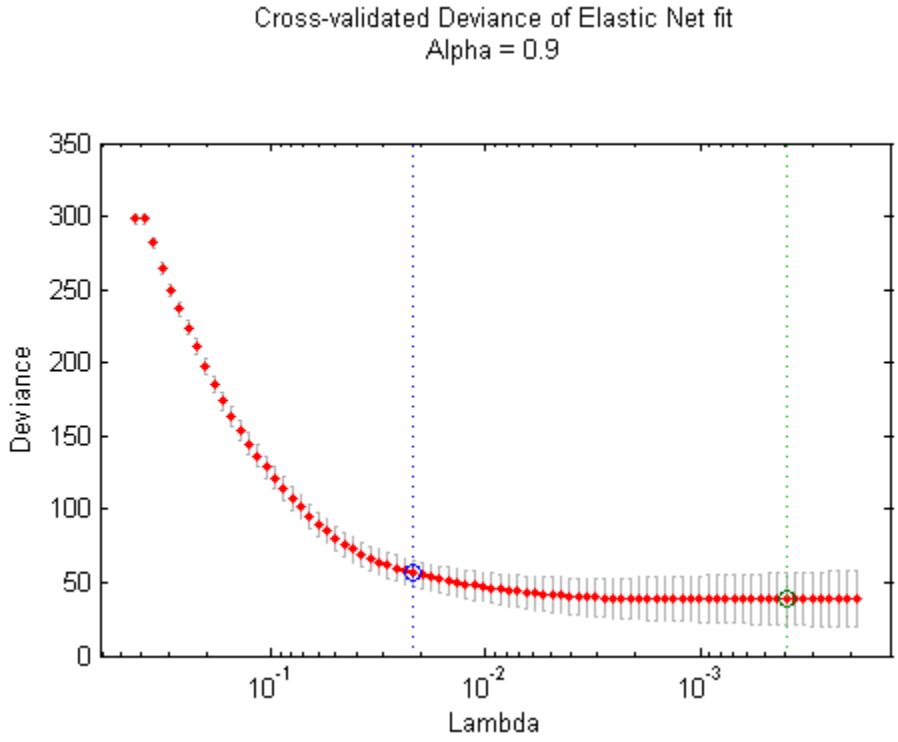
Fit a cross-validated set of regularized models. Use the `Alpha` parameter to favor retaining groups of highly correlated predictors, as opposed to eliminating all but one member of the group. Commonly, you use a relatively large value of `Alpha`.

```
rng('default') % for reproducibility
tic
[B,S] = lassoglm(obs,y,'binomial','NumLambda',100, ...
  'Alpha',0.9,'LambdaRatio',1e-4,'CV',10,'Options',opt);
toc
```

```
Elapsed time is 398.635386 seconds.
```

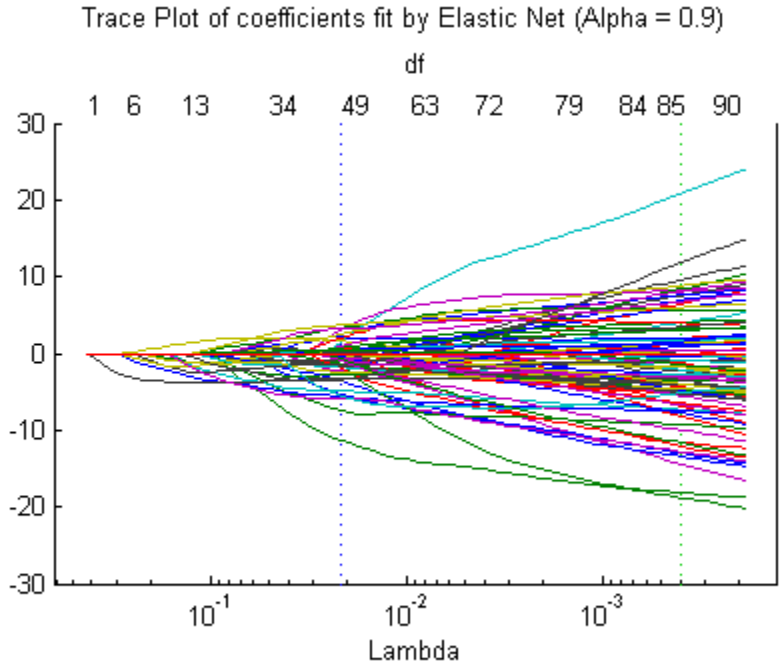
Examine cross-validation plot.

```
lassoPlot(B,S,'PlotType','CV');
```



Examine trace plot.

```
lassoPlot(B,S,'PlotType','Lambda','XScale','log')
```



The right (green) vertical dashed line represents the `Lambda` providing the smallest cross-validated deviance. The left (blue) dashed line has the minimal deviance plus no more than one standard deviation. This blue line has many fewer predictors:

```
[S.DF(S.Index1SE) S.DF(S.IndexMinDeviance)]
```

```
ans =

    50     86
```

You asked `lassoglm` to fit using 100 different `Lambda` values. How many did it use?

```
size(B)
```

```
ans =

        4000          84
```

`lassoglm` stopped after 84 values because the deviance was too small for small `Lambda` values. To avoid overfitting, `lassoglm` halts when the deviance of the fitted model is too small compared to the deviance in the binary responses, ignoring the predictor variables.

You can force `lassoglm` to include more terms by explicitly providing a set of `Lambda` values.

```
minLambda = min(S.Lambda);
explicitLambda = [minLambda*[.1 .01 .001] S.Lambda];
[B2,S2] = lassoglm(obs,y,'binomial','Lambda',explicitLambda,...
    'LambdaRatio',1e-4, 'CV',10,'Options',opt);
length(S2.Lambda)
```

```
ans =

    87
```

`lassoglm` used the three smaller values in fitting.

To save time, you can use:

- Fewer `Lambda`, meaning fewer fits
- Fewer cross-validation folds
- A larger value for `LambdaRatio`

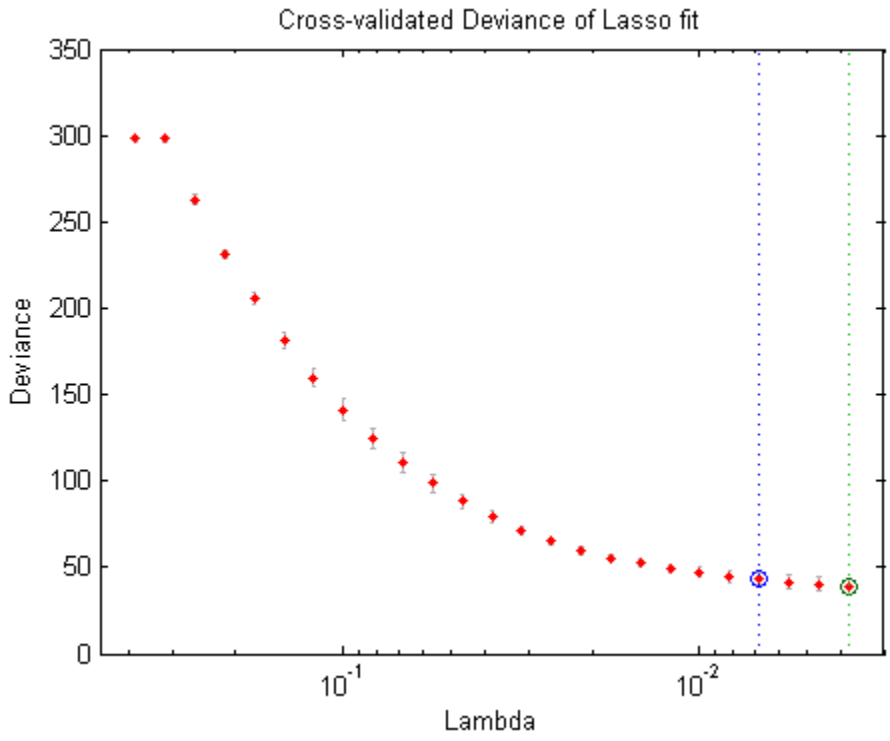
Use serial computation and all three of these time-saving methods:

```
tic
[Bquick,Squick] = lassoglm(obs,y,'binomial','NumLambda',25,...
    'LambdaRatio',1e-2,'CV',5);
toc
```

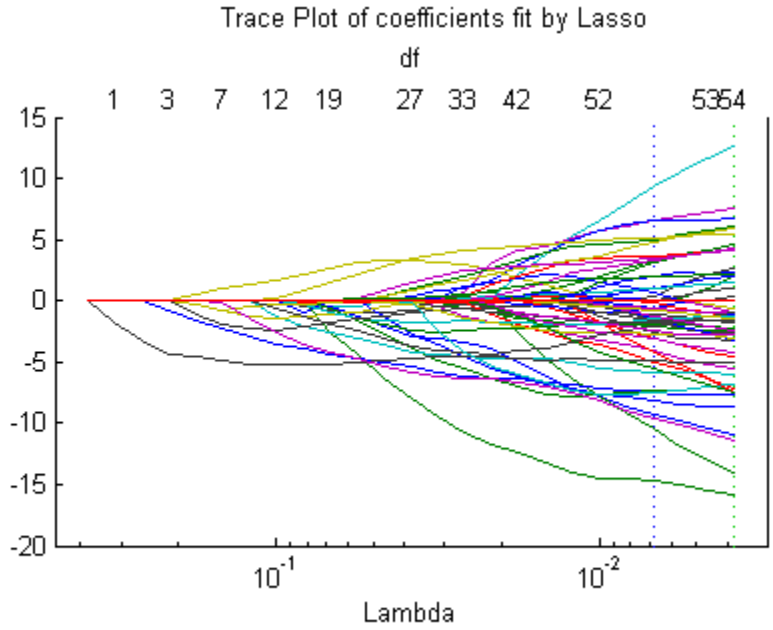
```
Elapsed time is 51.708074 seconds.
```

Graphically compare the new results to the first results.

```
lassoPlot(Bquick,Squick,'PlotType','CV');
```




```
lassoPlot(Bquick,Squick,'PlotType','Lambda','XScale','log')
```



The number of nonzero coefficients in the lowest plus one standard deviation model is around 50, similar to the first computation.

Generalized Linear Model Lasso and Elastic Net

Overview of Lasso and Elastic Net

Lasso is a regularization technique for estimating generalized linear models. Lasso includes a penalty term that constrains the size of the estimated coefficients. Therefore, it resembles ridge regression. Lasso is a *shrinkage estimator*: it generates coefficient estimates that are biased to be small. Nevertheless, a lasso estimator can have smaller error than an ordinary maximum likelihood estimator when you apply it to new data.

Unlike ridge regression, as the penalty term increases, the lasso technique sets more coefficients to zero. This means that the lasso estimator is a smaller model, with fewer predictors. As such, lasso is an alternative to stepwise regression and other model selection and dimensionality reduction techniques.

Elastic net is a related technique. Elastic net is akin to a hybrid of ridge regression and lasso regularization. Like lasso, elastic net can generate reduced models by generating zero-valued coefficients. Empirical studies suggest that the elastic net technique can outperform lasso on data with highly correlated predictors.

Definition of Lasso for Generalized Linear Models

For a nonnegative value of λ, `lasso` solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{N}\text{Deviance}\left(\beta_0,\beta\right)+\lambda\sum_{j=1}^{p}\left|\beta_j\right|\right),$$

where

- Deviance is the deviance of the model fit to the responses using intercept β_0 and predictor coefficients β. The formula for Deviance depends on the `distr` parameter you supply to `lassoglm`. Minimizing the λ-penalized deviance is equivalent to maximizing the λ-penalized log likelihood.
- N is the number of observations.
- λ is a nonnegative regularization parameter corresponding to one value of Lambda.
- Parameters β_0 and β are scalar and p-vector respectively.

As λ increases, the number of nonzero components of β decreases.

The lasso problem involves the L^1 norm of β, as contrasted with the elastic net algorithm.

Definition of Elastic Net for Generalized Linear Models

For an α strictly between 0 and 1, and a nonnegative λ, elastic net solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{N}\text{Deviance}\left(\beta_0,\beta\right)+\lambda P_\alpha\left(\beta\right)\right),$$

where

$$P_\alpha\left(\beta\right)=\frac{(1-\alpha)}{2}\|\beta\|_2^2+\alpha\|\beta\|_1=\sum_{j=1}^{p}\left(\frac{(1-\alpha)}{2}\beta_j^2+\alpha\left|\beta_j\right|\right).$$

Elastic net is the same as lasso when $\alpha = 1$. For other values of α, the penalty term $P_\alpha(\beta)$ interpolates between the L^1 norm of β and the squared L^2 norm of β. As α shrinks toward 0, elastic net approaches `ridge` regression.

References

[1] Tibshirani, R. *Regression Shrinkage and Selection via the Lasso.* Journal of the Royal Statistical Society, Series B, Vol. 58, No. 1, pp. 267–288, 1996.

[2] Zou, H. and T. Hastie. *Regularization and Variable Selection via the Elastic Net.* Journal of the Royal Statistical Society, Series B, Vol. 67, No. 2, pp. 301–320, 2005.

[3] Friedman, J., R. Tibshirani, and T. Hastie. *Regularization Paths for Generalized Linear Models via Coordinate Descent.* Journal of Statistical Software, Vol. 33, No. 1, 2010. http://www.jstatsoft.org/v33/i01

[4] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning,* 2nd edition. Springer, New York, 2008.

[5] McCullagh, P., and J. A. Nelder. *Generalized Linear Models,* 2nd edition. Chapman & Hall/CRC Press, 1989.

Generalized Linear Mixed-Effects Models

In this section...

What Are Generalized Linear Mixed-Effects Models?

Generalized linear mixed-effects (GLME) models describe the relationship between a response variable and independent variables using coefficients that can vary with respect to one or more grouping variables, for data with a response variable distribution other than normal. You can think of GLME models as extensions of generalized linear models (GLM) for data that are collected and summarized in groups. Alternatively, you can think of GLME models as a generalization of linear mixed-effects models (LME) for data where the response variable is not normally distributed.

A mixed-effects model consists of fixed-effects and random-effects terms. Fixed-effects terms are usually the conventional linear regression part of the model. Random-effects terms are associated with individual experimental units drawn at random from a population, and account for variations between groups that might affect the response. The random effects have prior distributions, whereas the fixed effects do not.

GLME Model Equations

The standard form of a generalized linear mixed-effects model is

$$y_i \mid b \sim Distr\left(\mu_i, \frac{\sigma^2}{w_i}\right)$$

$$g(\mu) = X\beta + Zb + \delta ,$$

where

- y is an n-by-1 response vector, and y_i is its ith element.
- b is the random-effects vector.
- *Distr* is a specified conditional distribution of y given b.
- μ is the conditional mean of y given b, and μ_i is its ith element.
- σ^2 is the dispersion parameter.
- w is the effective observation weight vector, and w_i is the weight for observation i.
  - For a binomial distribution, the effective observation weight is equal to the prior weight specified using the `'Weights'` name-value pair argument in `fitglme`, multiplied by the binomial size specified using the `'BinomialSize'` name-value pair argument.
  - For all other distributions, the effective observation weight is equal to the prior weight specified using the `'Weights'` name-value pair argument in `fitglme`.
- $g(\mu)$ is a link function that defines the relationship between the mean response μ and the linear combination of the predictors.
- X is an n-by-p fixed-effects design matrix.
- β is a p-by-1 fixed-effects vector.
- Z is an n-by-q random-effects design matrix.
- b is a q-by-1 random-effects vector.
- δ is a model offset vector.

The model for the mean response μ is

$$\mu = g^{-1}(\eta) ,$$

where g^{-1} is inverse of the link function $g(\mu)$, and $\hat{\eta}_{ME}$ is the linear predictor of the fixed and random effects of the generalized linear mixed-effects model

$$\eta = X\beta + Zb + \delta .$$

A GLME model is parameterized by β, θ, and σ^2.

The assumptions for generalized linear mixed-effects models are:

- The random effects vector b has the prior distribution:

  $$b \mid \sigma^2, \theta \sim N\left(0, \sigma^2 D(\theta)\right),$$

  where σ^2 is the dispersion parameter, and D is a symmetric and positive semidefinite matrix parameterized by an unconstrained parameter vector θ.
- The observations y_i are conditionally independent given b.

Prepare Data for Model Fitting

To fit a GLME model to your data, use `fitglme`. Format your input data using the `table` data type. Each row of the table represents one observation, and each column represents one predictor variable. For more information on creating and using `table`, see "Create a Table".

Input data can include continuous and grouping variables. `fitglme` assumes that predictors using the following data types are categorical:

- Logical
- Categorical
- String or character array

If the input data table contains any `NaN` values, then `fitglme` excludes that entire row of data from the fit. To exclude additional rows of data, you can use the `'Exclude'` name-value pair argument of `fitglme` when fitting the model.

Choose a Distribution Type for the Model

GLME models are used when the response data does not follow a normal distribution. Therefore, when fitting a model using `fitglme`, you must specify the response distribution type using the `'Distribution'` name-value pair argument. Often, the type of response data suggests the appropriate distribution type for the model.

Type of Response Data	Suggested Response Distribution Type
Any real number	`'Normal'`
Any positive number	`'Gamma'` or `'InverseGaussian'`

Type of Response Data	Suggested Response Distribution Type
Any nonnegative integer	`'Poisson'`
Integer from 0 to n, where n is a fixed positive value	`'Binomial'`

Choose a Link Function for the Model

GLME models use a link function, g, to map the relationship between the mean response and the linear combination of the predictors. By default, `fitglme` uses a predefined, commonly accepted link function based on the specified distribution of the response data, as shown in the following table. However, you can specify a different link function from the list of predefined functions, or define your own, using the `'Link'` name-value pair argument of `fitglme`.

Value	Description
`'comploglog'`	`g(mu) = log(-log(1-mu))`
`'identity'`	`g(mu) = mu` Canonical link for the normal distribution.
`'log'`	`g(mu) = log(mu)` Canonical link for the Poisson distribution.
`'logit'`	`g(mu) = log(mu/(1-mu))` Canonical link for the binomial distribution.
`'loglog'`	`g(mu) = log(-log(mu))`
`'probit'`	`g(mu) = norminv(mu)`
`'reciprocal'`	`g(mu) = mu.^(-1)`
Scalar value `P`	`g(mu) = mu.^P`
Structure `S`	A structure containing four fields whose values are function handles: • `S.Link` — Link function • `S.Derivative` — Derivative

Value	Description
	• `S.SecondDerivative` — Second derivative • `S.Inverse` — Inverse of link If `'FitMethod'` is `'MPL'` or `'REMPL'`, or if `S` represents a canonical link for the specified distribution, you can omit the specification of `S.SecondDerivative`.

When fitting a model to data, `fitglme` uses the canonical link function by default.

Distribution	Default Link Function
`'Normal'`	`'identity'`
`'Binomial'`	`'logit'`
`'Poisson'`	`'log'`
`'Gamma'`	`-1`
`'InverseGaussian'`	`-2`

The link functions `'comploglog'`, `'loglog'`, and `'probit'` are mainly useful for binomial models.

Specify the Model Formula

Model specification for `fitglme` uses Wilkinson notation, which is a string of the form `'y ~ terms'`, where `y` is the response variable name, and `terms` is written in the following notation.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1.*X2 (element-wise multiplication of X1 and X2)`
`X1:X2`	`X1.*X2` only

Wilkinson Notation	Factors in Standard Notation
`- X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `–1` in the formula.

For generalized linear mixed-effects models, the formula specification is of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` and `random` contain the fixed-effects and the random-effects terms, respectively.

Suppose the input data table contains the following:

- A response variable, `y`
- Predictor variables, `X1`, `X2`, ..., `XJ`, where J is the total number of predictor variables (including continuous and grouping variables).
- Grouping variables, `g1`, `g2`, ..., `gR`, where R is the number of grouping variables.

The grouping variables in `XJ` and `gR` can be categorical, logical, character arrays, or cell arrays of strings.

Then, in a formula of the form `'y ~ fixed + (random1|g1) + ... + (randomR|gR)'`, the term `fixed` corresponds to a specification of the fixed-effects design matrix `X`, `random1` is a specification of the random-effects design matrix `Z1` corresponding to grouping variable `g1`, and similarly `randomR` is a specification of the random-effects design matrix `ZR` corresponding to grouping variable `gR`. You can express the `fixed` and `random` terms using Wilkinson notation as follows.

Formula	Description
`'y ~ X1 + X2'`	Fixed effects for the intercept, `X1`, and `X2`. This formula is equivalent to `'y ~ 1 + X1 + X2'`.
`'y ~ -1 + X1 + X2'`	No intercept, with fixed effects for `X1` and `X2`. The implicit intercept term is suppressed by including `-1`.

Formula	Description
`'y ~ 1 + (1 | g1)'`	A fixed effect for the intercept, plus a random effect for the intercept for each level of the grouping variable `g1`.
`'y ~ X1 + (1 | g1)'`	Random intercept model with a fixed slope.
`'y ~ X1 + (X1 | g1)'`	Random intercept and slope, with possible correlation between them. This formula is equivalent to `'y ~ 1 + X1 + (1 + X1| g1)'`.
`'y ~ X1 + (1 | g1) + (-1 + X1 | g1)'`	Independent random-effects terms for intercept and slope.
`'y ~ 1 + (1 | g1) + (1 | g2) + (1 | g1:g2)'`	Random intercept model with independent main effects for `g1` and `g2`, plus an independent interaction effect.

For example, the sample data `mfr` contains simulated data from a manufacturing company that operates 50 factories across the world. Each factory runs a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches), and recorded data on processing time (`time_dev`), temperature (`temp_dev`), number of defects (`defects`), and a categorical variable indicating the raw materials supplier (`supplier`) for each batch.

To determine whether the new process (represented by the predictor variable `newprocess`) significantly reduces the number of defects, fit a GLME model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- μ_{ij} is the mean number of defects corresponding to factory i during batch j.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

Using Wilkinson notation, specify this model as:

```
'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|
factory)'
```

To account for the Poisson distribution of the response variable, when fitting the model using `fitglme`, specify the `'Distribution'` name-value pair argument as `'Poisson'`. By default, `fitglme` uses a log link function for response variables with a Poisson distribution.

Display the Model

The output of the fitting function `fitglme` provides information about generalized linear mixed-effects model.

Using the `mfr` manufacturing experiment data, fit a model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Specify the response distribution as Poisson, the link function as log, and the fit method as Laplace.

```
load mfr

glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

```
glme =


Generalized linear mixed-effects model fit by ML
```

```
Model information:
    Number of observations             100
    Fixed effects coefficients           6
    Random effects coefficients         20
    Covariance parameters                1
    Distribution                   Poisson
    Link                           Log
    FitMethod                      Laplace

Formula:
    defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1 | factory)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    416.35    434.58    -201.17          402.35

Fixed effects coefficients (95% CIs):
    Name                 Estimate     SE          tStat       DF    pValue
    '(Intercept)'           1.4689     0.15988      9.1875    94    9.8194e-15
    'newprocess'          -0.36766     0.17755     -2.0708    94      0.041122
    'time_dev'            -0.094521    0.82849    -0.11409    94       0.90941
    'temp_dev'             -0.28317     0.9617    -0.29444    94       0.76907
    'supplier_C'          -0.071868    0.078024     -0.9211    94       0.35936
    'supplier_B'           0.071072     0.07739     0.91836    94       0.36078


    Lower        Upper
       1.1515       1.7864
     -0.72019    -0.015134
      -1.7395       1.5505
      -2.1926       1.6263
     -0.22679     0.083051
    -0.082588      0.22473

Random effects covariance parameters:
Group: factory (20 Levels)
    Name1                Name2                Type         Estimate
    '(Intercept)'        '(Intercept)'        'std'        0.31381

Group: Error
    Name                      Estimate
    'sqrt(Dispersion)'        1
```

The `Model information` table displays the total number of observations in the sample data (100), the number of fixed- and random-effects coefficients (6 and 20, respectively), and the number of covariance parameters (1). It also indicates that the response variable has a `Poisson` distribution, the link function is `Log`, and the fit method is `Laplace`.

`Formula` indicates the model specification using Wilkinson's notation.

The `Model fit statistics` table displays statistics used to assess the goodness of fit of the model. This includes the Akaike information criterion (`AIC`), Bayesian information criterion (`BIC`) values, log likelihood (`LogLikelihood`), and deviance (`Deviance`) values.

The `Fixed effects coefficients` table indicates that `fitglme` returned 95% confidence intervals. It contains one row for each fixed-effects predictor, and each column contains statistics corresponding to that predictor. Column 1 (`Name`) contains the name of each fixed-effects coefficient, column 2 (`Estimate`) contains its estimated value, and column 3 (`SE`) contains the standard error of the coefficient. Column 4 (`tStat`) contains the *t*-statistic for a hypothesis test that the coefficient is equal to 0. Column 5 (`DF`) and column 6 (`pValue`) contain the degrees of freedom and *p*-value that correspond to the *t*-statistic, respectively. The last two columns (`Lower` and `Upper`) display the lower and upper limits, respectively, of the 95% confidence interval for each fixed-effects coefficient.

`Random effects covariance parameters` displays a table for each grouping variable (here, only `factory`), including its total number of levels (20), and the type and estimate of the covariance parameter. Here, `std` indicates that `fitglme` returns the standard deviation of the random effect associated with the factory predictor, which has an estimated value of 0.31381. It also displays a table containing the error parameter type (here, the square root of the dispersion parameter), and its estimated value of 1.

The standard display generated by `fitglme` does not provide confidence intervals for the random-effects parameters. To compute and display these values, use `covarianceParameters`.

Work with the Model

After you create a GLME model using `fitglme`, you can use additional functions to work with the model.

Inspect and Test Coefficients and Confidence Intervals

To extract estimates of the fixed- and random-effects coefficients, covariance parameters, design matrices, and related statistics:

- `fixedEffects` extracts estimated fixed-effects coefficients and related statistics from a fitted model. Related statistics include the standard error; the *t*-statistic, degrees of freedom, and *p*-value for a hypothesis test of whether each parameter is equal to 0; and the confidence intervals.
- `randomEffects` extracts estimated random-effects coefficients and related statistics from a fitted GLME model. Related statistics include the estimated empirical Bayes predictor (EBP) of each random effect, the square root of the conditional mean squared error of prediction (CMSEP) given the covariance parameters and the response; the *t*-statistic, estimated degrees of freedom, and *p*-value for a hypothesis test of whether each random effect is equal to 0; and the confidence intervals.
- `covarianceParameters` extracts estimated covariance parameters and related statistics from a fitted GLME model. Related statistics include estimate of the covariance parameter, and the confidence intervals.
- `designMatrix` extracts the fixed- and random-effects design matrices, or a specified subset thereof, from the fitted GLME model.

To conduct customized hypothesis tests for the significance of fixed- and random-effects coefficients, and to compute custom confidence intervals:

- `anova` performs a marginal *F*-test (hypothesis test) on fixed-effects terms, to determine if all coefficients representing the fixed-effects terms are equal to 0. You can use `anova` to test the combined significance of the coefficients of categorical predictors.
- `coefCI` computes confidence intervals for fixed- and random-effects parameters from a fitted GLME model. By default, `fitglme` computes 95% confidence intervals. Use `coefCI` to compute the boundaries at a different confidence level.
- `coefTest` performs custom hypothesis tests on fixed-effects or random-effects vectors of a fitted generalized linear mixed-effects model. For example, you can specify contrast matrices.

Generate New Response Values and Refit Model

To generate new response values, including fitted, predicted, and random responses, based on the fitted GLME model:

- `fitted` computes fitted response values using the original predictor values, and the estimated coefficient and parameter values from the fitted model.
- `predict` computes the predicted conditional or marginal mean of the response using either the original predictor values or new predictor values, and the estimated coefficient and parameter values from the fitted model.

- `random` generates random responses from a fitted model.
- `refit` creates a new fitted GLME model, based on the original model and a new response vector.

Inspect and Visualize Residuals

To extract and visualize residuals from the fitted GLME model:

- `residuals` extracts the raw or Pearson residuals from the fitted model. You can also specify whether to compute the conditional or marginal residuals.
- `plotResiduals` creates plots using the raw or Pearson residuals from the fitted model, including:
  - A histogram of the residuals
  - A scatterplot of the residuals versus fitted values
  - A scatterplot of residuals versus lagged residuals

See Also

`fitglme` | `GeneralizedLinearMixedModel`

Related Examples

- “Fit a Generalized Linear Mixed-Effects Model” on page 10-79

Estimating Parameters in Generalized Linear Mixed-Effects Models

In this section...

Model Form

The standard form of a generalized linear mixed-effects model is

where g is the link function and $\hat{\eta}_{ME}$ is the linear predictor of the fixed-and random-effects of the generalized linear mixed effects model, defined as

$$\hat{\eta}_{ME} = X\hat{\beta} + Z\hat{b} + \delta \ .$$

Here,

- X is an n-by-p fixed-effects design matrix
- β is a p-by-1 fixed-effects vector
- Z is an n-by-q random-effects design matrix
- b is a q-by-1 random-effects vector
- *offset* is an n-by-1 vector containing the offset variable in the fit.

The random-effects vector b is assumed to have the following prior distribution:

where D is a symmetric and positive semidefinite matrix, parameterized by component vector θ.

The observations yi are assumed to be conditional independent given b, which implies that

In this model, the parameters to estimate are the fixed-effects coefficients

The likelihood of y given β, θ, and τ^2 is

However, this integral is analytically intractable for generalized linear mixed-effects models. To solve this problem, use either the model approximation approach or the integral approximation approach.

Model Approximations

The maximum pseudolikelihood (MPL) and restricted maximum pseudolikelihood (REMPL) are model approximation approaches.

First, linearize the relationship between μ_i and β and b using a first-order Taylor series expansion of the general GLME equation . Write it in vector form as

Let and be the values of μ_i and η_i, evaluated at and . Then

Next, linearly approximating the equation around and , obtain

Then we get

Rewriting in a different form, we obtain

In vector form, this can be written as

where F is

This motivates the definition of a "pseudo" response y^p in terms of the original response vector y as

Similarly, we can obtain an approximation for the covariance

Together, the "pseudo" response y^p can be approximated using the equations

This final set of "pseudo" response equations looks like a weighted linear mixed-effects (LME) model, except that the distribution of the error term ε is unspecified. In GLME, we assume that the distribution of ε is Gaussian, which allows us to fit this "pseudo" model using standard weighted LME model fitting algorithms. This gives us the fitted values for , , , and . Then update and using the new fitted values and continue the process until convergence.

If the intermediate LME fits are done using maximum likelihood (ML), then the technique is called maximum pseudolikelihood (MPL). If the intermediate LME fits are done using restricted maximum likelihood (REML), then the technique is called

restricted maximum pseudolikelihood (REMPL). For more information on ML and REML, see “Estimating Parameters in Linear Mixed-Effects Models” on page 9-170.

Integral Approximations

Laplace approximation.

Fit a Generalized Linear Mixed-Effects Model

This example shows how to fit a generalized linear mixed-effects model (GLME) to sample data.

Load the sample data.

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

A manufacturing company operates 50 factories across the world, and each runs a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. However, the company wants to test the new process in select factories to ensure that it is effective before rolling it out to all 50 locations.

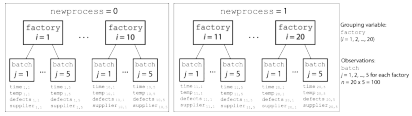
To test whether the new process significantly reduces the number of defects in each batch, the company selected 20 of its factories at random to participate in an experiment. Ten factories implemented the new process, while the other ten used the old process.

In each of the 20 factories (i = 1, 2, ..., 20), the company ran five batches (j = 1, 2, ..., 5) and recorded the following data in the table `mfr`:

- Flag to indicate use of the new process:
  - If the batch used the new process, then `newprocess = 1`
  - If the batch used the old process, then `newprocess = 0`
- Processing time for the batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Supplier of the chemical used in the batch (`supplier`)
  - `supplier` is a categorical variable with levels `A`, `B`, and `C`, where each level represents one of the three suppliers
- Number of defects in the batch (defects)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours and 20

degrees Celsius. The response variable `defects` has a Poisson distribution. This is simulated data.



The company wants to determine whether the new process significantly reduces the number of defects in each batch, while accounting for quality differences that might exist due to factory-specific variations in time, temperature, and supplier. The number of defects per batch can be modeled using a Poison distribution:

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

Use a generalized linear mixed-effects model to model the number of defects per batch:

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

Fit a GLME model and interpret the results.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept

grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

```
glme =


Generalized linear mixed-effects model fit by ML

Model information:
    Number of observations             100
    Fixed effects coefficients           6
    Random effects coefficients         20
    Covariance parameters                1
    Distribution                   Poisson
    Link                           Log
    FitMethod                      Laplace

Formula:
    defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1 | factory)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    416.35    434.58    -201.17          402.35

Fixed effects coefficients (95% CIs):
    Name                 Estimate     SE          tStat       DF    pValue
    '(Intercept)'           1.4689     0.15988      9.1875    94    9.8194e-15
    'newprocess'          -0.36766     0.17755     -2.0708    94      0.041122
    'time_dev'            -0.094521    0.82849     -0.11409   94      0.90941
    'temp_dev'            -0.28317      0.9617     -0.29444   94      0.76907
    'supplier_C'          -0.071868    0.078024    -0.9211    94      0.35936
    'supplier_B'           0.071072    0.07739      0.91836   94      0.36078


    Lower        Upper
       1.1515       1.7864
    -0.72019    -0.015134
     -1.7395       1.5505
     -2.1926       1.6263
```

```
     -0.22679     0.083051
    -0.082588      0.22473

Random effects covariance parameters:
Group: factory (20 Levels)
    Name1                Name2                Type         Estimate
    '(Intercept)'        '(Intercept)'        'std'        0.31381

Group: Error
    Name                      Estimate
    'sqrt(Dispersion)'        1
```

The `Model information` table displays the total number of observations in the sample data (100), the number of fixed- and random-effects coefficients (6 and 20, respectively), and the number of covariance parameters (1). It also indicates that the response variable has a `Poisson` distribution, the link function is `Log`, and the fit method is `Laplace`.

`Formula` indicates the model specification using Wilkinson's notation.

The `Model fit statistics` table displays statistics used to assess the goodness of fit of the model. This includes the Akaike information criterion (`AIC`), Bayesian information criterion (`BIC`) values, log likelihood (`LogLikelihood`), and deviance (`Deviance`) values.

The `Fixed effects coefficients` table indicates that `fitglme` returned 95% confidence intervals. It contains one row for each fixed-effects predictor, and each column contains statistics corresponding to that predictor. Column 1 (`Name`) contains the name of each fixed-effects coefficient, column 2 (`Estimate`) contains its estimated value, and column 3 (`SE`) contains the standard error of the coefficient. Column 4 (`tStat`) contains the *t*-statistic for a hypothesis test that the coefficient is equal to 0. Column 5 (`DF`) and column 6 (`pValue`) contain the degrees of freedom and *p*-value that correspond to the *t*-statistic, respectively. The last two columns (`Lower` and `Upper`) display the lower and upper limits, respectively, of the 95% confidence interval for each fixed-effects coefficient.

`Random effects covariance parameters` displays a table for each grouping variable (here, only `factory`), including its total number of levels (20), and the type and estimate of the covariance parameter. Here, `std` indicates that `fitglme` returns the standard deviation of the random effect associated with the factory predictor, which has an estimated value of 0.31381. It also displays a table containing the error parameter type (here, the square root of the dispersion parameter), and its estimated value of 1.

The standard display generated by `fitglme` does not provide confidence intervals for the random-effects parameters. To compute and display these values, use `covarianceParameters`.

Check significance of random effect.

To determine whether the random-effects intercept grouped by `factory` is statistically significant, compute the confidence intervals for the estimated covariance parameter.

```
[psi,dispersion,stats] = covarianceParameters(glme);
```

`covarianceParameters` returns the estimated covariance parameter in `psi`, the estimated dispersion parameter `dispersion`, and a cell array of related statistics `stats`. The first cell of `stats` contains statistics for `factory`, while the second cell contains statistics for the dispersion parameter.

Display the first cell of `stats` to see the confidence intervals for the estimated covariance parameter for `factory`.

```
stats{1}
```

```
ans =


    Covariance Type: Isotropic

    Group      Name1                Name2                Type
    factory    '(Intercept)'        '(Intercept)'        'std'


    Estimate    Lower      Upper
    0.31381     0.19253    0.51148
```

The columns `Lower` and `Upper` display the default 95% confidence interval for the estimated covariance parameter for `factory`. Because the interval [0.19253,0.51148] does not contain 0, the random-effects intercept is significant at the 5% significance level. Therefore, the random effect due to factory-specific variation must be considered before drawing any conclusions about the effectiveness of the new manufacturing process.

Compare two models.

Compare the mixed-effects model that includes a random-effects intercept grouped by `factory` with a model that does not include the random effect, to determine which model is a better fit for the data. Fit the first model, `FEglme`, using only the fixed-effects predictors `newprocess`, `time_dev`, `temp_dev`, and `supplier`. Fit the second model, `glme`, using these same fixed-effects predictors, but also including a random-effects intercept grouped by `factory`.

```
FEglme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier','Distr

glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Compare the two models using a likelihood ratio test. Specify `'CheckNesting'` as `true`, so `compare` returns a warning if the nesting requirements are not satisfied.

```
results = compare(FEglme,glme,'CheckNesting',true)
```

```
results =


    Theoretical Likelihood Ratio Test

    Model     DF    AIC       BIC       LogLik     LRStat    deltaDF
    FEglme    6     431.02    446.65    -209.51
    glme      7     416.35    434.58    -201.17    16.672    1


    pValue

    4.4435e-05
```

`compare` returns the degrees of freedom (`DF`), the Akaike information criterion (`AIC`), Bayesian information criterion (`BIC`), and log likelihood values for each model. `glme` has smaller AIC, BIC, and log likelihood values than `FEglme`, which indicates that `glme` (the model containing the random-effects term for intercept grouped by factory) is the better-fitting model for this data. Additionally, the small *p*-value indicates that `compare` rejects the null hypothesis that the response vector was generated by the fixed-effects-only model `FEglme`, in favor of the alternative that the response vector was generated by the mixed-effects model `glme`.

Plot the results.

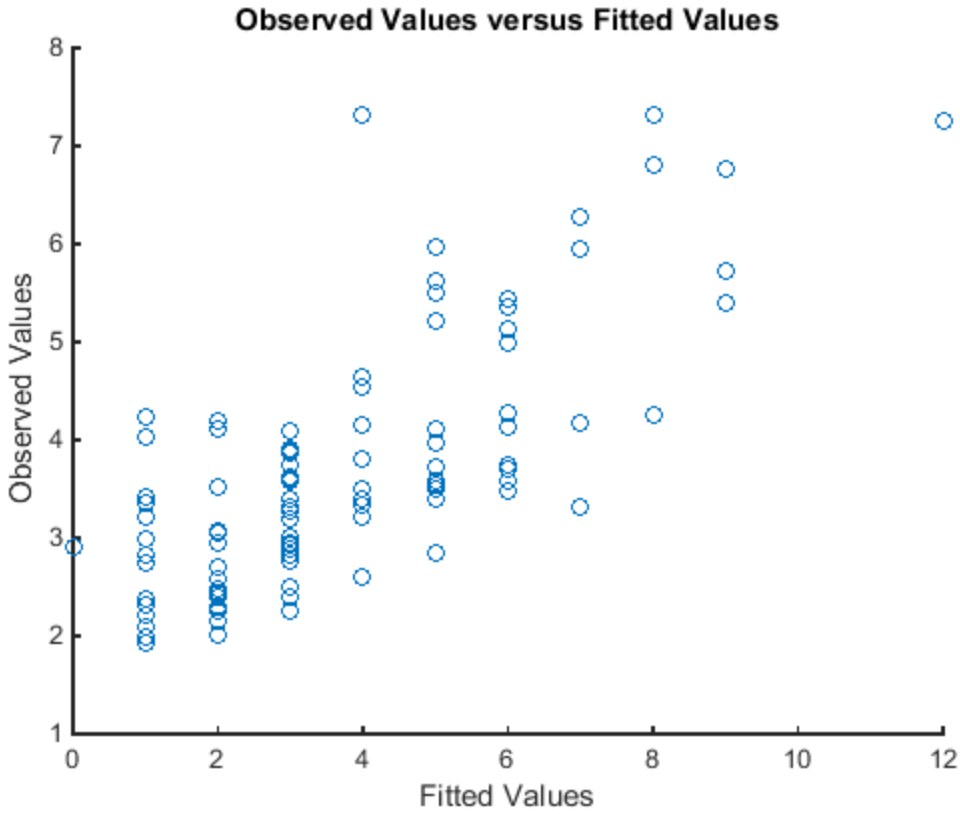
Generate the fitted conditional mean values for the model.

```
mufit = fitted(glme);
```

Plot the observed response values versus the fitted response values.

```
figure
scatter(mfr.defects,mufit)
title('Observed Values versus Fitted Values')
```

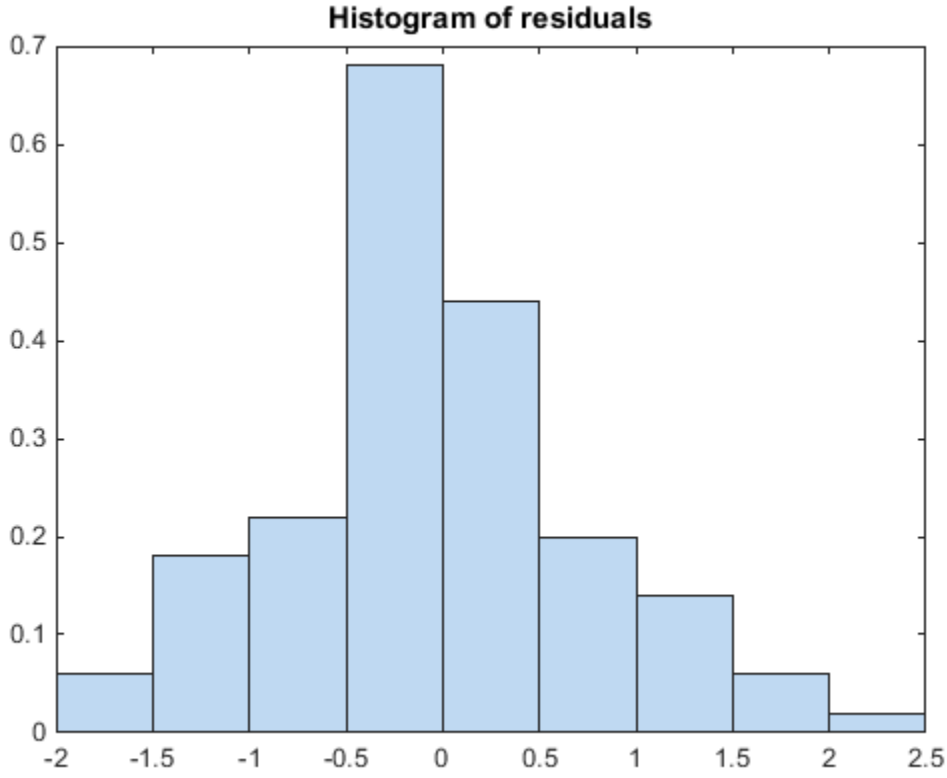
```
xlabel('Fitted Values')
ylabel('Observed Values')
```



Create diagnostic plots using conditional Pearson residuals to test model assumptions. Since raw residuals for generalized linear mixed-effects models do not have a constant variance across observations, use the conditional Pearson residuals instead.

Plot a histogram to visually confirm that the mean of the Pearson residuals is equal to 0. If the model is correct, we expect the Pearson residuals to be centered at 0.

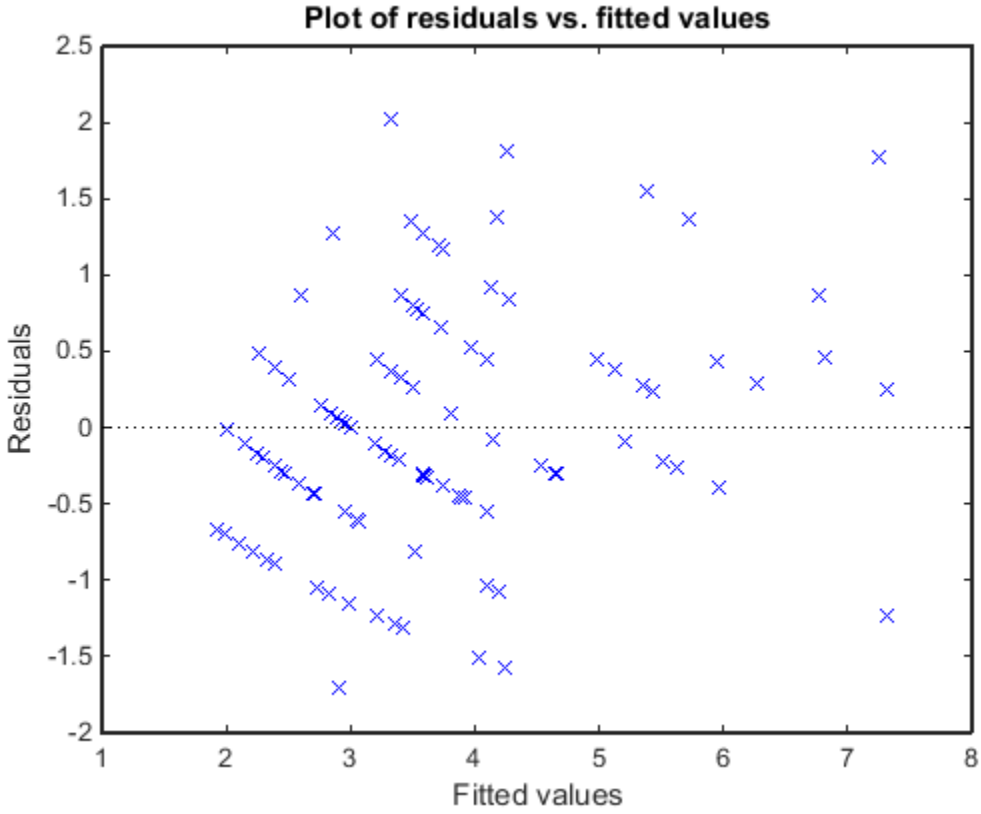
```
plotResiduals(glme,'histogram','ResidualType','Pearson')
```



The histogram shows that the Pearson residuals are centered at 0.

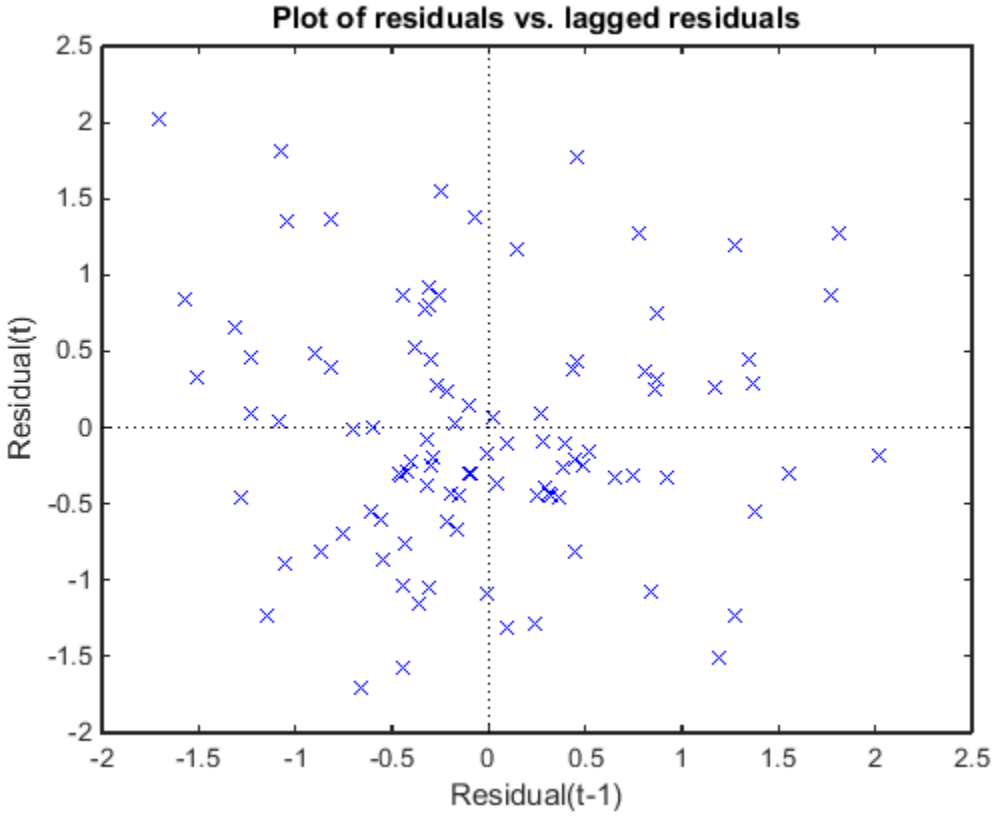
Plot the Pearson residuals versus the fitted values, to check for signs of nonconstant variance among the residuals (heteroscedasticity). We expect the conditional Pearson residuals to have a constant variance. Therefore, a plot of conditional Pearson residuals versus conditional fitted values should not reveal any systematic dependence on the conditional fitted values.

```
plotResiduals(glme,'fitted','ResidualType','Pearson')
```



The plot does not show a systematic dependence on the fitted values, so there are no signs of nonconstant variance among the residuals.

Plot the Pearson residuals versus lagged residuals, to check for correlation among the residuals. The conditional independence assumption in GLME implies that the conditional Pearson residuals are approximately uncorrelated.



There is no pattern to the plot, so there are no signs of correlation among the residuals.

See Also

`fitglme` | `GeneralizedLinearMixedModel`

More About

- "Generalized Linear Models" on page 10-12

Nonlinear Regression

Nonlinear Regression

In this section...

What Are Parametric Nonlinear Regression Models?

Parametric nonlinear models represent the relationship between a continuous response variable and one or more continuous predictor variables in the form
$y = f(X,\beta) + \varepsilon$,

where

- y is an n-by-1 vector of observations of the response variable.
- f is any function of X and β that evaluates each row of X along with the vector β to compute the prediction for the corresponding row of y.
- X is an n-by-p matrix of predictors, with one row for each observation, and one column for each predictor.
- β is a p-by-1 vector of unknown parameters to be estimated.
- ε is an n-by-1 vector of independent, identically distributed random disturbances.

In contrast, nonparametric models do not attempt to characterize the relationship between predictors and response with model parameters. Descriptions are often graphical, as in the case of "Classification Trees and Regression Trees" on page 16-33.

`fitnlm` attempts to find values of the parameters β that minimize the mean squared differences between the observed responses y and the predictions of the model $f(X,\beta)$. To do so, it needs a starting value `beta0` before iteratively modifying the vector β to a vector with minimal mean squared error.

Prepare Data

To begin fitting a regression, put your data into a form that fitting functions expect. All regression techniques begin with input data in an array `X` and response data in a separate vector `y`, or input data in a table or dataset array `tbl` and response data as a column in `tbl`. Each row of the input data represents one observation. Each column represents one predictor (variable).

For a table or dataset array `tbl`, indicate the response variable with the `'ResponseVar'` name-value pair:

```
mdl = fitlm(tbl,'ResponseVar','BloodPressure');
```

The response variable is the last column by default.

You cannot use numeric *categorical* predictors for nonlinear regression. A categorical predictor is one that takes values from a fixed set of possibilities.

Represent missing data as `NaN` for both input data and response data.

Dataset Array for Input and Response Data

For example, to create a dataset array from an Excel spreadsheet:

```
ds = dataset('XLSFile','hospital.xls',...
     'ReadObsNames',true);
```

To create a dataset array from workspace variables:

```
load carsmall
ds = dataset(Weight,Model_Year,MPG);
```

Table for Input and Response Data

To create a table from an Excel spreadsheet:

```
tbl = readtable('hospital.xls',...
     'ReadRowNames',true);
```

To create a table from workspace variables:

```
load carsmall
tbl = table(Weight,Model_Year,MPG);
```

Numeric Matrix for Input Data and Numeric Vector for Response

For example, to create numeric arrays from workspace variables:

```
load carsmall
X = [Weight Horsepower Cylinders Model_Year];
y = MPG;
```

To create numeric arrays from an Excel spreadsheet:

```
[X Xnames] = xlsread('hospital.xls');
y = X(:,4); % response y is systolic pressure
X(:,4) = []; % remove y from the X matrix
```

Notice that the nonnumeric entries, such as `sex`, do not appear in `X`.

Represent the Nonlinear Model

There are several ways to represent a nonlinear model. Use whichever is most convenient.

The nonlinear model is a required input to `fitnlm`, in the `modelfun` input.

`fitnlm` assumes that the response function $f(X,\beta)$ is smooth in the parameters β. If your function is not smooth, `fitnlm` can fail to provide optimal parameter estimates.

- "Function Handle to Anonymous Function or Function File" on page 11-4
- "String Representation of Formula" on page 11-5

Function Handle to Anonymous Function or Function File

The function handle `@modelfun(b,x)` accepts a vector `b` and matrix, table, or dataset array `x`. The function handle should return a vector `f` with the same number of rows as `x`. For example, the function file `hougen.m` computes

$$\text{hougen}(b,x) = \frac{b(1)x(2) - x(3)/b(5)}{1 + b(2)x(1) + b(3)x(2) + b(4)x(3)}.$$

Examine the function by entering `type hougen` at the MATLAB command line.

```
function yhat = hougen(beta,x)
%HOUGEN Hougen-Watson model for reaction kinetics.
```

```
%   YHAT = HOUGEN(BETA,X) gives the predicted values of the
%   reaction rate, YHAT, as a function of the vector of
%   parameters, BETA, and the matrix of data, X.
%   BETA must have 5 elements and X must have three
%   columns.
%
%   The model form is:
%   y = (b1*x2 - x3/b5)./(1+b2*x1+b3*x2+b4*x3)
%
%   Reference:
%      [1]  Bates, Douglas, and Watts, Donald, "Nonlinear
%      Regression Analysis and Its Applications", Wiley
%      1988 p. 271-272.

%   Copyright 1993-2004 The MathWorks, Inc.
%   B.A. Jones 1-06-95.

b1 = beta(1);
b2 = beta(2);
b3 = beta(3);
b4 = beta(4);
b5 = beta(5);

x1 = x(:,1);
x2 = x(:,2);
x3 = x(:,3);

yhat = (b1*x2 - x3/b5)./(1+b2*x1+b3*x2+b4*x3);
```

You can write an anonymous function that performs the same calculation as `hougen.m`.

```
modelfun = @(b,x)(b(1)*x(:,2) - x(:,3)/b(5))./...
(1 + b(2)*x(:,1) + b(3)*x(:,2) + b(4)*x(:,3));
```

String Representation of Formula

For data in a matrix `X` and response in a vector `y`:

- Represent the formula using `'x1'` as the first predictor (column) in `X`, `'x2'` as the second predictor, etc.
- Represent the vector of parameters to optimize as `'b1'`, `'b2'`, etc.
- Write the formula as `'y ~ (mathematical expressions)'`.

For example, to represent the response to the reaction data:

```
modelfun = 'y ~ (b1*x2 - x3/b5)/(1 + b2*x1 + b3*x2 + b4*x3)';
```

For data in a table or dataset array, you can use formulas represented as strings with the variable names from the table or dataset array. Put the response variable name at the left of the formula, followed by a ~, followed by a string representing the response formula.

This example shows how to create a string to represent the response to the `reaction` data that is in a dataset array.

1. Load the `reaction` data.

   ```
   load reaction
   ```

2. Put the data into a dataset array, where each variable has a name given in the `xn` or `yn` strings.

   ```
   ds = dataset({reactants,xn(1,:),xn(2,:),xn(3,:)},...
       {rate,yn});
   ```

3. Examine the first row of the dataset array.

   ```
   ds(1,:)

   ans =

       Hydrogen    n_Pentane    Isopentane    ReactionRate
       470         300          10            8.55
   ```

4. Write the `hougen` formula using names in the dataset array.

   ```
   modelfun = ['ReactionRate ~ (b1*n_Pentane - Isopentane/b5) /'...
   ' (1 + Hydrogen*b2 + n_Pentane*b3 + Isopentane*b4)']

   modelfun =
   ReactionRate ~ (b1*n_Pentane - Isopentane/b5) / ...
        (1 + Hydrogen*b2 + n_Pentane*b3 + Isopentane*b4)
   ```

Choose Initial Vector beta0

The initial vector for the fitting iterations, `beta0`, can greatly influence the quality of the resulting fitted model. `beta0` gives the dimensionality of the problem, meaning it needs the correct length. A good choice of `beta0` leads to a quick, reliable model, while a poor choice can lead to a long computation, or to an inadequate model.

It is difficult to give advice on choosing a good `beta0`. If you believe certain components of the vector should be positive or negative, set your `beta0` to have those characteristics. If you know the approximate value of other components, include them in `beta0`. However, if you don't know good values, try a random vector, such as

```
beta0 = randn(nVars,1);
% or
beta0 = 10*rand(nVars,1);
```

Fit Nonlinear Model to Data

The syntax for fitting a nonlinear regression model using a table or dataset array `tbl` is

```
mdl = fitnlm(tbl,modelfun,beta0)
```

The syntax for fitting a nonlinear regression model using a numeric array `X` and numeric response vector `y` is

```
mdl = fitnlm(X,y,modelfun,beta0)
```

For information on representing the input parameters, see "Prepare Data" on page 11-3, "Represent the Nonlinear Model" on page 11-4, and "Choose Initial Vector beta0" on page 11-6.

`fitnlm` assumes that the response variable in a table or dataset array `tbl` is the last column. To change this, use the `ResponseVar` name-value pair to name the response column.

Examine Quality and Adjust the Fitted Nonlinear Model

There are diagnostic plots to help you examine the quality of a model. `plotDiagnostics(mdl)` gives a variety of plots, including leverage and Cook's distance plots. `plotResiduals(mdl)` gives the difference between the fitted model and the data.

There are also properties of mdl that relate to the model quality. `mdl.RMSE` gives the root mean square error between the data and the fitted model. `mdl.Residuals.Raw` gives the raw residuals. `mdl.Diagnostics` contains several fields, such as Leverage and CooksDistance, that can help you identify particularly interesting observations.

This example shows how to examine a fitted nonlinear model using diagnostic, residual, and slice plots.

Load the sample data.

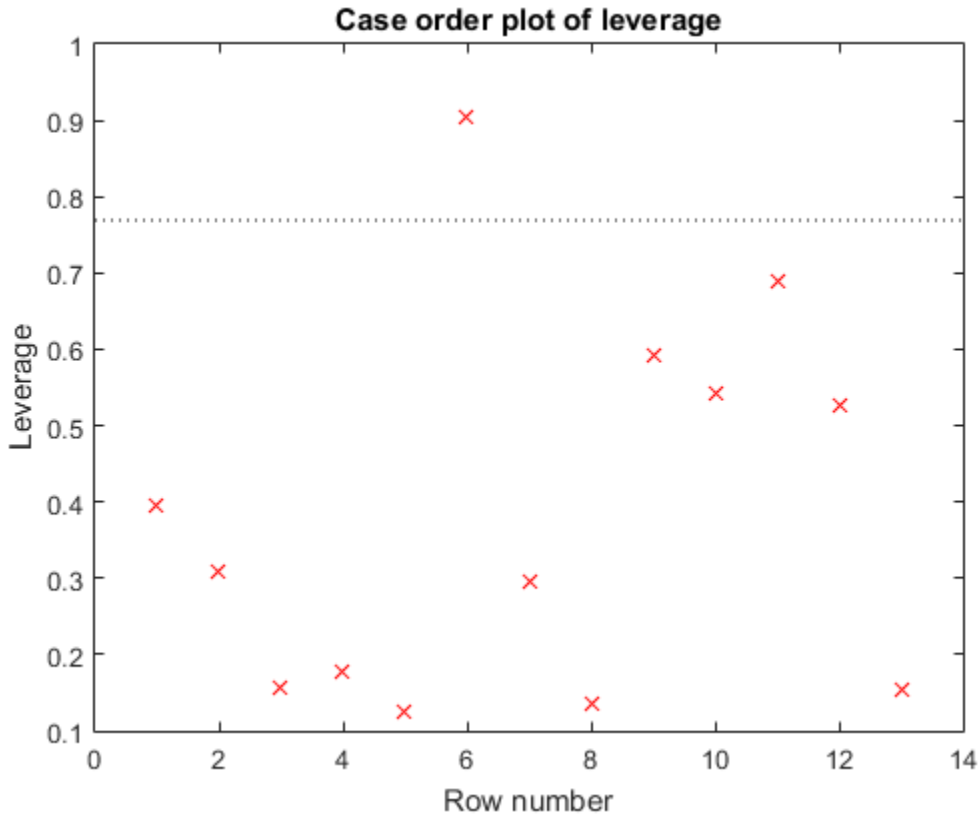
```
load reaction
```

Create a nonlinear model of rate as a function of `reactants` using the `hougen.m` function.

```
beta0 = ones(5,1);
mdl = fitnlm(reactants,...
    rate,@hougen,beta0);
```

Make a leverage plot of the data and model.

```
plotDiagnostics(mdl)
```



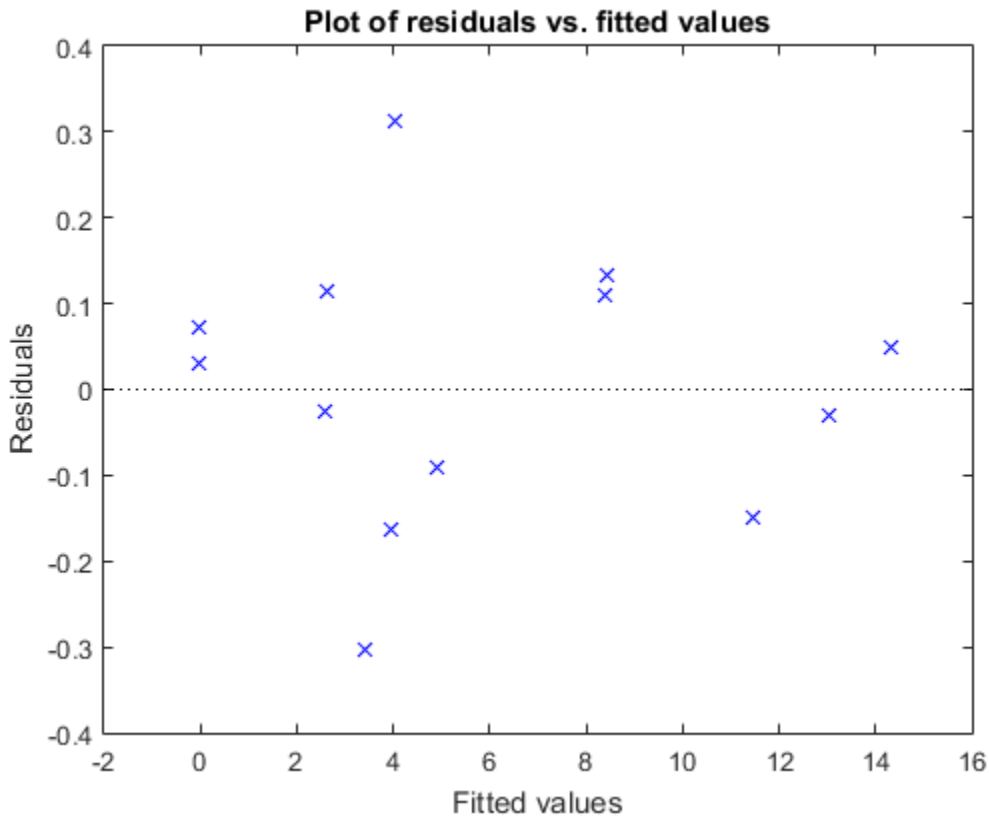
There is one point that has high leverage. Locate the point.

```
[~,maxl] = max(mdl.Diagnostics.Leverage)
```

```
maxl =

     6
```

Examine a residuals plot.

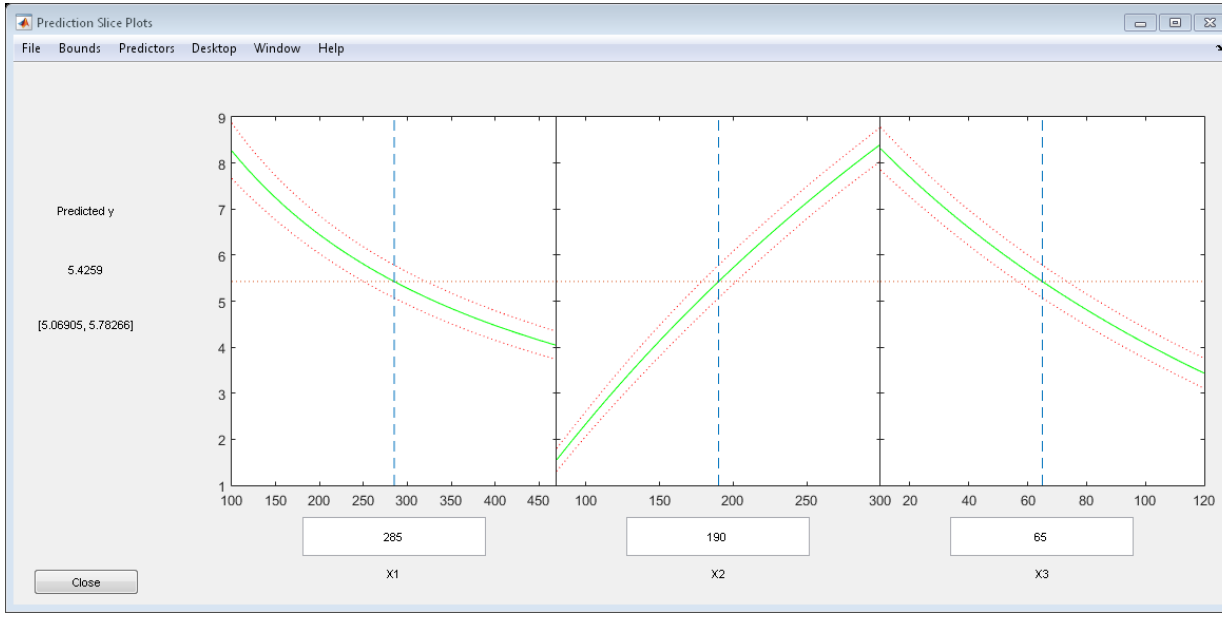
```
plotResiduals(mdl,'fitted')
```



Nothing stands out as an outlier.

Use a slice plot to show the effect of each predictor on the model.

```
plotSlice(mdl)
```



You can drag the vertical dashed blue lines to see the effect of a change in one predictor on the response. For example, drag the X2 line to the right, and notice that the slope of the X3 line changes.

Predict or Simulate Responses Using a Nonlinear Model

This example shows how to use the methods `predict` , `feval` , and `random` to predict and simulate responses to new data.

Randomly generate a sample from a Cauchy distribution.

```
rng('default')
X = rand(100,1);
```

```
X = tan(pi*X - pi/2);
```

Generate the response according to the model `y = b1*(pi /2 + atan((x - b2) / b3))` and add noise to the response.

```
modelfun = @(b,x) b(1) * ...
    (pi/2 + atan((x - b(2))/b(3)));
y = modelfun([12 5 10],X) + randn(100,1);
```

Fit a model starting from the arbitrary parameters $b = [1,1,1]$.

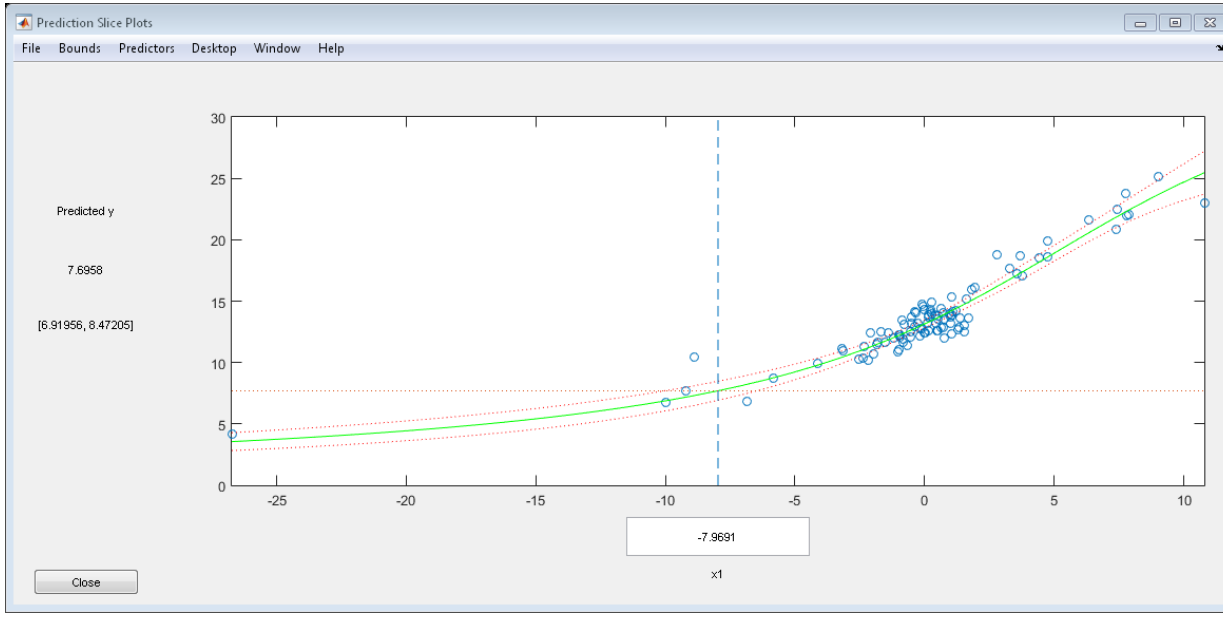
```
beta0 = [1 1 1]; % An arbitrary guess
mdl = fitnlm(X,y,modelfun,beta0)
```

```
mdl =


Nonlinear regression model:
    y ~ b1*(pi/2 + atan((x - b2)/b3))

Estimated Coefficients:
          Estimate      SE       tStat       pValue
          ________    _______    ______    __________

    b1    12.082      0.80028    15.097    3.3151e-27
    b2    5.0603       1.0825    4.6747    9.5063e-06
    b3      9.64      0.46499    20.732    2.0382e-37


Number of observations: 100, Error degrees of freedom: 97
Root Mean Squared Error: 1.02
R-Squared: 0.92,  Adjusted R-Squared 0.918
F-statistic vs. zero model: 6.45e+03, p-value = 1.72e-111
```

The fitted values are within a few percent of the parameters [12,5,10].

Examine the fit.

```
plotSlice(mdl)
```



predict

The `predict` method predicts the mean responses and, if requested, gives confidence bounds. Find the predicted response values and predicted confidence intervals about the response at *X* values [-15;5;12].

```
Xnew = [-15;5;12];
[ynew,ynewci] = predict(mdl,Xnew)
```

```
ynew =

    5.4122
   18.9022
   26.5161


ynewci =

    4.8233    6.0010
   18.4555   19.3490
   25.0170   28.0151
```

The confidence intervals are reflected in the slice plot.

feval

The `feval` method predicts the mean responses. `feval` is often more convenient to use than predict when you construct a model from a dataset array.

Create the nonlinear model from a dataset array.

```
ds = dataset({X,'X'},{y,'y'});
mdl2 = fitnlm(ds,modelfun,beta0);
```

Find the predicted model responses (CDF) at X values [-15;5;12].

```
Xnew = [-15;5;12];
ynew = feval(mdl2,Xnew)
```

```
ynew =

    5.4122
   18.9022
   26.5161
```

random

The `random` method simulates new random response values, equal to the mean prediction plus a random disturbance with the same variance as the training data.

```
Xnew = [-15;5;12];
ysim = random(mdl,Xnew)
```

```
ysim =

    6.0505
   19.0893
   25.4647
```

Rerun the random method. The results change.

```
ysim = random(mdl,Xnew)
```

```
ysim =

    6.3813
   19.2157
   26.6541
```

Nonlinear Regression Workflow

This example shows how to do a typical nonlinear regression workflow: import data, fit a nonlinear regression, test its quality, modify it to improve the quality, and make predictions based on the model.

Step 1. Prepare the data.

Load the `reaction` data

```
load reaction
```

Examine the data in the workspace. `reactants` is a matrix with 13 rows and 3 columns. Each row corresponds to one observation, and each column corresponds to one variable. The variable names are in `xn`:

```
xn
```

```
xn =

Hydrogen
n-Pentane
Isopentane
```

Similarly, `rate` is a vector of 13 responses, with the variable name in `yn`:

```
yn
```

```
yn =

Reaction Rate
```

The `hougen.m` file contains a nonlinear model of reaction rate as a function of the three predictor variables. For a 5-D vector b and 3-D vector x,

$$\text{hougen}(b,x) = \frac{b(1)x(2) - x(3)/b(5)}{1 + b(2)x(1) + b(3)x(2) + b(4)x(3)}.$$

As a start point for the solution, take `b` as a vector of ones.

```
beta0 = ones(5,1);
```

Step 2. Fit a nonlinear model to the data.

```
mdl = fitnlm(reactants,...
    rate,@hougen,beta0)

mdl =

Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1      1.2526     0.86702    1.4447    0.18654
    b2    0.062776    0.043562    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075158    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923

Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.193
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. constant model: 1.81e+03, p-value = 7.36e-12
```

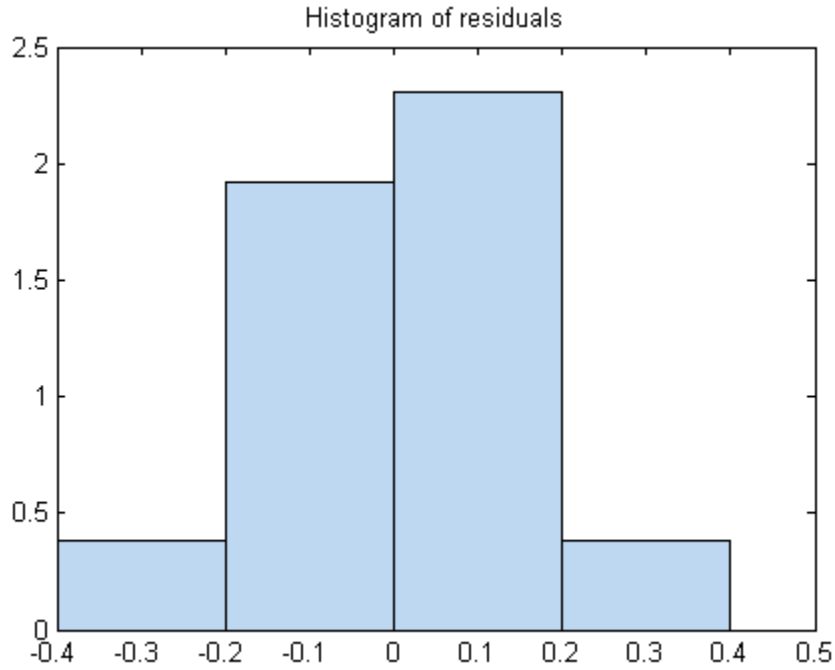
Step 3. Examine the quality of the model.

The root mean squared error is fairly low compared to the range of observed values.

```
[mdl.RMSE min(rate) max(rate)]

ans =

    0.1933    0.0200   14.3900
```

Examine a residuals plot.

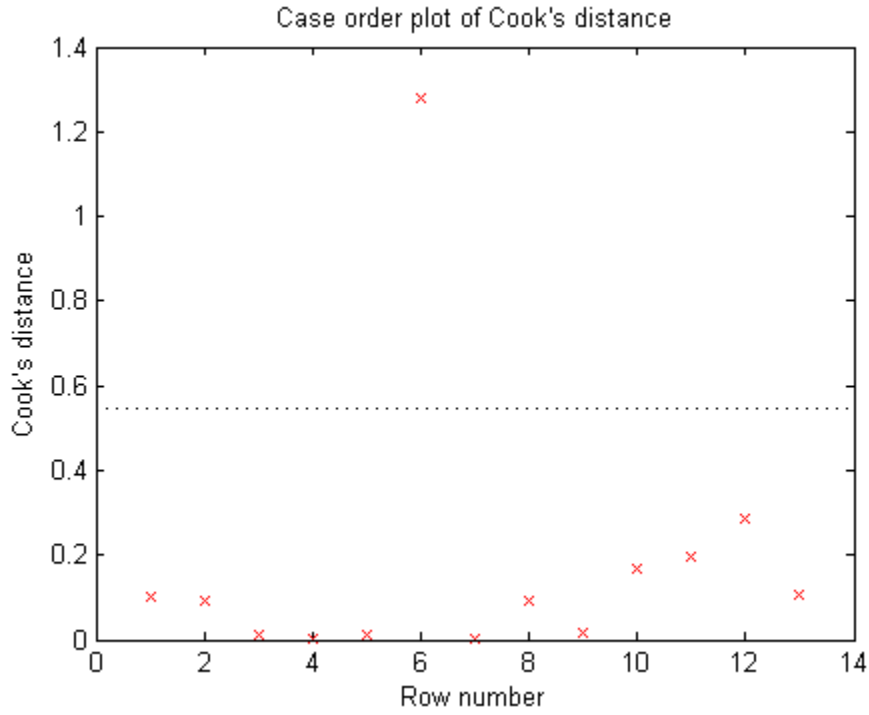
```
plotResiduals(mdl)
```



The model seems adequate for the data.

Examine a diagnostic plot to look for outliers.

```
plotDiagnostics(mdl,'cookd')
```



Observation 6 seems out of line.

Step 4. Remove the outlier.

Remove the outlier from the fit using the `Exclude` name-value pair.

```
mdl1 = fitnlm(reactants,...
    rate,@hougen,ones(5,1),'Exclude',6)
```

```
mdl1 =

Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1       0.619      0.4552    1.3598    0.21605
    b2    0.030377    0.023061    1.3172    0.22924
    b3    0.018927     0.01574    1.2024    0.26828
```

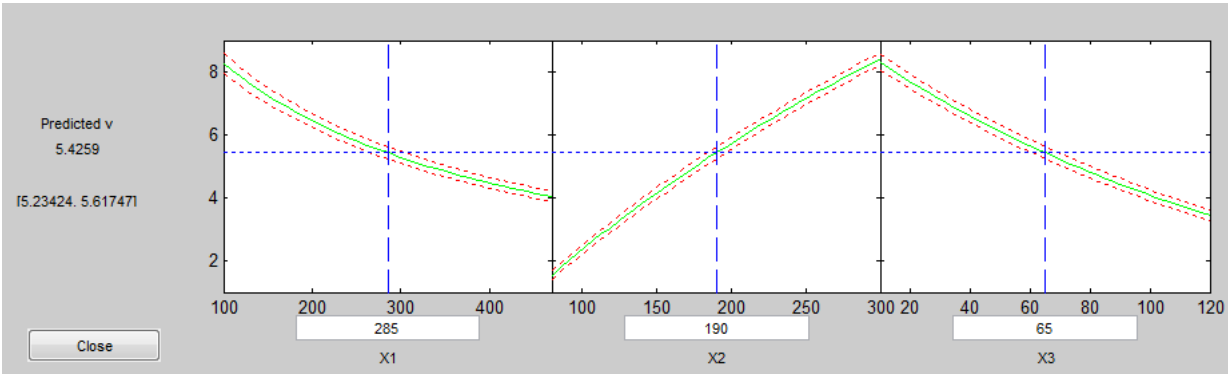
```
    b4     0.053411     0.041084        1.3     0.23476
    b5       2.4125       1.7903     1.3475      0.2198

Number of observations: 12, Error degrees of freedom: 7
Root Mean Squared Error: 0.198
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. constant model: 1.24e+03, p-value = 4.73e-10
```

The model coefficients changed quite a bit from those in `mdl`.

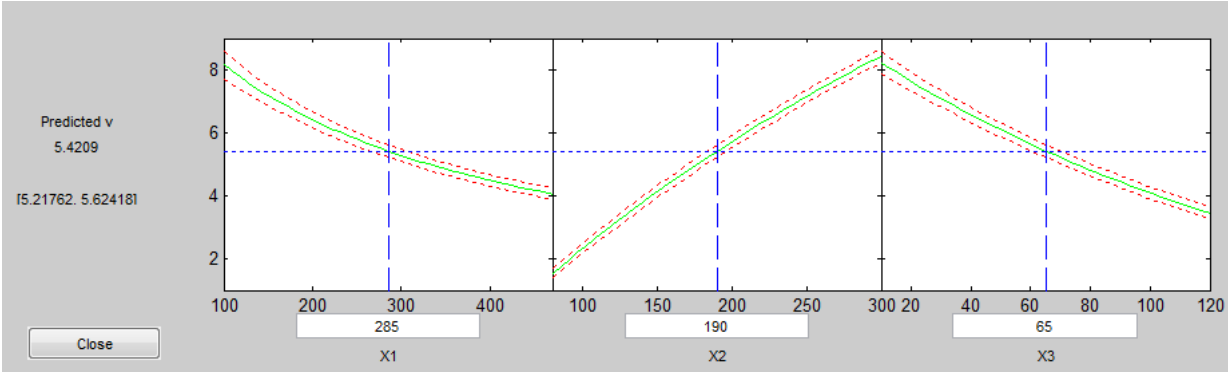
Step 5. Examine slice plots of both models.

To see the effect of each predictor on the response, make a slice plot using `plotSlice(mdl)`.

```
plotSlice(mdl)
```




```
plotSlice(mdl1)
```



The plots look very similar, with slightly wider confidence bounds for `mdl1`. This difference is understandable, since there is one less data point in the fit, representing over 7% fewer observations.

Step 6. Predict for new data.

Create some new data and predict the response from both models.

```
Xnew =  [200,200,200;100,200,100;500,50,5];
[ypred yci] = predict(mdl,Xnew)
```

```
ypred =

    1.8762
    6.2793
    1.6718


yci =

    1.6283    2.1242
    5.9789    6.5797
    1.5589    1.7846
```

```
[ypred1 yci1] = predict(mdl1,Xnew)
```

```
ypred1 =

    1.8984
    6.2555
    1.6594


yci1 =

    1.6260    2.1708
    5.9323    6.5787
    1.5345    1.7843
```

Even though the model coefficients are dissimilar, the predictions are nearly identical.

Mixed-Effects Models

In this section...

Introduction to Mixed-Effects Models

In statistics, an *effect* is anything that influences the value of a response variable at a particular setting of the predictor variables. Effects are translated into model parameters. In linear models, effects become coefficients, representing the proportional contributions of model terms. In nonlinear models, effects often have specific physical interpretations, and appear in more general nonlinear combinations.

Fixed effects represent population parameters, assumed to be the same each time data is collected. Estimating fixed effects is the traditional domain of regression modeling. *Random effects*, by comparison, are sample-dependent random variables. In modeling, random effects act like additional error terms, and their distributions and covariances must be specified.

For example, consider a model of the elimination of a drug from the bloodstream. The model uses time t as a predictor and the concentration of the drug C as the response. The nonlinear model term C_0e^{-rt} combines parameters C_0 and r, representing, respectively, an initial concentration and an elimination rate. If data is collected across multiple individuals, it is reasonable to assume that the elimination rate is a random variable r_i depending on individual i, varying around a population mean $\bar{r}$. The term C_0e^{-rt} becomes

$$C_0e^{-[\bar{r}+(r_i-\bar{r})]t} = C_0e^{-(\beta+b_i)t},$$

where $\beta = \bar{r}$ is a fixed effect and $b_i = r_i - \bar{r}$ is a random effect.

Random effects are useful when data falls into natural groups. In the drug elimination model, the groups are simply the individuals under study. More sophisticated models might group data by an individual's age, weight, diet, etc. Although the groups are not the focus of the study, adding random effects to a model extends the reliability of inferences beyond the specific sample of individuals.

Mixed-effects models account for both fixed and random effects. As with all regression models, their purpose is to describe a response variable as a function of the predictor variables. Mixed-effects models, however, recognize correlations within sample subgroups. In this way, they provide a compromise between ignoring data groups entirely and fitting each group with a separate model.

Mixed-Effects Model Hierarchy

Suppose data for a nonlinear regression model falls into one of m distinct groups $i = 1, ..., m$. To account for the groups in a model, write response j in group i as:

$$y_{ij} = f(\varphi, x_{ij}) + \varepsilon_{ij}$$

y_{ij} is the response, x_{ij} is a vector of predictors, φ is a vector of model parameters, and ε_{ij} is the measurement or process error. The index j ranges from 1 to n_i, where n_i is the number of observations in group i. The function f specifies the form of the model. Often, x_{ij} is simply an observation time t_{ij}. The errors are usually assumed to be independent and identically, normally distributed, with constant variance.

Estimates of the parameters in φ describe the population, assuming those estimates are the same for all groups. If, however, the estimates vary by group, the model becomes

$$y_{ij} = f(\varphi_i, x_{ij}) + \varepsilon_{ij}$$

In a mixed-effects model, φ_i may be a combination of a fixed and a random effect:

$$\varphi_i = \beta + b_i$$

The random effects b_i are usually described as multivariate normally distributed, with mean zero and covariance Ψ. Estimating the fixed effects β and the covariance of the random effects Ψ provides a description of the population that does not assume the parameters φ_i are the same across groups. Estimating the random effects b_i also gives a description of specific groups within the data.

Model parameters do not have to be identified with individual effects. In general, *design matrices* A and B are used to identify parameters with linear combinations of fixed and random effects:

$$\varphi_i = A\beta + Bb_i$$

If the design matrices differ among groups, the model becomes

$$\varphi_i = A_i\beta + B_ib_i$$

If the design matrices also differ among observations, the model becomes

$$\begin{aligned}\varphi_{ij} &= A_{ij}\beta + B_{ij}b_i\\ y_{ij} &= f(\varphi_{ij}, x_{ij}) + \varepsilon_{ij}\end{aligned}$$

Some of the group-specific predictors in x_{ij} may not change with observation j. Calling those v_i, the model becomes

$$y_{ij} = f(\varphi_{ij}, x_{ij}, v_i) + \varepsilon_{ij}$$

Specifying Mixed-Effects Models

Suppose data for a nonlinear regression model falls into one of m distinct groups $i = 1, ..., m$. (Specifically, suppose that the groups are not nested.) To specify a general nonlinear mixed-effects model for this data:

1. Define group-specific model parameters φ_i as linear combinations of fixed effects β and random effects b_i.

2 Define response values y_i as a nonlinear function f of the parameters and group-specific predictor variables X_i.

The model is:

$$\begin{aligned}\varphi_i &= A_i\beta + B_i b_i \\ y_i &= f(\varphi_i, X_i) + \varepsilon_i \\ b_i &\sim N(0, \Psi) \\ \varepsilon_i &\sim N(0, \sigma^2)\end{aligned}$$

This formulation of the nonlinear mixed-effects model uses the following notation:

φ_i	A vector of group-specific model parameters
β	A vector of fixed effects, modeling population parameters
b_i	A vector of multivariate normally distributed group-specific random effects
A_i	A group-specific design matrix for combining fixed effects
B_i	A group-specific design matrix for combining random effects
X_i	A data matrix of group-specific predictor values
y_i	A data vector of group-specific response values
f	A general, real-valued function of φ_i and X_i
ε_i	A vector of group-specific errors, assumed to be independent, identically, normally distributed, and independent of b_i
Ψ	A covariance matrix for the random effects
o^2	The error variance, assumed to be constant across observations

For example, consider a model of the elimination of a drug from the bloodstream. The model incorporates two overlapping phases:

- An initial phase p during which drug concentrations reach equilibrium with surrounding tissues
- A second phase q during which the drug is eliminated from the bloodstream

For data on multiple individuals i, the model is

$$y_{ij} = C_{pi}e^{-r_{pi}t_{ij}} + C_{qi}e^{-r_{qi}t_{ij}} + \varepsilon_{ij},$$

where y_{ij} is the observed concentration in individual i at time t_{ij}. The model allows for different sampling times and different numbers of observations for different individuals.

The elimination rates r_{pi} and r_{qi} must be positive to be physically meaningful. Enforce this by introducing the log rates $R_{pi} = \log(r_{pi})$ and $R_{qi} = \log(r_{qi})$ and reparametrizing the model:

$$y_{ij} = C_{pi}e^{-\exp(R_{pi})t_{ij}} + C_{qi}e^{-\exp(R_{qi})t_{ij}} + \varepsilon_{ij}$$

Choosing which parameters to model with random effects is an important consideration when building a mixed-effects model. One technique is to add random effects to all parameters, and use estimates of their variances to determine their significance in the model. An alternative is to fit the model separately to each group, without random effects, and look at the variation of the parameter estimates. If an estimate varies widely across groups, or if confidence intervals for each group have minimal overlap, the parameter is a good candidate for a random effect.

To introduce fixed effects β and random effects b_i for all model parameters, reexpress the model as follows:

$$\begin{aligned} y_{ij} &= [\bar{C}_p + (C_{pi} - \bar{C}_p)]e^{-\exp[\bar{R}_p + (R_{pi} - \bar{R}_p)]t_{ij}} + \\ &\quad [\bar{C}_q + (C_{qi} - \bar{C}_q)]e^{-\exp[\bar{R}_q + (R_{qi} - \bar{R}_q)]t_{ij}} + \varepsilon_{ij} \\ &= (\beta_1 + b_{1i})e^{-\exp(\beta_2 + b_{2i})t_{ij}} + \\ &\quad (\beta_3 + b_{3i})e^{-\exp(\beta_4 + b_{4i})t_{ij}} + \varepsilon_{ij} \end{aligned}$$

In the notation of the general model:

$$\beta = \begin{pmatrix} \beta_1 \\ \vdots \\ \beta_4 \end{pmatrix}, b_i = \begin{pmatrix} b_{i1} \\ \vdots \\ b_{i4} \end{pmatrix}, y_i = \begin{pmatrix} y_{i1} \\ \vdots \\ y_{in_i} \end{pmatrix}, X_i = \begin{pmatrix} t_{i1} \\ \vdots \\ t_{in_i} \end{pmatrix},$$

where n_i is the number of observations of individual i. In this case, the design matrices A_i and B_i are, at least initially, 4-by-4 identity matrices. Design matrices may be altered, as necessary, to introduce weighting of individual effects, or time dependency.

Fitting the model and estimating the covariance matrix Ψ often leads to further refinements. A relatively small estimate for the variance of a random effect suggests that it can be removed from the model. Likewise, relatively small estimates for covariances among certain random effects suggests that a full covariance matrix is unnecessary. Since random effects are unobserved, Ψ must be estimated indirectly. Specifying a diagonal or block-diagonal covariance pattern for Ψ can improve convergence and efficiency of the fitting algorithm.

Statistics and Machine Learning Toolbox functions `nlmefit` and `nlmefitsa` fit the general nonlinear mixed-effects model to data, estimating the fixed and random effects. The functions also estimate the covariance matrix Ψ for the random effects. Additional diagnostic outputs allow you to assess tradeoffs between the number of model parameters and the goodness of fit.

Specifying Covariate Models

If the model in "Specifying Mixed-Effects Models" on page 11-22 assumes a group-dependent covariate such as weight (w) the model becomes:

$$\begin{pmatrix}\varphi_1\\ \varphi_2\\ \varphi_3\end{pmatrix}=\begin{pmatrix}1 & 0 & 0 & w_i\\ 0 & 1 & 0 & 0\\ 0 & 0 & 1 & 0\end{pmatrix}\begin{pmatrix}\beta_1\\ \beta_2\\ \beta_3\\ \beta_4\end{pmatrix}+\begin{pmatrix}1 & 0 & 0\\ 0 & 1 & 0\\ 0 & 0 & 1\end{pmatrix}\begin{pmatrix}b_1\\ b_2\\ b_3\end{pmatrix}$$

Thus, the parameter φ_i for any individual in the `i`th group is:

$$\begin{pmatrix}\varphi_{1_i}\\ \varphi_{2_i}\\ \varphi_{3_i}\end{pmatrix}=\begin{pmatrix}\beta_1 + \beta_4 * w_i\\ \beta_2\\ \beta_3\end{pmatrix}+\begin{pmatrix}b_{1_i}\\ b_{2_i}\\ b_{3_i}\end{pmatrix}$$

To specify a covariate model, use the `'FEGroupDesign'` option.

`'FEGroupDesign'` is a `p-by-q-by-m` array specifying a different `p-by-q` fixed-effects design matrix for each of the `m` groups. Using the previous example, the array resembles the following:

1. Create the array.

```
% Number of parameters in the model (Phi)
num_params = 3;
% Number of covariates
num_cov = 1;
% Assuming number of groups in the data set is 7
num_groups = 7;
% Array of covariate values
covariates = [75; 52; 66; 55; 70; 58; 62 ];
A = repmat(eye(num_params, num_params+num_cov),...
[1,1,num_groups]);
A(1,num_params+1,1:num_groups) = covariates(:,1)
```

2. Create a `struct` with the specified design matrix.

```
options.FEGroupDesign = A;
```

3. Specify the arguments for `nlmefit` (or `nlmefitsa`) as shown in "Mixed-Effects Models Using nlmefit and nlmefitsa" on page 11-34.

Choosing nlmefit or nlmefitsa

Statistics and Machine Learning Toolbox provides two functions, `nlmefit` and `nlmefitsa` for fitting nonlinear mixed-effects models. Each function provides different capabilities, which may help you decide which to use.

Approximation Methods

`nlmefit` provides the following four approximation methods for fitting nonlinear mixed-effects models:

- `'LME'` — Use the likelihood for the linear mixed-effects model at the current conditional estimates of `beta` and `B`. This is the default.
- `'RELME'` — Use the restricted likelihood for the linear mixed-effects model at the current conditional estimates of `beta` and `B`.
- `'FO'` — First-order Laplacian approximation without random effects.
- `'FOCE'` — First-order Laplacian approximation at the conditional estimates of `B`.

`nlmefitsa` provides an additional approximation method, Stochastic Approximation Expectation-Maximization (SAEM) [24] with three steps :

1. Simulation: Generate simulated values of the random effects b from the posterior density $p(b \mid \Sigma)$ given the current parameter estimates.
2. Stochastic approximation: Update the expected value of the log likelihood function by taking its value from the previous step, and moving part way toward the average value of the log likelihood calculated from the simulated random effects.
3. Maximization step: Choose new parameter estimates to maximize the log likelihood function given the simulated values of the random effects.

Both `nlmefit` and `nlmefitsa` attempt to find parameter estimates to maximize a likelihood function, which is difficult to compute. `nlmefit` deals with the problem by approximating the likelihood function in various ways, and maximizing the approximate function. It uses traditional optimization techniques that depend on things like convergence criteria and iteration limits.

`nlmefitsa`, on the other hand, simulates random values of the parameters in such a way that in the long run they converge to the values that maximize the exact likelihood function. The results are random, and traditional convergence tests don't apply. Therefore `nlmefitsa` provides options to plot the results as the simulation progresses, and to restart the simulation multiple times. You can use these features to judge whether the results have converged to the accuracy you desire.

Parameters Specific to nlmefitsa

The following parameters are specific to `nlmefitsa`. Most control the stochastic algorithm.

- `CovO` — Initial value for the covariance matrix `PSI`. Must be an *r*-by-*r* positive definite matrix. If empty, the default value depends on the values of `BETAO`.
- `ComputeStdErrors` — `true` to compute standard errors for the coefficient estimates and store them in the output `STATS` structure, or `false` (default) to omit this computation.
- `LogLikMethod` — Specifies the method for approximating the log likelihood.
- `NBurnIn` — Number of initial burn-in iterations during which the parameter estimates are not recomputed. Default is 5.
- `NIterations` — Controls how many iterations are performed for each of three phases of the algorithm.
- `NMCMCIterations` — Number of Markov Chain Monte Carlo (MCMC) iterations.

Model and Data Requirements

There are some differences in the capabilities of `nlmefit` and `nlmefitsa`. Therefore some data and models are usable with either function, but some may require you to choose just one of them.

- **Error models** — `nlmefitsa` supports a variety of error models. For example, the standard deviation of the response can be constant, proportional to the function value, or a combination of the two. `nlmefit` fits models under the assumption that the standard deviation of the response is constant. One of the error models, `'exponential'`, specifies that the log of the response has a constant standard deviation. You can fit such models using `nlmefit` by providing the log response as input, and by rewriting the model function to produce the log of the nonlinear function value.
- **Random effects** — Both functions fit data to a nonlinear function with parameters, and the parameters may be simple scalar values or linear functions of covariates. `nlmefit` allows any coefficients of the linear functions to have both fixed and random effects. `nlmefitsa` supports random effects only for the constant (intercept) coefficient of the linear functions, but not for slope coefficients. So in the example in "Specifying Covariate Models" on page 11-25, `nlmefitsa` can treat only the first three beta values as random effects.

- **Model form** — `nlmefit` supports a very general model specification, with few restrictions on the design matrices that relate the fixed coefficients and the random effects to the model parameters. `nlmefitsa` is more restrictive:

  - The fixed effect design must be constant in every group (for every individual), so an observation-dependent design is not supported.
  - The random effect design must be constant for the entire data set, so neither an observation-dependent design nor a group-dependent design is supported.
  - As mentioned under **Random Effects**, the random effect design must not specify random effects for slope coefficients. This implies that the design must consist of zeros and ones.
  - The random effect design must not use the same random effect for multiple coefficients, and cannot use more than one random effect for any single coefficient.
  - The fixed effect design must not use the same coefficient for multiple parameters. This implies that it can have at most one nonzero value in each column.

  If you want to use `nlmefitsa` for data in which the covariate effects are random, include the covariates directly in the nonlinear model expression. Don't include the covariates in the fixed or random effect design matrices.

- **Convergence** — As described in the **Model form**, `nlmefit` and `nlmefitsa` have different approaches to measuring convergence. `nlmefit` uses traditional optimization measures, and `nlmefitsa` provides diagnostics to help you judge the convergence of a random simulation.

In practice, `nlmefitsa` tends to be more robust, and less likely to fail on difficult problems. However, `nlmefit` may converge faster on problems where it converges at all. Some problems may benefit from a combined strategy, for example by running `nlmefitsa` for a while to get reasonable parameter estimates, and using those as a starting point for additional iterations using `nlmefit`.

Using Output Functions with Mixed-Effects Models

The `Outputfcn` field of the `options` structure specifies one or more functions that the solver calls after each iteration. Typically, you might use an output function to plot points at each iteration or to display optimization quantities from the algorithm. To set up an output function:

1 Write the output function as a MATLAB file function or local function.

2 Use `statset` to set the value of `Outputfcn` to be a function handle, that is, the name of the function preceded by the `@` sign. For example, if the output function is `outfun.m`, the command

```
options = statset('OutputFcn', @outfun);
```

specifies `OutputFcn` to be the handle to `outfun`. To specify multiple output functions, use the syntax:

```
options = statset('OutputFcn',{@outfun, @outfun2});
```

3 Call the optimization function with `options` as an input argument.

For an example of an output function, see "Sample Output Function" on page 11-33.

Structure of the Output Function

The function definition line of the output function has the following form:

`stop = outfun(`*`beta`*`,`*`status`*`,`*`state`*`)`
where

- *beta* is the current fixed effects.
- *status* is a structure containing data from the current iteration. "Fields in status" on page 11-30 describes the structure in detail.
- *state* is the current state of the algorithm. "States of the Algorithm" on page 11-31 lists the possible values.
- *stop* is a flag that is `true` or `false` depending on whether the optimization routine should quit or continue. See "Stop Flag" on page 11-32 for more information.

The solver passes the values of the input arguments to `outfun` at each iteration.

Fields in status

The following table lists the fields of the `status` structure:

Field	Description
`procedure`	• `'ALT'` — alternating algorithm for the optimization of the linear mixed effects or restricted linear mixed effects approximations • `'LAP'` — optimization of the Laplacian approximation for first order or first order conditional estimation
`iteration`	An integer starting from 0.

Field	Description

`inner`	A structure describing the status of the inner iterations within the `ALT` and `LAP` procedures, with the fields:
	• `procedure` — When `procedure` is `'ALT'`:
	  • `'PNLS'` (penalized nonlinear least squares)
	  • `'LME'` (linear mixed-effects estimation)
	  • `'none'`
	When `procedure` is `'LAP'`,
	  • `'PNLS'` (penalized nonlinear least squares)
	  • `'PLM'` (profiled likelihood maximization)
	  • `'none'`
	• `state` — one of the following:
	  • `'init'`
	  • `'iter'`
	  • `'done'`
	  • `'none'`
	• `iteration` — an integer starting from 0, or `NaN`. For `nlmefitsa` with burn-in iterations, the output function is called after each of those iterations with a negative value for `STATUS.iteration`.

`fval`	The current log likelihood
`Psi`	The current random-effects covariance matrix
`theta`	The current parameterization of `Psi`
`mse`	The current error variance

States of the Algorithm

The following table lists the possible values for `state`:

state	Description
`'init'`	The algorithm is in the initial state before the first iteration.
`'iter'`	The algorithm is at the end of an iteration.

state	Description
'done'	The algorithm is in the final state after the last iteration.

The following code illustrates how the output function might use the value of `state` to decide which tasks to perform at the current iteration:

```
switch state
    case 'iter'
          % Make updates to plot or guis as needed
    case 'init'
          % Setup for plots or guis
    case 'done'
          % Cleanup of plots, guis, or final plot
otherwise
end
```

Stop Flag

The output argument `stop` is a flag that is `true` or `false`. The flag tells the solver whether it should quit or continue. The following examples show typical ways to use the `stop` flag.

Stopping an Optimization Based on Intermediate Results

The output function can stop the estimation at any iteration based on the values of arguments passed into it. For example, the following code sets stop to true based on the value of the log likelihood stored in the `'fval'` field of the status structure:

```
stop = outfun(beta,status,state)
stop = false;
% Check if loglikelihood is more than 132.
if status.fval > -132
    stop = true;
end
```

Stopping an Iteration Based on GUI Input

If you design a GUI to perform `nlmefit` iterations, you can make the output function stop when a user clicks a **Stop** button on the GUI. For example, the following code implements a dialog to cancel calculations:

```
function retval = stop_outfcn(beta,str,status)
persistent h stop;
if isequal(str.inner.state,'none')
```

```
    switch(status)
        case 'init'
            % Initialize dialog
            stop = false;
            h = msgbox('Press STOP to cancel calculations.',...
                'NLMEFIT: Iteration 0 ');
            button = findobj(h,'type','uicontrol');
            set(button,'String','STOP','Callback',@stopper)
            pos = get(h,'Position');
            pos(3) = 1.1 * pos(3);
            set(h,'Position',pos)
            drawnow
        case 'iter'
            % Display iteration number in the dialog title
            set(h,'Name',sprintf('NLMEFIT: Iteration %d',...
                str.iteration))
            drawnow;
        case 'done'
            % Delete dialog
            delete(h);
    end
end
if stop
    % Stop if the dialog button has been pressed
    delete(h)
end
retval = stop;

    function stopper(varargin)
        % Set flag to stop when button is pressed
        stop = true;
        disp('Calculation stopped.')
    end
end
```

Sample Output Function

`nmlefitoutputfcn` is the sample Statistics and Machine Learning Toolbox output function for `nlmefit` and `nlmefitsa`. It initializes or updates a plot with the fixed-effects (`BETA`) and variance of the random effects (`diag(STATUS.Psi)`). For `nlmefit`, the plot also includes the log-likelihood (`STATUS.fval`).

`nlmefitoutputfcn` is the default output function for `nlmefitsa`. To use it with `nlmefit`, specify a function handle for it in the options structure:

```
opt = statset('OutputFcn', @nlmefitoutputfcn, …)
beta = nlmefit(…, 'Options', opt, …)
```

To prevent `nlmefitsa` from using of this function, specify an empty value for the output function:

```
opt = statset('OutputFcn', [], …)
beta = nlmefitsa(…, 'Options', opt, …)
```

`nlmefitoutputfcn` stops `nlmefit` or `nlmefitsa` if you close the figure that it produces.

Mixed-Effects Models Using nlmefit and nlmefitsa

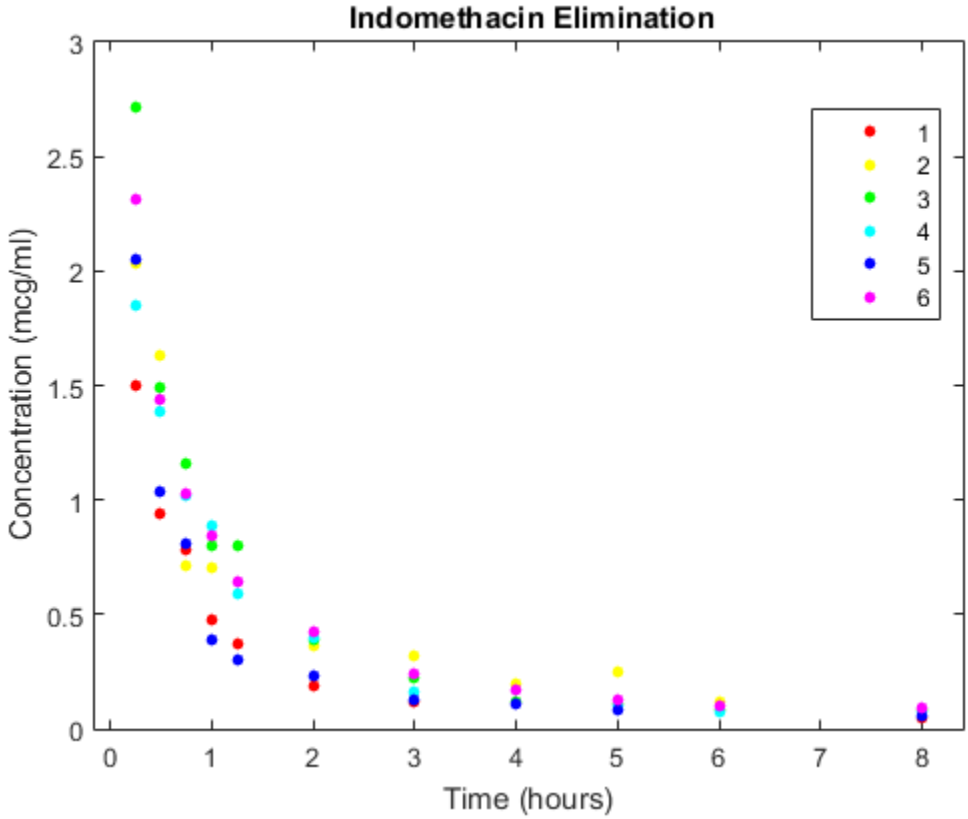
Load the sample data.

```
load indomethacin
```

The data in `indomethacin.mat` records concentrations of the drug indomethacin in the bloodstream of six subjects over eight hours.

Plot the scatter plot of indomethacin in the bloodstream grouped by subject.

```
gscatter(time,concentration,subject)
xlabel('Time (hours)')
ylabel('Concentration (mcg/ml)')
title('{\bf Indomethacin Elimination}')
hold on
```



`Specifying Mixed-Effects Models` page discusses a useful model for this type of data.

Construct the model via an anonymous function.

```
model = @(phi,t)(phi(1)*exp(-exp(phi(2))*t) + ...
                 phi(3)*exp(-exp(phi(4))*t));
```

Use the `nlinfit` function to fit the model to all of the data, ignoring subject-specific effects.

```
phi0 = [1 2 1 1];
[phi,res] = nlinfit(time,concentration,model,phi0);
```

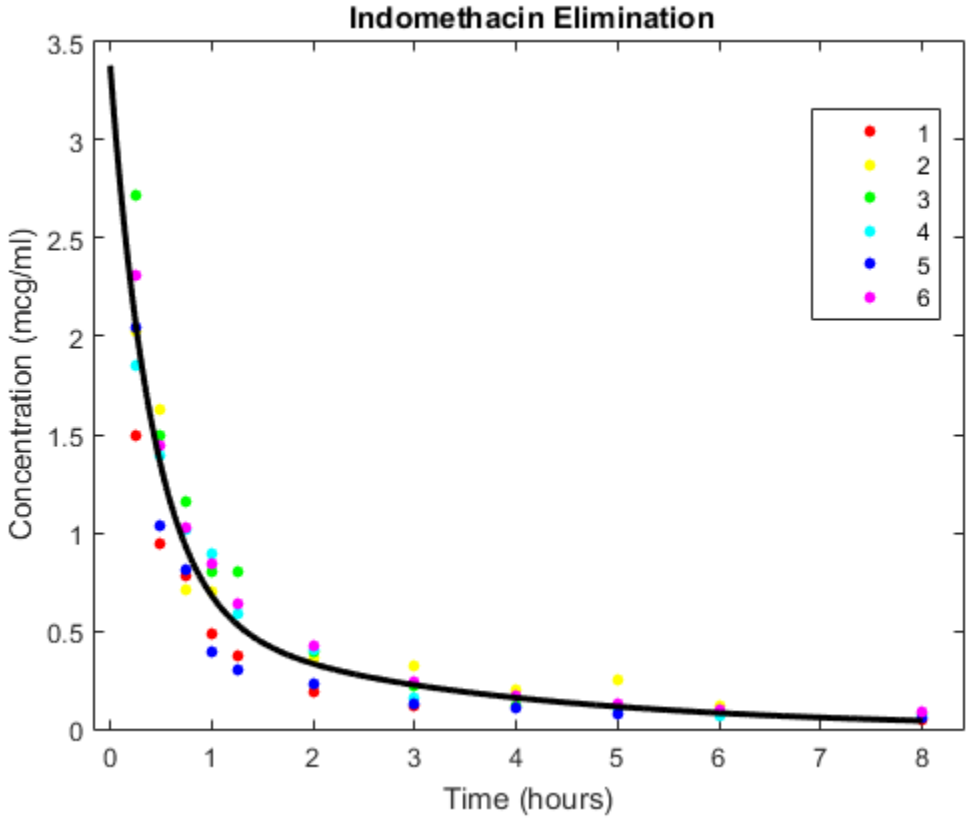
Compute the mean squared error.

```
numObs = length(time);
numParams = 4;
df = numObs-numParams;
mse = (res'*res)/df
```

```
mse =

    0.0304
```

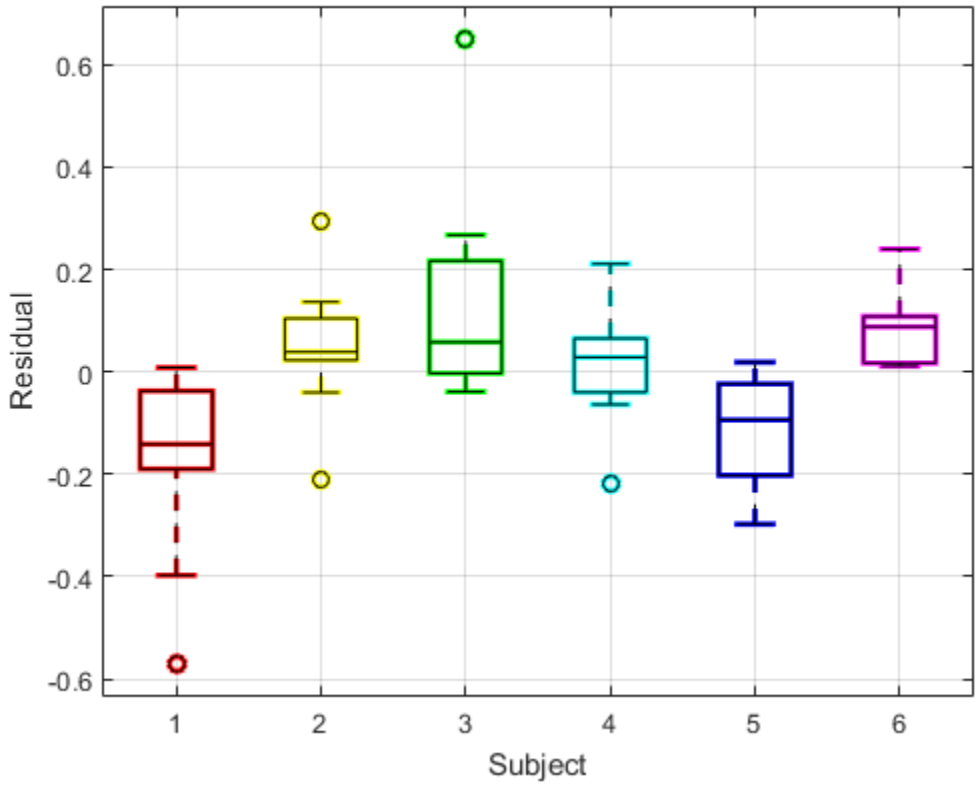
Super impose the model on the scatter plot of data.

```
tplot = 0:0.01:8;
plot(tplot,model(phi,tplot),'k','LineWidth',2)
hold off
```



Draw the box-plot of residuals by subject.

```
colors = 'rygcbm';
h = boxplot(res,subject,'colors',colors,'symbol','o');
set(h(~isnan(h)),'LineWidth',2)
hold on
boxplot(res,subject,'colors','k','symbol','ko')
grid on
xlabel('Subject')
ylabel('Residual')
hold off
```



The box plot of residuals by subject shows that the boxes are mostly above or below zero, indicating that the model has failed to account for subject-specific effects.

To account for subject-specific effects, fit the model separately to the data for each subject.

```
phi0 = [1 2 1 1];
PHI = zeros(4,6);
RES = zeros(11,6);
for I = 1:6
    tI = time(subject == I);
    cI = concentration(subject == I);
    [PHI(:,I),RES(:,I)] = nlinfit(tI,cI,model,phi0);
end
```

```
PHI
```

```
PHI =

    2.0293    2.8277    5.4683    2.1981    3.5661    3.0023
    0.5794    0.8013    1.7498    0.2423    1.0408    1.0882
    0.1915    0.4989    1.6757    0.2545    0.2915    0.9685
   -1.7878   -1.6354   -0.4122   -1.6026   -1.5069   -0.8731
```

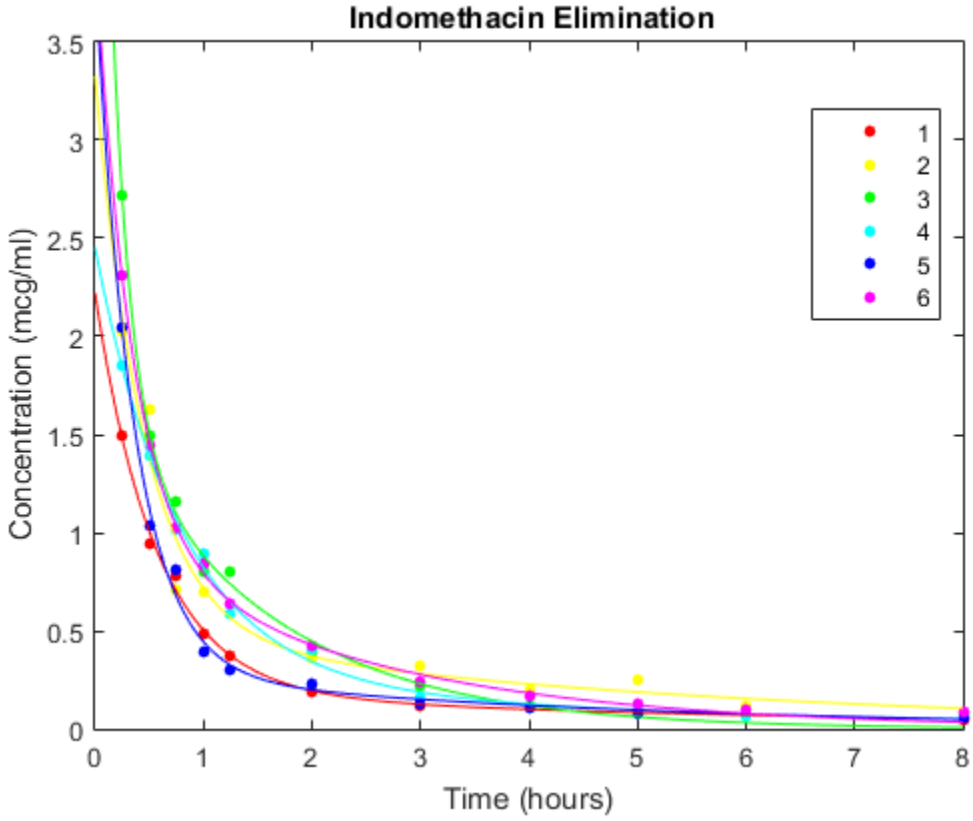
Compute the mean squared error.

```
numParams = 24;
df = numObs-numParams;
mse = (RES(:)'*RES(:))/df
```

```
mse =

    0.0057
```

Plot the scatter plot of the data and superimpose the model for each subject.

```
gscatter(time,concentration,subject)
xlabel('Time (hours)')
ylabel('Concentration (mcg/ml)')
title('{\bf Indomethacin Elimination}')
hold on
for I = 1:6
    plot(tplot,model(PHI(:,I),tplot),'Color',colors(I))
end
axis([0 8 0 3.5])
hold off
```

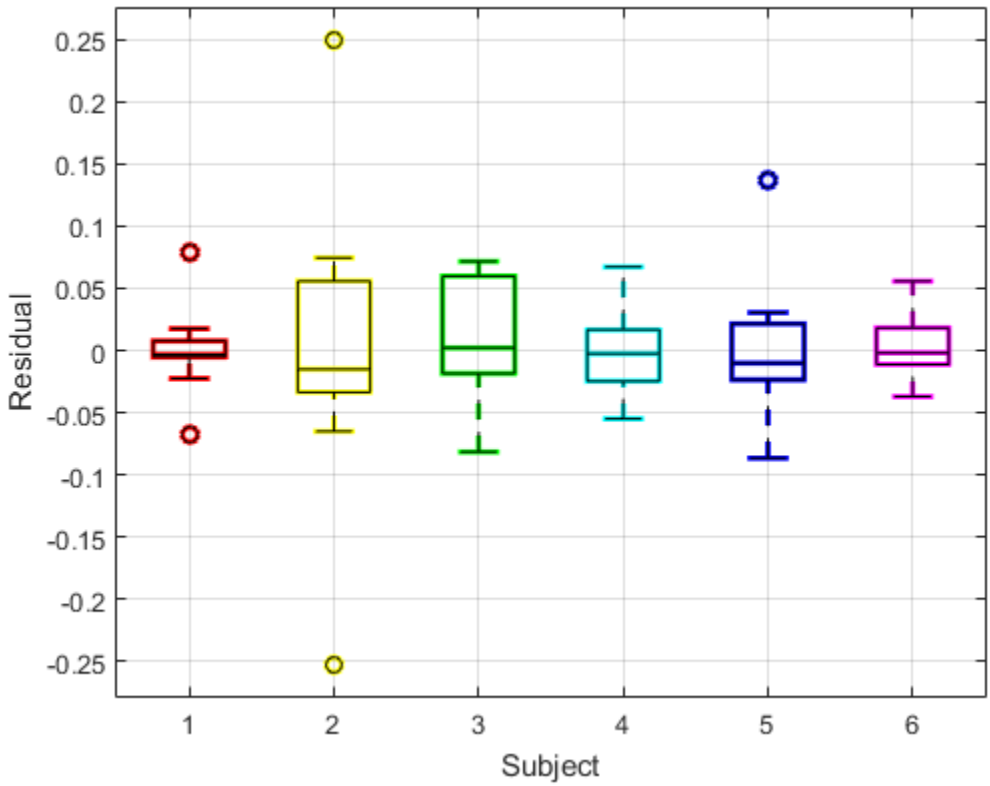


`PHI` gives estimates of the four model parameters for each of the six subjects. The estimates vary considerably, but taken as a 24-parameter model of the data, the mean-squared error of 0.0057 is a significant reduction from 0.0304 in the original four-parameter model.

Draw the box plot of residuals by subject.

```
h = boxplot(RES,'colors',colors,'symbol','o');
set(h(~isnan(h)),'LineWidth',2)
hold on
boxplot(RES,'colors','k','symbol','ko')
grid on
xlabel('Subject')
ylabel('Residual')
```

```
hold off
```



Now the box plot shows that the larger model accounts for most of the subject-specific effects. The spread of the residuals (the vertical scale of the box plot) is much smaller than in the previous box plot, and the boxes are now mostly centered on zero.

While the 24-parameter model successfully accounts for variations due to the specific subjects in the study, it does not consider the subjects as representatives of a larger population. The sampling distribution from which the subjects are drawn is likely more interesting than the sample itself. The purpose of mixed-effects models is to account for subject-specific variations more broadly, as random effects varying around population means.

Use the `nlmefit` function to fit a mixed-effects model to the data. You can also use `nlmefitsa` in place of `nlmefit` .

The following anonymous function, `nlme_model` , adapts the four-parameter model used by `nlinfit` to the calling syntax of `nlmefit` by allowing separate parameters for each individual. By default, `nlmefit` assigns random effects to all the model parameters. Also by default, `nlmefit` assumes a diagonal covariance matrix (no covariance among the random effects) to avoid overparametrization and related convergence issues.

```
nlme_model = @(PHI,t)(PHI(:,1).*exp(-exp(PHI(:,2)).*t) + ...
                      PHI(:,3).*exp(-exp(PHI(:,4)).*t));
phi0 = [1 2 1 1];
[phi,PSI,stats] = nlmefit(time,concentration,subject, ...
                          [],nlme_model,phi0)
```

```
phi =

    2.8277
    0.7729
    0.4606
   -1.3459


PSI =

    0.3264         0         0         0
         0    0.0250         0         0
         0         0    0.0124         0
         0         0         0    0.0000


stats =

           dfe: 57
          logl: 54.5882
           mse: 0.0066
          rmse: 0.0787
    errorparam: 0.0815
           aic: -91.1765
           bic: -93.0506
          covb: [4x4 double]
        sebeta: [0.2558 0.1066 0.1092 0.2244]
          ires: [66x1 double]
```

```
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]
```

The mean-squared error of 0.0066 is comparable to the 0.0057 of the 24-parameter model without random effects, and significantly better than the 0.0304 of the four-parameter model without random effects.

The estimated covariance matrix `PSI` shows that the variance of the fourth random effect is essentially zero, suggesting that you can remove it to simplify the model. To do this, use the `'REParamsSelect'` name-value pair to specify the indices of the parameters to be modeled with random effects in `nlmefit` .

```
[phi,PSI,stats] = nlmefit(time,concentration,subject, ...
                          [],nlme_model,phi0, ...
                          'REParamsSelect',[1 2 3])
```

```
phi =

    2.8277
    0.7728
    0.4605
   -1.3460


PSI =

    0.3270         0         0
         0    0.0250         0
         0         0    0.0124


stats =

           dfe: 58
          logl: 54.5875
           mse: 0.0066
          rmse: 0.0780
    errorparam: 0.0815
           aic: -93.1750
           bic: -94.8410
```

```
          covb: [4x4 double]
        sebeta: [0.2560 0.1066 0.1092 0.2244]
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]
```

The log-likelihood `logl` is almost identical to what it was with random effects for all of the parameters, the Akaike information criterion `aic` is reduced from -91.1765 to -93.1750, and the Bayesian information criterion `bic` is reduced from -93.0506 to -94.8410. These measures support the decision to drop the fourth random effect.

Refitting the simplified model with a full covariance matrix allows for identification of correlations among the random effects. To do this, use the `CovPattern` parameter to specify the pattern of nonzero elements in the covariance matrix.

```
[phi,PSI,stats] = nlmefit(time,concentration,subject, ...
                          [],nlme_model,phi0, ...
                          'REParamsSelect',[1 2 3], ...
                          'CovPattern',ones(3))
```

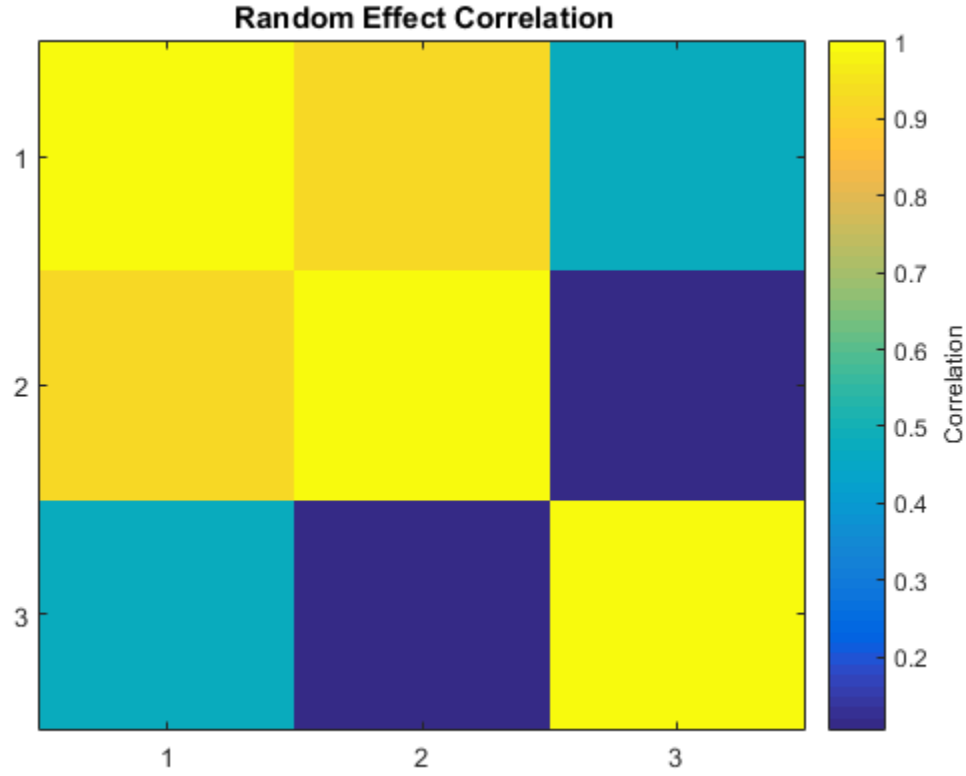
```
phi =

    2.8163
    0.8251
    0.5553
   -1.1505


PSI =

    0.4733    0.1145    0.0494
    0.1145    0.0324    0.0029
    0.0494    0.0029    0.0225


stats =

           dfe: 55
          logl: 58.4293
           mse: 0.0061
```

```
          rmse: 0.0783
    errorparam: 0.0781
           aic: -94.8585
           bic: -97.1492
          covb: [4x4 double]
        sebeta: [0.3017 0.1104 0.1167 0.1680]
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]
```

The estimated covariance matrix `PSI` shows that the random effects on the first two parameters have a relatively strong correlation, and both have a relatively weak correlation with the last random effect. This structure in the covariance matrix is more apparent if you convert `PSI` to a correlation matrix using `corrcov` .

```
RHO = corrcov(PSI)
clf;
imagesc(RHO)
set(gca,'XTick',[1 2 3],'YTick',[1 2 3])
title('{\bf Random Effect Correlation}')
h = colorbar;
set(get(h,'YLabel'),'String','Correlation');
```

```
RHO =

    1.0000    0.9241    0.4786
    0.9241    1.0000    0.1068
    0.4786    0.1068    1.0000
```



Incorporate this structure into the model by changing the specification of the covariance pattern to block-diagonal.

```
P = [1 1 0;1 1 0;0 0 1] % Covariance pattern
[phi,PSI,stats,b] = nlmefit(time,concentration,subject, ...
                            [],nlme_model,phi0, ...
                            'REParamsSelect',[1 2 3], ...
                            'CovPattern',P)
```

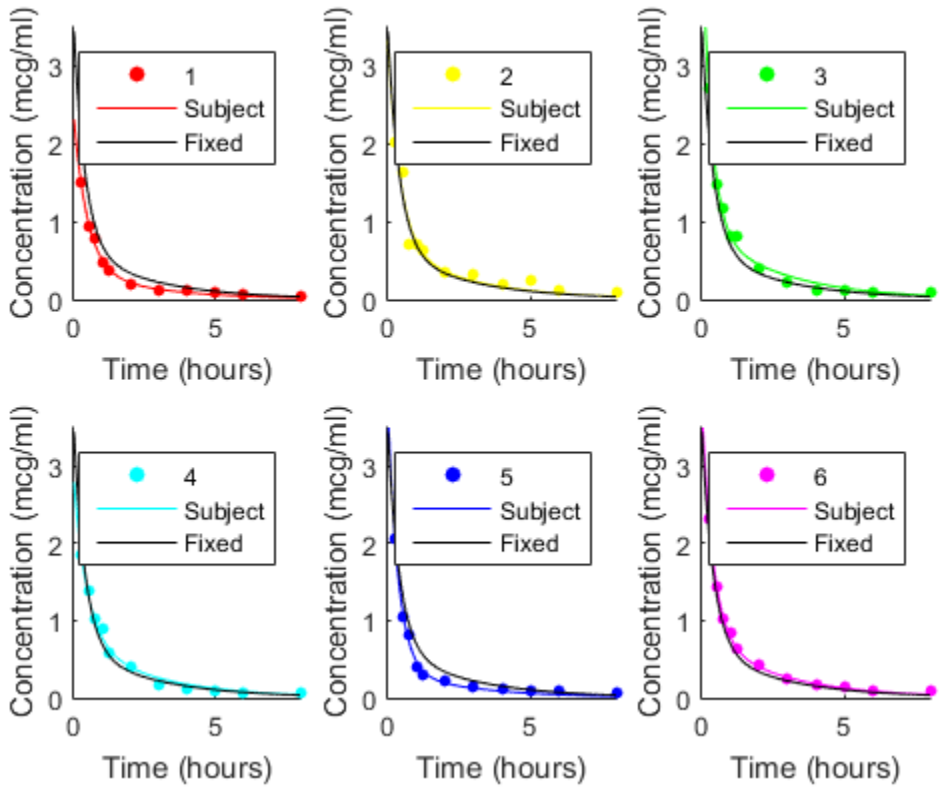
```
P =

     1     1     0
     1     1     0
```

```
     0     0     1


phi =

    2.7830
    0.8981
    0.6581
   -1.0000


PSI =

    0.5180    0.1069         0
    0.1069    0.0221         0
         0         0    0.0454


stats =

           dfe: 57
          logl: 58.0804
           mse: 0.0061
          rmse: 0.0768
    errorparam: 0.0782
           aic: -98.1608
           bic: -100.0350
          covb: [4x4 double]
        sebeta: [0.3171 0.1073 0.1384 0.1453]
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]


b =

   -0.8507   -0.1563    1.0427   -0.7559    0.5652    0.1550
   -0.1756   -0.0323    0.2152   -0.1560    0.1167    0.0320
   -0.2756    0.0519    0.2620    0.1064   -0.2835    0.1389
```

The block-diagonal covariance structure reduces `aic` from -94.9462 to -98.1608 and `bic` from -97.2368 to -100.0350 without significantly affecting the log-likelihood. These measures support the covariance structure used in the final model. The output `b` gives predictions of the three random effects for each of the six subjects. These are combined with the estimates of the fixed effects in `phi` to produce the mixed-effects model.

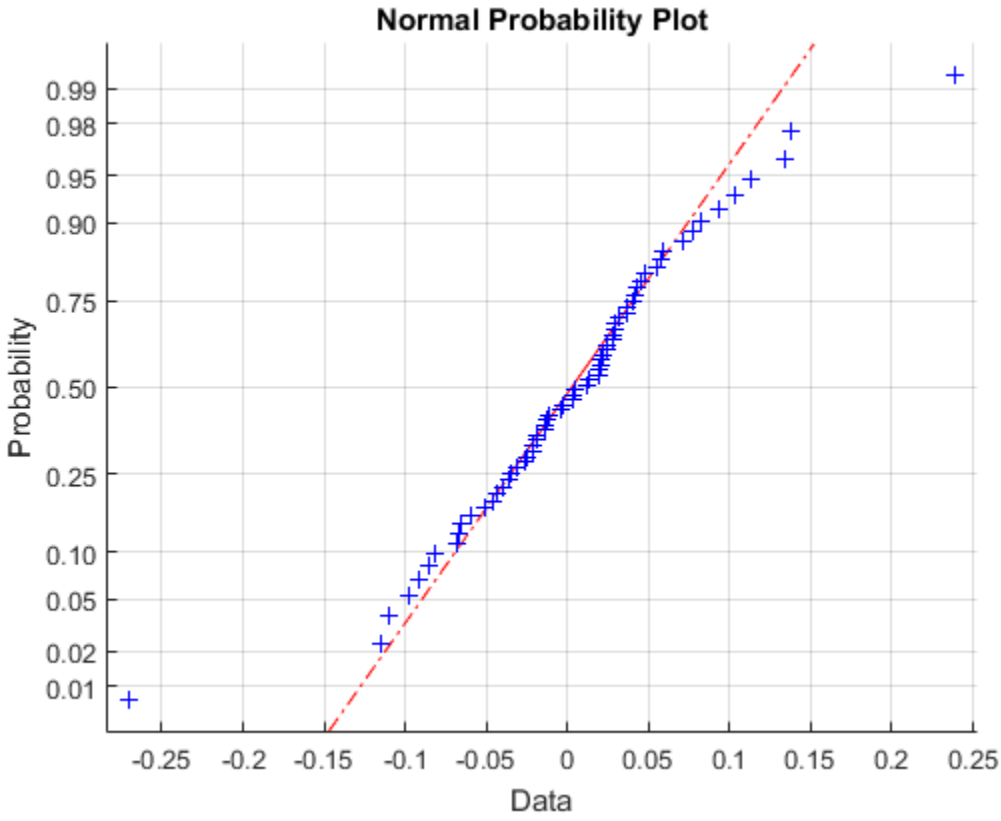
Plot the mixed-effects model for each of the six subjects. For comparison, the model without random effects is also shown.

```
PHI = repmat(phi,1,6) + ...                 % Fixed effects
      [b(1,:);b(2,:);b(3,:);zeros(1,6)];    % Random effects
RES = zeros(11,6); % Residuals
colors = 'rygcbm';
for I = 1:6
    fitted_model = @(t)(PHI(1,I)*exp(-exp(PHI(2,I))*t) + ...
                        PHI(3,I)*exp(-exp(PHI(4,I))*t));
    tI = time(subject == I);
    cI = concentration(subject == I);
    RES(:,I) = cI - fitted_model(tI);

    subplot(2,3,I)
    scatter(tI,cI,20,colors(I),'filled')
    hold on
    plot(tplot,fitted_model(tplot),'Color',colors(I))
    plot(tplot,model(phi,tplot),'k')
    axis([0 8 0 3.5])
    xlabel('Time (hours)')
    ylabel('Concentration (mcg/ml)')
    legend(num2str(I),'Subject','Fixed')
end
```



If obvious outliers in the data (visible in previous box plots) are ignored, a normal probability plot of the residuals shows reasonable agreement with model assumptions on the errors.

```
clf; normplot(RES(:))
```



Examining Residuals for Model Verification

You can examine the `stats` structure, which is returned by both `nlmefit` and `nlmefitsa`, to determine the quality of your model. The `stats` structure contains fields with conditional weighted residuals (`cwres` field) and individual weighted residuals (`iwres` field). Since the model assumes that residuals are normally distributed, you can examine the residuals to see how well this assumption holds.

This example generates synthetic data using normal distributions. It shows how the fit statistics look:

- Good when testing against the same type of model as generates the data

- Poor when tested against incorrect data models

1. Initialize a 2-D model with 100 individuals:

```
nGroups = 100; % 100 Individuals
nlmefun = @(PHI,t)(PHI(:,1)*5 + PHI(:,2)^2.*t); % Regression fcn
REParamSelect = [1  2]; % Both Parameters have random effect
errorParam = .03;
beta0 = [ 1.5  5]; % Parameter means
psi = [ 0.35  0; ...  % Covariance Matrix
       0   0.51 ];
time =[0.25;0.5;0.75;1;1.25;2;3;4;5;6];
nParameters = 2;
rng(0,'twister') % for reproducibility
```

2. Generate the data for fitting with a proportional error model:

```
b_i = mvnrnd(zeros(1, numel(REParamSelect)), psi, nGroups);
individualParameters = zeros(nGroups,nParameters);
individualParameters(:, REParamSelect) = ...
     bsxfun(@plus,beta0(REParamSelect), b_i);

groups = repmat(1:nGroups,numel(time),1);
groups = vertcat(groups(:));

y = zeros(numel(time)*nGroups,1);
x = zeros(numel(time)*nGroups,1);
for i = 1:nGroups
    idx = groups == i;
    f = nlmefun(individualParameters(i,:), time);
    % Make a proportional error model for y:
    y(idx) = f + errorParam*f.*randn(numel(f),1);
    x(idx) = time;
end

P = [ 1 0 ; 0 1 ];
```

3. Fit the data using the same regression function and error model as the model generator:

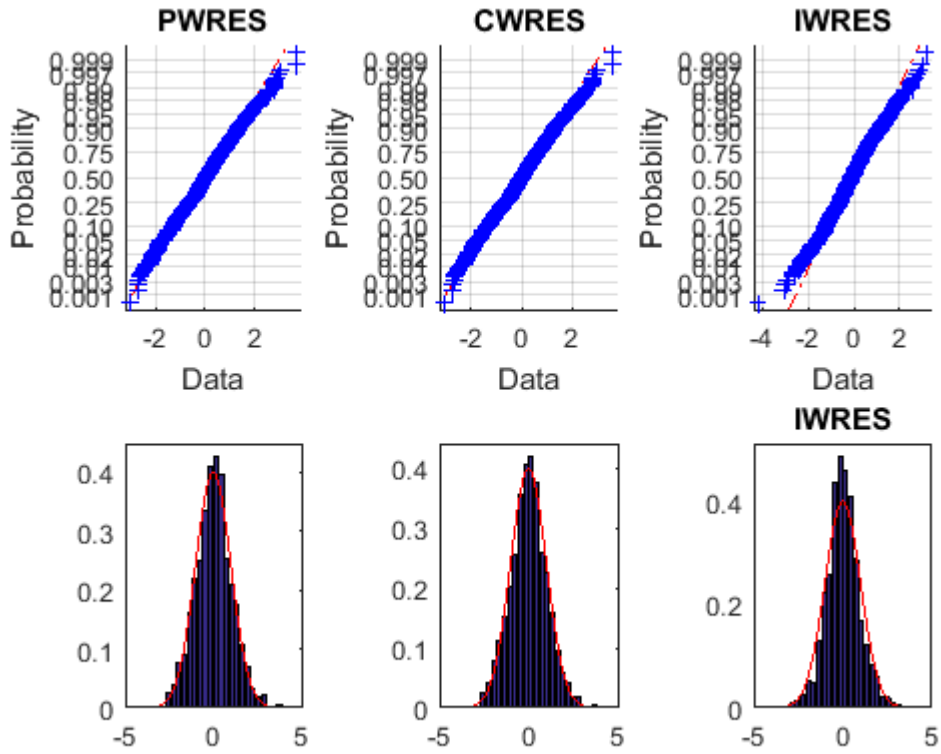
```
[~,~,stats] = nlmefit(x,y,groups, ...
    [],nlmefun,[1 1],'REParamsSelect',REParamSelect,...
    'ErrorModel','Proportional','CovPattern',P);
```

4. Create a plotting routine by copying the following function definition, and creating a file `plotResiduals.m` on your MATLAB path:

```
function plotResiduals(stats)
pwres = stats.pwres;
iwres = stats.iwres;
cwres = stats.cwres;
figure
subplot(2,3,1);
normplot(pwres); title('PWRES')
subplot(2,3,4);
createhistplot(pwres);

subplot(2,3,2);
normplot(cwres); title('CWRES')
subplot(2,3,5);
createhistplot(cwres);

subplot(2,3,3);
normplot(iwres); title('IWRES')
subplot(2,3,6);
createhistplot(iwres); title('IWRES')

function createhistplot(pwres)
h = histogram(pwres);

% x is the probability/height for each bin
x = h.Values/sum(h.Values*h.BinWidth)

% n is the center of each bin
n = h.BinEdges + (0.5*h.BinWidth)
n(end) = [];

bar(n,x);
ylim([0 max(x)*1.05]);
hold on;
x2 = -4:0.1:4;
f2 = normpdf(x2,0,1);
plot(x2,f2,'r');
end

end
```

5 Plot the residuals using the `plotResiduals` function:

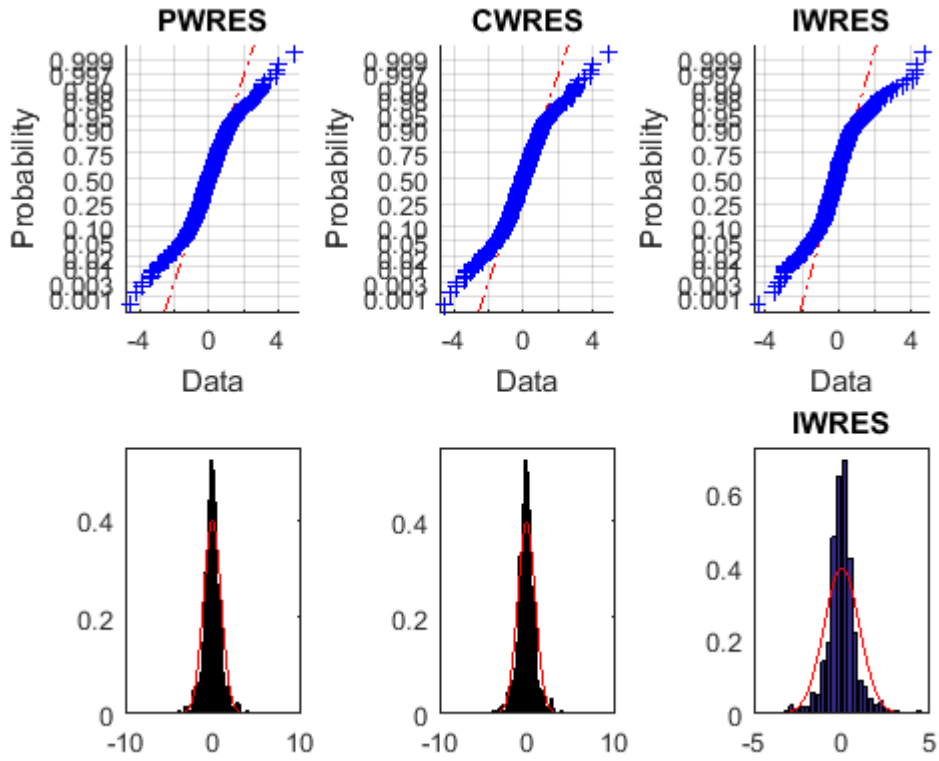
```
plotResiduals(stats);
```



The upper probability plots look straight, meaning the residuals are normally distributed. The bottom histogram plots match the superimposed normal density plot. So you can conclude that the error model matches the data.

6 For comparison, fit the data using a constant error model, instead of the proportional model that created the data:

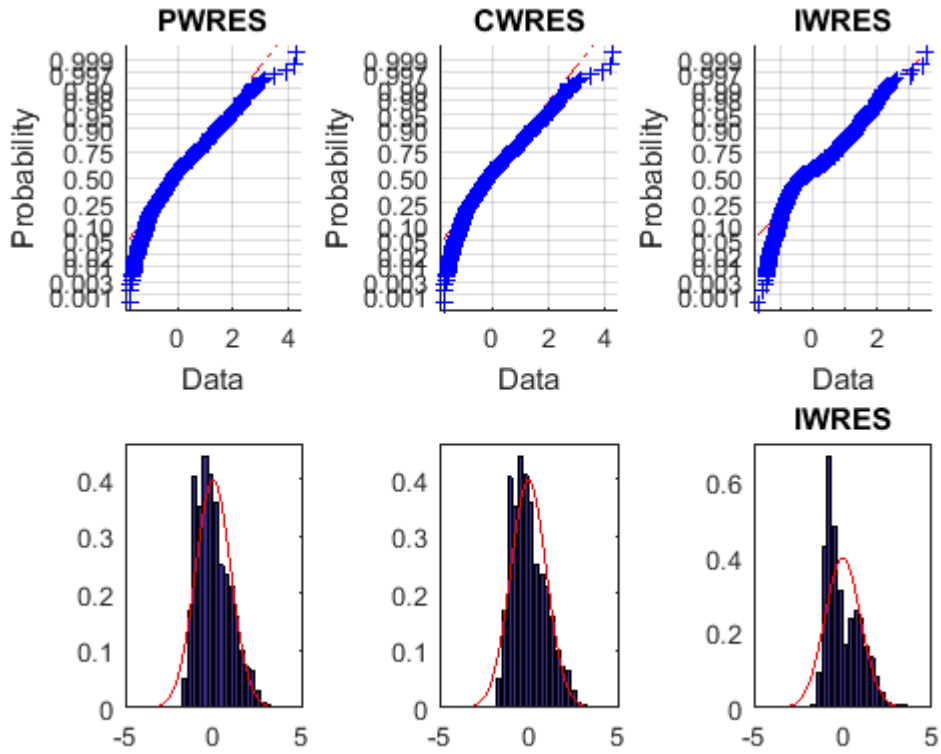
```
[~,~,stats] = nlmefit(x,y,groups, ...
    [],nlmefun,[0 0],'REParamsSelect',REParamSelect,...
    'ErrorModel','Constant','CovPattern',P);
plotResiduals(stats);
```



The upper probability plots are not straight, indicating the residuals are not normally distributed. The bottom histogram plots are fairly close to the superimposed normal density plots.

7 For another comparison, fit the data to a different structural model than created the data:

```
nlmefun2 = @(PHI,t)(PHI(:,1)*5 + PHI(:,2).*t.^4);
[~,~,stats] = nlmefit(x,y,groups, ...
    [],nlmefun2,[0 0],'REParamsSelect',REParamSelect,...
    'ErrorModel','constant', 'CovPattern',P);
plotResiduals(stats);
```



Not only are the upper probability plots not straight, but the histogram plot is quite skewed compared to the superimposed normal density. These residuals are not normally distributed, and do not match the model.

Pitfalls in Fitting Nonlinear Models by Transforming to Linearity

This example shows pitfalls that can occur when fitting a nonlinear model by transforming to linearity. Imagine that we have collected measurements on two variables, x and y, and we want to model y as a function of x. Assume that x is measured exactly, while measurements of y are affected by additive, symmetric, zero-mean errors.

```
x = [5.72 4.22 5.72 3.59 5.04 2.66 5.02 3.11 0.13 2.26 ...
     5.39 2.57 1.20 1.82 3.23 5.46 3.15 1.84 0.21 4.29 ...
     4.61 0.36 3.76 1.59 1.87 3.14 2.45 5.36 3.44 3.41]';
y = [2.66 2.91 0.94 4.28 1.76 4.08 1.11 4.33 8.94 5.25 ...
     0.02 3.88 6.43 4.08 4.90 1.33 3.63 5.49 7.23 0.88 ...
     3.08 8.12 1.22 4.24 6.21 5.48 4.89 2.30 4.13 2.17]';
```

Let's also assume that theory tells us that these data should follow a model of exponential decay, y = p1*exp(p2*x), where p1 is positive and p2 is negative. To fit this model, we could use nonlinear least squares.

```
modelFun = @(p,x) p(1)*exp(p(2)*x);
```

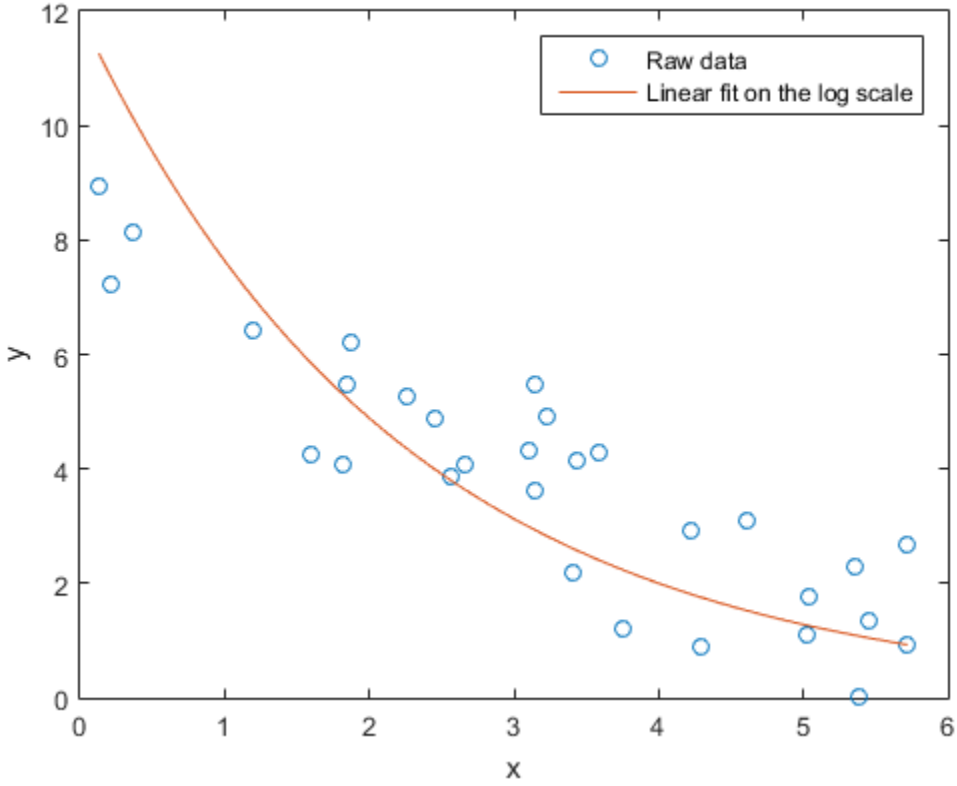
But the nonlinear model can also be transformed to a linear one by taking the log on both sides, to get log(y) = log(p1) + p2*x. That's tempting, because we can fit that linear model by ordinary linear least squares. The coefficients we'd get from a linear least squares would be log(p1) and p2.

```
paramEstsLin = [ones(size(x)), x] \ log(y);
paramEstsLin(1) = exp(paramEstsLin(1))
```

```
paramEstsLin =

   11.9312
   -0.4462
```

How did we do? We can superimpose the fit on the data to find out.

```
xx = linspace(min(x), max(x));
yyLin = modelFun(paramEstsLin, xx);
plot(x,y,'o', xx,yyLin,'-');
xlabel('x'); ylabel('y');
legend({'Raw data','Linear fit on the log scale'},'location','NE');
```

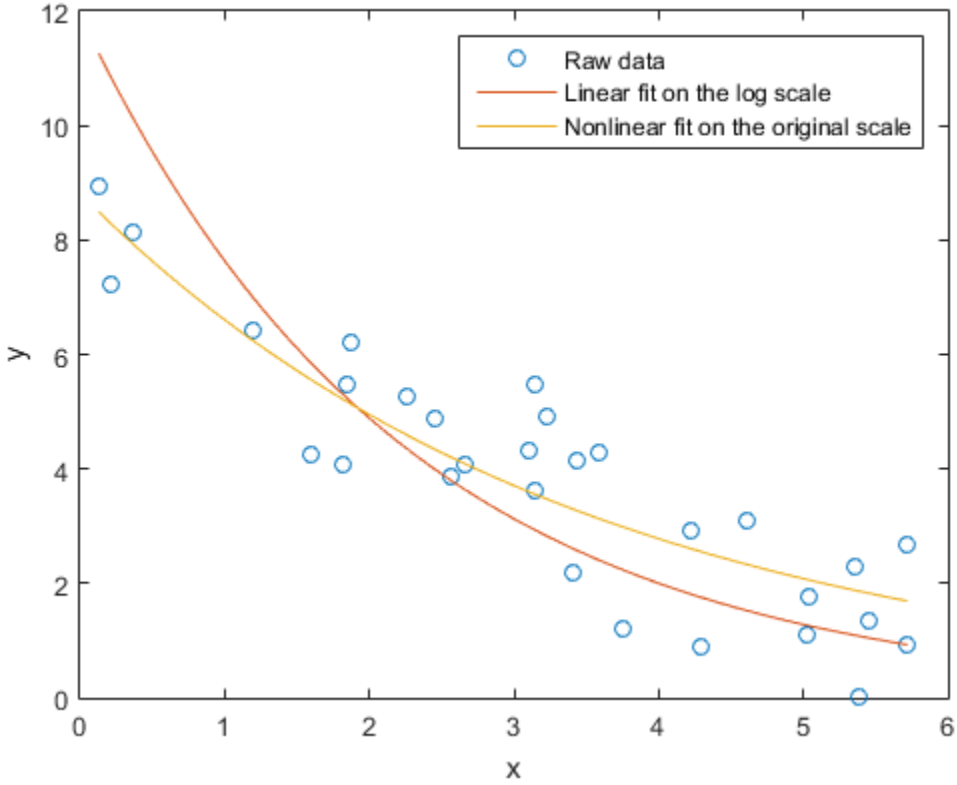


Something seems to have gone wrong, because the fit doesn't really follow the trend that we can see in the raw data. What kind of fit would we get if we used `nlinfit` to do nonlinear least squares instead? We'll use the previous fit as a rough starting point, even though it's not a great fit.

```
paramEsts = nlinfit(x, y, modelFun, paramEstsLin)
```

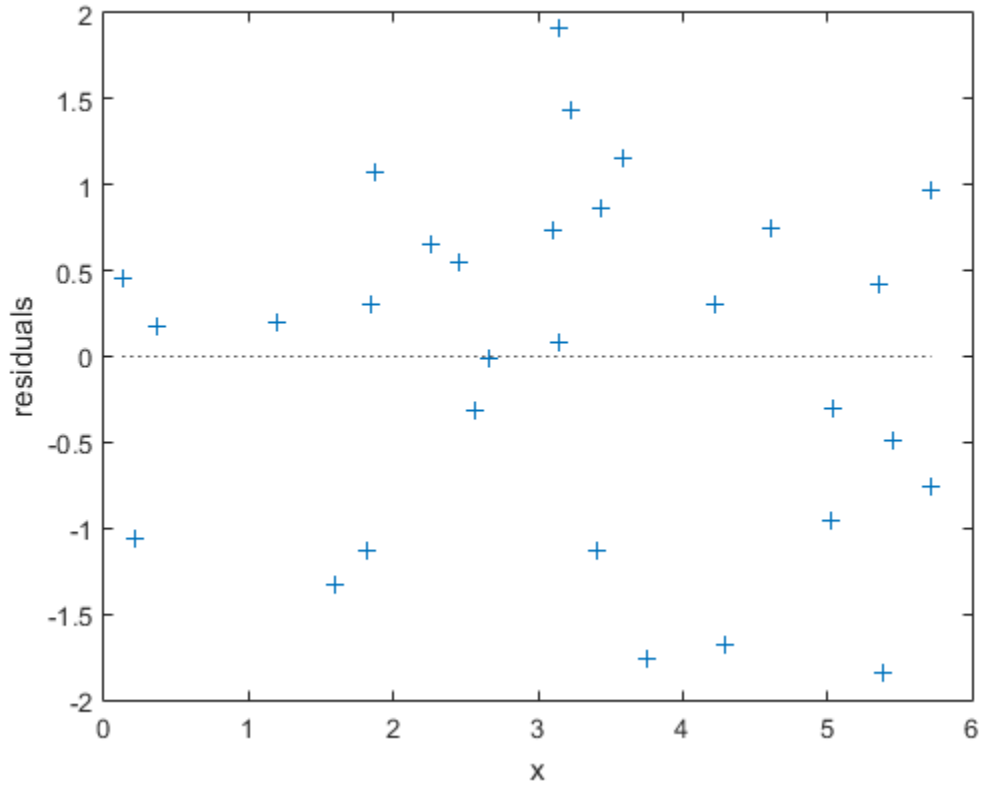
```
paramEsts =

    8.8145
   -0.2885
```

```
yy = modelFun(paramEsts,xx);
plot(x,y,'o', xx,yyLin,'-', xx,yy,'-');
xlabel('x'); ylabel('y');
legend({'Raw data','Linear fit on the log scale',  ...
 'Nonlinear fit on the original scale'},'location','NE');
```



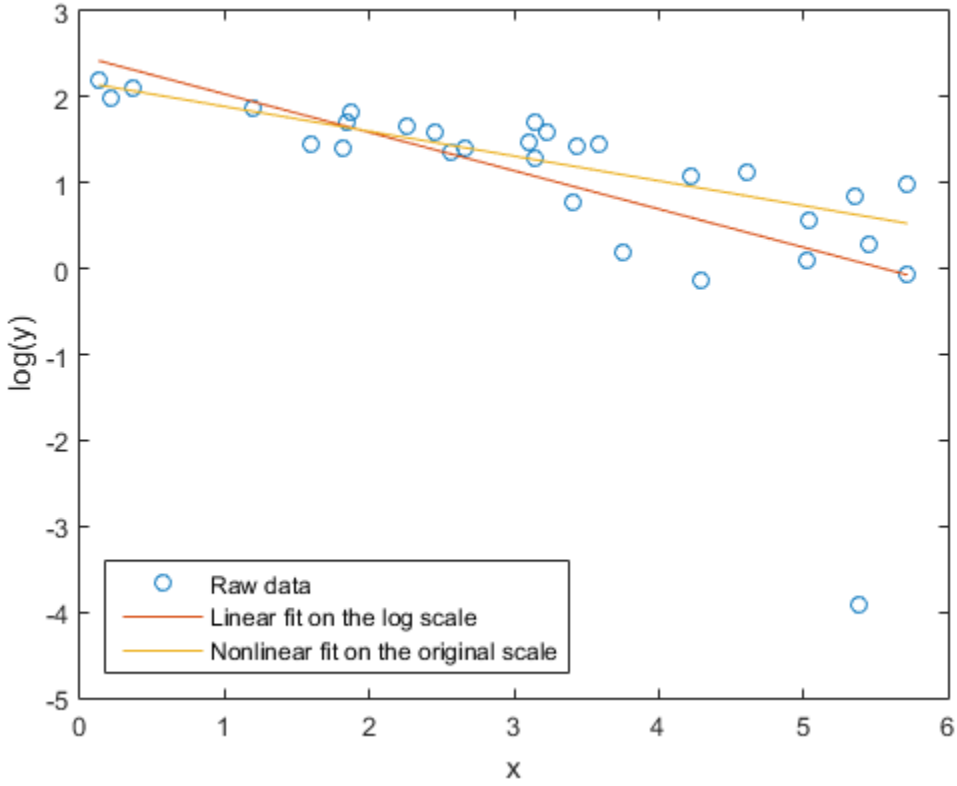
The fit using `nlinfit` more or less passes through the center of the data point scatter. A residual plot shows something approximately like an even scatter about zero.

```
r = y-modelFun(paramEsts,x);
plot(x,r,'+', [min(x) max(x)],[0 0],'k:');
xlabel('x'); ylabel('residuals');
```



So what went wrong with the linear fit? The problem is in log transform. If we plot the data and the two fits on the log scale, we can see that there's an extreme outlier.

```
plot(x,log(y),'o', xx,log(yyLin),'-', xx,log(yy),'-');
xlabel('x'); ylabel('log(y)');
ylim([-5,3]);
legend({'Raw data', 'Linear fit on the log scale',  ...
 'Nonlinear fit on the original scale'},'location','SW');
```

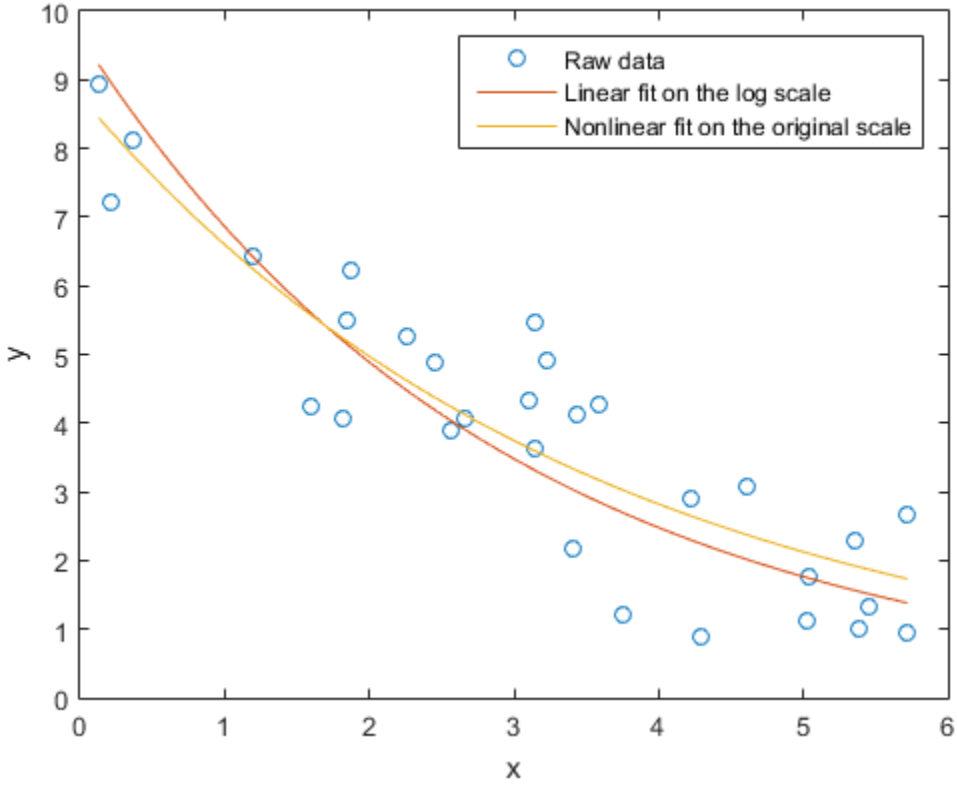


That observation is not an outlier in the original data, so what happened to make it one on the log scale? The log transform is exactly the right thing to straighten out the trend line. But the log is a very nonlinear transform, and so symmetric measurement errors on the original scale have become asymmetric on the log scale. Notice that the outlier had the smallest y value on the original scale -- close to zero. The log transform has "stretched out" that smallest y value more than its neighbors. We made the linear fit on the log scale, and so it is very much affected by that outlier.

Had the measurement at that one point been slightly different, the two fits might have been much more similar. For example,

```
y(11) = 1;
paramEsts = nlinfit(x, y, modelFun, [10;-.3])
```

```
paramEsts =

    8.7618
   -0.2833


paramEstsLin = [ones(size(x)), x] \ log(y);
paramEstsLin(1) = exp(paramEstsLin(1))


paramEstsLin =

    9.6357
   -0.3394


yy = modelFun(paramEsts,xx);
yyLin = modelFun(paramEstsLin, xx);
plot(x,y,'o', xx,yyLin,'-', xx,yy,'-');
xlabel('x'); ylabel('y');
legend({'Raw data', 'Linear fit on the log scale',  ...
 'Nonlinear fit on the original scale'},'location','NE');
```



Still, the two fits are different. Which one is "right"? To answer that, suppose that instead of additive measurement errors, measurements of y were affected by multiplicative errors. These errors would not be symmetric, and least squares on the original scale would not be appropriate. On the other hand, the log transform would make the errors symmetric on the log scale, and the linear least squares fit on that scale is appropriate.

So, which method is "right" depends on what assumptions you are willing to make about your data. In practice, when the noise term is small relative to the trend, the log transform is "locally linear" in the sense that y values near the same x value will not be stretched out too asymmetrically. In that case, the two methods lead to essentially the same fit. But when the noise term is not small, you should consider what assumptions are realistic, and choose an appropriate fitting method.

Survival Analysis

What Is Survival Analysis?

In this section...

Introduction

Survival analysis is time-to-event analysis, that is, when the outcome of interest is the time until an event occurs. Examples of time-to-events are the time until infection, reoccurrence of a disease, or recovery in health sciences, duration of unemployment in economics, time until the failure of a machine part or lifetime of light bulbs in engineering, and so on. Survival analysis is a part of reliability studies in engineering. In this case, it is usually used to study the lifetime of industrial components. In reliability analyses, survival times are usually called failure times as the variable of interest is how much time a component functions properly before it fails.

Survival analysis consists of parametric, semiparametric, and nonparametric methods. You can use these to estimate the most commonly used measures in survival studies, survivor and hazard functions, compare them for different groups, and assess the relationship of predictor variables to survival time. Some statistical probability distributions describe survival times well. Commonly used distributions are exponential, Weibull, lognormal, Burr, and Birnbaum-Saunders distributions. Statistics and Machine Learning Toolbox functions `ecdf` and `ksdensity` compute the empirical and kernel density estimates of the cdf, cumulative hazard, and survivor functions. `coxphfit` fits the Cox proportional hazards model to the data.

Censoring

One important concept in survival analysis is censoring. The survival times of some individuals might not be fully observed due to different reasons. In life sciences, this might happen when the survival study (e.g., the clinical trial) stops before the full survival times of all individuals can be observed, or a person drops out of a study, or for long-term studies, when the patient is lost to follow up. In the industrial context, not all

components might have failed before the end of the reliability study. In such cases, the individual survives beyond the time of the study, and the exact survival time is unknown. This is called right censoring.

During a survival study either the individual is observed to fail at time T, or the observation on that individual ceases at time c. Then the observation is $\min(T,c)$ and an indicator variable I_c shows if the individual is censored or not. The calculations for hazard and survivor functions must be adjusted to account for censoring. Statistics and Machine Learning Toolbox functions such as `ecdf`, `ksdensity`, `coxphfit`, `mle` account for censoring.

Data

Survival data usually consists of the time until an event of interest occurs and the censoring information for each individual or component. The following table shows the fictitious unemployment time of individuals in a 6-month study. Two individuals are right censored (indicated by a censoring value of 1). One individual was still unemployed after the 24th week, when the study ended. Contact with the other censored individual was lost at the end of the 21st week.

Unemployment Time (Weeks)	Censoring
14	0
23	0
7	0
21	1
19	0
16	0
24	1
8	0

Survival data might also include the number of failures at a certain time (the number of times a particular survival or failure time was observed). The following table shows the simulated time until a light-emitting diodes drops to 70% of its full light output level, in hours, in an accelerated life test.

Failure Time (hrs)	Frequency
8600	6

Failure Time (hrs)	Frequency
15300	19
22000	11
28600	20
35300	17
42000	14
48700	8
55400	2
62100	0
68800	2

Data might also have information on the predictor variables, to use in semi-parametric regression-like methods such as Cox proportional hazards regression.

Time Until Recovery (weeks)	Censoring	Gender	Systolic Blood Pressure	Diastolic Blood Pressure
12	1	Male	124	93
20	0	Female	109	77
7	0	Female	125	83
13	0	Male	117	75
9	1	Male	122	80
15	0	Female	121	70
17	1	Male	130	88
8	0	Female	115	82
14	0	Male	118	86

Survivor Function

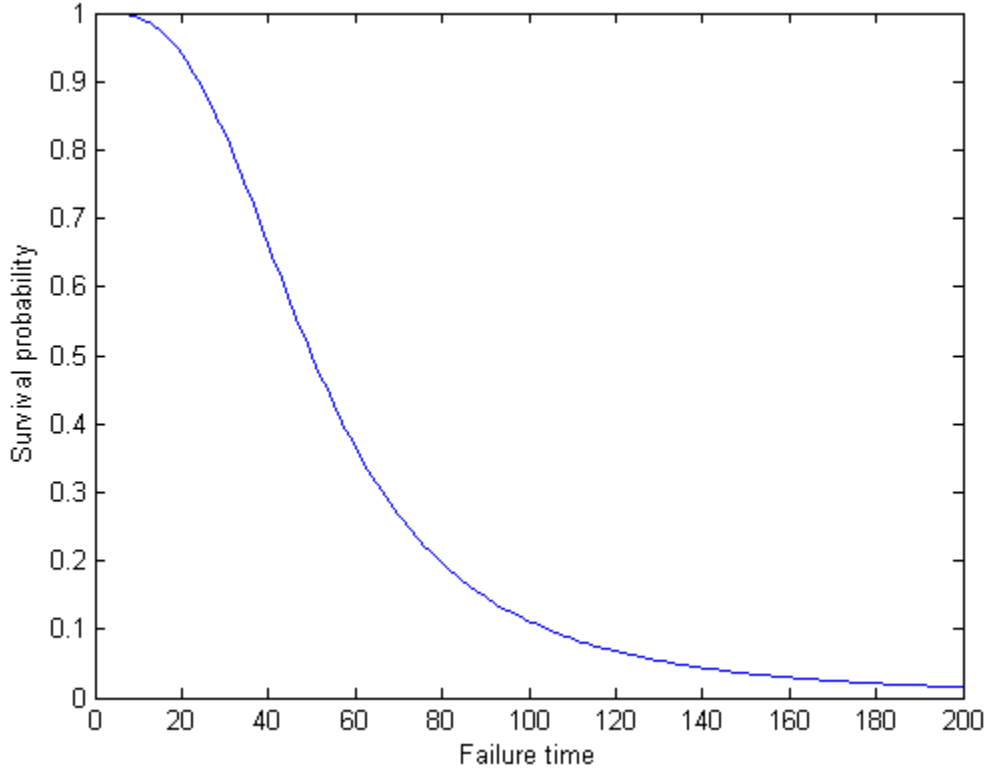
The survivor function is the probability of survival as a function of time. It is also called the survival function. It gives the probability that the survival time of an individual exceeds a certain value. Since the cumulative distribution function, $F(t)$, is

the probability that the survival time is less than or equal to a given point in time, the survival function for a continuous distribution, $S(t)$, is the complement of the cumulative distribution function:

$S(t) = 1 - F(t)$.

For example, for data coming from a Burr distribution with parameters 50, 3, and 1, you can calculate and plot the survivor function.

```
x = 0:0.1:200;
figure()
plot(x,1-cdf('Burr',x,50,3,1))
xlabel('Failure time');
ylabel('Survival probability');
```



The survivor function is also related to the hazard function. If the data has the hazard function, $h(t)$, then the survivor function is

$$S(t) = \exp\left(-\int_0^t h(u)\,du \right),$$

which corresponds to

$$S(t) = \exp\left(-H(t)\right),$$

where $H(t)$ is the cumulative hazard function.

Hazard Function

The hazard function gives the instantaneous failure rate of an individual conditioned on the fact that the individual survived until a given time. That is,

$$h(t) = \lim_{\Delta t \to 0} \frac{P\left(t \le T < t + \Delta t \mid T \ge t\right)}{\Delta t},$$

where Δt is a very small time interval. The hazard rate, therefore, is sometimes called the conditional failure rate. The hazard function always takes a positive value. However, these values do not correspond to probabilities and might be greater than 1.

The hazard function is related to the probability density function, $f(t)$, cumulative distribution function, $F(t)$, and survivor function, $S(t)$, as follows:

$$h(t) = \frac{f(t)}{S(t)} = \frac{f(t)}{1 - F(t)},$$

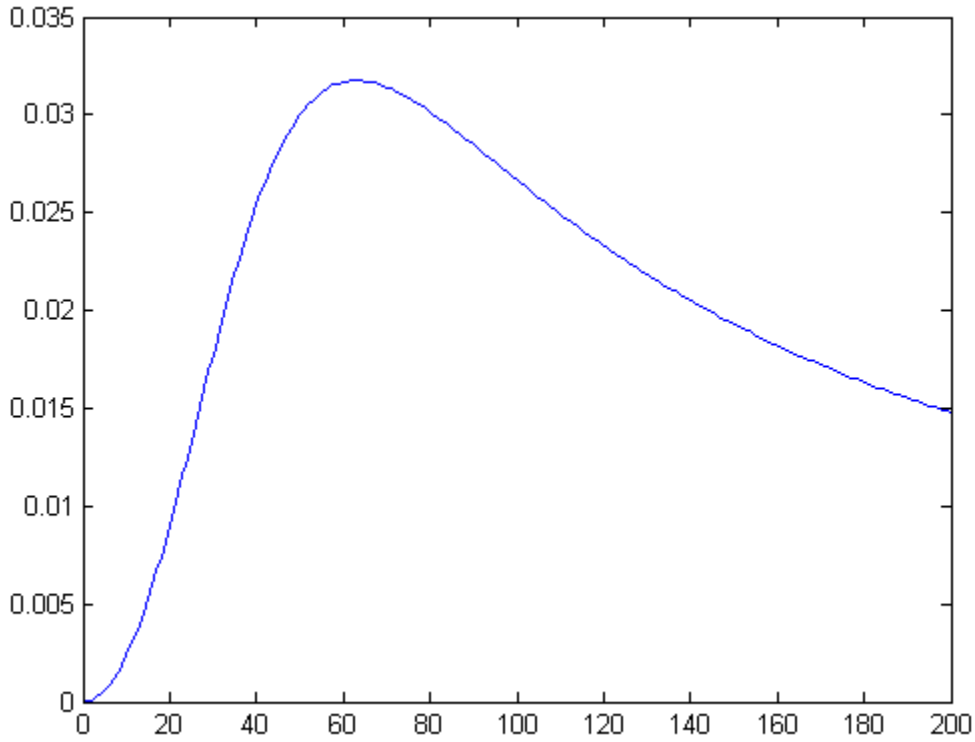
which is also equivalent to

$$h(t) = -\frac{d}{dt} \ln S(t).$$

So, if you know the shape of the survival function, you can also derive the corresponding hazard function.

For example, for data coming from a Burr distribution with parameters 50, 3, and 1, you can calculate and plot the hazard function.

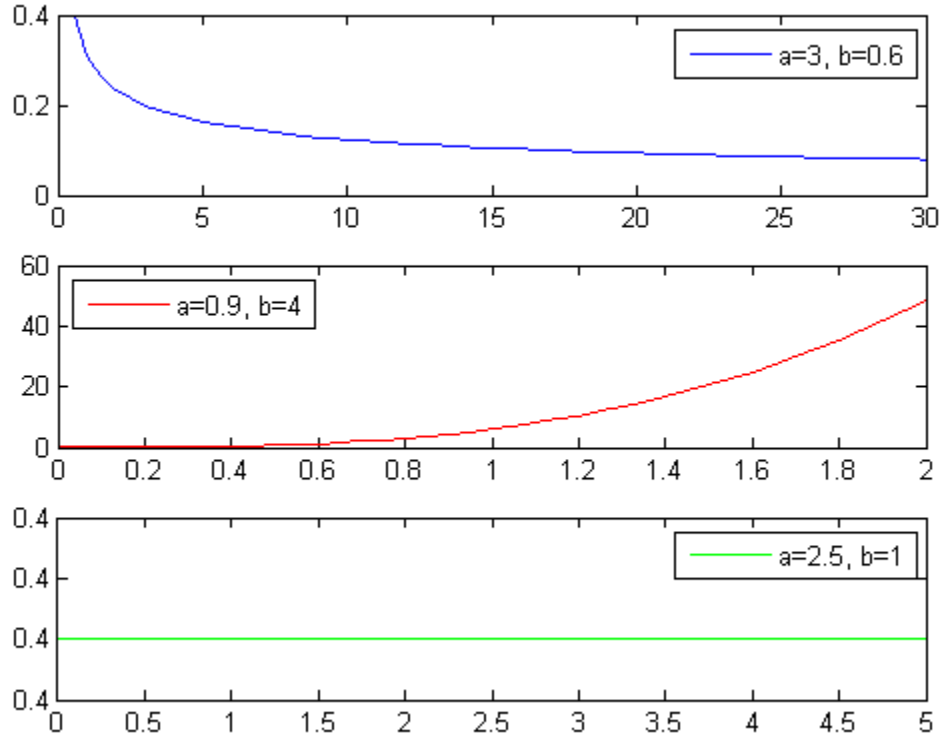
```
x = 0:1:200;
Burrhazard = pdf('Burr',x,50,3,1)./(1-cdf('Burr',x,50,3,1));
figure()
plot(x,Burrhazard)
xlabel('Failure time');
ylabel('Hazard rate');
```



There are different types of hazard functions. The previous figure shows a situation when the hazard rate increases for the early time periods and then gradually decreases.

The hazard rate might also be monotonically decreasing, increasing, or constant over time. The following figure shows examples of different types of hazard functions for data coming from different Weibull distributions.

```
ax1 = subplot(3,1,1);
x1 = 0:0.5:30;
hazard1 = pdf('wbl',x1,3,0.6)./(1-cdf('wbl',x1,3,0.6));
plot(x1,hazard1)

ax2 = subplot(3,1,2);
x2 = 0:0.05:2;
hazard2 = pdf('wbl',x2,0.9,4)./(1-cdf('wbl',x2,0.9,4));
plot(x2,hazard2,'color','r')

ax3 = subplot(3,1,3);
x3 = 0:0.05:5;
hazard3 = pdf('wbl',x3,2.5,1)./(1-cdf('wbl',x3,2.5,1));
plot(x3,hazard3)

set(ax1,'Ylim',[0 0.4]);
legend(ax1,'a=3, b=0.6');
legend(ax2,'a=0.9, b=4','location','northwest');
legend(ax3,'a=2.5, b=1');
```



In the third case, the Weibull distribution has a shape parameter value of 1, which corresponds to the exponential distribution. The exponential distribution always has a constant hazard rate over time.

References

[1] Cox, D. R., and D. Oakes. *Analysis of Survival Data*. London: Chapman & Hall, 1984.

[2] Lawless, J. F. *Statistical Models and Methods for Lifetime Data*. Hoboken, NJ: Wiley-Interscience, 2002.

[3] Kleinbaum, D. G., and M. Klein. *Survival Analysis*. Statistics for Biology and Health. 2nd edition. Springer, 2005.

See Also

`coxphfit` | `ecdf` | `ksdensity`

Related Examples

- "Hazard and Survivor Functions for Different Groups" on page 12-18
- "Survivor Functions for Two Groups" on page 12-25
- "Cox Proportional Hazards Model for Censored Data" on page 12-33

More About

- "Kaplan-Meier Method" on page 12-11
- "Cox Proportional Hazards Regression" on page 12-30

Kaplan-Meier Method

Use the Kaplan-Meier nonparametric method to estimate the empirical hazard, survivor, and cumulative distribution functions. The Statistics and Machine Learning Toolbox function `ecdf` produces the empirical cumulative hazard, survivor, and cumulative distribution functions. The Kaplan-Meier estimator for the survivor function is also called the *product-limit estimator*.

The Kaplan-Meier method uses survival data summarized in life tables. Life tables order data according to ascending failure times, but you don't have to enter the failure/survival times in an ordered manner to use `ecdf`.

A life table usually consists of:

- Failure times
- Number of items failed at a time/time period
- Number of items censored at a time/time period
- Number of items at risk at the beginning of a time/time period

The number at risk is the total number of survivors at the beginning of each period. The number at risk at the beginning of the first period is all individuals in the lifetime study. At the beginning of each remaining period, the number at risk is reduced by the number of failures plus individuals censored at the end of the previous period.

This life table shows fictitious survival data. At the beginning of the first failure time, there are seven items at risk. At time 4, three fail. So at the beginning of time 7, there are four items at risk. Only one fails at time 7, so the number at risk at the beginning of time 11 is three. Two fail at time 11, so at the beginning of time 12, the number at risk is one. The remaining item fails at time 12.

Failure Time (t)	Number Failed	Number at Risk
4	3	7
7	1	4
11	2	3
12	1	1

You can estimate the hazard, cumulative hazard, survival, and cumulative distribution functions using the life tables as described next.

Cumulative Hazard Rate (Failure Rate)

The hazard rate at each period is the number of failures in the given period divided by the number of surviving individuals at the beginning of the period (number at risk).

Failure Time (t)	Hazard Rate ($h(t)$)	Cumulative Hazard Rate
0	0	0
t_1	d_1/r_1	d_1/r_1
t_2	d_2/r_2	$h(t_1) + d_2/r_2$
...	...	...
t_n	d_n/r_n	$h(t_{n-1}) + d_n/r_n$

Survival Probability

For each period, the survival probability is the product of the complement of hazard rates. The initial survival probability at the beginning of the first time period is 1. If the hazard rate for the each period is $h(t_i)$, then the survivor probability is as shown.

Time (t)	Survival Probability ($S(t)$)
0	1
t_1	$1*(1 - h(t_1))$
t_2	$S(t_1)*(1 - h(t_2))$
...	...
t_n	$S(t_{n-1})*(1 - h(t_n))$

Cumulative Distribution Function

Because the cumulative distribution function (cdf) and the survivor function are complements of each other, you can find the cdf from the life tables using $F(t) = 1 - S(t)$.

You can compute the cumulative hazard rate, survival rate, and cumulative distribution function for the simulated data in the first table on this page as follows.

t	Number Failed (d)	Number at Risk (r)	Hazard Rate	Survival Probability	Cumulative Distribution Function
4	3	7	3/7	$1 - 3/7 = 4/7 = 0.5714$	0.4286

t	Number Failed (*d*)	Number at Risk (*r*)	Hazard Rate	Survival Probability	Cumulative Distribution Function
7	1	4	1/4	4/7*(1 – 1/4) = 3/7 = .4286	0.5714
11	2	3	2/3	3/7*(1 – 2/3) = 1/7 = 0.1429	0.8571
12	1	1	1/1	1/7*(1 – 1) = 0	1

This rates in this example are based on the discrete failure times, and hence the calculations do not necessarily follow the derivative-based definition in “What Is Survival Analysis?” on page 12-2

Here is how you can enter the data and calculate these measures using `ecdf`. The data does not necessarily have to be in ascending order. Suppose the failure times are stored in an array `y`.

```
y = [4 7 11 12];
freq = [3 1 2 1];
[f,x] = ecdf(y,'frequency',freq)
```

```
f =

         0
    0.4286
    0.5714
    0.8571
    1.0000


x =

     4
     4
     7
    11
    12
```

When you have censored data, the life table might look like the following:

Time (*t*)	Number failed (*d*)	Censoring	Number at Risk (*r*)	Hazard Rate	Survival Probability	Cumulative Distribution Function
4	2	1	7	2/7	1 – 2/7 = 0.7143	0.2857
7	1	0	4	1/4	0.7143*(1 – 1/4) = 0.5357	0.4643
11	1	1	3	2/3	0.5357*(1 – 1/3) = 0.3571	0.6429
12	1	0	1	1/1	0.3571*(1 – 1) = 0	1.0000

At any given time, the censored items are also considered in the total of number at risk, and the hazard rate formula is based on the number failed and the total number at risk. While updating the number at risk at the beginning of each period, the total number failed and censored in the previous period is reduced from the number at risk at the beginning of that period.

While using `ecdf`, you must also enter the censoring information using an array of binary variables. Enter 1 for censored data, and enter 0 for exact failure time.

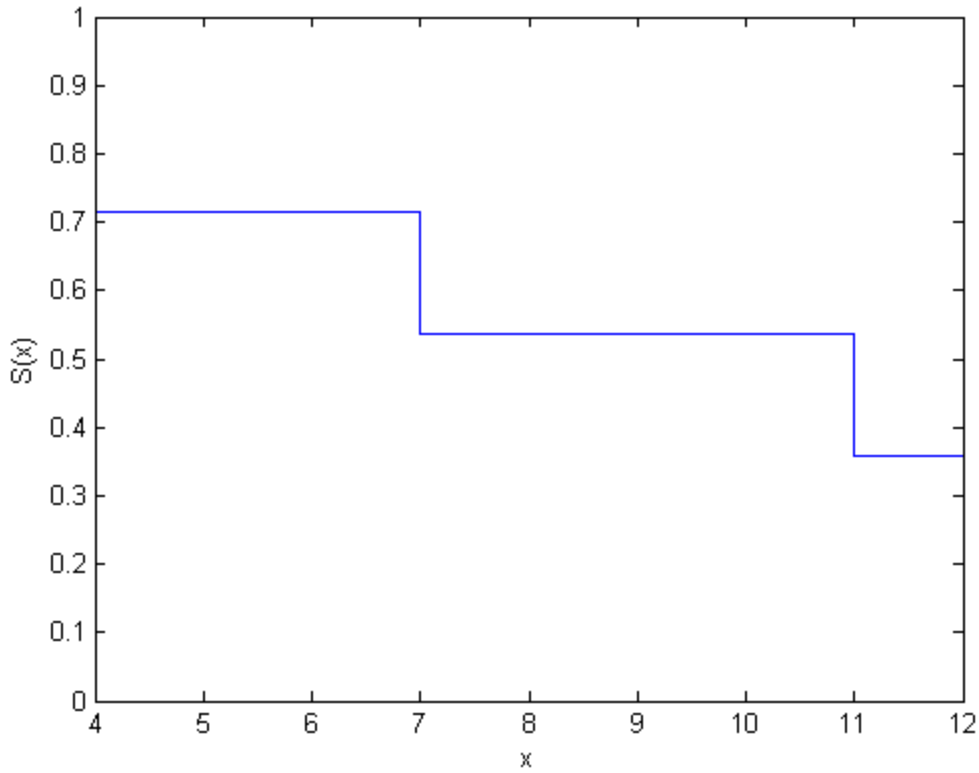
```
y = [4 4 4 7 11 11 12];
cens = [0 1 0 0 1 0 0];
[f,x] = ecdf(y,'censoring',cens)
```

```
f =

         0
    0.2857
    0.4643
    0.6429
    1.0000

x =

     4
     4
     7
    11
```

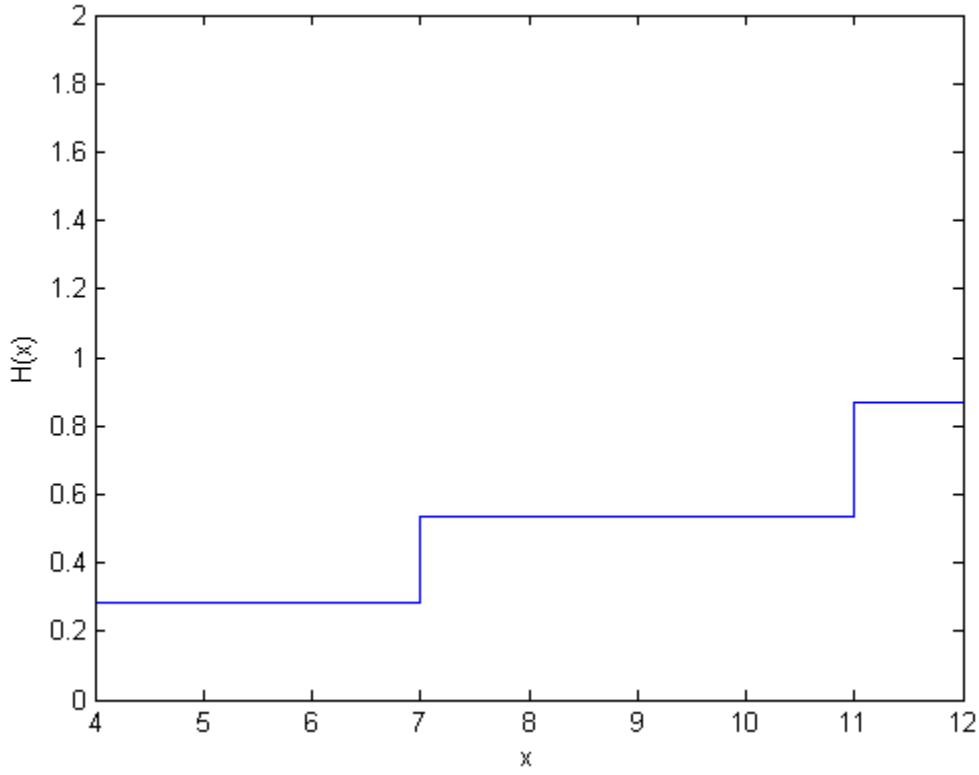
12

`ecdf`, by default, produces the cumulative distribution function values. You have to specify the survivor function or the hazard function using optional name-value pair arguments. You can also plot the results as follows.

```
figure()
ecdf(y,'censoring',cens,'function','survivor');
```




```
figure()
ecdf(y,'censoring',cens,'function','cumulative hazard');
```



References

[1] Cox, D. R., and D. Oakes. *Analysis of Survival Data*. London: Chapman & Hall, 1984.

[2] Lawless, J. F. *Statistical Models and Methods for Lifetime Data*. Hoboken, NJ: Wiley-Interscience, 2002.

[3] Kleinbaum, D. G., and M. Klein. *Survival Analysis*. Statistics for Biology and Health. 2nd edition. Springer, 2005.

See Also

`coxphfit` | `ecdf` | `ksdensity`

Related Examples

- "Hazard and Survivor Functions for Different Groups" on page 12-18
- "Survivor Functions for Two Groups" on page 12-25
- "Cox Proportional Hazards Model for Censored Data" on page 12-33

More About

- "What Is Survival Analysis?" on page 12-2
- "Cox Proportional Hazards Regression" on page 12-30

Hazard and Survivor Functions for Different Groups

This example shows how to estimate and plot the cumulative hazard and survivor functions for different groups.

Step 1. Load and organize sample data.

Load the sample data.

```
load(fullfile(matlabroot,'examples','stats','readmissiontimes.mat'))
```

The data has readmission times of patients with information on their gender, age, weight, smoking status, and censorship. This is simulated data.

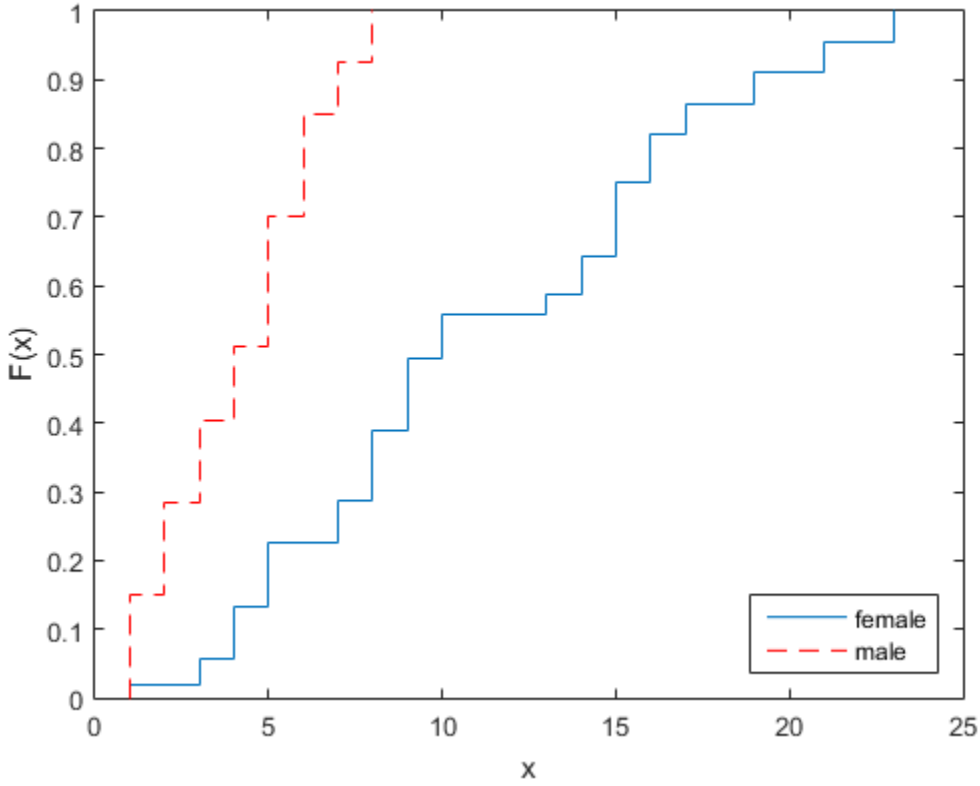
Create a matrix of readmission times and censoring for each gender.

```
female = [ReadmissionTime(Sex==1),Censored(Sex==1)];
male = [ReadmissionTime(Sex==0),Censored(Sex==0)];
```

Step 2. Estimate and plot cumulative distribution function for each gender.

Plot the Kaplan-Meier estimate of the cumulative distribution function for female and male patients.

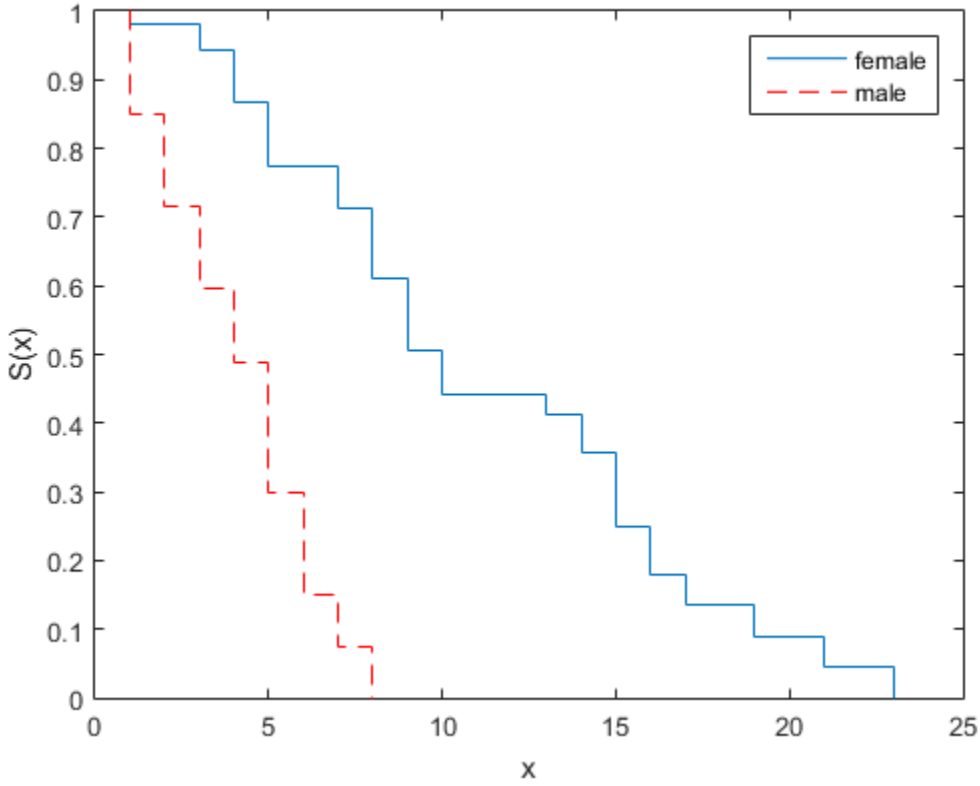
```
figure()
ecdf(gca,female(:,1),'Censoring',female(:,2));
hold on
[f,x] = ecdf(male(:,1),'Censoring',male(:,2));
stairs(x,f,'--r')
hold off
legend('female','male','Location','SouthEast')
```



Step 3. Plot survivor functions.

Compare the survivor functions for female and male patients.

```
figure()
ax1 = gca;
ecdf(ax1,female(:,1),'Censoring',female(:,2),'function','survivor');
hold on
[f,x] = ecdf(male(:,1),'Censoring',male(:,2),'function','survivor');
stairs(x,f,'--r')
legend('female','male')
```



This figure shows that readmission times are shorter for male patients than female patients.

Step 4. Fit Weibull survivor functions.

Fit Weibull distributions to readmission times of female and male patients.

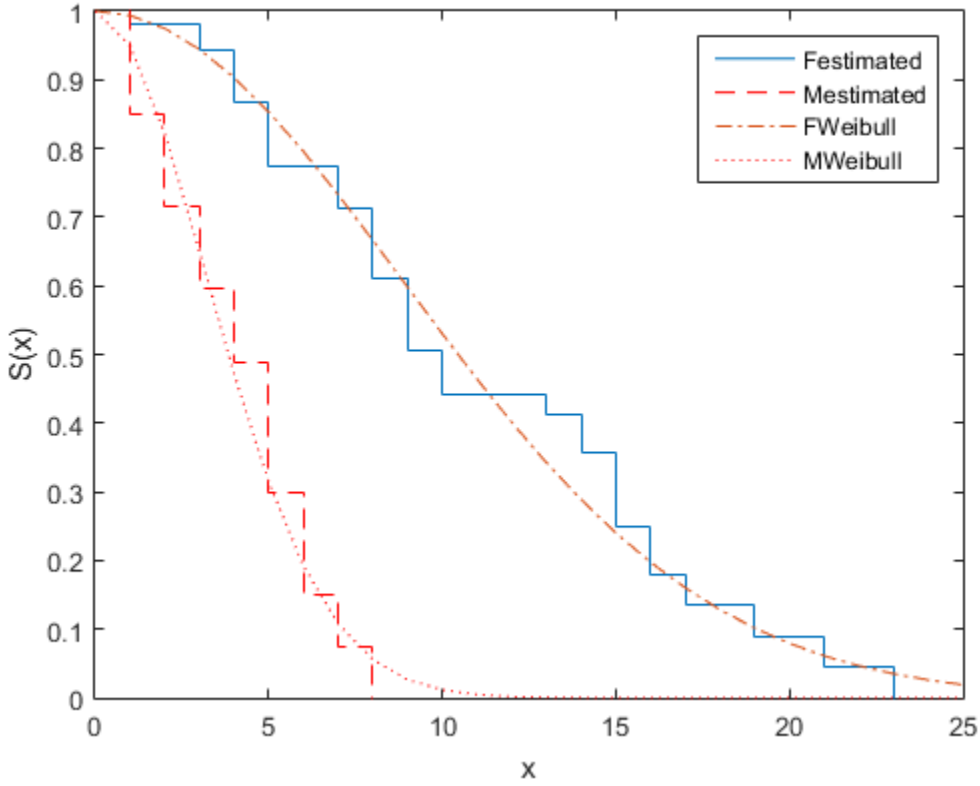
```
pd = fitdist(female(:,1),'wbl','Censoring',female(:,2))
```

```
pd =

  WeibullDistribution
```

```
  Weibull distribution
    A = 12.5593   [10.749, 14.6745]
    B = 1.99834   [1.56489, 2.55185]


pd2 = fitdist(male(:,1),'wbl','Censoring',male(:,2))


pd2 =

  WeibullDistribution

  Weibull distribution
    A = 4.63991   [3.91039, 5.50551]
    B = 1.94422   [1.48496, 2.54552]


pd2 = fitdist(male(:,1),'wbl','Censoring',male(:,2))


pd2 =

  WeibullDistribution

  Weibull distribution
    A = 4.63991   [3.91039, 5.50551]
    B = 1.94422   [1.48496, 2.54552]
```

Plot the Weibull survivor functions for female and male patients on estimated survivor functions.

```
plot(0:1:25,1-cdf('wbl',0:1:25,12.5593,1.99834),'-.')
plot(0:1:25,1-cdf('wbl',0:1:25,4.63991,1.94422),':r')
hold off
legend('Festimated','Mestimated','FWeibull','MWeibull')
```



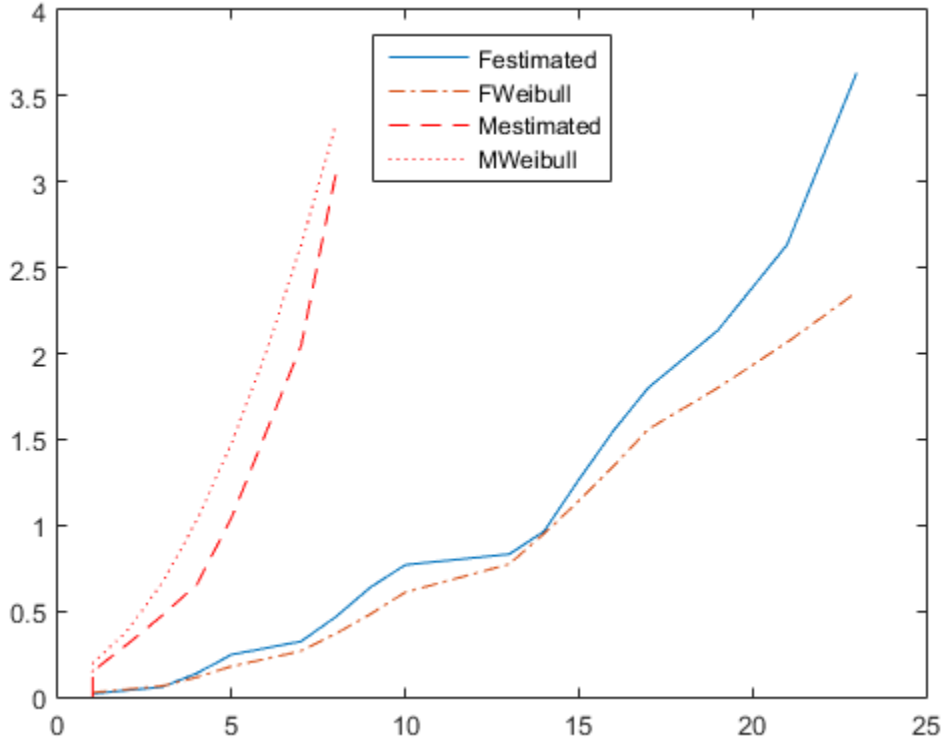
Weibull distribution provides a good fit for the data.

Step 5. Estimate cumulative hazard and fit Weibull cumulative hazard functions.

Estimate the cumulative hazard function for the genders and fit Weibull cumulative hazard functions.

```
figure()
[f,x] = ecdf(female(:,1),'Censoring',female(:,2),...
'function','cumhazard');
plot(x,f)
hold on
plot(x,cumsum(pdf(pd,x)./(1-cdf(pd,x))),'-.')
[f,x] = ecdf(male(:,1),'Censoring',male(:,2),...
```

```
'function','cumhazard');
plot(x,f,'--r')
plot(x,cumsum(pdf(pd2,x)./(1-cdf(pd2,x))),':r')
legend('Festimated','FWeibull','Mestimated','MWeibull',...
'Location','North')
```



See Also

`coxphfit` | `ecdf` | `ksdensity`

Related Examples

- “Survivor Functions for Two Groups” on page 12-25

- "Cox Proportional Hazards Model for Censored Data" on page 12-33

More About

- "What Is Survival Analysis?" on page 12-2
- "Kaplan-Meier Method" on page 12-11
- "Cox Proportional Hazards Regression" on page 12-30

Survivor Functions for Two Groups

This example shows how to find the empirical survivor functions and the parametric survivor functions using the Burr type XII distribution fit to data for two groups.

Step 1. Load and prepare sample data.

Load the sample data.

```
load(fullfile(matlabroot,'examples','stats','lightbulb.mat'))
```

The first column of the data has the lifetime (in hours) of two types of light bulbs. The second column has information about the type of light bulb. 1 indicates fluorescent bulbs whereas 0 indicates the incandescent bulb. The third column has censoring information. 1 indicates censored data, and 0 indicates the exact failure time. This is simulated data.

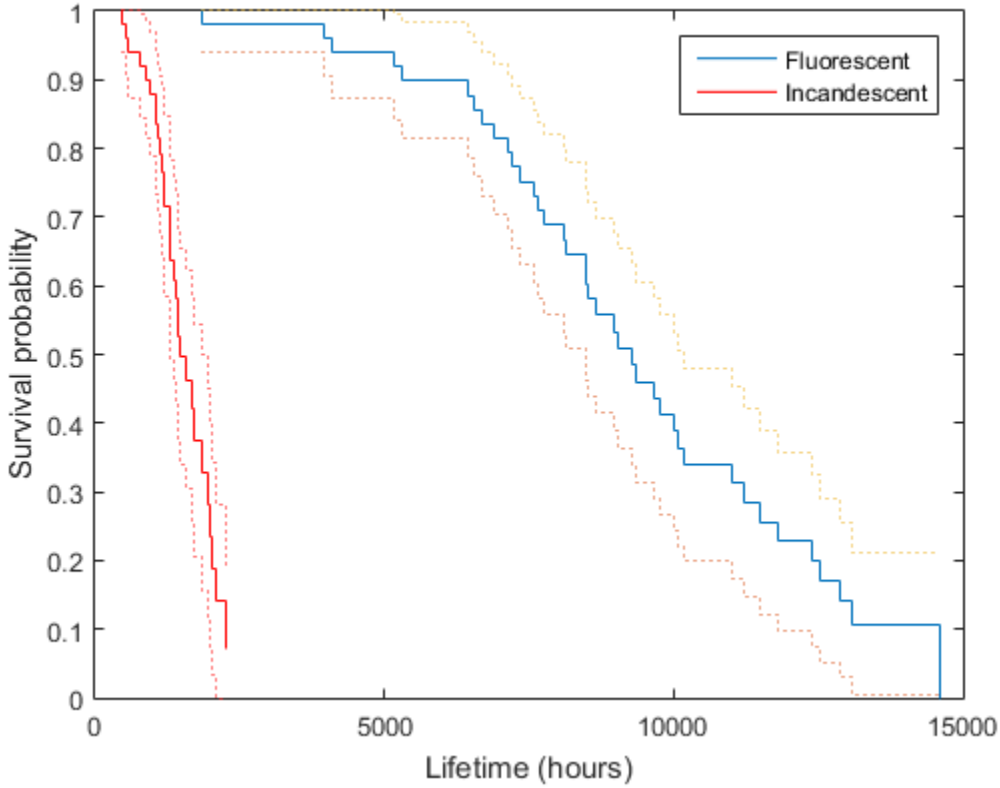
Create a variable for each light bulb type and also include the censorship information.

```
fluo = [lightbulb(lightbulb(:,2)==0,1),...
   lightbulb(lightbulb(:,2)==0,3)];
insc = [lightbulb(lightbulb(:,2)==1,1),...
   lightbulb(lightbulb(:,2)==1,3)];
```

Step 2. Plot estimated survivor functions.

Plot the estimated survivor functions for the two different types of light bulbs.

```
figure()
[f,x,flow,fup] = ecdf(fluo(:,1),'censoring',fluo(:,2),...
    'function','survivor');
ax1 = stairs(x,f);
hold on
stairs(x,flow,':')
stairs(x,fup,':')
[f,x,flow,fup] = ecdf(insc(:,1),'censoring',insc(:,2),...
    'function','survivor');
ax2 = stairs(x,f,'color','r');
stairs(x,flow,':r')
stairs(x,fup,':r')
legend([ax1,ax2],{'Fluorescent','Incandescent'})
xlabel('Lifetime (hours)')
ylabel('Survival probability')
```



You can see that the survival probability of incandescent light bulbs is much smaller than that of fluorescent light bulbs.

Step 3. Fit Burr Type XII distribution.

Fit Burr distribution to the lifetime data of fluorescent and incandescent type bulbs.

```
pd = fitdist(fluo(:,1),'burr','Censoring',fluo(:,2))
```

```
pd =

  BurrDistribution
```

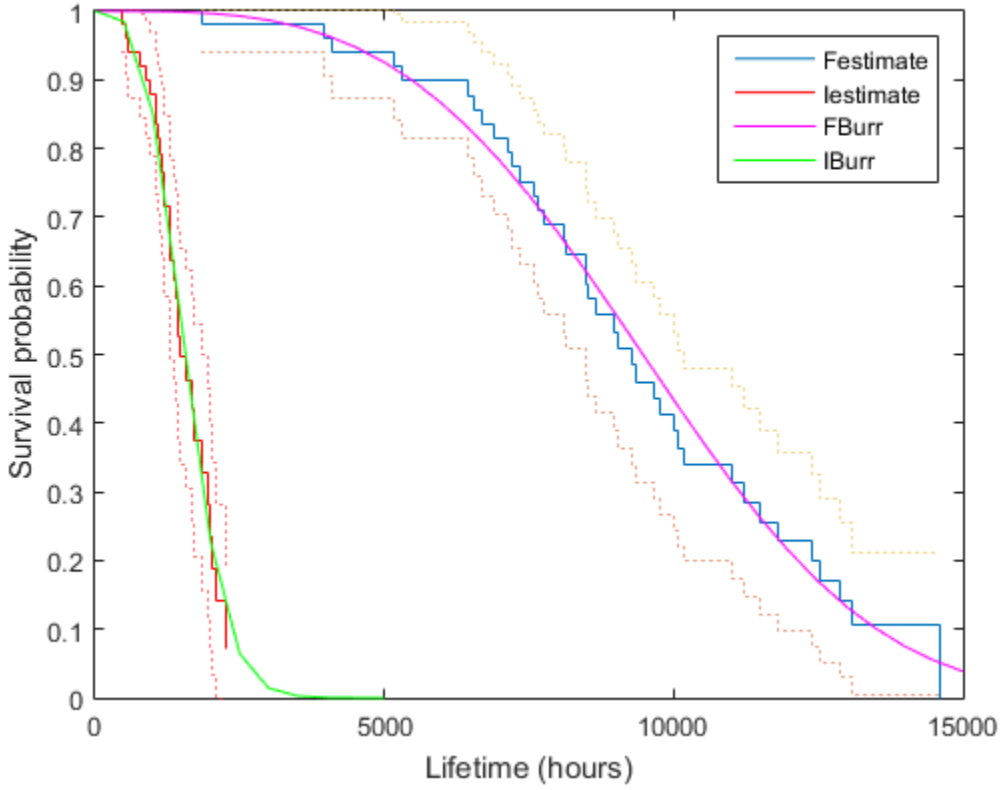
```
  Burr distribution
    alpha = 29143.5   [0.903899, 9.39642e+08]
        c = 3.44582   [2.13013, 5.57417]
        k =  33.704   [8.10669e-14, 1.40126e+16]
```

```
pd2 = fitdist(insc(:,1),'burr','Censoring',insc(:,2))
```

```
pd2 =

  BurrDistribution

  Burr distribution
    alpha = 2650.76   [430.773, 16311.4]
        c = 3.41898   [2.16794, 5.39197]
        k =  4.5891   [0.0307809, 684.185]
```

Superimpose Burr type XII survivor functions.

```
ax3 = plot(0:500:15000,1-cdf('burr',0:500:15000,29143.5,...
   3.44582,33.704),'m');
ax4 = plot(0:500:5000,1-cdf('burr',0:500:5000,2650.76,...
   3.41898,4.5891),'g');
legend([ax1;ax2;ax3;ax4],'Festimate','Iestimate','FBurr','IBurr')
```



Burr distribution provides a good fit for the lifetime of light bulbs in this example.

Step 4. Fit a Cox proportional hazards model.

Fit a Cox proportional hazards regression where the type of the bulb is the explanatory variable.

```
[b,logl,H,stats] = coxphfit(lightbulb(:,2),lightbulb(:,1),...
'Censoring',lightbulb(:,3));
stats
```

```
stats =
```

```
    covb: 1.0757
    beta: 4.7262
      se: 1.0372
       z: 4.5568
       p: 5.1936e-06
```

The p-value, p, indicates that the type of light bulb is statistically significant. The estimate of the hazard ratio is $exp(b)$ = 112.8646. This means that the hazard for the incandescent bulbs is 112.86 times the hazard for the fluorescent bulbs.

See Also

`coxphfit` | `ecdf` | `ksdensity`

Related Examples

- “Hazard and Survivor Functions for Different Groups” on page 12-18
- “Cox Proportional Hazards Model for Censored Data” on page 12-33

More About

- “What Is Survival Analysis?” on page 12-2
- “Kaplan-Meier Method” on page 12-11
- “Cox Proportional Hazards Regression” on page 12-30

Cox Proportional Hazards Regression

Cox proportional hazards regression is a semiparametric method for adjusting survival rate estimates to quantify the effect of predictor variables. The method represents the effects of explanatory variables as a multiplier of a common baseline hazard function, $h_0(t)$. The hazard function is the nonparametric part of the Cox proportional hazards regression function, whereas the impact of the predictor variables is a loglinear regression. For a baseline relative to 0, this model corresponds to

$$h_X(t) = h_0(t)e^{\sum_i X_i b_i},$$

where $h_X(t)$ is the hazard rate at X and $h_0(t)$ is the baseline hazard rate function.

The Cox proportional hazards model relates the hazard rate for individuals or items at the value X, to the hazard rate for individuals or items at the baseline value. It produces an estimate for the hazard ratio, $HR = h_X(t)/h_0(t)$. The model is based on the assumption that the baseline hazard function depends on time, t, but the predictor variables do not. This is also called the proportional hazards assumption, which states that the hazard rate does not change over time for any individual. The hazard ratio represents the relative risk of instant failure for individuals or items having the predictive variable value X compared to the ones having the baseline values. For example, if the predictive variable is smoking status, where nonsmoking is the baseline category, the hazard ratio shows the relative instant failure rate of smokers compared to the baseline category, that is, nonsmokers.

For a baseline relative to X^* and the predictor variable value X, the hazard ratio is

$$HR = \frac{h_X(t)}{h_{X^*}(t)} = \exp\left[\sum_i \left(X_i - X_i^*\right) b_i\right].$$

For example, if the baseline is the mean values of the predictor variables (`mean(X)`), then the hazard rate model becomes

$$h_X(t) = h_{\bar{X}}(t)\exp\left[\sum_i \left(X_i - \bar{X}\right) b_i\right].$$

Hazard rates are related to survival rates, such that the survival rate at time t for an individual with the explanatory variable value x is

$$S_X(t) = S_0(t)^{HR_X(t)},$$

where $S_0(t)$ is the survivor function with the baseline hazard rate function $h_0(t)$, and $HR_x(t)$ is the hazard ratio of the predictor variable value x relative to the baseline value.

A point estimate of the effect of each explanatory variable, that is, the estimated hazard ratio for the effect of each explanatory variable is exp(b), given all other variables are held constant, where b is the coefficient estimate for that variable. The coefficient estimates are found by maximizing the likelihood function of the model. The likelihood function for the proportional hazards regression model is based on the observed order of events. It is the product of likelihood of a failure estimated for each failure time. If there are n failures at n distinct failure times, then the likelihood is

$$L = \left[\frac{h(t_1)}{\sum_{i=1}^{n} h(t_i)}\right] \times \left[\frac{h(t_2)}{\sum_{i=2}^{n} h(t_i)}\right] \times \cdots \times \left[\frac{h(t_n)}{h(t_n)}\right].$$

You can use a likelihood ratio test to assess the significance of adding a term or terms in a model. Consider the two models where the first model has p predictive variables and the second model has $p + r$ predictive variables. Then, comparing the two models, $-2*(L_1/L_2)$ has a chi-square distribution with r degrees of freedom (the number of terms being tested).

References

[1] Cox, D. R., and D. Oakes. *Analysis of Survival Data*. London: Chapman & Hall, 1984.

[2] Lawless, J. F. *Statistical Models and Methods for Lifetime Data*. Hoboken, NJ: Wiley-Interscience, 2002.

[3] Kleinbaum, D. G., and M. Klein. *Survival Analysis*. Statistics for Biology and Health. 2nd edition. Springer, 2005.

See Also

`coxphfit` | `ecdf` | `ksdensity`

Related Examples

- "Hazard and Survivor Functions for Different Groups" on page 12-18
- "Survivor Functions for Two Groups" on page 12-25
- "Cox Proportional Hazards Model for Censored Data" on page 12-33

More About

- "What Is Survival Analysis?" on page 12-2
- "Kaplan-Meier Method" on page 12-11

Cox Proportional Hazards Model for Censored Data

This example shows how to construct a Cox proportional hazards model, and assess the significance of the predictor variables.

Step 1. Load sample data.

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load readmissiontimes
```

The response variable is `Readmission Time`, which shows the readmission times for 100 patients. The predictor variables are `Age`, `Sex`, `Weight`, and the smoking status of each patient, `Smoker`. 1 indicates the patient is a smoker, and 0 indicates that the patient does not smoke. The column vector `Censored` has the censorship information for each patient, where 1 indicates censored data, and 0 indicates the exact readmission times are observed. This is simulated data.

Step 2. Fit Cox proportional hazards function.

Fit a Cox proportional hazard function with the variable Sex as the predictor variable, taking the censoring into account.

```
X = Sex;
[b,logl,H,stats] = coxphfit(X,ReadmissionTime,...
'censoring',Censored);
```

Assess the statistical significance of the term Sex.

```
stats
```

```
stats =

    covb: 0.1016
    beta: -1.7642
      se: 0.3188
       z: -5.5335
       p: 3.1392e-08
```

The *p*-value, p, indicates that the term Sex is statistically significant.

Save the loglikelihood value with a different name. You will use this to assess the significance of the extended models.

```
loglSex = logl
```

```
loglSex =

 -262.1365
```

Step 3. Add Age and Weight to the model.

Fit a Cox proportional hazards model with the variables Sex, Age, and Weight.

```
X = [Sex Age Weight];
[b,logl,H,stats] = coxphfit(X,ReadmissionTime,...
'censoring',Censored);
```

Assess the significance of the terms.

```
stats.beta
```

```
ans =

   -0.5441
    0.0143
    0.0250
```

```
stats.p
```

```
ans =

    0.4953
    0.3842
    0.0960
```

None of the terms, adjusted for others, is statistically significant.

Assess the significance of the terms using the log likelihood ratio. You can assess the significance of the new model using the likelihood ratio statistic. First find the difference between the log-likelihood statistic of the model without the terms Age and Weight and the log-likelihood of the model with Sex, Age, and Weight.

```
-2*[loglSex - logl]
```

```
ans =

    3.6705
```

Now, compute the *p*-value for the likelihood ratio statistic. The likelihood ratio statistic has a Chi-square distribution with a degrees of freedom equal to the number of predictor variables being assessed. In this case, the degrees of freedom is 2.

```
p = 1 - cdf('chi2',3.6705,2)
```

```
p =

    0.1596
```

The *p*-value of 0.1596 indicates that the terms Age and Weight are not statistically significant, given the term Sex in the model.

Step 4. Add Smoker to the model.

Fit a Cox proportional hazards model with the variables Sex and Smoker.

```
X = [Sex Smoker];
[b,logl,H,stats] = coxphfit(X,ReadmissionTime,...
'censoring',Censored);
```

Assess the significance of the terms in the model.

```
stats.p
```

```
ans =

    0.0000
    0.0148
```

Compare this model to the first model where Sex is the only term.

```
 -2*[loglSex - logl]
```

```
ans =

    5.5789
```

Compute the *p*-value for the likelihood ratio statistic. The likelihood ratio statistic has a Chi-square distribution with a degree of freedom of 1.

```
p = 1 - cdf('chi2',5.5789,1)
```

```
p =

    0.0182
```

The p-value of 0.0182 indicates that Sex and Smoker are statistically significant given the other is in the model. The model with Sex and Smoker is a better fit compared to the model with only Sex.

Request the coefficient estimates.

```
 stats.beta
```

```
ans =

   -1.7165
    0.6338
```

The default baseline is the mean of `X`, so the final model for the hazard ratio is

$$HR = \frac{h_X(t)}{h_{\bar{X}}(t)} = \exp\left[\beta_s\left(X_s - \bar{X}_s\right) + \beta_a\left(X_a - \bar{X}_a\right)\right].$$

Fit a Cox ph model with a baseline of 0.

```
X = [Sex Smoker];
[b,logl,H,stats] = coxphfit(X,ReadmissionTime,...
'censoring',Censored,'baseline',0);
```

The model for the hazard ratio is

$$HR = \frac{h_X(t)}{h_0(t)} = \exp\left[\beta_s X_s + \beta_a X_a\right].$$

Request the coefficient estimates.

```
 stats.beta
```

```
ans =

   -1.7165
    0.6338
```

The coefficients are not affected, but the hazard rate differs from when the baseline is the mean of X.

See Also

`coxphfit` | `ecdf` | `ksdensity`

Related Examples

- "Hazard and Survivor Functions for Different Groups" on page 12-18
- "Survivor Functions for Two Groups" on page 12-25

More About

- "What Is Survival Analysis?" on page 12-2
- "Kaplan-Meier Method" on page 12-11
- "Cox Proportional Hazards Regression" on page 12-30

Multivariate Methods

Introduction to Multivariate Methods

Large, high-dimensional data sets are common in the modern era of computer-based instrumentation and electronic data storage. High-dimensional data present many challenges for statistical visualization, analysis, and modeling.

Data visualization, of course, is impossible beyond a few dimensions. As a result, pattern recognition, data preprocessing, and model selection must rely heavily on numerical methods.

A fundamental challenge in high-dimensional data analysis is the so-called *curse of dimensionality*. Observations in a high-dimensional space are necessarily sparser and less representative than those in a low-dimensional space. In higher dimensions, data over-represent the edges of a sampling distribution, because regions of higher-dimensional space contain the majority of their volume near the surface. (A d-dimensional spherical shell has a volume, relative to the total volume of the sphere, that approaches 1 as d approaches infinity.) In high dimensions, typical data points at the interior of a distribution are sampled less frequently.

Often, many of the dimensions in a data set—the measured features—are not useful in producing a model. Features may be irrelevant or redundant. Regression and classification algorithms may require large amounts of storage and computation time to process raw data, and even if the algorithms are successful the resulting models may contain an incomprehensible number of terms.

Because of these challenges, multivariate statistical methods often begin with some type of *dimension reduction*, in which data are approximated by points in a lower-dimensional space. Dimension reduction is the goal of the methods presented in this chapter. Dimension reduction often leads to simpler models and fewer measured variables, with consequent benefits when measurements are expensive and visualization is important.

Multivariate Linear Regression

In this section...

Multivariate Linear Regression Model

The multivariate linear regression model expresses a d-dimensional continuous response vector as a linear combination of predictor terms plus a vector of error terms with a multivariate normal distribution. Let $\mathbf{y}_i = (y_{i1},\ldots,y_{id})'$ denote the response vector for observation i, $i = 1,\ldots,n$. In the most general case, given the d-by-K design matrix $\mathbf{X}_i$ and the K-by-1 vector of coefficients β, the multivariate linear regression model is

$$\mathbf{y}_i = \mathbf{X}_i\beta + \varepsilon_i,$$

where the d-dimensional vector of error terms follows a multivariate normal distribution,

$$\varepsilon_i \sim MVN_d(\mathbf{0},\Sigma).$$

The model assumes independence between observations, meaning the error variance-covariance matrix for the n stacked d-dimensional response vectors is

$$\mathbf{I}_n \otimes \Sigma = \begin{pmatrix} \Sigma & & 0 \\ & \ddots & \\ 0 & & \Sigma \end{pmatrix}.$$

If $\mathbf{y}$ denotes the nd-by-1 vector of stacked d-dimensional responses, and $\mathbf{X}$ denotes the nd-by-K matrix of stacked design matrices, then the distribution of the response vector is

$$\mathbf{y} \sim MVN_{nd}(\mathbf{X}\beta, \mathbf{I}_n \otimes \Sigma).$$

Solving Multivariate Regression Problems

To fit multivariate linear regression models of the form

$$\mathbf{y}_i = \mathbf{X}_i\beta + \varepsilon_i,\ \varepsilon_i \sim MVN_d(\mathbf{0},\Sigma)$$

in Statistics and Machine Learning Toolbox, use `mvregress`. This function fits multivariate regression models with a diagonal (heteroscedastic) or unstructured (heteroscedastic and correlated) error variance-covariance matrix, Σ, using least squares or maximum likelihood estimation.

Many variations of multivariate regression might not initially appear to be of the form supported by `mvregress`, such as:

- Multivariate general linear model
- Multivariate analysis of variance (MANOVA)
- Longitudinal analysis
- Panel data analysis
- Seemingly unrelated regression (SUR)
- Vector autoregressive (VAR) model

In many cases, you can frame these problems in the form used by `mvregress` (but `mvregress` does not support parameterized error variance-covariance matrices). For the special case of one-way MANOVA, you can alternatively use `manova1`. Econometrics Toolbox™ has functions for VAR estimation.

Note: The multivariate linear regression model is distinct from the multiple linear regression model, which models a *univariate* continuous response as a linear combination of exogenous terms plus an independent and identically distributed error term. To fit a multiple linear regression model, use `LinearModel.fit`.

See Also

`LinearModel.fit` | `manova1` | `mvregress` | `mvregresslike`

Related Examples

- “Set Up Multivariate Regression Problems” on page 13-15

- "Multivariate General Linear Model" on page 13-29
- "Fixed Effects Panel Model with Concurrent Correlation" on page 13-34
- "Longitudinal Analysis" on page 13-42

More About

- "Estimation of Multivariate Regression Models" on page 13-6

Estimation of Multivariate Regression Models

In this section...

Least Squares Estimation

Ordinary Least Squares

When you fit multivariate linear regression models using `mvregress`, you can use the optional name-value pair `'algorithm','cwls'` to choose least squares estimation. In this case, by default, `mvregress` returns ordinary least squares (OLS) estimates using $\Sigma = \mathbf{I}_d$. Alternatively, if you specify a covariance matrix for weighting, you can return covariance-weighted least squares (CWLS) estimates. If you combine OLS and CWLS, you can get feasible generalized least squares (FGLS) estimates.

The OLS estimate for the coefficient vector is the vector $\mathbf{b}$ that minimizes

$$\sum_{i=1}^{n}(\mathbf{y}_i - \mathbf{X}_i\mathbf{b})'(\mathbf{y}_i - \mathbf{X}_i\mathbf{b}).$$

Let $\mathbf{y}$ denote the nd-by-1 vector of stacked d-dimensional responses, and $\mathbf{X}$ denote the nd-by-K matrix of stacked design matrices. The K-by-1 vector of OLS regression coefficient estimates is

$$\mathbf{b}_{OLS} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}.$$

This is the first `mvregress` output.

Given $\Sigma = \mathbf{I}_d$ (the `mvregress` OLS default), the variance-covariance matrix of the OLS estimates is

$$V(\mathbf{b}_{OLS}) = (\mathbf{X}'\mathbf{X})^{-1}.$$

This is the fourth `mvregress` output. The standard errors of the OLS regression coefficients are the square root of the diagonal of this variance-covariance matrix.

If your data is not scaled such that $\Sigma = \sigma^2\mathbf{I}_d$, then you can multiply the `mvregress` variance-covariance matrix by the mean squared error (MSE), an unbiased estimate of σ^2. To compute the MSE, return the n-by-d matrix of residuals, $\mathbf{E}$ (the third `mvregress` output). Then,

$$\text{MSE} = \frac{\sum_{i=1}^{n} \mathbf{e}_i\mathbf{e}_i'}{n-K},$$

where $\mathbf{e}_i = (\mathbf{y}_i - \mathbf{X}_i\beta)'$ is the ith row of $\mathbf{E}$.

Covariance-Weighted Least Squares

For most multivariate problems, an identity error covariance matrix is insufficient, and leads to inefficient or biased standard error estimates. You can specify a matrix for CWLS estimation using the optional name-value pair argument `covar0`, for example, an invertible d-by-d matrix named $\mathbf{C}_0$. Usually, $\mathbf{C}_0$ is a diagonal matrix such that the inverse matrix $\mathbf{C}_0^{-1}$ contains weights for each dimension to model heteroscedasticity. However, $\mathbf{C}_0$ can also be a nondiagonal matrix that models correlation.

Given $\mathbf{C}_0$, the CWLS solution is the vector $\mathbf{b}$ that minimizes

$$\sum_{i=1}^{n} (\mathbf{y}_i - \mathbf{X}_i\mathbf{b})'\mathbf{C}_0(\mathbf{y}_i - \mathbf{X}_i\mathbf{b}).$$

In this case, the K-by-1 vector of CWLS regression coefficient estimates is

$$\mathbf{b}_{CWLS} = \left(\mathbf{X}'(\mathbf{I}_n \otimes \mathbf{C}_0)^{-1}\mathbf{X}\right)^{-1}\mathbf{X}'(\mathbf{I}_n \otimes \mathbf{C}_0)^{-1}\mathbf{y}.$$

This is the first `mvregress` output.

If $\Sigma = \mathbf{C}_0$, this is the generalized least squares (GLS) solution. The corresponding variance-covariance matrix of the CWLS estimates is

$$V(\mathbf{b}_{CWLS}) = \left(\mathbf{X}'(\mathbf{I}_n \otimes \mathbf{C}_0)^{-1}\mathbf{X}\right)^{-1}.$$

This is the fourth `mvregress` output. The standard errors of the CWLS regression coefficients are the square root of the diagonal of this variance-covariance matrix.

If you only know the error covariance matrix up to a proportion, that is, $\Sigma = \sigma^2\mathbf{C}_0$, you can multiply the `mvregress` variance-covariance matrix by the MSE, as described in "Ordinary Least Squares" on page 13-6.

Error Covariance Estimation

Regardless of which least squares method you use, the estimate for the error variance-covariance matrix is

$$\hat{\Sigma} = \begin{pmatrix} \hat{\sigma}_1^2 & \hat{\sigma}_{12} & \cdots & \hat{\sigma}_{1d} \\ \hat{\sigma}_{12} & \hat{\sigma}_2^2 & \cdots & \hat{\sigma}_{2d} \\ \vdots & \vdots & \ddots & \vdots \\ \hat{\sigma}_{1d} & \hat{\sigma}_{2d} & \cdots & \hat{\sigma}_d^2 \end{pmatrix} = \frac{\mathbf{E}'\mathbf{E}}{n},$$

where $\mathbf{E}$ is the n-by-d matrix of residuals. The ith row of $\mathbf{E}$ is $\mathbf{e}_i = (\mathbf{y}_i - \mathbf{X}_i\mathbf{b})'$.

The error covariance estimate, $\hat{\Sigma}$, is the second `mvregress` output, and the matrix of residuals, $\mathbf{E}$, is the third output. If you specify the optional name-value pair `'covtype','diagonal'`, then `mvregress` returns $\hat{\Sigma}$ with zeros in the off-diagonal entries,

$$\hat{\Sigma} = \begin{pmatrix} \hat{\sigma}_1^2 & & 0 \\ & \ddots & \\ 0 & & \hat{\sigma}_d^2 \end{pmatrix}.$$

Feasible Generalized Least Squares

The generalized least squares estimate is the CWLS estimate with a known covariance matrix. That is, given Σ is known, the GLS solution is

$$\mathbf{b}_{GLS} = \left(\mathbf{X}'(\mathbf{I}_n \otimes \Sigma)^{-1}\mathbf{X}\right)^{-1}\mathbf{X}'(\mathbf{I}_n \otimes \Sigma)^{-1}\mathbf{y},$$

with variance-covariance matrix

$$V(\mathbf{b}_{GLS}) = \left(\mathbf{X}'(\mathbf{I}_n \otimes \Sigma)^{-1}\mathbf{X}\right)^{-1}.$$

In most cases, the error covariance is unknown. The feasible generalized least squares (FGLS) estimate uses $\hat{\Sigma}$ in place of Σ. You can obtain two-step FGLS estimates as follows:

1. Perform OLS regression, and return an estimate $\hat{\Sigma}$.
2. Perform CWLS regression, using $\mathbf{C}_0 = \hat{\Sigma}$.

You can also iterate between these two steps until convergence is reached.

For some data, the OLS estimate $\hat{\Sigma}$ is positive semidefinite, and has no unique inverse. In this case, you cannot get the FGLS estimate using `mvregress`. As an alternative, you can use `lscov`, which uses a generalized inverse to return weighted least squares solutions for positive semidefinite covariance matrices.

Panel Corrected Standard Errors

An alternative to FGLS is to use OLS coefficient estimates (which are consistent) and make a standard error correction to improve efficiency. One such standard error adjustment—which does not require inversion of the covariance matrix—is panel corrected standard errors (PCSE) [1]. The panel corrected variance-covariance matrix for OLS estimates is

$$V_{pcse}(\mathbf{b}_{OLS}) = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'(\mathbf{I}_n \otimes \Sigma)\mathbf{X}(\mathbf{X}'\mathbf{X}).$$

The PCSE are the square root of the diagonal of this variance-covariance matrix. “Fixed Effects Panel Model with Concurrent Correlation” on page 13-34 illustrates PCSE computation.

Maximum Likelihood Estimation

Maximum Likelihood Estimates

The default estimation algorithm used by `mvregress` is maximum likelihood estimation (MLE). The loglikelihood function for the multivariate linear regression model is

$$\log L(\beta,\Sigma|\mathbf{y},\mathbf{X}) = \frac{1}{2}nd\log(2\pi) + \frac{1}{2}n\log(\det(\Sigma)) + \frac{1}{2}\sum_{i=1}^{n}(\mathbf{y}_i - \mathbf{X}_i\beta)'\Sigma^{-1}(\mathbf{y}_i - \mathbf{X}_i\beta).$$

The MLEs for β and Σ are the values that maximize the loglikelihood objective function.

`mvregress` finds the MLEs using an iterative two-stage algorithm. At iteration $m + 1$, the estimates are

$$\mathbf{b}_{MLE}^{(m+1)} = \left(\mathbf{X}'\left(\mathbf{I}_n \otimes \Sigma^{(m)}\right)^{-1}\mathbf{X}\right)^{-1}\mathbf{X}'\left(\mathbf{I}_n \otimes \Sigma^{(m)}\right)^{-1}\mathbf{y}$$

and

$$\hat{\Sigma}^{(m+1)} = \frac{1}{n}\sum_{i=1}^{n}\left(\mathbf{y}_i - \mathbf{X}_i\mathbf{b}_{MLE}^{(m+1)}\right)\left(\mathbf{y}_i - \mathbf{X}_i\mathbf{b}_{MLE}^{(m+1)}\right)'.$$

The algorithm terminates when the changes in the coefficient estimates and loglikelihood objective function are less than a specified tolerance, or when the specified maximum number of iterations is reached. The optional name-value pair arguments for changing these convergence criteria are `tolbeta`, `tolobj`, and `maxiter`, respectively.

Standard Errors

The variance-covariance matrix of the MLEs is an optional `mvregress` output. By default, `mvregress` returns the variance-covariance matrix for only the regression coefficients, but you can also get the variance-covariance matrix of $\hat{\Sigma}$ using the optional name-value pair `'vartype','full'`. In this case, `mvregress` returns the variance-covariance matrix for all K regression coefficients, and d or $d(d+1)/2$ covariance terms (depending on whether the error covariance is diagonal or full).

By default, the variance-covariance matrix is the inverse of the observed Fisher information matrix (the `'hessian'` option). You can request the expected Fisher information matrix using the optional name-value pair `'vartype','fisher'`. Provided there is no missing response data, the observed and expected Fisher information matrices are the same. If response data is missing, the observed Fisher information accounts for the added uncertainty due to the missing values, whereas the expected Fisher information matrix does not.

The variance-covariance matrix for the regression coefficient MLEs is

$$V(\mathbf{b}_{MLE}) = \left(\mathbf{X}'(\mathbf{I}_n \otimes \Sigma)^{-1}\mathbf{X}\right)^{-1},$$

evaluated at the MLE of the error covariance matrix. This is the fourth `mvregress` output. The standard errors of the MLEs are the square root of the diagonal of this variance-covariance matrix.

For $\hat{\Sigma}$, let θ denote the vector of parameters in the estimated error variance-covariance matrix. For example, if $d = 2$, then:

- If the estimated covariance matrix is diagonal, then $\theta = (\sigma_1^2, \sigma_2^2)$.
- If the estimated covariance matrix is full, then $\theta = (\sigma_1^2, \sigma_{12}, \sigma_2^2)$.

The Fisher information matrix for θ, $I(\theta)$, has elements

$$I(\theta)_{u,v} = \frac{1}{2} tr\left(\Sigma^{-1} \frac{\partial \Sigma}{\partial \theta_u} \Sigma^{-1} \frac{\partial \Sigma}{\partial \theta_v} \right),\ u,v = 1,\ldots,n_\theta,$$

where n_θ is the length of θ (either d or $d(d+1)/2$). The resulting variance-covariance matrix is

$$V(\theta) = I(\theta)^{-1}.$$

When you request the full variance-covariance matrix, `mvregress` returns (as the fourth output) the block diagonal matrix

$$\begin{pmatrix} V(\mathbf{b}_{MLE}) & \mathbf{0} \\ \mathbf{0} & V(\theta) \end{pmatrix}.$$

Missing Response Data

Expectation/Conditional Maximization

If any response values are missing, indicated by `NaN`, `mvregress` uses an expectation/conditional maximization (ECM) algorithm for estimation (if enough data is available). In this case, the algorithm is iterative for both least squares and maximum likelihood estimation. During each iteration, `mvregress` imputes missing response values using their conditional expectation.

Consider organizing the data so that the joint distribution of the missing and observed responses, denoted $\tilde{\mathbf{y}}$ and $\mathbf{y}$ respectively, can be written as

$$\begin{pmatrix} \tilde{\mathbf{y}} \\ \mathbf{y} \end{pmatrix} \sim MVN\left\{ \begin{pmatrix} \tilde{\mathbf{X}}\beta \\ \mathbf{X}\beta \end{pmatrix}, \begin{pmatrix} \Sigma_{\tilde{y}} & \Sigma_{\tilde{y}y} \\ \Sigma_{y\tilde{y}} & \Sigma_y \end{pmatrix} \right\}.$$

Using properties of the multivariate normal distribution, the conditional expectation of the missing responses given the observed responses is

$$\mathrm{E}\left(\tilde{\mathbf{y}}|\mathbf{y}\right) = \tilde{\mathbf{X}}\beta + \Sigma_{\tilde{y}y}\Sigma_{y}^{-1}(\mathbf{y} - \mathbf{X}\beta).$$

Also, the variance-covariance matrix of the conditional distribution is

$$\mathrm{COV}(\tilde{\mathbf{y}}|\mathbf{y}) = \Sigma_{\tilde{y}} - \Sigma_{\tilde{y}y}\Sigma_{y}^{-1}\Sigma_{y\tilde{y}}.$$

At each iteration of the ECM algorithm, `mvregress` uses the parameter values from the previous iteration to:

- Update the regression coefficients using the combined vector of observed responses and conditional expectations of missing responses.
- Update the variance-covariance matrix, adjusting for missing responses using the variance-covariance matrix of the conditional distribution.

Finally, the residuals that `mvregress` returns for missing responses are the difference between the conditional expectation and the fitted value, both evaluated at the final parameter estimates.

If you prefer to ignore any observations that have missing response values, use the name-value pair `'algorithm','mvn'`. Note that `mvregress` always ignores observations that have missing predictor values.

Observed Information Matrix

By default, `mvregress` uses the observed Fisher information matrix (the `'hessian'` option) to compute the variance-covariance matrix of the regression parameters. This accounts for the additional uncertainty due to missing response values.

The observed information matrix includes contributions from only the observed responses. That is, the observed Fisher information matrix for the parameters in the error variance-covariance matrix has elements

$$I(\theta)_{u,v} = \frac{1}{2}\sum_{i=1}^{n} tr\left(\Sigma_i^{-1}\frac{\partial\Sigma_i}{\partial\theta_u}\Sigma_i^{-1}\frac{\partial\Sigma_i}{\partial\theta_v}\right),\ u,v = 1,\ldots,n_\theta,$$

where $\hat{\Sigma}_i$ is the subset of $\hat{\Sigma}$ corresponding to the observed responses in $\mathbf{y}_i$.

For example, if $d = 3$, but y_{i2} is missing, then

$$\hat{\Sigma}_i = \begin{pmatrix} \hat{\sigma}_1^2 & \hat{\sigma}_{13} \\ \hat{\sigma}_{13} & \hat{\sigma}_3^2 \end{pmatrix}.$$

The observed Fisher information for the regression coefficients has similar contributions from the design and covariance matrices.

References

[1] Beck, N. and J. N. Katz. *What to Do (and Not to Do) with Time-Series-Cross-Section Data in Comparative Politics*. American Political Science Review, Vol. 89, No. 3, pp. 634–647, 1995.

See Also

`mvregress` | `mvregresslike`

Related Examples

- "Set Up Multivariate Regression Problems" on page 13-15
- "Multivariate General Linear Model" on page 13-29
- "Fixed Effects Panel Model with Concurrent Correlation" on page 13-34
- "Longitudinal Analysis" on page 13-42

More About

- "Multivariate Linear Regression" on page 13-3

Set Up Multivariate Regression Problems

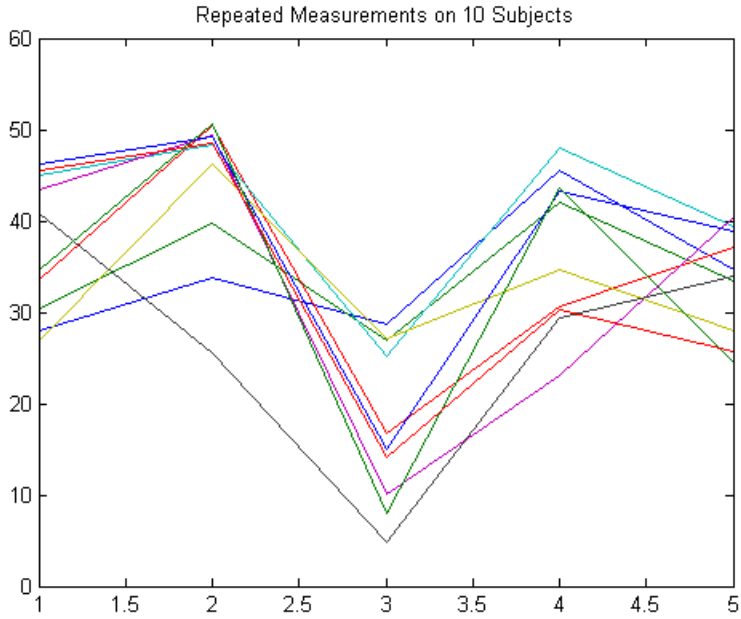
In this section...

Response Matrix

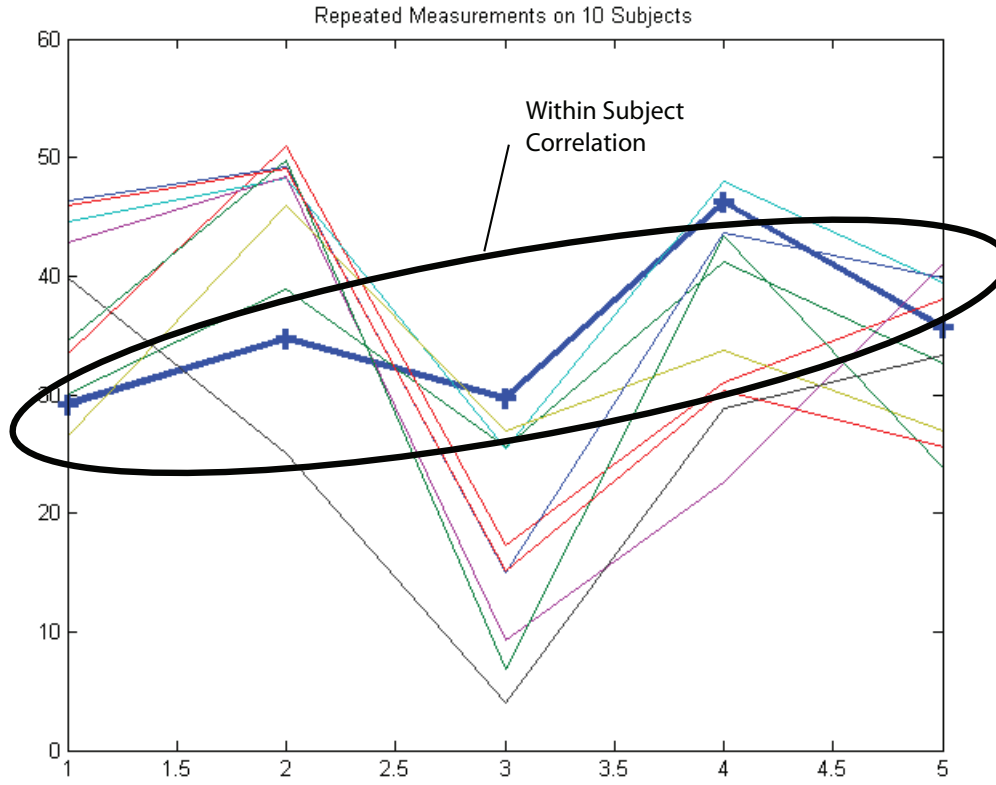
To fit a multivariate linear regression model using `mvregress`, you must set up your response matrix and design matrices in a particular way. Given properly formatted inputs, `mvregress` can handle a variety of multivariate regression problems.

`mvregress` expects the n observations of potentially correlated d-dimensional responses to be in an n-by-d matrix, named `Y`, for example. That is, set up your responses so that the dependency structure is between observations in the same *row*. If you specify `Y` as a vector of length n (either a row or column vector), then `mvregress` assumes that $d = 1$, and treats the elements as n independent observations. It does *not* model the vector as one realization of a correlated series (such as a time series).

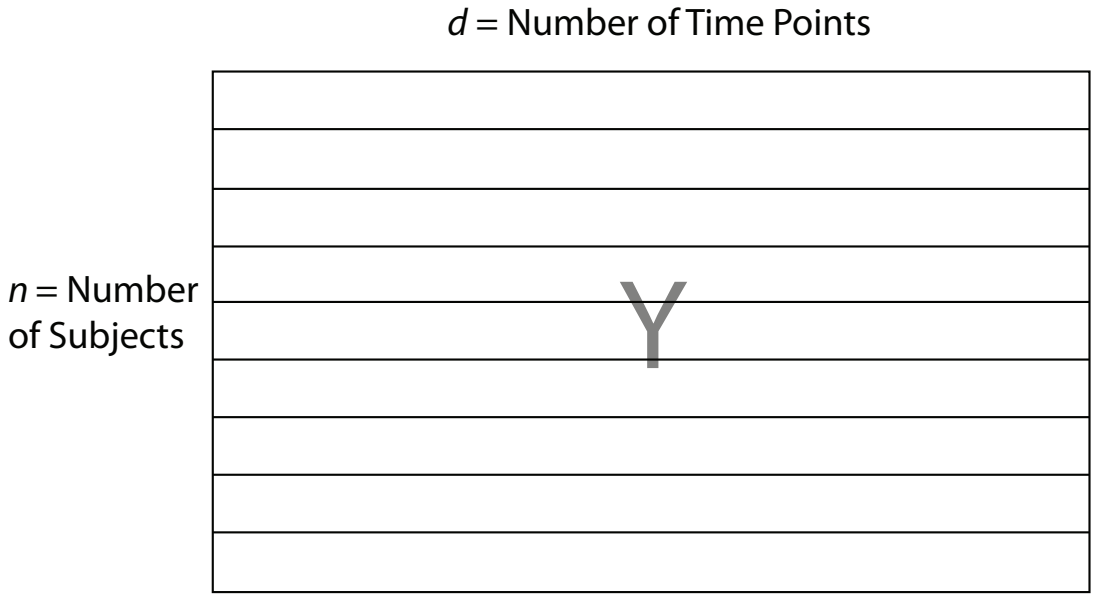
To illustrate how to set up a response matrix, suppose that your multivariate responses are repeated measurements made on subjects at multiple time points, as in the following figure.



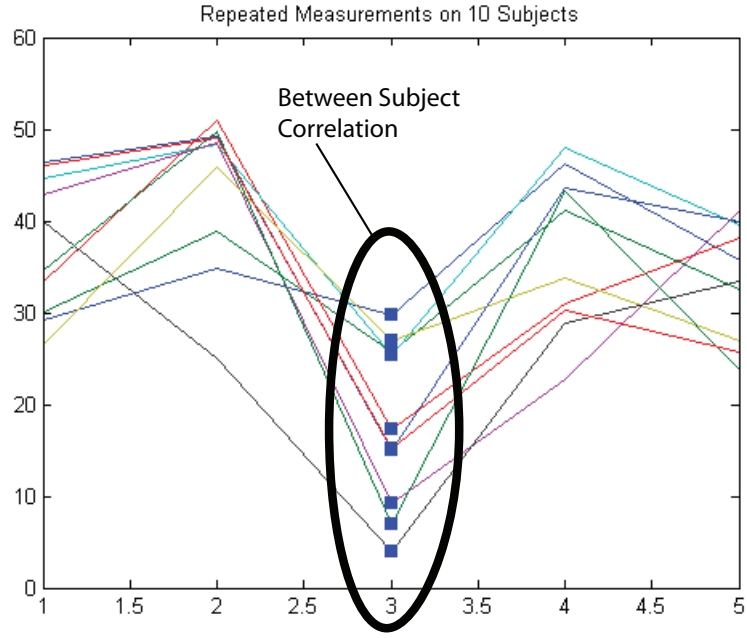
Suppose that observations within a subject are correlated.



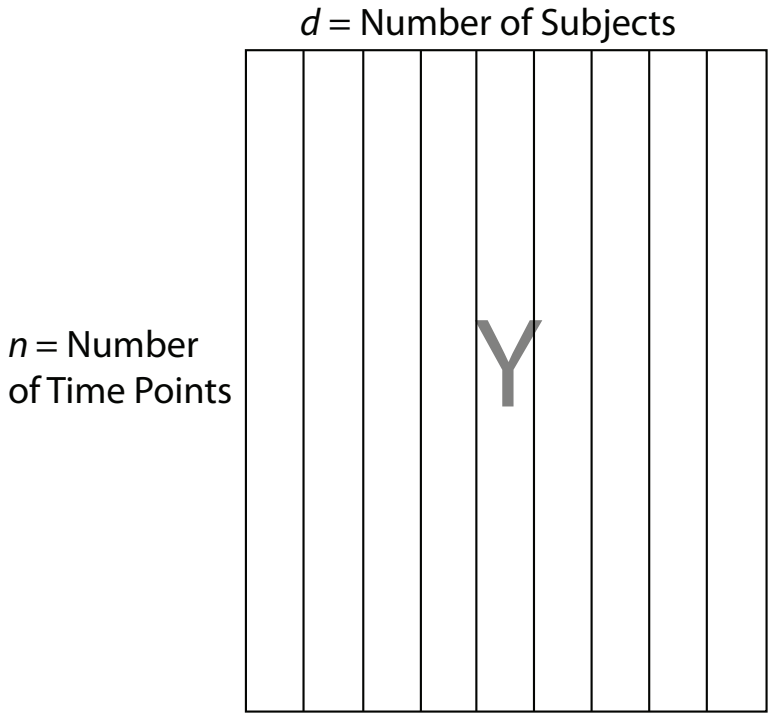
In this case, set up the response matrix Y such that each row corresponds to a subject, and each column corresponds to a time point.



Then again, suppose that observations made on subjects at the same time are correlated (concurrent correlation).



In this case, set up the response matrix Y such that each row corresponds to a time point, and each column corresponds to a subject.



Design Matrices

In the multivariate linear regression model, each d-dimensional response has a corresponding design matrix. Depending on the model, the design matrix might be comprised of exogenous predictor variables, dummy variables, lagged responses, or a combination of these and other covariate terms.

- If $d > 1$ and all d dimensions have the same design matrix, then specify one n-by-p design matrix, where p is the number of predictor variables. To determine an intercept for each dimension, add a column of ones to the design matrix. In this case, `mvregress` applies the design matrix to all d dimensions.
- If $d > 1$ and all d dimensions do not have the same design matrix, then specify the design matrices using a length-n cell array of d-by-K arrays, named `X`, for example. K is the total number of regression coefficients in the model. Note that the rows of the arrays in `X` correspond to the columns of the response matrix, `Y`.

$$X = \left\{ \underset{d \times K}{\mathbf{X}_1}, \underset{d \times K}{\mathbf{X}_2}, \ldots, \underset{d \times K}{\mathbf{X}_n} \right\}$$

If all n observations have the same design matrix, you can specify a cell array containing one d-by-K design matrix. In this case, `mvregress` applies the design matrix to all n observations. For example, this situation might arise if the predictors are functions of time, and all observations were measured at the same time points.

- In the special case that $d = 1$, you can specify one n-by-K design matrix (not in a cell array). However, you should consider using `fitlm` to fit regression models to univariate, continuous responses.

The following sections illustrate how to set up the some common multivariate regression problems for estimation using `mvregress`.

Common Multivariate Regression Problems

Multivariate General Linear Model

The multivariate general linear model is of the form

$$\mathbf{Y}_{n\times d} = \mathbf{X}_{n\times(p+1)}\mathbf{B}_{(p+1)\times d} + \mathbf{E}_{n\times d}.$$

In expanded form,

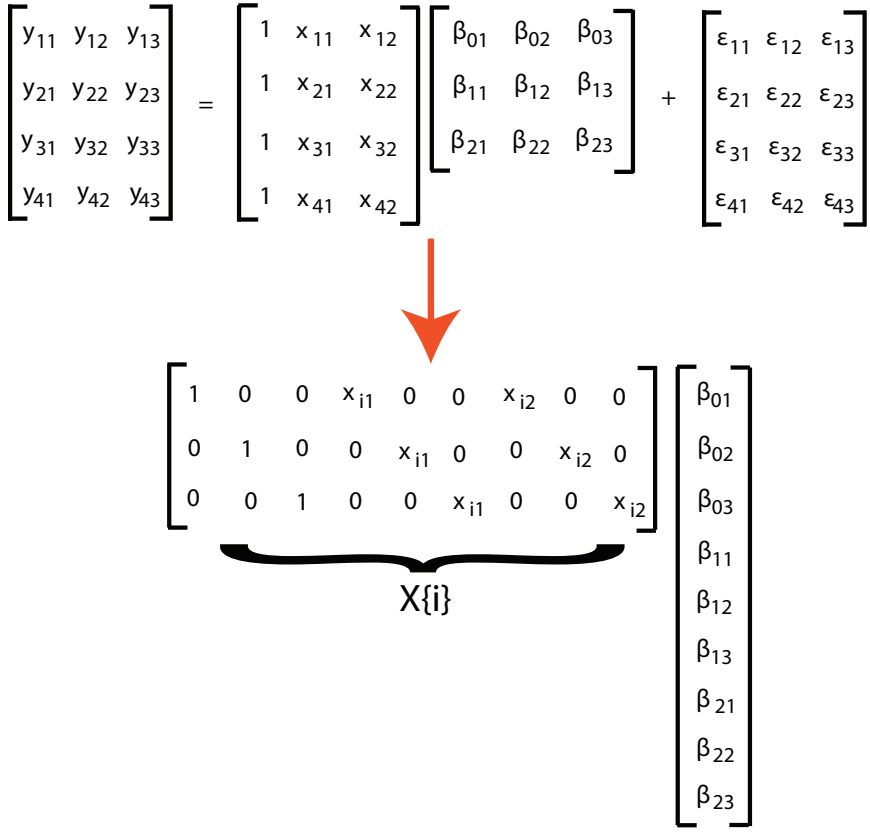
$$\begin{bmatrix} y_{11} & y_{12} & \cdots & y_{1d} \\ y_{21} & y_{22} & \cdots & y_{2d} \\ \vdots & \vdots & \ddots & \vdots \\ y_{n1} & y_{n2} & \cdots & y_{nd} \end{bmatrix} = \begin{bmatrix} 1 & x_{11} & x_{12} & \cdots & x_{1p} \\ 1 & x_{21} & x_{22} & \cdots & x_{2p} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & x_{n1} & x_{n2} & \cdots & x_{np} \end{bmatrix} \begin{bmatrix} \beta_{01} & \beta_{02} & \cdots & \beta_{0d} \\ \beta_{11} & \beta_{12} & \cdots & \beta_{1d} \\ \vdots & \vdots & \ddots & \vdots \\ \beta_{p1} & \beta_{p2} & \cdots & \beta_{pd} \end{bmatrix} + \begin{bmatrix} \varepsilon_{11} & \varepsilon_{12} & \cdots & \varepsilon_{1d} \\ \varepsilon_{21} & \varepsilon_{22} & \cdots & \varepsilon_{2d} \\ \vdots & \vdots & \ddots & \vdots \\ \varepsilon_{n1} & \varepsilon_{n2} & \cdots & \varepsilon_{nd} \end{bmatrix}.$$

That is, each d-dimensional response has an intercept and p predictor variables, and each dimension has its own set of regression coefficients. In this form, the least squares solution is `B = X\Y`. To estimate this model using `mvregress`, use the n-by-d matrix of responses, as above.

If all d dimensions have the same design matrix, use the n-by-(p+1) design matrix, as above. Adding a column of ones to the p predictor variables computes the intercept for each dimension.

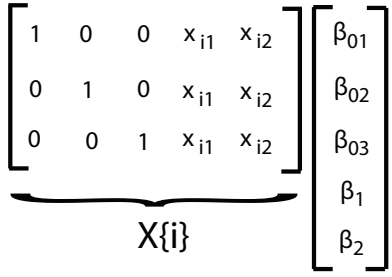
If all d dimensions do not have the same design matrix, reformat the n-by-(p + 1) design matrix into a length-n cell array of d-by-K matrices. Here, $K = (p + 1)d$ for an intercept and slopes for each dimension.

For example, suppose $n = 4$, $d = 3$, and $p = 2$ (two predictor terms in addition to an intercept). This figure shows how to format the ith element in the cell array.



If you prefer, you can reshape the K-by-1 vector of coefficients back into a $(p + 1)$-by-d matrix after estimation.

To put constraints on the model parameters, adjust the design matrix accordingly. For example, suppose that the three dimensions in the previous example have a common slope. That is, $\beta_{11} = \beta_{12} = \beta_{13} = \beta_1$ and $\beta_{21} = \beta_{22} = \beta_{23} = \beta_2$. In this case, each design matrix is 3-by-5, as shown in the following figure.



Longitudinal Analysis

In a longitudinal analysis, you might measure responses on n subjects at d time points, with correlation between observations made on the same subject. For example, suppose that you measure responses y_{ij} at times t_{ij}, $i = 1,...,n$ and $j = 1,...,d$. In addition, suppose that each subject is in one of two groups (such as male or female), specified by the indicator variable G_i. You could model y_{ij} as a function of G_i and t_{ij}, with group-specific intercepts and slopes, as follows:

$$y_{ij} = \beta_0 + \beta_1 G_i + \beta_2 t_{ij} + \beta_3 G_i \times t_{ij} + \varepsilon_{ij}, i = 1,\ldots,n; j = 1,\ldots,d,$$

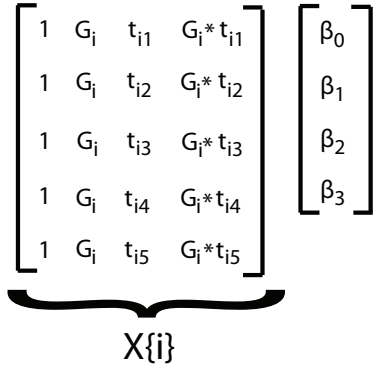
where

$$\varepsilon_i = (\varepsilon_{i1},\ldots,\varepsilon_{id})' \sim MVN(\mathbf{0},\Sigma).$$

Most longitudinal models include time as an explicit predictor.

To fit this model using `mvregress`, arrange the responses in an n-by-d matrix, where n is the number of subjects and d is the number of time points. Specify the design matrices in an n-length cell array of d-by-K matrices, where here $K = 4$ for the four regression coefficients.

For example, suppose $d = 5$ (five observations per subject). The ith design matrix and corresponding parameter vector for the specified model are shown in the following figure.



Panel Analysis

In a panel analysis, you might measure responses and covariates on d subjects (such as individuals or countries) at n time points. For example, suppose you measure responses y_{tj} and covariates x_{tj} on subjects $j = 1,...,d$ at times $t = 1,...,n$. A fixed effects panel model, with subject-specific fixed effects, and concurrent correlation might look like:

$$y_{tj} = \alpha_j + \beta x_{tj} + \varepsilon_{tj},$$

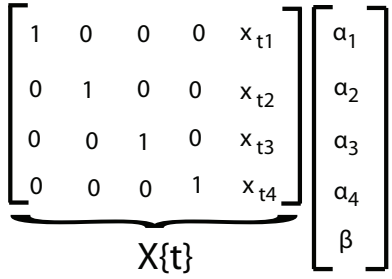
where

$$\varepsilon_t = (\varepsilon_{t1},...,\varepsilon_{td})' \sim MVN(\mathbf{0},\Sigma).$$

In contrast to longitudinal models, the panel analysis model typically includes covariates measured at each time point, instead of using time as an explicit predictor.

To fit this model using `mvregress`, arrange the responses in an n-by-d matrix, such that each column corresponds to a subject. Specify the design matrices in an n-length cell array of d-by-K matrices, where here $K = d + 1$ for the d intercepts and a slope term.

For example, suppose $d = 4$ (four subjects). The tth design matrix and corresponding parameter vector are shown in the following figure.



Seemingly Unrelated Regression

In a seemingly unrelated regression (SUR), you model d separate regressions, each with its own intercept and slope, but a common error variance-covariance matrix. For example, suppose you measure responses y_{ij} and covariates x_{ij} for regression models j = 1,...,d, with i = 1,...,n observations to fit each regression. The SUR model might look like:

$$y_{ij} = \beta_{0j} + \beta_j x_{ij} + \varepsilon_{ij},$$

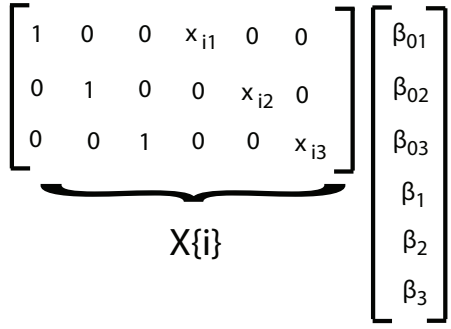
where

$$\varepsilon_i = (\varepsilon_{i1},\ldots,\varepsilon_{id})' \sim MVN(\mathbf{0},\Sigma).$$

This model is very similar to the multivariate general linear model, except that it has different covariates for each dimension.

To fit this model using `mvregress`, arrange the responses in an n-by-d matrix, such that each column has the data for the jth regression model. Specify the design matrices in an n-length cell array of d-by-K matrices, where here $K = 2d$ for d intercepts and d slopes.

For example, suppose d = 3 (three regressions). The ith design matrix and corresponding parameter vector are shown in the following figure.



Vector Autoregressive Model

The VAR(p) vector autoregressive model expresses d-dimensional time series responses as a linear function of p lagged d-dimensional responses from previous times. For example, suppose you measure responses y_{tj} for time series $j = 1,...,d$ at times $t = 1,...,n$. The VAR(p) model might look like:

$$\begin{bmatrix} y_{t1} \\ y_{t2} \\ \vdots \\ y_{td} \end{bmatrix} = \begin{bmatrix} c_1 \\ c_2 \\ \vdots \\ c_d \end{bmatrix} + \begin{bmatrix} \varphi_{11}^{(1)} & \varphi_{12}^{(1)} & \cdots & \varphi_{1d}^{(1)} \\ \vdots & \vdots & \ddots & \vdots \\ \varphi_{d1}^{(1)} & \varphi_{d2}^{(1)} & \cdots & \varphi_{dd}^{(1)} \end{bmatrix} \begin{bmatrix} y_{t-1,1} \\ y_{t-1,2} \\ \vdots \\ y_{t-1,d} \end{bmatrix} + \cdots + \begin{bmatrix} \varphi_{11}^{(p)} & \varphi_{12}^{(p)} & \cdots & \varphi_{1d}^{(p)} \\ \vdots & \vdots & \ddots & \vdots \\ \varphi_{d1}^{(p)} & \varphi_{d2}^{(p)} & \cdots & \varphi_{dd}^{(p)} \end{bmatrix} \begin{bmatrix} y_{t-p,1} \\ y_{t-p,2} \\ \vdots \\ y_{t-p,d} \end{bmatrix} + \begin{bmatrix} \varepsilon_{t1} \\ \varepsilon_{t2} \\ \vdots \\ \varepsilon_{td} \end{bmatrix},$$

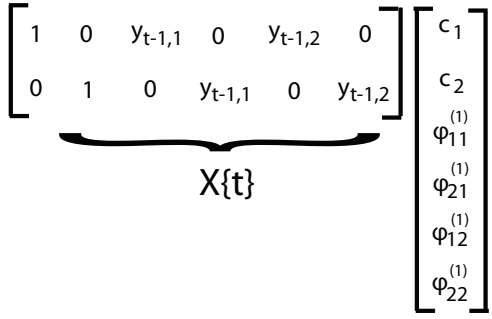
where

$$\varepsilon_t = (\varepsilon_{t1},...,\varepsilon_{td})' \sim MVN(\mathbf{0},\Sigma).$$

When estimating vector autoregressive models, you typically need to use the first p observations to initiate the model, or provide some other presample response values.

To fit this model using `mvregress`, arrange the responses in an n-by-d matrix, such that each column corresponds to a time series. Specify the design matrices in an n-length cell array of d-by-K matrices, where here $K = d + pd^2$.

For example, suppose $d = 2$ (two time series) and $p = 1$ (one lag). The tth design matrix and corresponding parameter vector are shown in the following figure.



Alternatively, Econometrics Toolbox has functions for fitting and forecasting VAR(*p*) models, including the option to specify exogenous predictor variables.

See Also

`mvregress` | `mvregresslike`

Related Examples

- "Multivariate General Linear Model" on page 13-29
- "Fixed Effects Panel Model with Concurrent Correlation" on page 13-34
- "Longitudinal Analysis" on page 13-42

More About

- "Multivariate Linear Regression" on page 13-3
- "Estimation of Multivariate Regression Models" on page 13-6

Multivariate General Linear Model

This example shows how to set up a multivariate general linear model for estimation using `mvregress`.

Load sample data.

This data contains measurements on a sample of 205 auto imports from 1985.

Here, model the bivariate response of city and highway MPG (columns 14 and 15).

For predictors, use wheel base (column 3), curb weight (column 7), and fuel type (column 18). The first two predictors are continuous, and for this example are centered and scaled. Fuel type is a categorical variable with two categories (`11` and `20`), so a dummy indicator variable is needed for the regression.

```
load('imports-85')
Y = X(:,14:15);
[n,d] = size(Y);

X1 = zscore(X(:,3));
X2 = zscore(X(:,7));
X3 = X(:,18)==20;

Xmat = [ones(n,1) X1 X2 X3];
```

The variable `X3` is coded to have value `1` for the fuel type 20, and value `0` otherwise.

For convenience, the three predictors (wheel base, curb weight, and fuel type indicator) are combined into one design matrix, with an added intercept term.

Set up design matrices.

Given these predictors, the multivariate general linear model for the bivariate MPG response is

$$\begin{bmatrix} y_{11} & y_{12} \\ y_{21} & y_{22} \\ \vdots & \vdots \\ y_{n1} & y_{n2} \end{bmatrix} = \begin{bmatrix} 1 & x_{11} & x_{12} & x_{13} \\ 1 & x_{21} & x_{22} & x_{23} \\ \vdots & \vdots & \vdots & \vdots \\ 1 & x_{n1} & x_{n2} & x_{n3} \end{bmatrix} \begin{bmatrix} \beta_{01} & \beta_{02} \\ \beta_{11} & \beta_{12} \\ \beta_{21} & \beta_{22} \\ \beta_{31} & \beta_{32} \end{bmatrix} + \begin{bmatrix} \varepsilon_{11} & \varepsilon_{12} \\ \varepsilon_{21} & \varepsilon_{22} \\ \vdots & \vdots \\ \varepsilon_{n1} & \varepsilon_{n2} \end{bmatrix},$$

where $\varepsilon_i = (\varepsilon_{i1}, \varepsilon_{i2})' \sim MVN(\mathbf{0}, \Sigma)$. There are $K = 8$ regression coefficients in total.

Create a length $n = 205$ cell array of 2-by-8 (d-by-K) matrices for use with `mvregress`. The ith matrix in the cell array is

$$X\{i\} = \begin{bmatrix} 1 & 0 & x_{i1} & 0 & x_{i2} & 0 & x_{i3} & 0 \\ 0 & 1 & 0 & x_{i1} & 0 & x_{i2} & 0 & x_{i3} \end{bmatrix}.$$

```
Xcell = cell(1,n);
for i = 1:n
    Xcell{i} = [kron([Xmat(i,:)],eye(d))];
end
```

Given this specification of the design matrices, the corresponding parameter vector is

$$\beta = \begin{bmatrix} \beta_{01} \\ \beta_{02} \\ \beta_{11} \\ \beta_{12} \\ \beta_{21} \\ \beta_{22} \\ \beta_{31} \\ \beta_{32} \end{bmatrix}.$$

Estimate regression coefficients.

Fit the model using maximum likelihood estimation.

```
[beta,sigma,E,V] = mvregress(Xcell,Y);
beta
```

```
beta =

   33.5476
   38.5720
    0.9723
    0.3950
   -6.3064
   -6.3584
   -9.2284
   -8.6663
```

These coefficient estimates show:

- The expected city and highway MPG for cars of average wheel base, curb weight, and fuel type 11 are `33.5` and `38.6`, respectively. For fuel type 20, the expected city and highway MPG are `33.5476 - 9.2284 = 24.3192` and `38.5720 - 8.6663 = 29.9057`.
- An increase of one standard deviation in curb weight has almost the same effect on expected city and highway MPG. Given all else is equal, the expected MPG decreases by about `6.3` with each one standard deviation increase in curb weight, for both city and highway MPG.
- For each one standard deviation increase in wheel base, the expected city MPG increases `0.972`, while the expected highway MPG increases by only `0.395`, given all else is equal.

Compute standard errors.

The standard errors for the regression coefficients are the square root of the diagonal of the variance-covariance matrix, `V`.

```
se = sqrt(diag(V))
```

```
se =

    0.7365
    0.7599
    0.3589
    0.3702
    0.3497
    0.3608
    0.7790
    0.8037
```

Reshape coefficient matrix.

You can easily reshape the regression coefficients into the original 4-by-2 matrix.

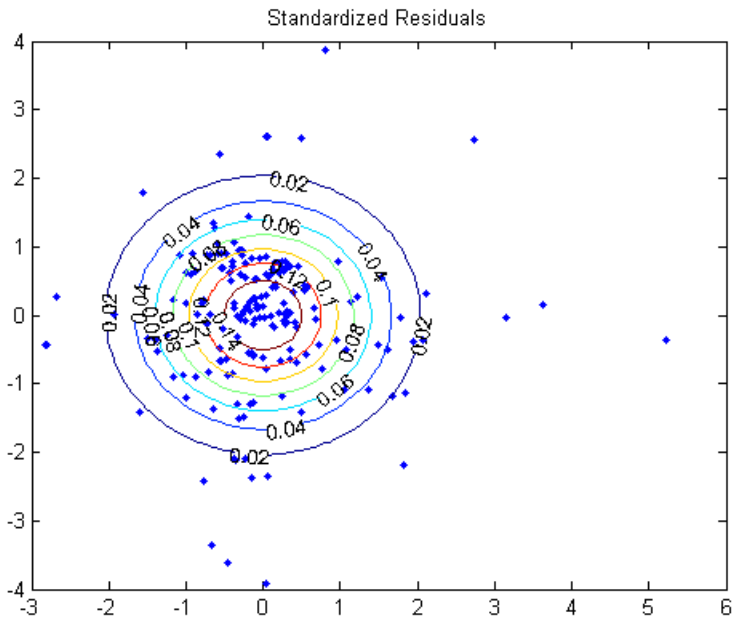
```
B = reshape(beta,2,4)'
```

```
B =

   33.5476   38.5720
    0.9723    0.3950
   -6.3064   -6.3584
   -9.2284   -8.6663
```

Check model assumptions.

Under the model assumptions, $\mathbf{z} = \mathbf{E}\Sigma^{-1/2}$ should be independent, with a bivariate standard normal distribution. In this 2-D case, you can assess the validity of this assumption using a scatter plot.

```
z = E/chol(sigma);
figure()
plot(z(:,1),z(:,2),'.')
title('Standardized Residuals')
hold on

% Overlay standard normal contours
z1 = linspace(-5,5);
z2 = linspace(-5,5);
[zx,zy] = meshgrid(z1,z2);
zgrid = [reshape(zx,100^2,1),reshape(zy,100^2,1)];
zn = reshape(mvnpdf(zgrid),100,100);
[c,h] = contour(zx,zy,zn);
clabel(c,h)
```



Several residuals are larger than expected, but overall, there is little evidence against the multivariate normality assumption.

See Also

`mvregress` | `mvregresslike`

Related Examples

- "Set Up Multivariate Regression Problems" on page 13-15
- "Fixed Effects Panel Model with Concurrent Correlation" on page 13-34
- "Longitudinal Analysis" on page 13-42

More About

- "Multivariate Linear Regression" on page 13-3
- "Estimation of Multivariate Regression Models" on page 13-6

Fixed Effects Panel Model with Concurrent Correlation

This example shows how to perform panel data analysis using `mvregress`. First, a fixed effects model with concurrent correlation is fit by ordinary least squares (OLS) to some panel data. Then, the estimated error covariance matrix is used to get panel corrected standard errors for the regression coefficients.

Load sample data.

Navigate to the folder containing sample data. Load the sample panel data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
load('panelData')
```

The dataset array, `panelData`, contains yearly observations on eight cities for 6 years. This is simulated data.

Define variables.

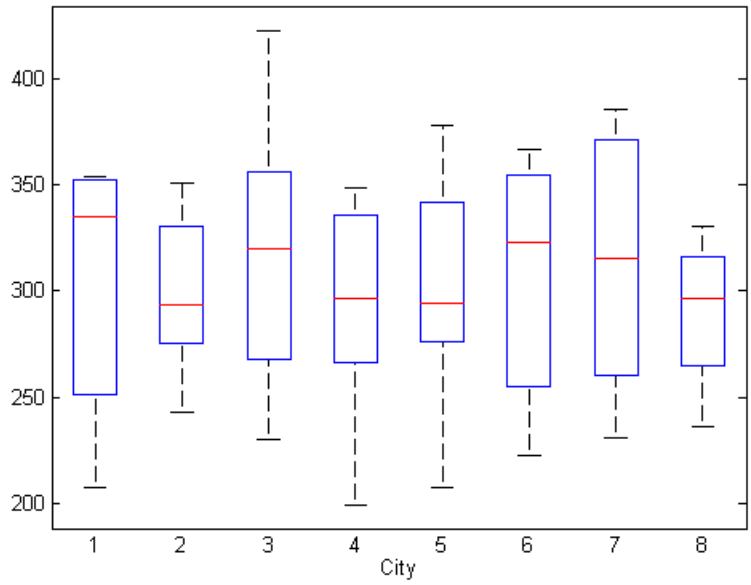
The first variable, `Growth`, measures economic growth (the response variable). The second and third variables are city and year indicators, respectively. The last variable, `Employ`, measures employment (the predictor variable).

```
y = panelData.Growth;
city = panelData.City;
year = panelData.Year;
x = panelData.Employ;
```

Plot data grouped by category.

To look for potential city-specific fixed effects, create a box plot of the response grouped by city.

```
figure()
boxplot(y,city)
xlabel('City')
```

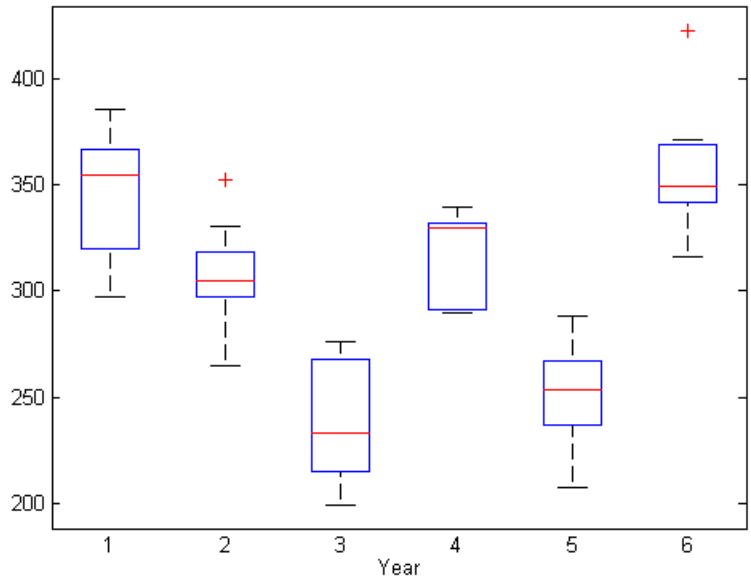


There does not appear to be any systematic differences in the mean response among cities.

Plot data grouped by a different category.

To look for potential year-specific fixed effects, create a box plot of the response grouped by year.

```
figure()
boxplot(y,year)
xlabel('Year')
```



Some evidence of systematic differences in the mean response between years seems to exist.

Format response data.

Let y_{ij} denote the response for city $j = 1,...,d$, in year $i = 1,...,n$. Similarly, x_{ij} is the corresponding value of the predictor variable. In this example, $n = 6$ and $d = 8$.

Consider fitting a year-specific fixed effects model with a constant slope and concurrent correlation among cities in the same year,

$$y_{ij} = \alpha_i + \beta_1 x_{ij} + \varepsilon_{ij},\ i = 1,\ldots,n, j = 1,\ldots,d,$$

where $\varepsilon_i = (\varepsilon_{i1},\ldots,\varepsilon_{id})' \sim MVN(\mathbf{0},\Sigma)$. The concurrent correlation accounts for any unmeasured, time-static factors that might impact growth similarly for some cities. For example, cities with close spatial proximity might be more likely to have similar economic growth.

To fit this model using `mvregress`, reshape the response data into an n-by-d matrix.

```
n = 6; d = 8;
Y = reshape(y,n,d);
```

Format design matrices.

Create a length-n cell array of d-by-K design matrices. For this model, there are $K = 7$ parameters ($d = 6$ intercept terms and a slope).

Suppose the vector of parameters is arranged as

$$\beta = \begin{pmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_6 \\ \beta_1 \end{pmatrix}.$$

In this case, the first design matrix for year 1 looks like

$$X\{1\} = \begin{pmatrix} 1 & 0 & \cdots & 0 & x_{11} \\ 1 & 0 & \cdots & 0 & x_{12} \\ \vdots & \vdots & \cdots & 0 & \vdots \\ 1 & 0 & \cdots & 0 & x_{18} \end{pmatrix},$$

and the second design matrix for year 2 looks like

$$X\{2\} = \begin{pmatrix} 0 & 1 & 0 & \cdots & 0 & x_{21} \\ 0 & 1 & 0 & \cdots & 0 & x_{22} \\ \vdots & \vdots & 0 & \cdots & 0 & \vdots \\ 0 & 1 & 0 & \cdots & 0 & x_{28} \end{pmatrix}.$$

The design matrices for the remaining 4 years are similar.

```
K = 7; N = n*d;
X = cell(n,1);
for i = 1:n
    x0 = zeros(d,K-1);
    x0(:,i) = 1;
    X{i} = [x0,x(i:n:N)];
end
```

Fit the model.

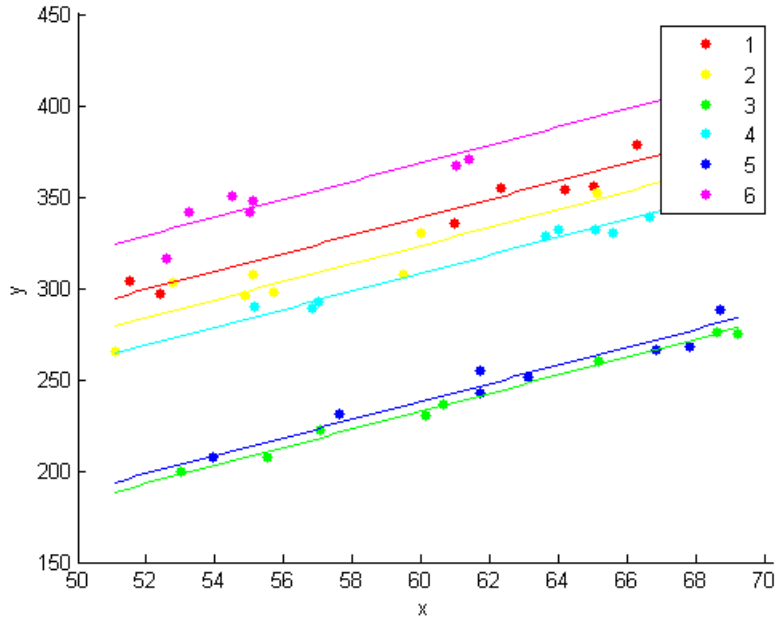
Fit the model using ordinary least squares (OLS).

```
[b,sig,E,V] = mvregress(X,Y,'algorithm','cwls');
b
```

```
b =

   41.6878
   26.1864
  -64.5107
   11.0924
  -59.1872
   71.3313
    4.9525
```

Plot fitted model.

```
xx = linspace(min(x),max(x));
axx = repmat(b(1:K-1),1,length(xx));
bxx = repmat(b(K)*xx,n,1);
yhat =  axx + bxx;

figure()
hPoints = gscatter(x,y,year);
hold on
hLines = plot(xx,yhat);
for i=1:n
   set(hLines(i),'color',get(hPoints(i),'color'));
end
hold off
```

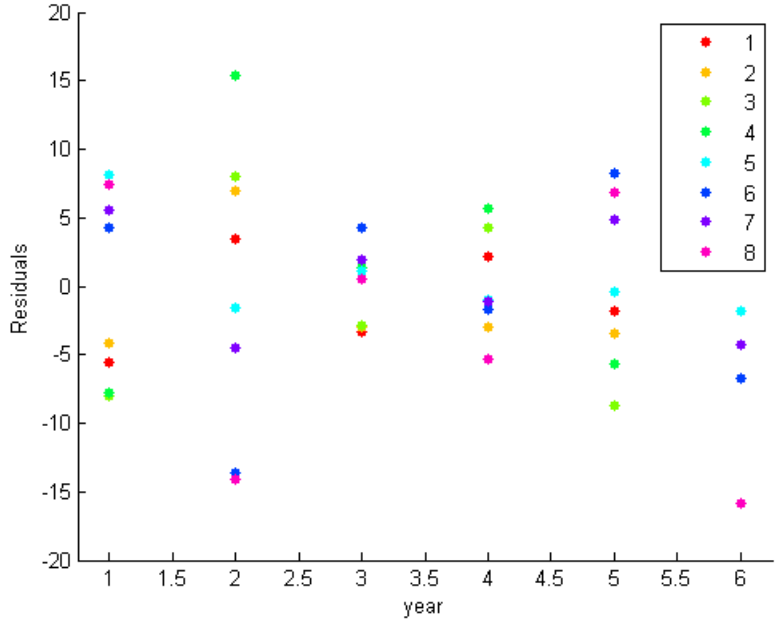


The model with year-specific intercepts and common slope appears to fit the data quite well.

Residual correlation.

Plot the residuals, grouped by year.

```
figure()
gscatter(year,E(:),city)
ylabel('Residuals')
```



The residual plot suggests concurrent correlation is present. For examples, cities 1, 2, 3, and 4 are consistently above or below average as a group in any given year. The same is true for the collection of cities 5, 6, 7, and 8. As seen in the exploratory plots, there are no systematic city-specific effects.

Panel corrected standard errors.

Use the estimated error variance-covariance matrix to compute panel corrected standard errors for the regression coefficients.

```
XX = cell2mat(X);
S = kron(eye(n),sig);
Vpcse = inv(XX'*XX)*XX'*S*XX*inv(XX'*XX);
se = sqrt(diag(Vpcse))
```

```
se =

    9.3750
    8.6698
    9.3406
```

```
    9.4286
    9.5729
    8.8207
    0.1527
```

See Also

`mvregress` | `mvregresslike`

Related Examples

- "Set Up Multivariate Regression Problems" on page 13-15
- "Multivariate General Linear Model" on page 13-29
- "Longitudinal Analysis" on page 13-42

More About

- "Multivariate Linear Regression" on page 13-3
- "Estimation of Multivariate Regression Models" on page 13-6

Longitudinal Analysis

This example shows how to perform longitudinal analysis using `mvregress`.

Load sample data.

Navigate to the folder containing sample data. Load the sample longitudinal data.

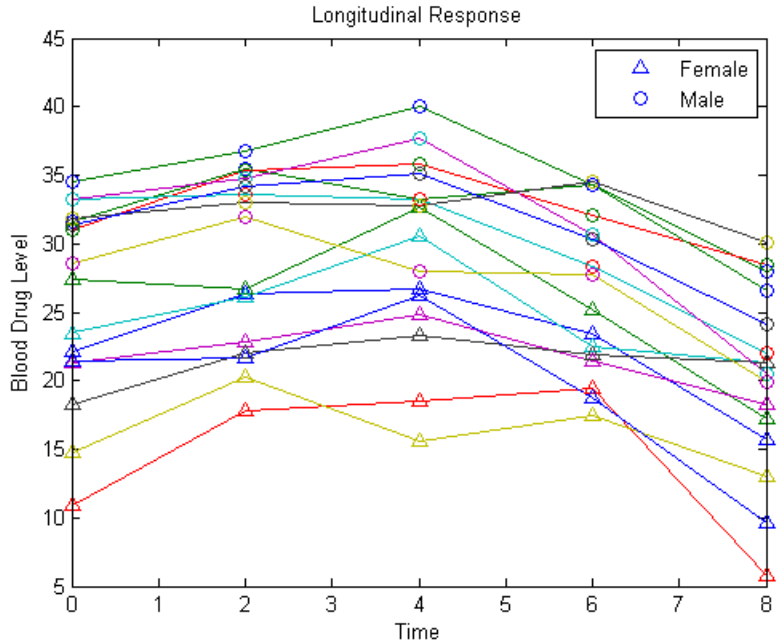
```
cd(matlabroot)
cd('help/toolbox/stats/examples')
load('longitudinalData')
```

The matrix `Y` contains response data for 16 individuals. The response is the blood level of a drug measured at five time points (t = 0, 2, 4, 6, and 8). Each row of `Y` corresponds to an individual, and each column corresponds to a time point. The first eight subjects are female, and the second eight subjects are male. This is simulated data.

Plot data.

Plot the data for all 16 subjects.

```
figure()
t = [0,2,4,6,8];
plot(t,Y)
hold on

hf = plot(t,Y(1:8,:),'^');
hm = plot(t,Y(9:16,:),'o');
legend([hf(1),hm(1)],'Female','Male','Location','NorthEast')

title('Longitudinal Response')
ylabel('Blood Drug Level')
xlabel('Time')
hold off
```



Define design matrices.

Let y_{ij} denote the response for individual $i = 1,...,n$ measured at times t_{ij}, $j = 1,...,d$. In this example, $n = 16$ and $d = 5$. Let G_i denote the gender of individual i, where $G_i = 1$ for males and 0 for females.

Consider fitting a quadratic longitudinal model, with a separate slope and intercept for each gender,

$$y_{ij} = \beta_0 + \beta_1 G_i + \beta_2 t_{ij} + \beta_3 t_{ij}^2 + \beta_4 G_i \times t_{ij} + \beta_5 G_i \times t_{ij}^2 + \varepsilon_{ij},$$

where $\varepsilon_i = (\varepsilon_{i1},\ldots,\varepsilon_{id})' \sim MVN(\mathbf{0},\Sigma)$. The error correlation accounts for clustering within an individual.

To fit this model using `mvregress`, the response data should be in an n-by-d matrix. `Y` is already in the proper format.

Next, create a length-n cell array of d-by-K design matrices. For this model, there are K = 6 parameters.

For individual i, the 5-by-6 design matrix is

$$X\{i\} = \begin{pmatrix} 1 & G_i & t_{i1} & t_{i1}^2 & G_i \times t_{i1} & G_i \times t_{i1}^2 \\ 1 & G_i & t_{i2} & t_{i2}^2 & G_i \times t_{i2} & G_i \times t_{i2}^2 \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1 & G_i & t_{i5} & t_{i5}^2 & G_i \times t_{i5} & G_i \times t_{i5}^2 \end{pmatrix},$$

corresponding to the parameter vector

$$\beta = \begin{pmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_5 \end{pmatrix}.$$

The matrix `X1` has the design matrix for a female, and `X2` has the design matrix for a male.

Create a cell array of design matrices. The first eight individuals are females, and the second eight are males.

```
X = cell(8,1);
X(1:8) = {X1};
X(9:16) = {X2};
```

Fit the model.

Fit the model using maximum likelihood estimation. Display the estimated coefficients and standard errors.

```
[b,sig,E,V,loglikF] = mvregress(X,Y);
[b sqrt(diag(V))]

ans =
```

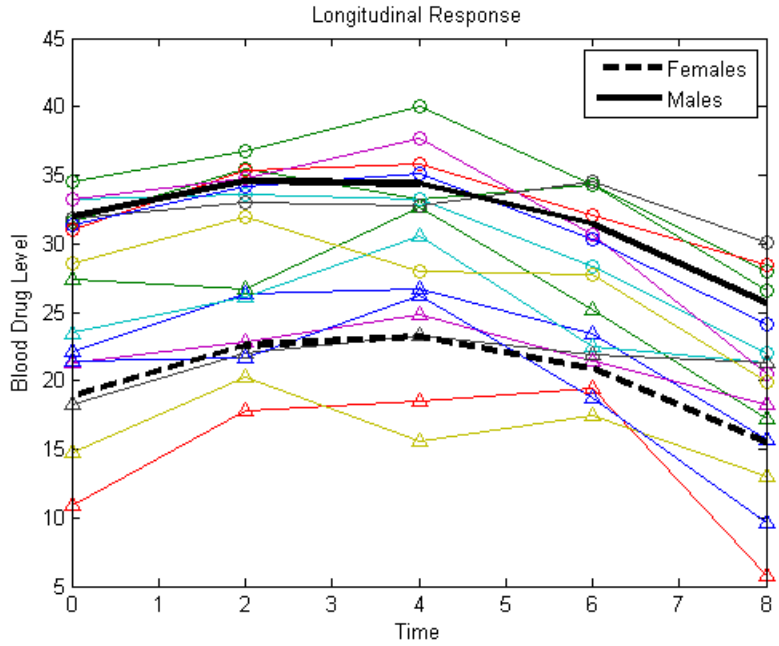
```
   18.8619    0.7432
   13.0942    1.0511
    2.5968    0.2845
   -0.3771    0.0398
   -0.5929    0.4023
    0.0290    0.0563
```

The coefficients on the interaction terms (in the last two rows of `b`) do not appear significant. You can use the value of the loglikelihood objective function for this fit, `loglikF`, to compare this model to one without the interaction terms using a likelihood ratio test.

Plot fitted model.

Plot the fitted lines for females and males.

```
Yhatf = X1*b;
Yhatm = X2*b;

figure()
plot(t,Y)
hold on

plot(t,Y(1:8,:),'^',t,Y(9:16,:),'o')

hf = plot(t,Yhatf,'k--','LineWidth',3);
hm = plot(t,Yhatm,'k','LineWidth',3);
legend([hf,hm],'Females','Males','Location','NorthEast')

title('Longitudinal Response')
ylabel('Blood Drug Level')
xlabel('Time')
hold off
```



Define a reduced model.

Fit the model without interaction terms,

$$y_{ij} = \beta_0 + \beta_1 G_i + \beta_2 t_{ij} + \beta_3 t_{ij}^2 + \varepsilon_{ij},$$

where $\varepsilon_i = (\varepsilon_{i1},\ldots,\varepsilon_{id})' \sim MVN(\mathbf{0},\Sigma)$.

This model has four coefficients, which correspond to the first four columns of the design matrices `X1` and `X2` (for females and males, respectively).

```
X1R = X1(:,1:4);
X2R = X2(:,1:4);

XR = cell(8,1);
XR(1:8) = {X1R};
XR(9:16) = {X2R};
```

Fit the reduced model.

Fit this model using maximum likelihood estimation. Display the estimated coefficients and their standard errors.

```
[bR,sigR,ER,VR,loglikR] = mvregress(XR,Y);
[bR,sqrt(diag(VR))]
```

```
ans =

   19.3765    0.6898
   12.0936    0.8591
    2.2919    0.2139
   -0.3623    0.0283
```

Conduct a likelihood ratio test.

Compare the two models using a likelihood ratio test. The null hypothesis is that the reduced model is sufficient. The alternative is that the reduced model is inadequate (compared to the full model with the interaction terms).

The likelihood ratio test statistic is compared to a chi-squared distribution with two degrees of freedom (for the two coefficients being dropped).

```
LR = 2*(loglikF-loglikR);
pval = 1 - chi2cdf(LR,2)
```

```
pval =

    0.0803
```

The *p*-value `0.0803` indicates that the null hypothesis is not rejected at the 5% significance level. Therefore, there is insufficient evidence that the extra terms improve the fit.

See Also

`mvregress` | `mvregresslike`

Related Examples

- "Set Up Multivariate Regression Problems" on page 13-15
- "Multivariate General Linear Model" on page 13-29
- "Fixed Effects Panel Model with Concurrent Correlation" on page 13-34

More About

- "Multivariate Linear Regression" on page 13-3
- "Estimation of Multivariate Regression Models" on page 13-6

Multidimensional Scaling

In this section...

Introduction to Multidimensional Scaling

One of the most important goals in visualizing data is to get a sense of how near or far points are from each other. Often, you can do this with a scatter plot. However, for some analyses, the data that you have might not be in the form of points at all, but rather in the form of pairwise similarities or dissimilarities between cases, observations, or subjects. There are no points to plot.

Even if your data are in the form of points rather than pairwise distances, a scatter plot of those data might not be useful. For some kinds of data, the relevant way to measure how near two points are might not be their Euclidean distance. While scatter plots of the raw data make it easy to compare Euclidean distances, they are not always useful when comparing other kinds of inter-point distances, city block distance for example, or even more general dissimilarities. Also, with a large number of variables, it is very difficult to visualize distances unless the data can be represented in a small number of dimensions. Some sort of dimension reduction is usually necessary.

Multidimensional scaling (MDS) is a set of methods that address all these problems. MDS allows you to visualize how near points are to each other for many kinds of distance or dissimilarity metrics and can produce a representation of your data in a small number of dimensions. MDS does not require raw data, but only a matrix of pairwise distances or dissimilarities.

Classical Multidimensional Scaling

Introduction to Classical Multidimensional Scaling

This example shows how to use `cmdscale` to perform classical (metric) multidimensional scaling, also known as principal coordinates analysis.

`cmdscale` takes as an input a matrix of inter-point distances and creates a configuration of points. Ideally, those points are in two or three dimensions, and the Euclidean distances between them reproduce the original distance matrix. Thus, a scatter plot of the points created by `cmdscale` provides a visual representation of the original distances.

As a very simple example, you can reconstruct a set of points from only their inter-point distances. First, create some four dimensional points with a small component in their fourth coordinate, and reduce them to distances.

```
rng default;  % For reproducibility
X = [normrnd(0,1,10,3),normrnd(0,.1,10,1)];
D = pdist(X,'euclidean');
```

Next, use `cmdscale` to find a configuration with those inter-point distances. `cmdscale` accepts distances as either a square matrix, or, as in this example, in the vector upper-triangular form produced by `pdist`.

```
[Y,eigvals] = cmdscale(D);
```

`cmdscale` produces two outputs. The first output, `Y`, is a matrix containing the reconstructed points. The second output, `eigvals`, is a vector containing the sorted eigenvalues of what is often referred to as the "scalar product matrix," which, in the simplest case, is equal to `Y*Y'`. The relative magnitudes of those eigenvalues indicate the relative contribution of the corresponding columns of `Y` in reproducing the original distance matrix `D` with the reconstructed points.

```
format short g
[eigvals eigvals/max(abs(eigvals))]
```

```
ans =

        35.41            1
       11.158      0.31511
       1.6894      0.04771
       0.1436    0.0040553
```

```
   7.9529e-15    2.246e-16
    4.564e-15   1.2889e-16
   2.6538e-15   7.4944e-17
  -2.2475e-17  -6.3471e-19
  -3.6359e-16  -1.0268e-17
  -3.3335e-15  -9.4139e-17
```

If `eigvals` contains only positive and zero (within round-off error) eigenvalues, the columns of `Y` corresponding to the positive eigenvalues provide an exact reconstruction of `D`, in the sense that their inter-point Euclidean distances, computed using `pdist`, for example, are identical (within round-off) to the values in `D`.

```
maxerr4 = max(abs(D - pdist(Y)))   % Exact reconstruction
```

```
maxerr4 =

   3.5527e-15
```

If two or three of the eigenvalues in `eigvals` are much larger than the rest, then the distance matrix based on the corresponding columns of `Y` nearly reproduces the original distance matrix `D`. In this sense, those columns form a lower-dimensional representation that adequately describes the data. However it is not always possible to find a good low-dimensional reconstruction.

```
maxerr3 = max(abs(D - pdist(Y(:,1:3))))  % Good reconstruction in 3D
maxerr2 = max(abs(D - pdist(Y(:,1:2))))  % Poor reconstruction in 2D
```

```
maxerr3 =

     0.043142


maxerr2 =

      0.98315
```

The reconstruction in three dimensions reproduces `D` very well, but the reconstruction in two dimensions has errors that are of the same order of magnitude as the largest values in `D`.

```
max(max(D))

ans =

       5.8974
```

Often, `eigvals` contains some negative eigenvalues, indicating that the distances in `D` cannot be reproduced exactly. That is, there might not be any configuration of points whose inter-point Euclidean distances are given by `D`. If the largest negative eigenvalue is small in magnitude relative to the largest positive eigenvalues, then the configuration returned by `cmdscale` might still reproduce `D` well.

Example: Multidimensional Scaling

This example shows how to construct a map of 10 US cities based on the distances between those cities, using `cmdscale`.

First, create the distance matrix and pass it to `cmdscale`. In this example, `D` is a full distance matrix: it is square and symmetric, has positive entries off the diagonal, and has zeros on the diagonal.

```
cities = ...
{'Atl','Chi','Den','Hou','LA','Mia','NYC','SF','Sea','WDC'};
D = [    0  587 1212  701 1936  604  748 2139 2182   543;
       587    0  920  940 1745 1188  713 1858 1737   597;
      1212  920    0  879  831 1726 1631  949 1021  1494;
       701  940  879    0 1374  968 1420 1645 1891  1220;
      1936 1745  831 1374    0 2339 2451  347  959  2300;
       604 1188 1726  968 2339    0 1092 2594 2734   923;
       748  713 1631 1420 2451 1092    0 2571 2408   205;
      2139 1858  949 1645  347 2594 2571    0  678  2442;
      2182 1737 1021 1891  959 2734 2408  678    0  2329;
       543  597 1494 1220 2300  923  205 2442 2329     0];
[Y,eigvals] = cmdscale(D);
```

Next, look at the eigenvalues returned by `cmdscale`. Some of these are negative, indicating that the original distances are not Euclidean. This is because of the curvature of the earth.

```
format short g
[eigvals eigvals/max(abs(eigvals))]
```

```
ans =

   9.5821e+06            1
   1.6868e+06      0.17604
       8157.3    0.0008513
       1432.9   0.00014954
       508.67   5.3085e-05
       25.143    2.624e-06
   3.3906e-10   3.5385e-17
       -897.7  -9.3685e-05
      -5467.6   -0.0005706
       -35479   -0.0037026
```

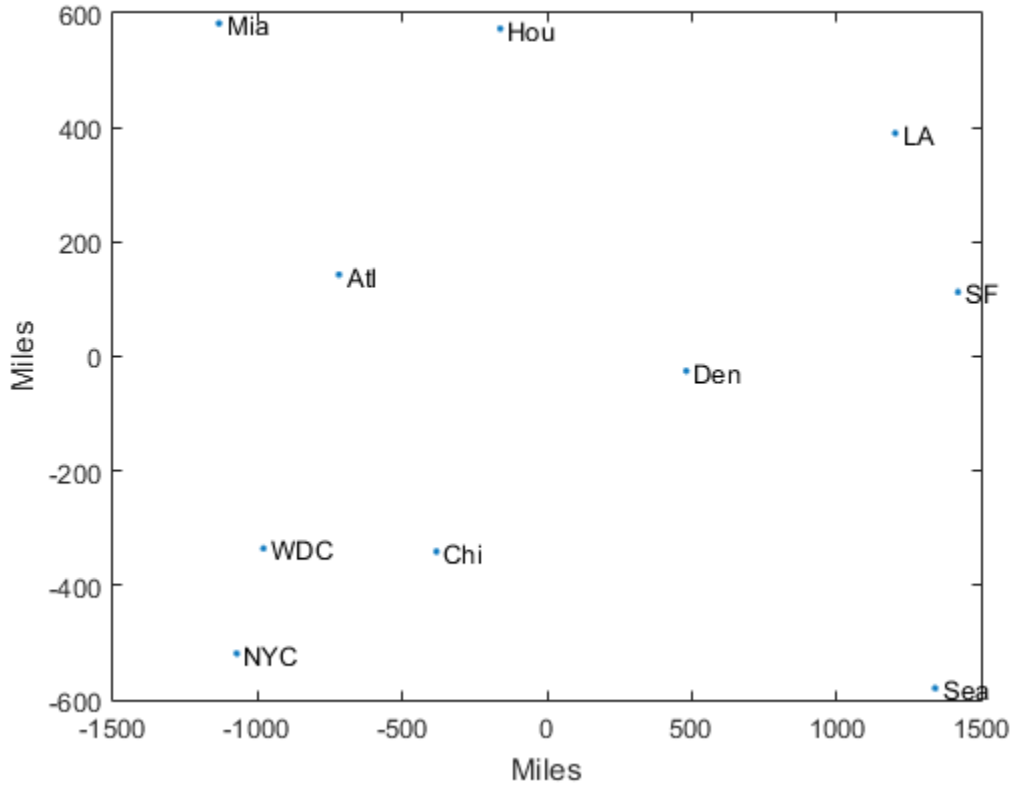
However, in this case, the two largest positive eigenvalues are much larger in magnitude than the remaining eigenvalues. So, despite the negative eigenvalues, the first two coordinates of `Y` are sufficient for a reasonable reproduction of `D`.

```
Dtriu = D(find(tril(ones(10),-1)))';
maxrelerr = max(abs(Dtriu-pdist(Y(:,1:2))))./max(Dtriu)
```

```
maxrelerr =

    0.0075371
```

Here is a plot of the reconstructed city locations as a map. The orientation of the reconstruction is arbitrary.

```
plot(Y(:,1),Y(:,2),'.')
text(Y(:,1)+25,Y(:,2),cities)
xlabel('Miles')
ylabel('Miles')
```



Nonclassical Multidimensional Scaling

The function `mdscale` performs nonclassical multidimensional scaling. As with `cmdcale`, you use `mdscale` either to visualize dissimilarity data for which no "locations" exist, or to visualize high-dimensional data by reducing its dimensionality. Both functions take a matrix of dissimilarities as an input and produce a configuration of points. However, `mdscale` offers a choice of different criteria to construct the configuration, and allows missing data and weights.

For example, the cereal data include measurements on 10 variables describing breakfast cereals. You can use `mdscale` to visualize these data in two dimensions. First, load the data. For clarity, this example code selects a subset of 22 of the observations.

```
load cereal.mat
X = [Calories Protein Fat Sodium Fiber ...
    Carbo Sugars Shelf Potass Vitamins];
% Take a subset from a single manufacturer
mfg1 = strcmp('G',cellstr(Mfg));
X = X(mfg1,:);
size(X)
ans =
    22 10
```

Then use `pdist` to transform the 10-dimensional data into dissimilarities. The output from `pdist` is a symmetric dissimilarity matrix, stored as a vector containing only the (23*22/2) elements in its upper triangle.

```
dissimilarities = pdist(zscore(X),'cityblock');
size(dissimilarities)
ans =
     1   231
```

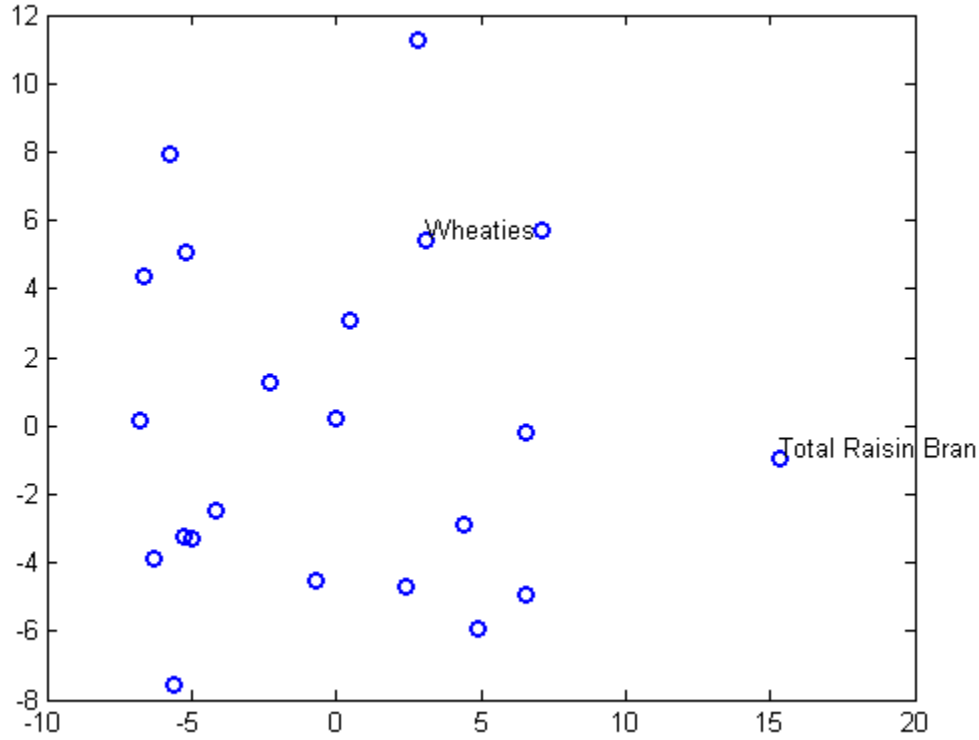
This example code first standardizes the cereal data, and then uses city block distance as a dissimilarity. The choice of transformation to dissimilarities is application-dependent, and the choice here is only for simplicity. In some applications, the original data are already in the form of dissimilarities.

Next, use `mdscale` to perform metric MDS. Unlike `cmdscale`, you must specify the desired number of dimensions, and the method to use to construct the output configuration. For this example, use two dimensions. The metric STRESS criterion is a common method for computing the output; for other choices, see the `mdscale` reference page in the online documentation. The second output from `mdscale` is the value of that criterion evaluated for the output configuration. It measures the how well the inter-point distances of the output configuration approximate the original input dissimilarities:

```
[Y,stress] =...
mdscale(dissimilarities,2,'criterion','metricstress');
stress
stress =
    0.1856
```

A scatterplot of the output from `mdscale` represents the original 10-dimensional data in two dimensions, and you can use the `gname` function to label selected points:

```
plot(Y(:,1),Y(:,2),'o','LineWidth',2);
gname(Name(mfg1))
```



Nonmetric Multidimensional Scaling

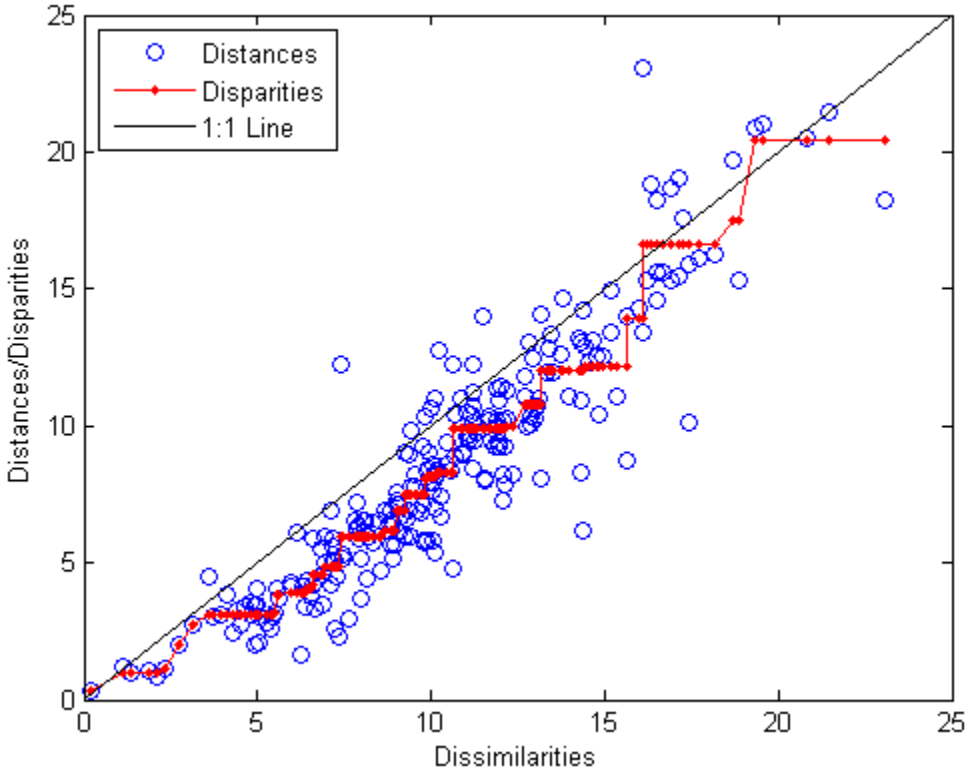
Metric multidimensional scaling creates a configuration of points whose inter-point distances approximate the given dissimilarities. This is sometimes too strict a requirement, and non-metric scaling is designed to relax it a bit. Instead of trying to approximate the dissimilarities themselves, non-metric scaling approximates a nonlinear, but monotonic, transformation of them. Because of the monotonicity, larger or smaller distances on a plot of the output will correspond to larger or smaller dissimilarities, respectively. However, the nonlinearity implies that `mdscale` only attempts to preserve the ordering of dissimilarities. Thus, there may be contractions or expansions of distances at different scales.

You use `mdscale` to perform nonmetric MDS in much the same way as for metric scaling. The nonmetric STRESS criterion is a common method for computing the output; for more choices, see the `mdscale` reference page in the online documentation. As with metric scaling, the second output from `mdscale` is the value of that criterion evaluated for the output configuration. For nonmetric scaling, however, it measures the how well the inter-point distances of the output configuration approximate the disparities. The disparities are returned in the third output. They are the transformed values of the original dissimilarities:

```
[Y,stress,disparities] = ...
mdscale(dissimilarities,2,'criterion','stress');
stress
stress =
    0.1562
```

To check the fit of the output configuration to the dissimilarities, and to understand the disparities, it helps to make a Shepard plot:

```
distances = pdist(Y);
[dum,ord] = sortrows([disparities(:) dissimilarities(:)]);
plot(dissimilarities,distances,'bo', ...
     dissimilarities(ord),disparities(ord),'r.-', ...
     [0 25],[0 25],'k-')
xlabel('Dissimilarities')
ylabel('Distances/Disparities')
legend({'Distances' 'Disparities' '1:1 Line'},...
       'Location','NorthWest');
```



This plot shows that `mdscale` has found a configuration of points in two dimensions whose inter-point distances approximates the disparities, which in turn are a nonlinear transformation of the original dissimilarities. The concave shape of the disparities as a function of the dissimilarities indicates that fit tends to contract small distances relative to the corresponding dissimilarities. This may be perfectly acceptable in practice.

`mdscale` uses an iterative algorithm to find the output configuration, and the results can often depend on the starting point. By default, `mdscale` uses `cmdscale` to construct an initial configuration, and this choice often leads to a globally best solution. However, it is possible for `mdscale` to stop at a configuration that is a local minimum of the criterion. Such cases can be diagnosed and often overcome by running `mdscale` multiple times with different starting points. You can do this using the `'start'` and `'replicates'` parameters. The following code runs five replicates of MDS, each starting at a different

randomly-chosen initial configuration. The criterion value is printed out for each replication; `mdscale` returns the configuration with the best fit.

```
opts = statset('Display','final');
[Y,stress] =...
mdscale(dissimilarities,2,'criterion','stress',...
'start','random','replicates',5,'Options',opts);

35 iterations, Final stress criterion = 0.156209
31 iterations, Final stress criterion = 0.156209
48 iterations, Final stress criterion = 0.171209
33 iterations, Final stress criterion = 0.175341
32 iterations, Final stress criterion = 0.185881
```

Notice that `mdscale` finds several different local solutions, some of which do not have as low a stress value as the solution found with the `cmdscale` starting point.

Procrustes Analysis

In this section...

Compare Landmark Data

The `procrustes` function analyzes the distribution of a set of shapes using Procrustes analysis. This analysis method matches landmark data (geometric locations representing significant features in a given shape) to calculate the best shape-preserving Euclidian transformations. These transformations minimize the differences in location between compared landmark data.

Procrustes analysis is also useful in conjunction with multidimensional scaling. In "Example: Multidimensional Scaling" on page 13-52 there is an observation that the orientation of the reconstructed points is arbitrary. Two different applications of multidimensional scaling could produce reconstructed points that are very similar in principle, but that look different because they have different orientations. The `procrustes` function transforms one set of points to make them more comparable to the other.

Data Input

The `procrustes` function takes two matrices as input:

- The target shape matrix X has dimension $n \times p$, where n is the number of landmarks in the shape and p is the number of measurements per landmark.
- The comparison shape matrix Y has dimension $n \times q$ with $q \le p$. If there are fewer measurements per landmark for the comparison shape than the target shape ($q < p$), the function adds columns of zeros to Y, yielding an $n \times p$ matrix.

The equation to obtain the transformed shape, Z, is

$$Z = bYT + c$$

where:

- b is a scaling factor that stretches ($b > 1$) or shrinks ($b < 1$) the points.
- T is the orthogonal rotation and reflection matrix.
- c is a matrix with constant values in each column, used to shift the points.

The `procrustes` function chooses b, T, and c to minimize the distance between the target shape X and the transformed shape Z as measured by the least squares criterion:

$$\sum_{i=1}^{n}\sum_{j=1}^{p}(X_{ij}-Z_{ij})^2$$

Preprocess Data for Accurate Results

Procrustes analysis is appropriate when all `p` measurement dimensions have similar scales. The analysis would be inaccurate, for example, if the columns of Z had different scales:

- The first column is measured in milliliters ranging from 2,000 to 6,000.
- The second column is measured in degrees Celsius ranging from 10 to 25.
- The third column is measured in kilograms ranging from 50 to 230.

In such cases, standardize your variables by:

1. Subtracting the sample mean from each variable.
2. Dividing each resultant variable by its sample standard deviation.

Use the `zscore` function to perform this standardization.

Compare Handwritten Shapes

In this example, use Procrustes analysis to compare two handwritten number threes. Visually and analytically explore the effects of forcing size and reflection changes as follows:

- "Step 1: Load and Display the Original Data" on page 13-62

Step 1: Load and Display the Original Data

Input landmark data for two handwritten number threes:

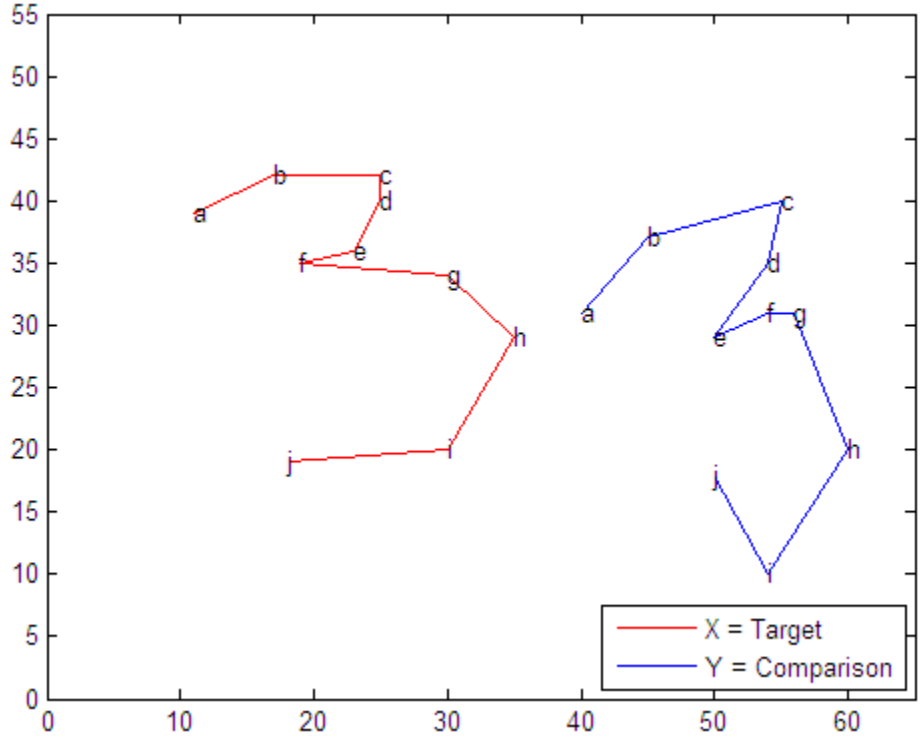
```
A = [11 39;17 42;25 42;25 40;23 36;19 35;30 34;35 29;...
30 20;18 19];
B = [15 31;20 37;30 40;29 35;25 29;29 31;31 31;35 20;...
29 10;25 18];
```

Create `X` and `Y` from `A` and `B`, moving `B` to the side to make each shape more visible:

```
X = A;
Y = B + repmat([25 0], 10,1);
```

Plot the shapes, using letters to designate the landmark points. Lines in the figure join the points to indicate the drawing path of each shape.

```
plot(X(:,1), X(:,2),'r-', Y(:,1), Y(:,2),'b-');
text(X(:,1), X(:,2),('abcdefghij')')
text(Y(:,1), Y(:,2),('abcdefghij')')
legend('X = Target','Y = Comparison','location','SE')
set(gca,'YLim',[0 55],'XLim',[0 65]);
```



Step 2: Calculate the Best Transformation

Use Procrustes analysis to find the transformation that minimizes distances between landmark data points.

Call `procrustes` as follows:

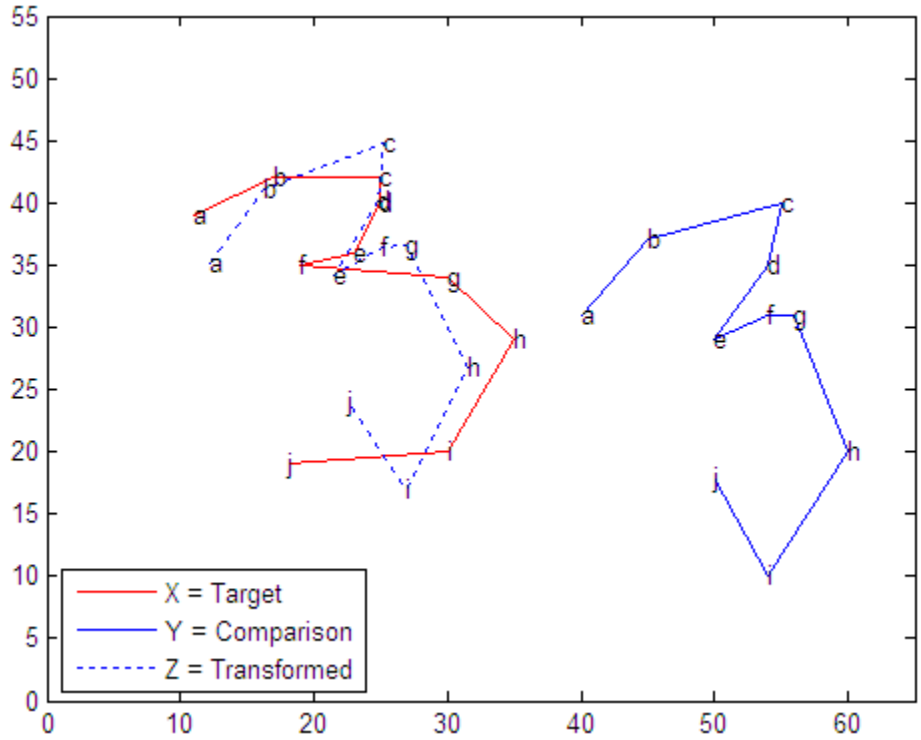
```
[d, Z, tr] = procrustes(X,Y);
```

The outputs of the function are:

- `d` – A standardized dissimilarity measure.)
- `Z` – A matrix of the transformed landmarks.
- `tr` – A structure array of the computed transformation with fields `T`, `b`, and `c` which correspond to the transformation equation, Equation 13-1.

Visualize the transformed shape, `Z`, using a dashed blue line:

```
plot(X(:,1), X(:,2),'r-', Y(:,1), Y(:,2),'b-',...
Z(:,1),Z(:,2),'b:');
text(X(:,1), X(:,2),('abcdefghij')')
text(Y(:,1), Y(:,2),('abcdefghij')')
text(Z(:,1), Z(:,2),('abcdefghij')')
legend('X = Target','Y = Comparison',...
'Z = Transformed','location','SW')
set(gca,'YLim',[0 55],'XLim',[0 65]);
```



Step 3: Examine the Similarity of the Two Shapes

Use two different numerical values to assess the similarity of the target shape and the transformed shape.

Dissimilarity Measure d

The dissimilarity measure `d` gives a number between 0 and 1 describing the difference between the target shape and the transformed shape. Values near 0 imply more similar shapes, while values near 1 imply dissimilarity. For this example:

```
d =
     0.1502
```

The small value of `d` in this case shows that the two shapes are similar.

`procrustes` calculates `d` by comparing the sum of squared deviations between the set of points with the sum of squared deviations of the original points from their column means:

```
numerator = sum(sum((X-Z).^2))
numerator =

  166.5321

denominator = sum(sum(bsxfun(@minus,X,mean(X)).^2))
denominator =

  1.1085e+003

ratio = numerator/denominator
ratio =

    0.1502
```

Note: The resulting measure `d` is independent of the scale of the size of the shapes and takes into account only the similarity of landmark data. "Examine the Scaling Measure b" on page 13-65 shows how to examine the size similarity of the shapes.

Examine the Scaling Measure b

The target and comparison threes in the previous figure visually show that the two numbers are of a similar size. The closeness of calculated value of the scaling factor `b` to 1 supports this observation as well:

```
tr.b
ans =
    0.9291
```

The sizes of the target and comparison shapes appear similar. This visual impression is reinforced by the value of b = 0.93, which implies that the best transformation results in shrinking the comparison shape by a factor .93 (only 7%).

Step 4: Restrict the Form of the Transformations

Explore the effects of manually adjusting the scaling and reflection coefficients.

Fix the Scaling Factor b = 1

Force b to equal 1 (set `'Scaling'` to `false`) to examine the amount of dissimilarity in size of the target and transformed figures:

```
ds = procrustes(X,Y,'Scaling',false)
ds =
    0.1552
```

In this case, setting `'Scaling'` to `false` increases the calculated value of d only 0.0049, which further supports the similarity in the size of the two number threes. A larger increase in d would have indicated a greater size discrepancy.

Force a Reflection in the Transformation

This example requires only a rotation, not a reflection, to align the shapes. You can show this by observing that the determinant of the matrix T is 1 in this analysis:

```
det(tr.T)
ans =
    1.0000
```

If you need a reflection in the transformation, the determinant of T is -1. You can force a reflection into the transformation as follows:

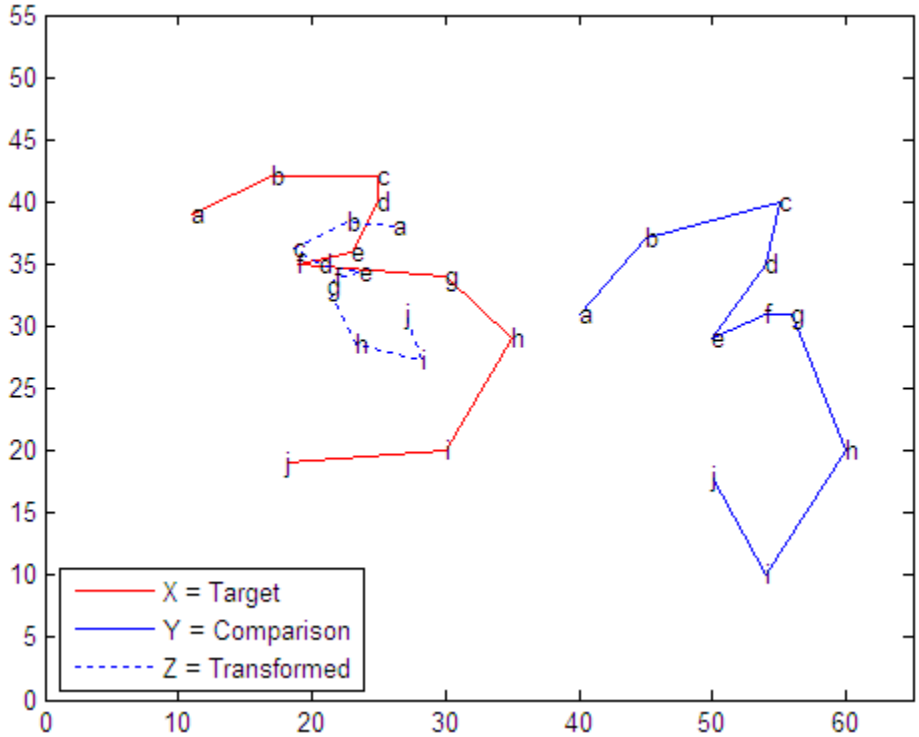
```
[dr,Zr,trr] = procrustes(X,Y,'Reflection',true);
dr
dr =

    0.8130
```

The d value increases dramatically, indicating that a forced reflection leads to a poor transformation of the landmark points. A plot of the transformed shape shows a similar result:

- The landmark data points are now further away from their target counterparts.

- The transformed three is now an undesirable mirror image of the target three.

```
plot(X(:,1), X(:,2),'r-', Y(:,1), Y(:,2),'b-',...
Zr(:,1),Zr(:,2),'b:');
text(X(:,1), X(:,2),('abcdefghij')')
text(Y(:,1), Y(:,2),('abcdefghij')')
text(Zr(:,1), Zr(:,2),('abcdefghij')')
legend('X = Target','Y = Comparison',...
'Z = Transformed','location','SW')
set(gca,'YLim',[0 55],'XLim',[0 65]);
```



It appears that the shapes might be better matched if you flipped the transformed shape upside down. Flipping the shapes would make the transformation even worse, however, because the landmark data points would be further away from their target counterparts. From this example, it is clear that manually adjusting the scaling and reflection parameters is generally not optimal.

Feature Selection

In this section...

Introduction to Feature Selection

Feature selection reduces the dimensionality of data by selecting only a subset of measured features (predictor variables) to create a model. Selection criteria usually involve the minimization of a specific measure of predictive error for models fit to different subsets. Algorithms search for a subset of predictors that optimally model measured responses, subject to constraints such as required or excluded features and the size of the subset.

Feature selection is preferable to feature transformation when the original units and meaning of features are important and the modeling goal is to identify an influential subset. When categorical features are present, and numerical transformations are inappropriate, feature selection becomes the primary means of dimension reduction.

Sequential Feature Selection

Introduction to Sequential Feature Selection

A common method of feature selection is *sequential feature selection*. This method has two components:

- An objective function, called the *criterion*, which the method seeks to minimize over all feasible feature subsets. Common criteria are mean squared error (for regression models) and misclassification rate (for classification models).
- A sequential search algorithm, which adds or removes features from a candidate subset while evaluating the criterion. Since an exhaustive comparison of the criterion value at all 2^n subsets of an n-feature data set is typically infeasible (depending on the size of n and the cost of objective calls), sequential searches move in only one direction, always growing or always shrinking the candidate set.

The method has two variants:

- *Sequential forward selection* (*SFS*), in which features are sequentially added to an empty candidate set until the addition of further features does not decrease the criterion.
- *Sequential backward selection* (*SBS*), in which features are sequentially removed from a full candidate set until the removal of further features increase the criterion.

Stepwise regression is a sequential feature selection technique designed specifically for least-squares fitting. The functions `stepwise` and `stepwisefit` make use of optimizations that are only possible with least-squares criteria. Unlike generalized sequential feature selection, stepwise regression may remove features that have been added or add features that have been removed.

The Statistics and Machine Learning Toolbox function `sequentialfs` carries out sequential feature selection. Input arguments include predictor and response data and a function handle to a file implementing the criterion function. Optional inputs allow you to specify SFS or SBS, required or excluded features, and the size of the feature subset. The function calls `cvpartition` and `crossval` to evaluate the criterion at different candidate sets.

Example: Sequential Feature Selection

For example, consider a data set with 100 observations of 10 predictors. The following generates random data from a logistic model, with a binomial distribution of responses at each set of values for the predictors. Some coefficients are set to zero so that not all of the predictors affect the response:

```
n = 100;
m = 10;
X = rand(n,m);
b = [1 0 0 2 .5 0 0 0.1 0 1];
Xb = X*b';
p = 1./(1+exp(-Xb));
N = 50;
y = binornd(N,p);
```

The `glmfit` function fits a logistic model to the data:

```
Y = [y N*ones(size(y))];
[b0,dev0,stats0] = glmfit(X,Y,'binomial');

% Display coefficient estimates and their standard errors:
```

```
model0 = [b0 stats0.se]
model0 =
    0.3115    0.2596
    0.9614    0.1656
   -0.1100    0.1651
   -0.2165    0.1683
    1.9519    0.1809
    0.5683    0.2018
   -0.0062    0.1740
    0.0651    0.1641
   -0.1034    0.1685
    0.0017    0.1815
    0.7979    0.1806

% Display the deviance of the fit:
dev0
dev0 =
  101.2594
```

This is the full model, using all of the features (and an initial constant term). Sequential feature selection searches for a subset of the features in the full model with comparative predictive power.

First, you must specify a criterion for selecting the features. The following function, which calls `glmfit` and returns the deviance of the fit (a generalization of the residual sum of squares) is a useful criterion in this case:

```
function dev = critfun(X,Y)

[b,dev] = glmfit(X,Y,'binomial');
```

You should create this function as a file on the MATLAB path.

The function `sequentialfs` performs feature selection, calling the criterion function via a function handle:

```
maxdev = chi2inv(.95,1);
opt = statset('display','iter',...
              'TolFun',maxdev,...
              'TolTypeFun','abs');

inmodel = sequentialfs(@critfun,X,Y,...
                       'cv','none',...
                       'nullmodel',true,...
```

```
                    'options',opt,...
                    'direction','forward');

Start forward sequential feature selection:
Initial columns included:  none
Columns that can not be included:  none
Step 1, used initial columns, criterion value 309.118
Step 2, added column 4, criterion value 180.732
Step 3, added column 1, criterion value 138.862
Step 4, added column 10, criterion value 114.238
Step 5, added column 5, criterion value 103.503
Final columns included:  1 4 5 10
```

The iterative display shows a decrease in the criterion value as each new feature is added to the model. The final result is a reduced model with only four of the original ten features: columns `1`, `4`, `5`, and `10` of `X`. These features are indicated in the logical vector `inmodel` returned by `sequentialfs`.

The deviance of the reduced model is higher than for the full model, but the addition of any other single feature would not decrease the criterion by more than the absolute tolerance, `maxdev`, set in the options structure. Adding a feature with no effect reduces the deviance by an amount that has a chi-square distribution with one degree of freedom. Adding a significant feature results in a larger change. By setting `maxdev` to `chi2inv(.95,1)`, you instruct `sequentialfs` to continue adding features so long as the change in deviance is more than would be expected by random chance.

The reduced model (also with an initial constant term) is:

```
[b,dev,stats] = glmfit(X(:,inmodel),Y,'binomial');

% Display coefficient estimates and their standard errors:
model = [b stats.se]
model =
    0.0784    0.1642
    1.0040    0.1592
    1.9459    0.1789
    0.6134    0.1872
    0.8245    0.1730
```

Feature Transformation

In this section...

Introduction to Feature Transformation

Feature transformation is a group of methods that create new features (predictor variables). The methods are useful for dimension reduction when the transformed features have a descriptive power that is more easily ordered than the original features. In this case, less descriptive features can be dropped from consideration when building models.

Feature transformation methods are contrasted with the methods presented in "Feature Selection" on page 13-68, where dimension reduction is achieved by computing an optimal subset of predictive features measured in the original data.

The methods presented in this section share some common methodology. Their goals, however, are essentially different:

- Nonnegative matrix factorization is used when model terms must represent nonnegative quantities, such as physical quantities.
- Principal component analysis is used to summarize data in fewer dimensions, for example, to visualize it.
- Factor analysis is used to build explanatory models of data correlations.

Nonnegative Matrix Factorization

Introduction to Nonnegative Matrix Factorization

Nonnegative matrix factorization (*NMF*) is a dimension-reduction technique based on a low-rank approximation of the feature space. Besides providing a reduction in the number of features, NMF guarantees that the features are nonnegative, producing additive models that respect, for example, the nonnegativity of physical quantities.

Given a nonnegative m-by-n matrix X and a positive integer $k < \min(m,n)$, NMF finds nonnegative m-by-k and k-by-n matrices W and H, respectively, that minimize the norm of the difference $X - WH$. W and H are thus approximate nonnegative factors of X.

The k columns of W represent transformations of the variables in X; the k rows of H represent the coefficients of the linear combinations of the original n variables in X that produce the transformed variables in W. Since k is generally smaller than the rank of X, the product WH provides a compressed approximation of the data in X. A range of possible values for k is often suggested by the modeling context.

The Statistics and Machine Learning Toolbox function `nnmf` carries out nonnegative matrix factorization. `nnmf` uses one of two iterative algorithms that begin with random initial values for W and H. Because the norm of the residual $X - WH$ may have local minima, repeated calls to `nnmf` may yield different factorizations. Sometimes the algorithm converges to a solution of lower rank than k, which may indicate that the result is not optimal.

Example: Nonnegative Matrix Factorization

For example, consider the five predictors of biochemical oxygen demand in the data set `moore.mat`.

```
load moore
X = moore(:,1:5);
rng('default'); % For reproducibility
```

The following uses `nnmf` to compute a rank-two approximation of `X` with a multiplicative update algorithm that begins from five random initial values for `W` and `H`.

```
opt = statset('MaxIter',10,'Display','final');
[W0,H0] = nnmf(X,2,'replicates',5,'options',opt,'algorithm','mult');
```

```
    rep    iteration     rms resid    |delta x|
      1       10       358.296    0.00190554
      2       10       78.3556   0.000351747
```

```
      3       10      230.962    0.0172839
      4       10      326.347   0.00739552
      5       10      361.547   0.00705539
Final root mean square residual = 78.3556
```

The `'mult'` algorithm is sensitive to initial values, which makes it a good choice when using `'replicates'` to find `W` and `H` from multiple random starting values.

Now perform the factorization using an alternating least-squares algorithm, which converges faster and more consistently. Run 100 times more iterations, beginning from the initial `W0` and `H0` identified above.

```
opt = statset('Maxiter',1000,'Display','final');
[W,H] = nnmf(X,2,'w0',W0,'h0',H0,'options',opt,'algorithm','als');
```

```
    rep    iteration    rms resid   |delta x|
      1        2      77.5315  0.000830334
Final root mean square residual = 77.5315
```

The two columns of `W` are the transformed predictors. The two rows of `H` give the relative contributions of each of the five predictors in `X` to the predictors in `W`.

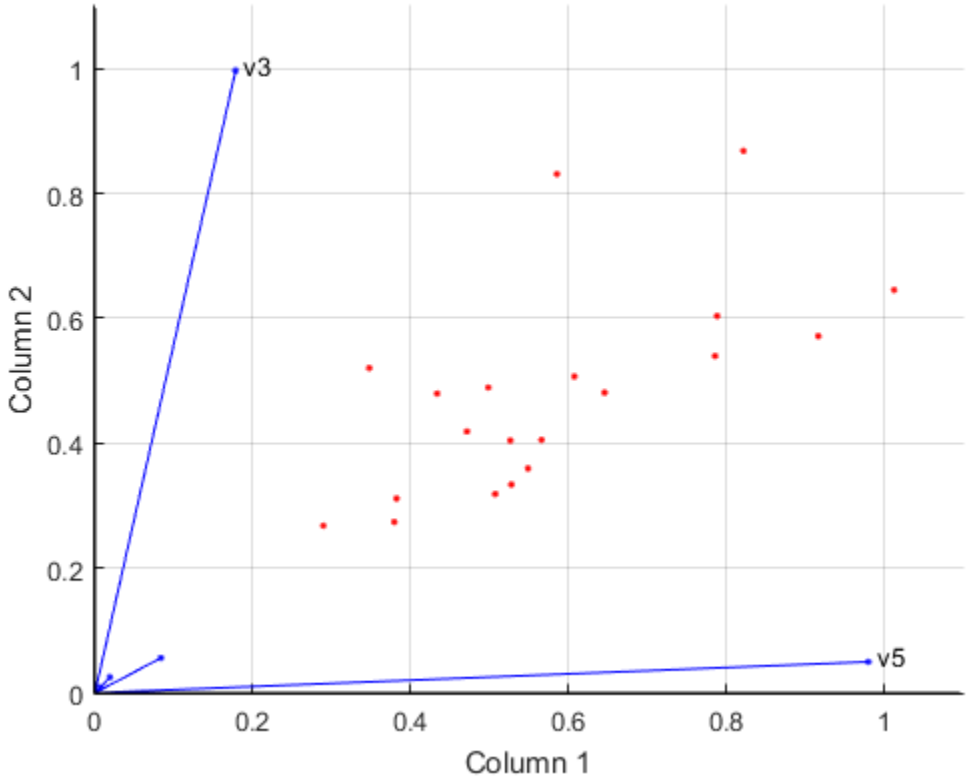
```
H
```

```
H =

    0.0835    0.0190    0.1782    0.0072    0.9802
    0.0559    0.0250    0.9969    0.0085    0.0497
```

The fifth predictor in `X` (weight `0.9802`) strongly influences the first predictor in `W`. The third predictor in `X` (weight `0.9969`) strongly influences the second predictor in `W`.

Visualize the relative contributions of the predictors in `X` with a `biplot`, showing the data and original variables in the column space of `W`.

```
biplot(H','scores',W,'varlabels',{'','','v3','','v5'});
axis([0 1.1 0 1.1])
xlabel('Column 1')
ylabel('Column 2')
```



Principal Component Analysis (PCA)

One of the difficulties inherent in multivariate statistics is the problem of visualizing data that has many variables. The MATLAB function `plot` displays a graph of the relationship between two variables. The `plot3` and `surf` commands display different three-dimensional views. But when there are more than three variables, it is more difficult to visualize their relationships.

Fortunately, in data sets with many variables, groups of variables often move together. One reason for this is that more than one variable might be measuring the same driving principle governing the behavior of the system. In many systems there are only a few such driving forces. But an abundance of instrumentation enables you to measure dozens

of system variables. When this happens, you can take advantage of this redundancy of information. You can simplify the problem by replacing a group of variables with a single new variable.

Principal component analysis is a quantitatively rigorous method for achieving this simplification. The method generates a new set of variables, called *principal components*. Each principal component is a linear combination of the original variables. All the principal components are orthogonal to each other, so there is no redundant information. The principal components as a whole form an orthogonal basis for the space of the data.

There are an infinite number of ways to construct an orthogonal basis for several columns of data. What is so special about the principal component basis?

The first principal component is a single axis in space. When you project each observation on that axis, the resulting values form a new variable. And the variance of this variable is the maximum among all possible choices of the first axis.

The second principal component is another axis in space, perpendicular to the first. Projecting the observations on this axis generates another new variable. The variance of this variable is the maximum among all possible choices of this second axis.

The full set of principal components is as large as the original set of variables. But it is commonplace for the sum of the variances of the first few principal components to exceed 80% of the total variance of the original data. By examining plots of these few new variables, researchers often develop a deeper understanding of the driving forces that generated the original data.

You can use the function `pca` to find the principal components. To use `pca`, you need to have the actual measured data you want to analyze. However, if you lack the actual data, but have the sample covariance or correlation matrix for the data, you can still use the function `pcacov` to perform a principal components analysis. See the reference page for `pcacov` for a description of its inputs and outputs.

Quality of Life in U.S. Cities

This example shows how to perform a weighted principal components analysis and interpret the results.

Load sample data.

Load the sample data. The data includes ratings for 9 different indicators of the quality of life in 329 U.S. cities. These are climate, housing, health, crime, transportation,

education, arts, recreation, and economics. For each category, a higher rating is better. For example, a higher rating for crime means a lower crime rate.

Display the `categories` variable.

```
load cities
categories
```

```
categories =
   climate
   housing
   health
   crime
   transportation
   education
   arts
   recreation
   economics
```

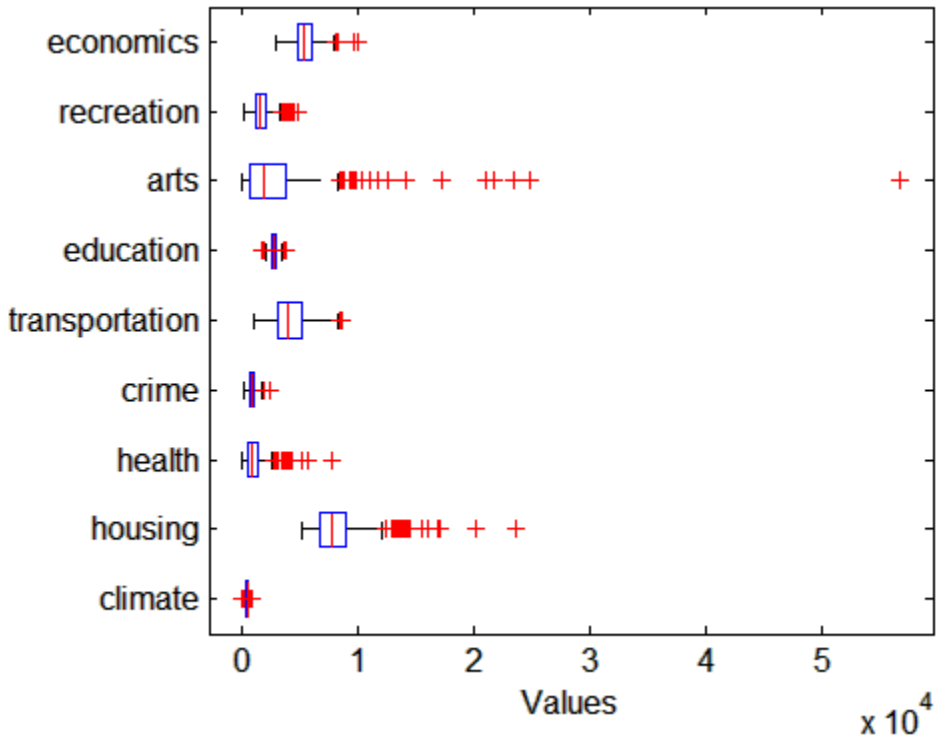
In total, the `cities` data set contains three variables:

- `categories`, a string matrix containing the names of the indices
- `names`, a string matrix containing the 329 city names
- `ratings`, the data matrix with 329 rows and 9 columns

Plot data.

Make a boxplot to look at the distribution of the `ratings` data.

```
figure()
boxplot(ratings,'orientation','horizontal','labels',categories)
```



There is more variability in the ratings of the arts and housing than in the ratings of crime and climate.

Check pairwise correlation.

Check the pairwise correlation between the variables.

```
C = corr(ratings,ratings);
```

The correlation among some variables is as high as 0.85. Principal components analysis constructs independent new variables which are linear combinations of the original variables.

Compute principal components.

When all variables are in the same unit, it is appropriate to compute principal components for raw data. When the variables are in different units or the difference in

the variance of different columns is substantial (as in this case), scaling of the data or use of weights is often preferable.

Perform the principal component analysis by using the inverse variances of the ratings as weights.

```
w = 1./var(ratings);
[wcoeff,score,latent,tsquared,explained] = pca(ratings,...
'VariableWeights',w);
```

Or equivalently:

```
[wcoeff,score,latent,tsquared,explained] = pca(ratings,...
'VariableWeights','variance');
```

The following sections explain the five outputs of `pca`.

Component coefficients.

The first output, `wcoeff`, contains the coefficients of the principal components.

The first three principal component coefficient vectors are:

```
c3 = wcoeff(:,1:3)
```

```
c3 = wcoeff(:,1:3)
c3 =

   1.0e+03 *

    0.0249   -0.0263   -0.0834
    0.8504   -0.5978   -0.4965
    0.4616    0.3004   -0.0073
    0.1005   -0.1269    0.0661
    0.5096    0.2606    0.2124
    0.0883    0.1551    0.0737
    2.1496    0.9043   -0.1229
    0.2649   -0.3106   -0.0411
    0.1469   -0.5111    0.6586
```

These coefficients are weighted, hence the coefficient matrix is not orthonormal.

Transform coefficients.

Transform the coefficients so that they are orthonormal.

```
coefforth = inv(diag(std(ratings)))*wcoeff;
```

Note that if you use a weights vector, `w`, while conducting the `pca`, then

```
coefforth = diag(sqrt(w))*wcoeff;
```

Check coefficients are orthonormal.

The transformed coefficients are now orthonormal.

```
I = c3'*c3

I =
    1.0000   -0.0000   -0.0000
   -0.0000    1.0000   -0.0000
   -0.0000   -0.0000    1.0000
```

Component scores.

The second output, `score`, contains the coordinates of the original data in the new coordinate system defined by the principal components. The `score` matrix is the same size as the input data matrix. You can also obtain the component scores using the orthonormal coefficients and the standardized ratings as follows.

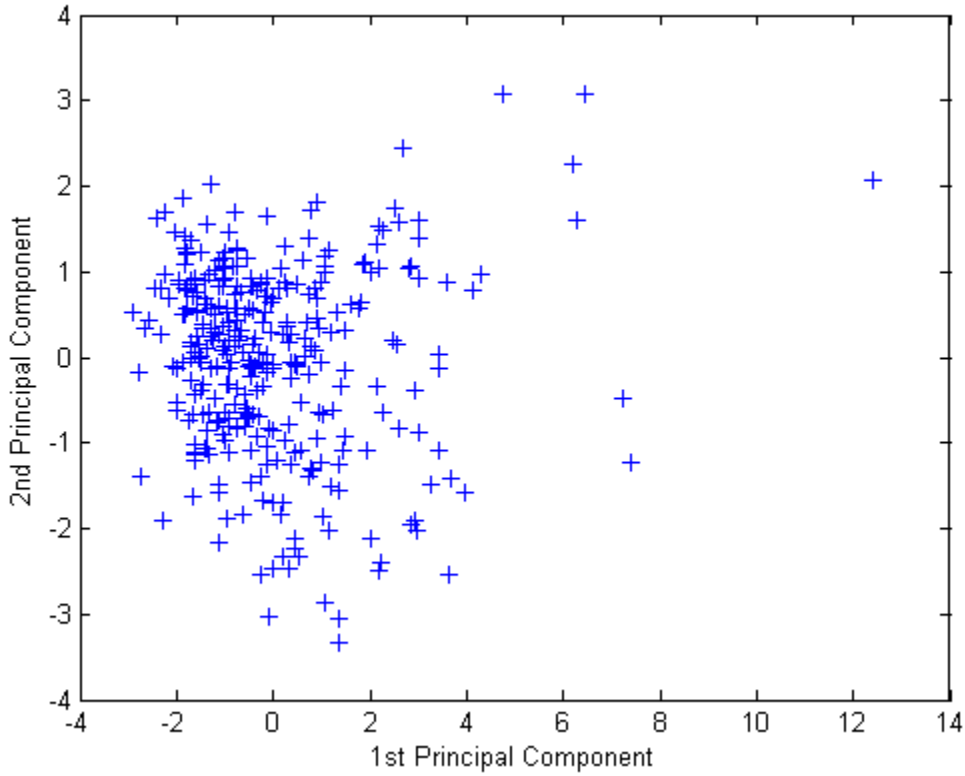
```
cscores = zscore(ratings)*coefforth;
```

`cscores` and `score` are identical matrices.

Plot component scores.

Create a plot of the first two columns of `score`.

```
figure()
plot(score(:,1),score(:,2),'+')
xlabel('1st Principal Component')
ylabel('2nd Principal Component')
```



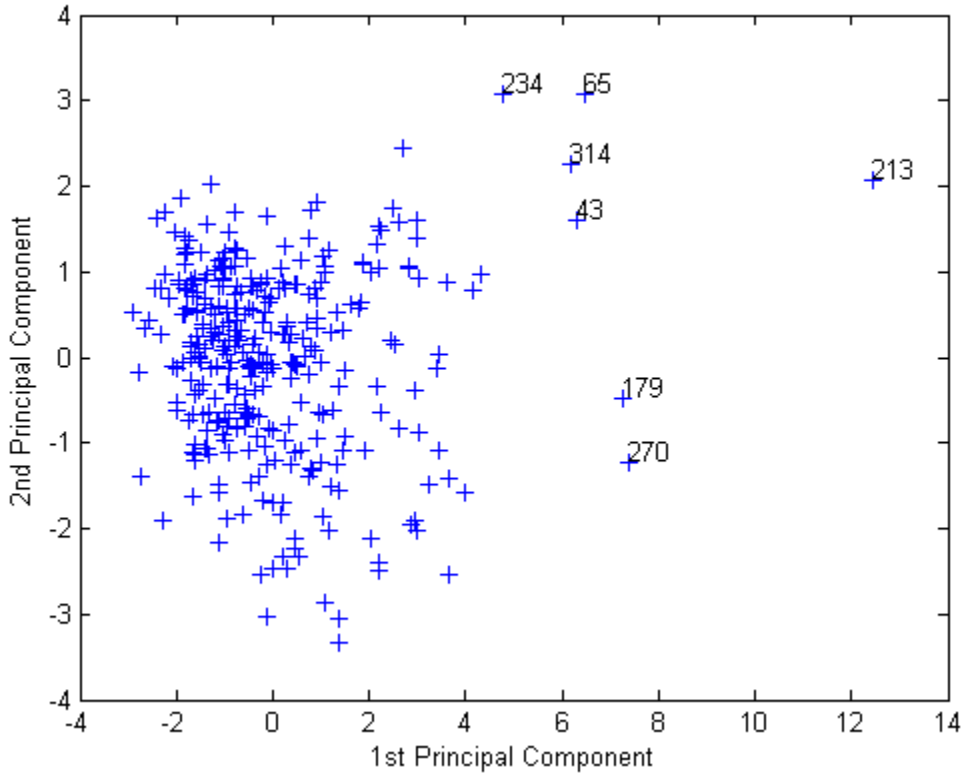
This plot shows the centered and scaled ratings data projected onto the first two principal components. `pca` computes the scores to have mean zero.

Explore plot interactively.

Note the outlying points in the right half of the plot. You can graphically identify these points as follows.

```
gname
```

Move your cursor over the plot and click once near the rightmost seven points. This labels the points by their row numbers as in the following figure.



After labeling points, press **Return**.

Extract observation names.

Create an index variable containing the row numbers of all the cities you chose and get the names of the cities.

```
metro = [43 65 179 213 234 270 314];
names(metro,:)
```

```
ans =
   Boston, MA
   Chicago, IL
   Los Angeles, Long Beach, CA
```

```
New York, NY
Philadelphia, PA-NJ
San Francisco, CA
Washington, DC-MD-VA
```

These labeled cities are some of the biggest population centers in the United States and they appear more extreme than the remainder of the data.

Component variances.

The third output, `latent`, is a vector containing the variance explained by the corresponding principal component. Each column of `score` has a sample variance equal to the corresponding row of `latent`.

```
latent
```

```
latent =

    3.4083
    1.2140
    1.1415
    0.9209
    0.7533
    0.6306
    0.4930
    0.3180
    0.1204
```

Percent variance explained.

The fifth output, `explained`, is a vector containing the percent variance explained by the corresponding principal component.

```
explained
```

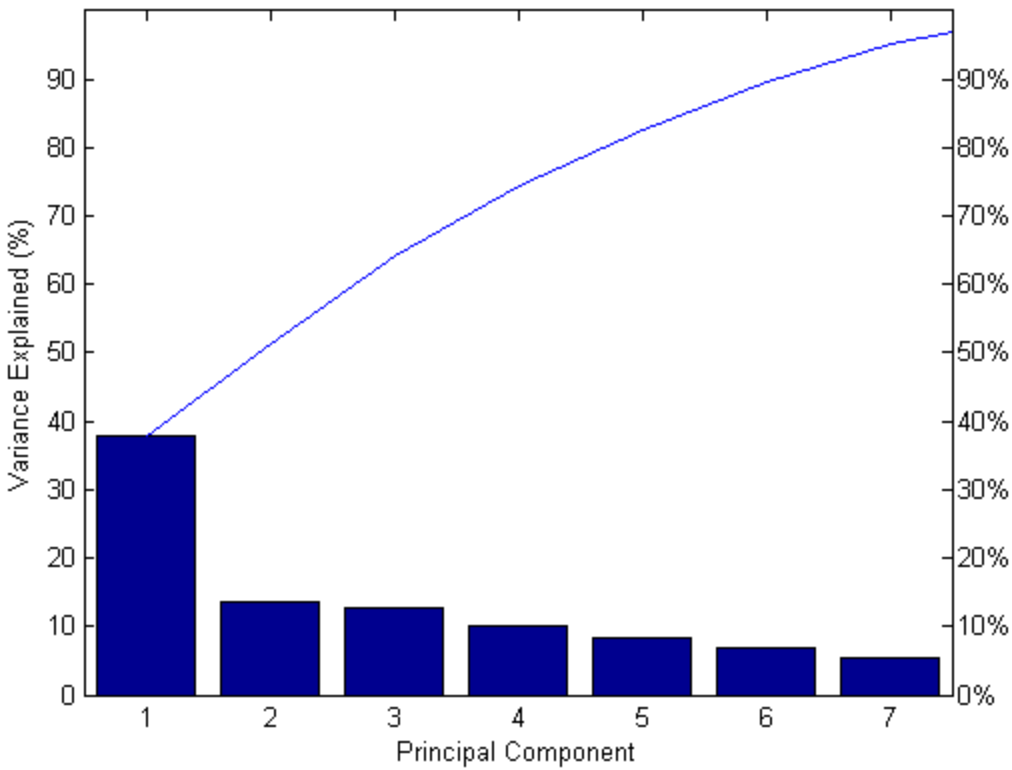
```
explained =

   37.8699
   13.4886
   12.6831
   10.2324
    8.3698
    7.0062
    5.4783
```

```
    3.5338
    1.3378
```

Create scree plot.

Make a scree plot of the percent variability explained by each principal component.

```
figure()
pareto(explained)
xlabel('Principal Component')
ylabel('Variance Explained (%)')
```



This scree plot only shows the first seven (instead of the total nine) components that explain 95% of the total variance. The only clear break in the amount of variance

accounted for by each component is between the first and second components. However, the first component by itself explains less than 40% of the variance, so more components might be needed. You can see that the first three principal components explain roughly two-thirds of the total variability in the standardized ratings, so that might be a reasonable way to reduce the dimensions.

Hotelling's T-squared statistic.

The last output from `pca` is `tsquared`, which is Hotelling's T^2, a statistical measure of the multivariate distance of each observation from the center of the data set. This is an analytical way to find the most extreme points in the data.

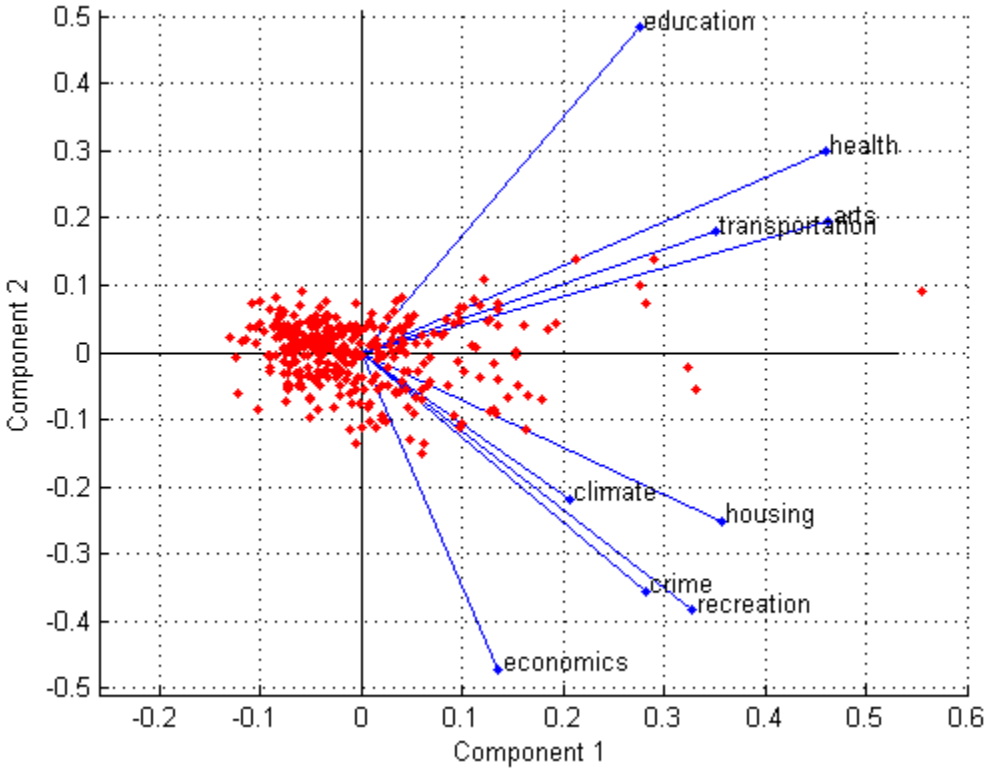
```
[st2,index] = sort(tsquared,'descend'); % sort in descending order
extreme = index(1);
names(extreme,:)

ans =

New York, NY
```

The ratings for New York are the furthest from the average U.S. city.

Visualize the results.

Visualize both the orthonormal principal component coefficients for each variable and the principal component scores for each observation in a single plot.

```
biplot(coefforth(:,1:2),'scores',score(:,1:2),'varlabels',categories);
axis([-.26 0.6 -.51 .51]);
```



All nine variables are represented in this bi-plot by a vector, and the direction and length of the vector indicate how each variable contributes to the two principal components in the plot. For example, the first principal component, on the horizontal axis, has positive coefficients for all nine variables. That is why the nine vectors are directed into the right half of the plot. The largest coefficients in the first principal component are the third and seventh elements, corresponding to the variables `health` and `arts`.

The second principal component, on the vertical axis, has positive coefficients for the variables `education`, `health`, `arts`, and `transportation`, and negative coefficients for the remaining five variables. This indicates that the second component distinguishes among cities that have high values for the first set of variables and low for the second, and cities that have the opposite.

The variable labels in this figure are somewhat crowded. You can either exclude the `VarLabels` parameter when making the plot, or select and drag some of the labels to better positions using the Edit Plot tool from the figure window toolbar.

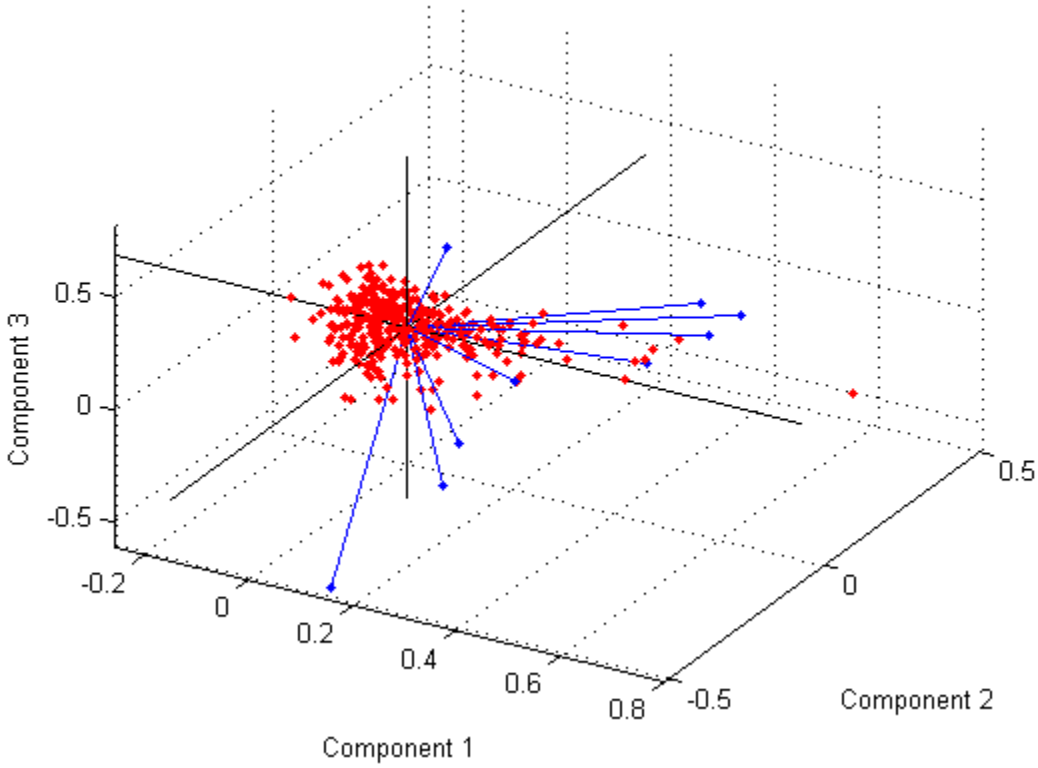
This 2-D bi-plot also includes a point for each of the 329 observations, with coordinates indicating the score of each observation for the two principal components in the plot. For example, points near the left edge of this plot have the lowest scores for the first principal component. The points are scaled with respect to the maximum score value and maximum coefficient length, so only their relative locations can be determined from the plot.

You can identify items in the plot by selecting **Tools**>`Data Cursor` from the figure window. By clicking a variable (vector), you can read that variable's coefficients for each principal component. By clicking an observation (point), you can read that observation's scores for each principal component.

Create a three-dimensional bi-plot.

You can also make a bi-plot in three dimensions.

```
figure()
biplot(coefforth(:,1:3),'scores',score(:,1:3),'obslabels',names);
axis([-.26 0.8 -.51 .51 -.61 .81]);
view([30 40]);
```



This graph is useful if the first two principal coordinates do not explain enough of the variance in your data. You can also rotate the figure to see it from different angles by selecting the**Tools**> `Rotate 3D`.

Factor Analysis

Introduction to Factor Analysis

Multivariate data often includes a large number of measured variables, and sometimes those variables overlap, in the sense that groups of them might be dependent. For

example, in a decathlon, each athlete competes in 10 events, but several of them can be thought of as speed events, while others can be thought of as strength events, etc. Thus, you can think of a competitor's 10 event scores as largely dependent on a smaller set of three or four types of athletic ability.

Factor analysis is a way to fit a model to multivariate data to estimate just this sort of interdependence. In a factor analysis model, the measured variables depend on a smaller number of unobserved (latent) factors. Because each factor might affect several variables in common, they are known as *common factors*. Each variable is assumed to be dependent on a linear combination of the common factors, and the coefficients are known as *loadings*. Each measured variable also includes a component due to independent random variability, known as *specific variance* because it is specific to one variable.

Specifically, factor analysis assumes that the covariance matrix of your data is of the form

$$\sum_x = \Lambda\Lambda^T + \Psi$$

where Λ is the matrix of loadings, and the elements of the diagonal matrix Ψ are the specific variances. The function `factoran` fits the Factor Analysis model using maximum likelihood.

Example: Factor Analysis

Factor Loadings

Over the course of 100 weeks, the percent change in stock prices for ten companies has been recorded. Of the ten companies, the first four can be classified as primarily technology, the next three as financial, and the last three as retail. It seems reasonable that the stock prices for companies that are in the same sector might vary together as economic conditions change. Factor Analysis can provide quantitative evidence that companies within each sector do experience similar week-to-week changes in stock price.

In this example, you first load the data, and then call `factoran`, specifying a model fit with three common factors. By default, `factoran` computes rotated estimates of the

loadings to try and make their interpretation simpler. But in this example, you specify an unrotated solution.

```
load stockreturns

[Loadings,specificVar,T,stats] = factoran(stocks,3,'rotate','none');
```

The first two `factoran` return arguments are the estimated loadings and the estimated specific variances. Each row of the loadings matrix represents one of the ten stocks, and each column corresponds to a common factor. With unrotated estimates, interpretation of the factors in this fit is difficult because most of the stocks contain fairly large coefficients for two or more factors.

```
Loadings
```

```
Loadings =

    0.8885    0.2367   -0.2354
    0.7126    0.3862    0.0034
    0.3351    0.2784   -0.0211
    0.3088    0.1113   -0.1905
    0.6277   -0.6643    0.1478
    0.4726   -0.6383    0.0133
    0.1133   -0.5416    0.0322
    0.6403    0.1669    0.4960
    0.2363    0.5293    0.5770
    0.1105    0.1680    0.5524
```

Note "Factor Rotation" on page 13-91 helps to simplify the structure in the `Loadings` matrix, to make it easier to assign meaningful interpretations to the factors.

From the estimated specific variances, you can see that the model indicates that a particular stock price varies quite a lot beyond the variation due to the common factors.

```
specificVar
```

```
specificVar =

    0.0991
    0.3431
```

```
    0.8097
    0.8559
    0.1429
    0.3691
    0.6928
    0.3162
    0.3311
    0.6544
```

A specific variance of 1 would indicate that there is *no* common factor component in that variable, while a specific variance of 0 would indicate that the variable is *entirely* determined by common factors. These data seem to fall somewhere in between.

The *p* value returned in the `stats` structure fails to reject the null hypothesis of three common factors, suggesting that this model provides a satisfactory explanation of the covariation in these data.

```
stats.p
```

```
ans =

    0.8144
```

To determine whether fewer than three factors can provide an acceptable fit, you can try a model with two common factors. The *p* value for this second fit is highly significant, and rejects the hypothesis of two factors, indicating that the simpler model is not sufficient to explain the pattern in these data.

```
[Loadings2,specificVar2,T2,stats2] = factoran(stocks, 2,'rotate','none');

stats2.p
```

```
ans =

   3.5610e-06
```

Factor Rotation

As the results illustrate, the estimated loadings from an unrotated factor analysis fit can have a complicated structure. The goal of factor rotation is to find a parameterization in

which each variable has only a small number of large loadings. That is, each variable is affected by a small number of factors, preferably only one. This can often make it easier to interpret what the factors represent.

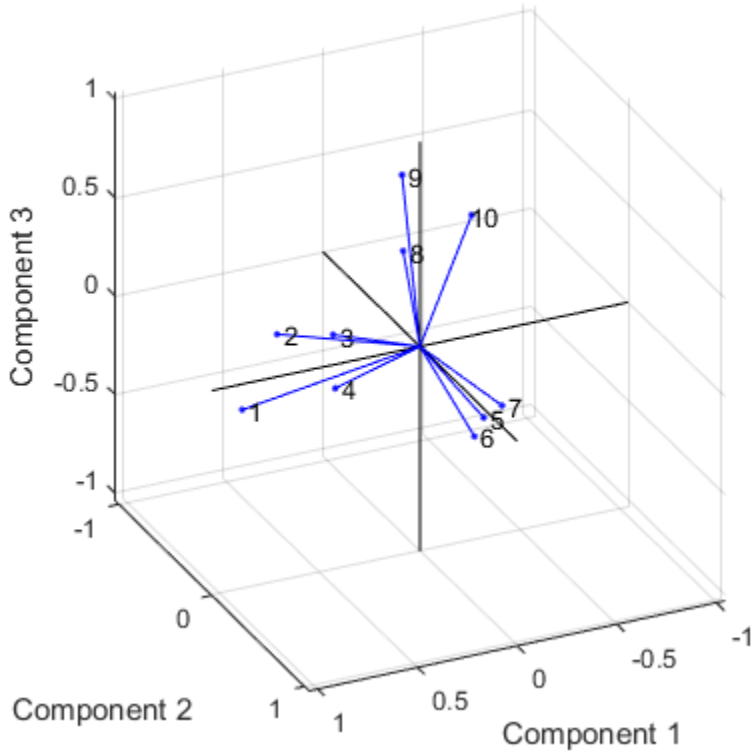
If you think of each row of the loadings matrix as coordinates of a point in *M*-dimensional space, then each factor corresponds to a coordinate axis. Factor rotation is equivalent to rotating those axes and computing new loadings in the rotated coordinate system. There are various ways to do this. Some methods leave the axes orthogonal, while others are oblique methods that change the angles between them. For this example, you can rotate the estimated loadings by using the promax criterion, a common oblique method.

```
[LoadingsPM,specVarPM] = factoran(stocks,3,'rotate','promax');
LoadingsPM
```

```
LoadingsPM =

    0.9452    0.1214   -0.0617
    0.7064   -0.0178    0.2058
    0.3885   -0.0994    0.0975
    0.4162   -0.0148   -0.1298
    0.1021    0.9019    0.0768
    0.0873    0.7709   -0.0821
   -0.1616    0.5320   -0.0888
    0.2169    0.2844    0.6635
    0.0016   -0.1881    0.7849
   -0.2289    0.0636    0.6475
```

Promax rotation creates a simpler structure in the loadings, one in which most of the stocks have a large loading on only one factor. To see this structure more clearly, you can use the `biplot` function to plot each stock using its factor loadings as coordinates.

```
biplot(LoadingsPM,'varlabels',num2str((1:10)'));
axis square
view(155,27);
```



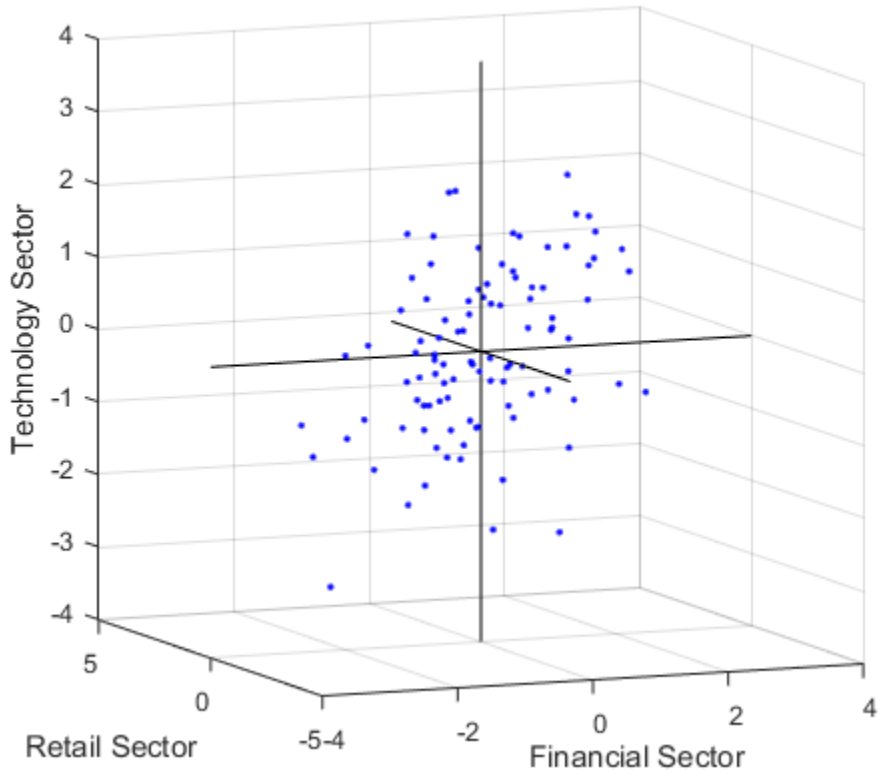
This plot shows that promax has rotated the factor loadings to a simpler structure. Each stock depends primarily on only one factor, and it is possible to describe each factor in terms of the stocks that it affects. Based on which companies are near which axes, you could reasonably conclude that the first factor axis represents the financial sector, the second retail, and the third technology. The original conjecture, that stocks vary primarily within sector, is apparently supported by the data.

Factor Scores

Sometimes, it is useful to be able to classify an observation based on its factor scores. For example, if you accepted the three-factor model and the interpretation of the rotated factors, you might want to categorize each week in terms of how favorable it was for each of the three stock sectors, based on the data from the 10 observed stocks.

Because the data in this example are the raw stock price changes, and not just their correlation matrix, you can have `factoran` return estimates of the value of each of the three rotated common factors for each week. You can then plot the estimated scores to see how the different stock sectors were affected during each week.

```
[LoadingsPM,specVarPM,TPM,stats,F] = factoran(stocks, 3,'rotate','promax');

plot3(F(:,1),F(:,2),F(:,3),'b.')
line([-4 4 NaN 0 0 NaN 0 0], [0 0 NaN -4 4 NaN 0 0],[0 0 NaN 0 0 NaN -4 4], 'Color','bl
xlabel('Financial Sector')
ylabel('Retail Sector')
zlabel('Technology Sector')
grid on
axis square
view(-22.5, 8)
```



Oblique rotation often creates factors that are correlated. This plot shows some evidence of correlation between the first and third factors, and you can investigate further by computing the estimated factor correlation matrix.

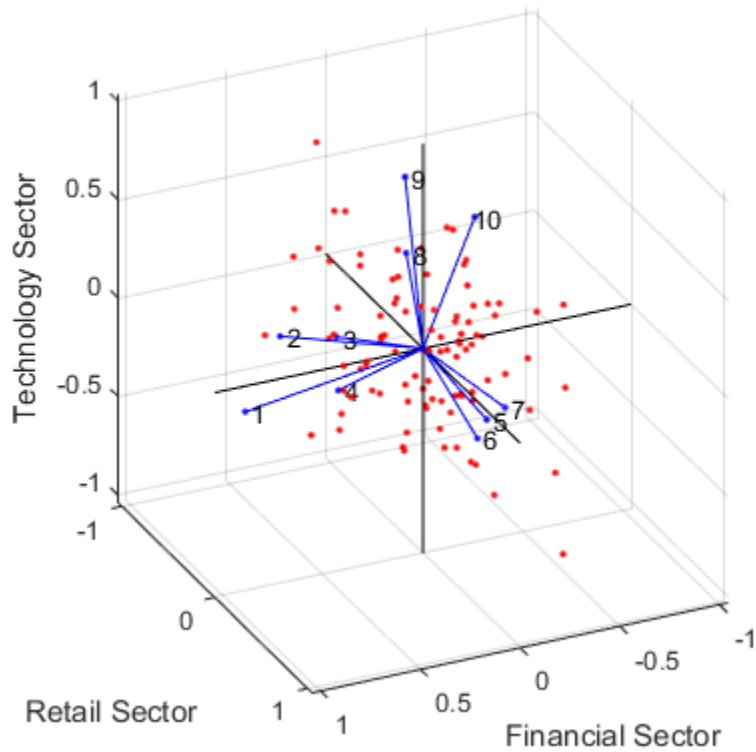
```
inv(TPM'*TPM)
```

```
ans =

    1.0000    0.1559    0.4082
    0.1559    1.0000   -0.0559
    0.4082   -0.0559    1.0000
```

Visualize the Results

You can use the `biplot` function to help visualize both the factor loadings for each variable and the factor scores for each observation in a single plot. For example, the following command plots the results from the factor analysis on the stock data and labels each of the 10 stocks.

```
biplot(LoadingsPM,'scores',F,'varlabels',num2str((1:10)'))
xlabel('Financial Sector')
ylabel('Retail Sector')
zlabel('Technology Sector')
axis square
view(155,27)
```



In this case, the factor analysis includes three factors, and so the biplot is three-dimensional. Each of the 10 stocks is represented in this plot by a vector, and the direction and length of the vector indicates how each stock depends on the underlying factors. For example, you have seen that after promax rotation, the first four stocks have positive loadings on the first factor, and unimportant loadings on the other two factors. That first factor, interpreted as a financial sector effect, is represented in this biplot as one of the horizontal axes. The dependence of those four stocks on that factor corresponds to the four vectors directed approximately along that axis. Similarly, the dependence of stocks 5, 6, and 7 primarily on the second factor, interpreted as a retail sector effect, is represented by vectors directed approximately along that axis.

Each of the 100 observations is represented in this plot by a point, and their locations indicate the score of each observation for the three factors. For example, points near the top of this plot have the highest scores for the technology sector factor. The points are scaled to fit within the unit square, so only their relative locations can be determined from the plot.

You can use the **Data Cursor** tool from the **Tools** menu in the figure window to identify the items in this plot. By clicking a stock (vector), you can read off that stock's loadings for each factor. By clicking an observation (point), you can read off that observation's scores for each factor.

Partial Least Squares Regression and Principal Components Regression

This example shows how to apply Partial Least Squares Regression (PLSR) and Principal Components Regression (PCR), and discusses the effectiveness of the two methods. PLSR and PCR are both methods to model a response variable when there are a large number of predictor variables, and those predictors are highly correlated or even collinear. Both methods construct new predictor variables, known as components, as linear combinations of the original predictor variables, but they construct those components in different ways. PCR creates components to explain the observed variability in the predictor variables, without considering the response variable at all. On the other hand, PLSR does take the response variable into account, and therefore often leads to models that are able to fit the response variable with fewer components. Whether or not that ultimately translates into a more parsimonious model, in terms of its practical use, depends on the context.

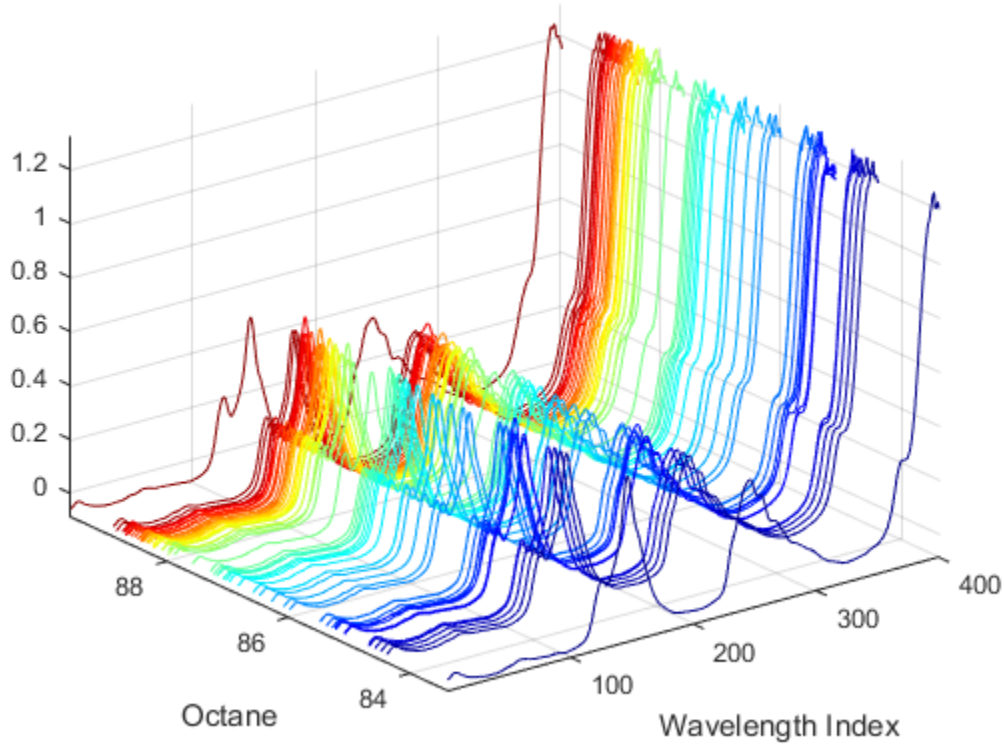
Loading the Data

Load a data set comprising spectral intensities of 60 samples of gasoline at 401 wavelengths, and their octane ratings. These data are described in Kalivas, John H., "Two Data Sets of Near Infrared Spectra," Chemometrics and Intelligent Laboratory Systems, v.37 (1997) pp.255-259.

```
load spectra
whos NIR octane
```

```
  Name         Size              Bytes  Class     Attributes

  NIR         60x401            192480  double
  octane      60x1                 480  double
```

```
[dummy,h] = sort(octane);
oldorder = get(gcf,'DefaultAxesColorOrder');
set(gcf,'DefaultAxesColorOrder',jet(60));
plot3(repmat(1:401,60,1)',repmat(octane(h),1,401)',NIR(h,:)');
set(gcf,'DefaultAxesColorOrder',oldorder);
xlabel('Wavelength Index'); ylabel('Octane'); axis('tight');
grid on
```



Fitting the Data with Two Components

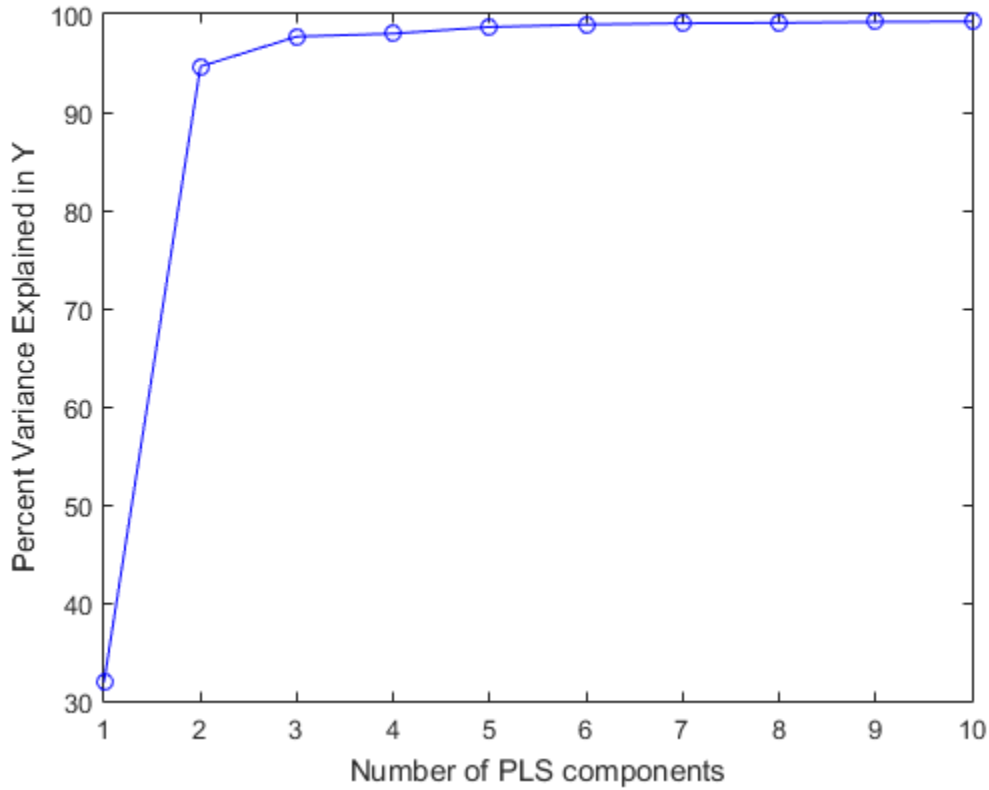
Use the `plsregress` function to fit a PLSR model with ten PLS components and one response.

```
X = NIR;
y = octane;
[n,p] = size(X);
[Xloadings,Yloadings,Xscores,Yscores,betaPLS10,PLSPctVar] = plsregress(...
 X,y,10);
```

Ten components may be more than will be needed to adequately fit the data, but diagnostics from this fit can be used to make a choice of a simpler model with fewer

components. For example, one quick way to choose the number of components is to plot the percent of variance explained in the response variable as a function of the number of components.

```
plot(1:10,cumsum(100*PLSPctVar(2,:)),'-bo');
xlabel('Number of PLS components');
ylabel('Percent Variance Explained in Y');
```



In practice, more care would probably be advisable in choosing the number of components. Cross-validation, for instance, is a widely-used method that will be illustrated later in this example. For now, the above plot suggests that PLSR with two components explains most of the variance in the observed `y`. Compute the fitted response values for the two-component model.

```
[Xloadings,Yloadings,Xscores,Yscores,betaPLS] = plsregress(X,y,2);
yfitPLS = [ones(n,1) X]*betaPLS;
```

Next, fit a PCR model with two principal components. The first step is to perform Principal Components Analysis on `X`, using the `pca` function, and retaining two principal components. PCR is then just a linear regression of the response variable on those two components. It often makes sense to normalize each variable first by its standard deviation when the variables have very different amounts of variability, however, that is not done here.

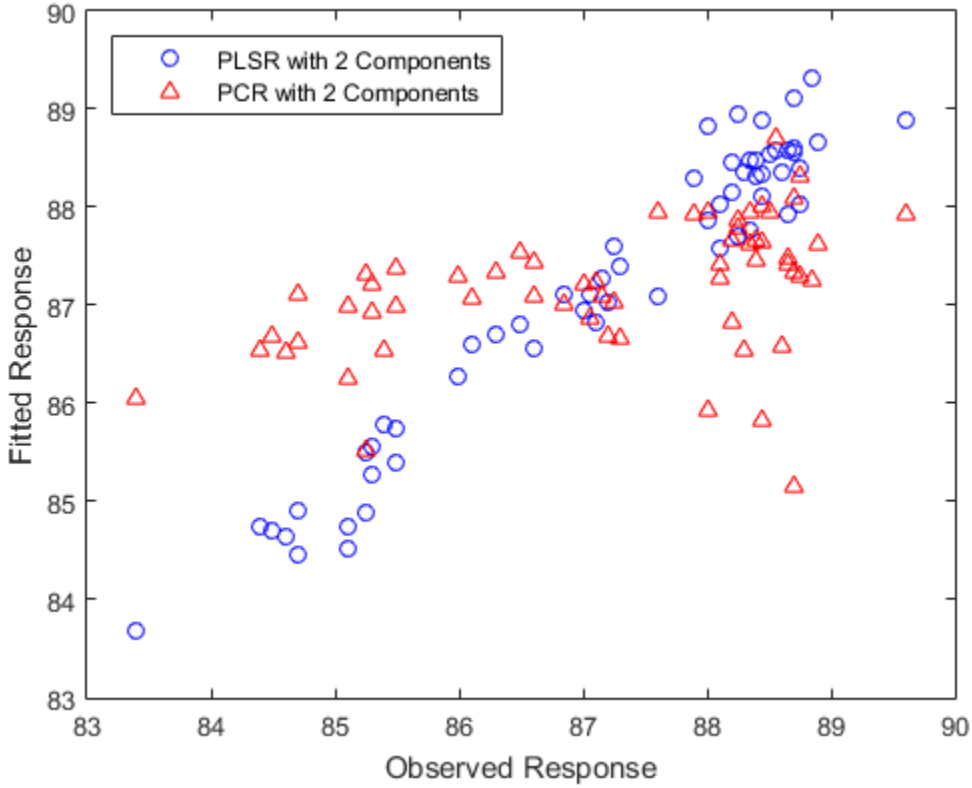
```
[PCALoadings,PCAScores,PCAVar] = pca(X,'Economy',false);
betaPCR = regress(y-mean(y), PCAScores(:,1:2));
```

To make the PCR results easier to interpret in terms of the original spectral data, transform to regression coefficients for the original, uncentered variables.

```
betaPCR = PCALoadings(:,1:2)*betaPCR;
betaPCR = [mean(y) - mean(X)*betaPCR; betaPCR];
yfitPCR = [ones(n,1) X]*betaPCR;
```

Plot fitted vs. observed response for the PLSR and PCR fits.

```
plot(y,yfitPLS,'bo',y,yfitPCR,'r^');
xlabel('Observed Response');
ylabel('Fitted Response');
legend({'PLSR with 2 Components' 'PCR with 2 Components'},  ...
 'location','NW');
```



In a sense, the comparison in the plot above is not a fair one -- the number of components (two) was chosen by looking at how well a two-component PLSR model predicted the response, and there's no reason why the PCR model should be restricted to that same number of components. With the same number of components, however, PLSR does a much better job at fitting `y`. In fact, looking at the horizontal scatter of fitted values in the plot above, PCR with two components is hardly better than using a constant model. The r-squared values from the two regressions confirm that.

```
TSS = sum((y-mean(y)).^2);
RSS_PLS = sum((y-yfitPLS).^2);
rsquaredPLS = 1 - RSS_PLS/TSS
```

```
rsquaredPLS =
```

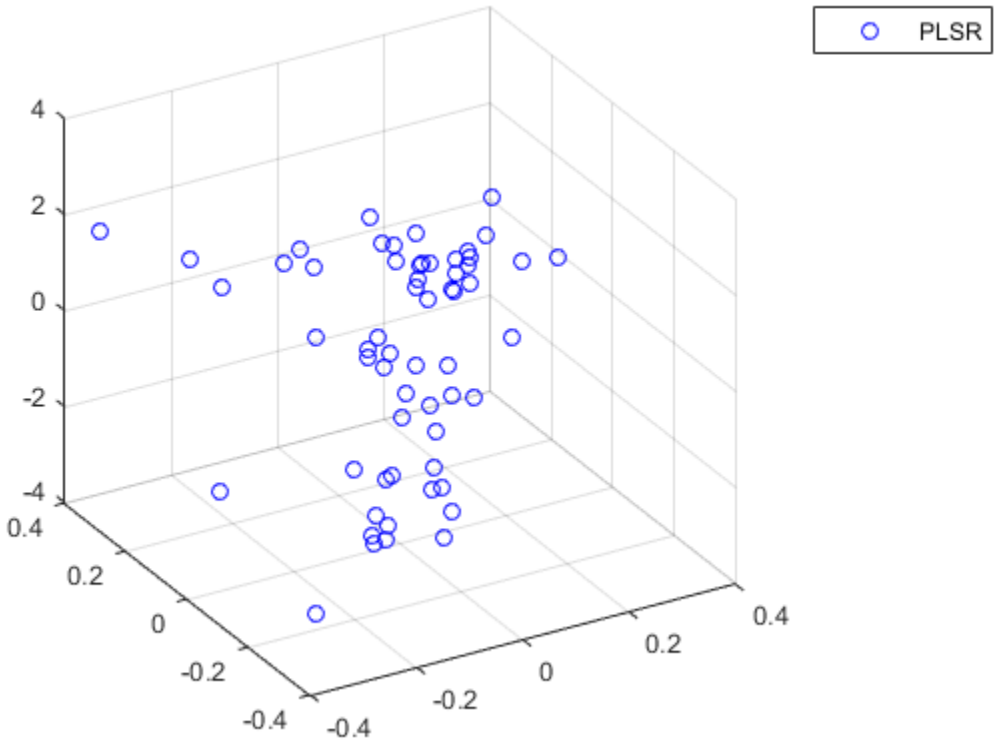
```
    0.9466
```

```
RSS_PCR = sum((y-yfitPCR).^2);
rsquaredPCR = 1 - RSS_PCR/TSS
```

```
rsquaredPCR =

    0.1962
```

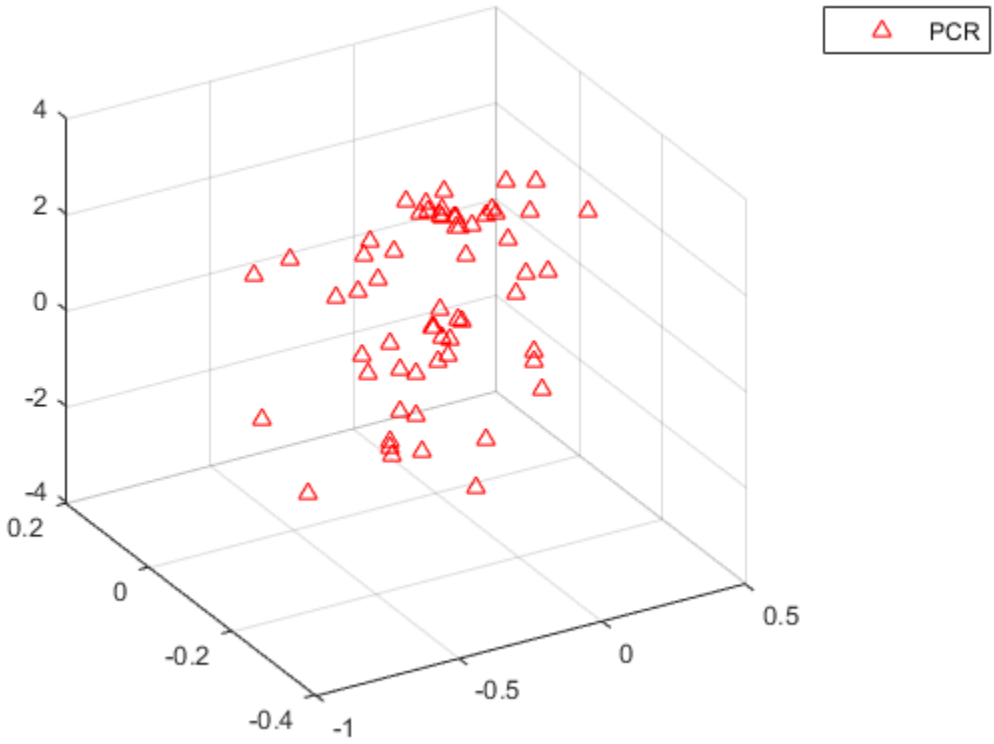
Another way to compare the predictive power of the two models is to plot the response variable against the two predictors in both cases.

```
plot3(Xscores(:,1),Xscores(:,2),y-mean(y),'bo');
legend('PLSR');
grid on; view(-30,30);
```



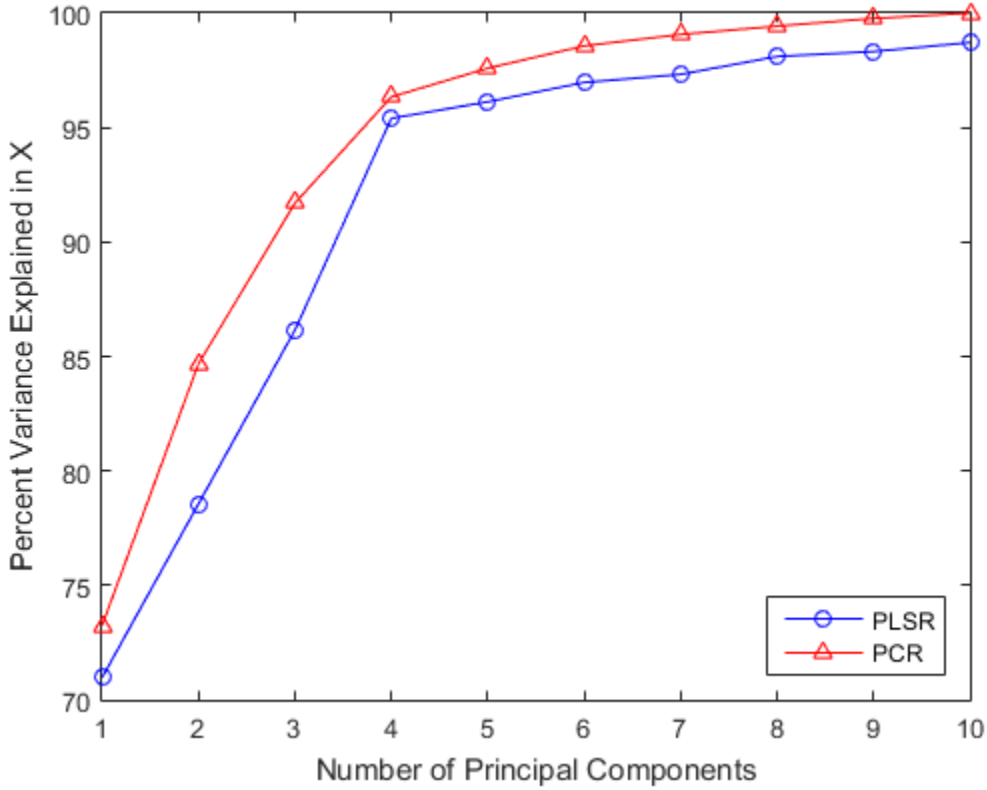
It's a little hard to see without being able to interactively rotate the figure, but the PLSR plot above shows points closely scattered about a plane. On the other hand, the PCR plot below shows a cloud of points with little indication of a linear relationship.

```
plot3(PCAScores(:,1),PCAScores(:,2),y-mean(y),'r^');
legend('PCR');
grid on; view(-30,30);
```



Notice that while the two PLS components are much better predictors of the observed `y`, the following figure shows that they explain somewhat less variance in the observed `X` than the first two principal components used in the PCR.

```
plot(1:10,100*cumsum(PLSPctVar(1,:)),'b-o',1:10,  ...
 100*cumsum(PCAVar(1:10))/sum(PCAVar(1:10)),'r-^');
xlabel('Number of Principal Components');
ylabel('Percent Variance Explained in X');
legend({'PLSR' 'PCR'},'location','SE');
```



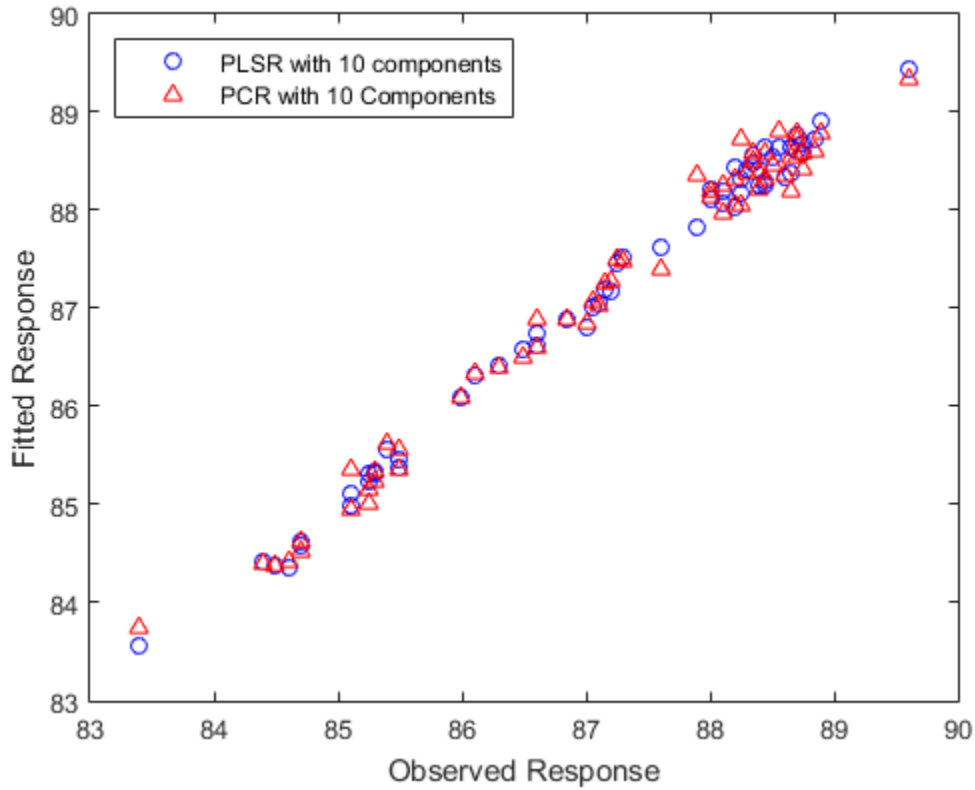
The fact that the PCR curve is uniformly higher suggests why PCR with two components does such a poor job, relative to PLSR, in fitting `y`. PCR constructs components to best explain `X`, and as a result, those first two components ignore the information in the data that is important in fitting the observed `y`.

Fitting with More Components

As more components are added in PCR, it will necessarily do a better job of fitting the original data `y`, simply because at some point most of the important predictive information in `X` will be present in the principal components. For example, the following figure shows that the difference in residuals for the two methods is much less dramatic when using ten components than it was for two components.

```
yfitPLS10 = [ones(n,1) X]*betaPLS10;
```

```
betaPCR10 = regress(y-mean(y), PCAScores(:,1:10));
betaPCR10 = PCALoadings(:,1:10)*betaPCR10;
betaPCR10 = [mean(y) - mean(X)*betaPCR10; betaPCR10];
yfitPCR10 = [ones(n,1) X]*betaPCR10;
plot(y,yfitPLS10,'bo',y,yfitPCR10,'r^');
xlabel('Observed Response');
ylabel('Fitted Response');
legend({'PLSR with 10 components' 'PCR with 10 Components'},  ...
 'location','NW');
```



Both models fit y fairly accurately, although PLSR still makes a slightly more accurate fit. However, ten components is still an arbitrarily-chosen number for either model.

Choosing the Number of Components with Cross-Validation

It's often useful to choose the number of components to minimize the expected error when predicting the response from future observations on the predictor variables. Simply using a large number of components will do a good job in fitting the current observed data, but is a strategy that leads to overfitting. Fitting the current data too well results in a model that does not generalize well to other data, and gives an overly-optimistic estimate of the expected error.

Cross-validation is a more statistically sound method for choosing the number of components in either PLSR or PCR. It avoids overfitting data by not reusing the same data to both fit a model and to estimate prediction error. Thus, the estimate of prediction error is not optimistically biased downwards.

`plsregress` has an option to estimate the mean squared prediction error (MSEP) by cross-validation, in this case using 10-fold C-V.

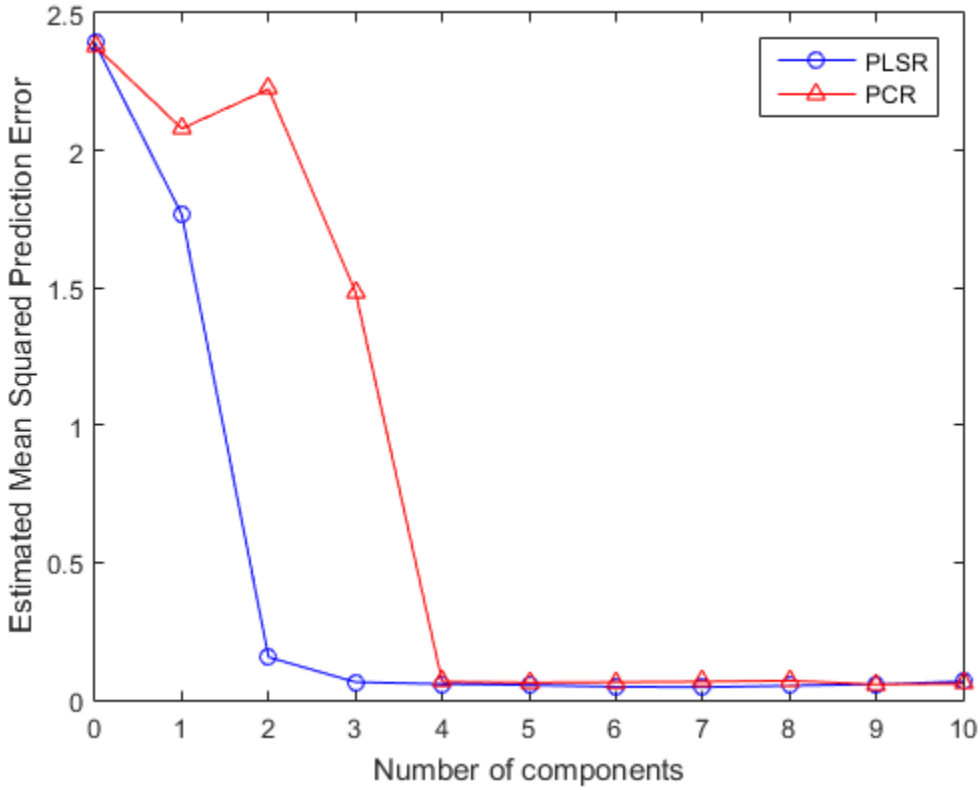
```
[Xl,Yl,Xs,Ys,beta,pctVar,PLSmsep] = plsregress(X,y,10,'CV',10);
```

For PCR, `crossval` combined with a simple function to compute the sum of squared errors for PCR, can estimate the MSEP, again using 10-fold cross-validation.

```
PCRmsep = sum(crossval(@pcrsse,X,y,'KFold',10),1) / n;
```

The MSEP curve for PLSR indicates that two or three components does about as good a job as possible. On the other hand, PCR needs four components to get the same prediction accuracy.

```
plot(0:10,PLSmsep(2,:),'b-o',0:10,PCRmsep,'r-^');
xlabel('Number of components');
ylabel('Estimated Mean Squared Prediction Error');
legend({'PLSR' 'PCR'},'location','NE');
```



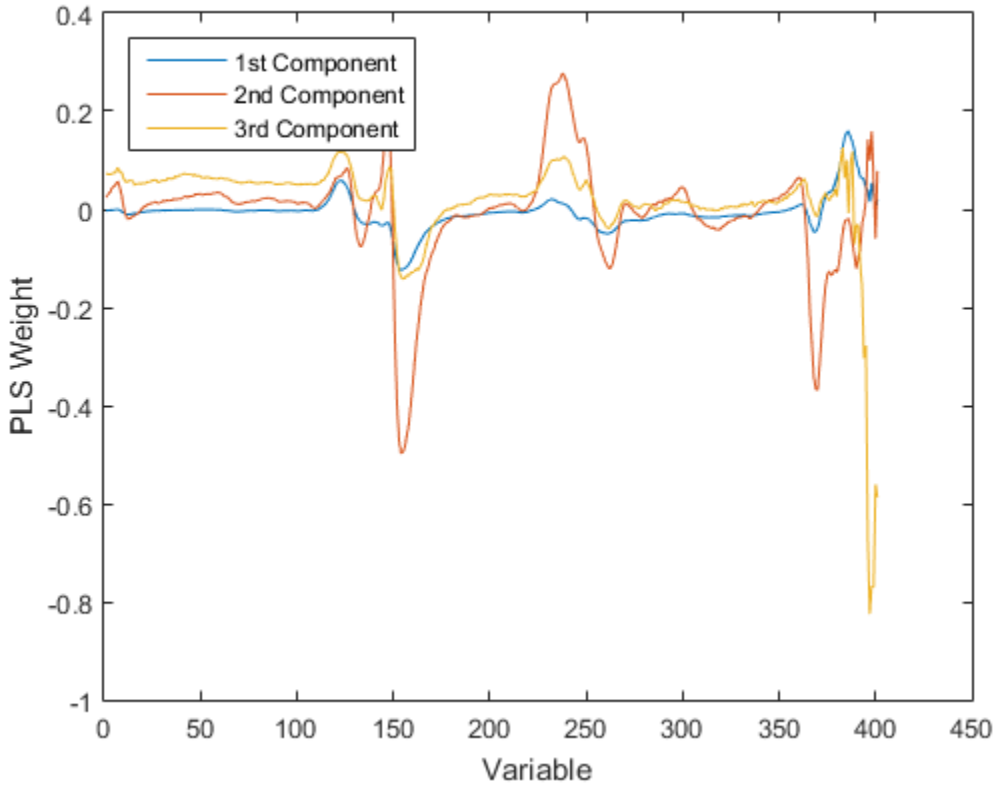
In fact, the second component in PCR *increases* the prediction error of the model, suggesting that the combination of predictor variables contained in that component is not strongly correlated with `y`. Again, that's because PCR constructs components to explain variation in `X`, not `y`.

Model Parsimony

So if PCR requires four components to get the same prediction accuracy as PLSR with three components, is the PLSR model more parsimonious? That depends on what aspect of the model you consider.

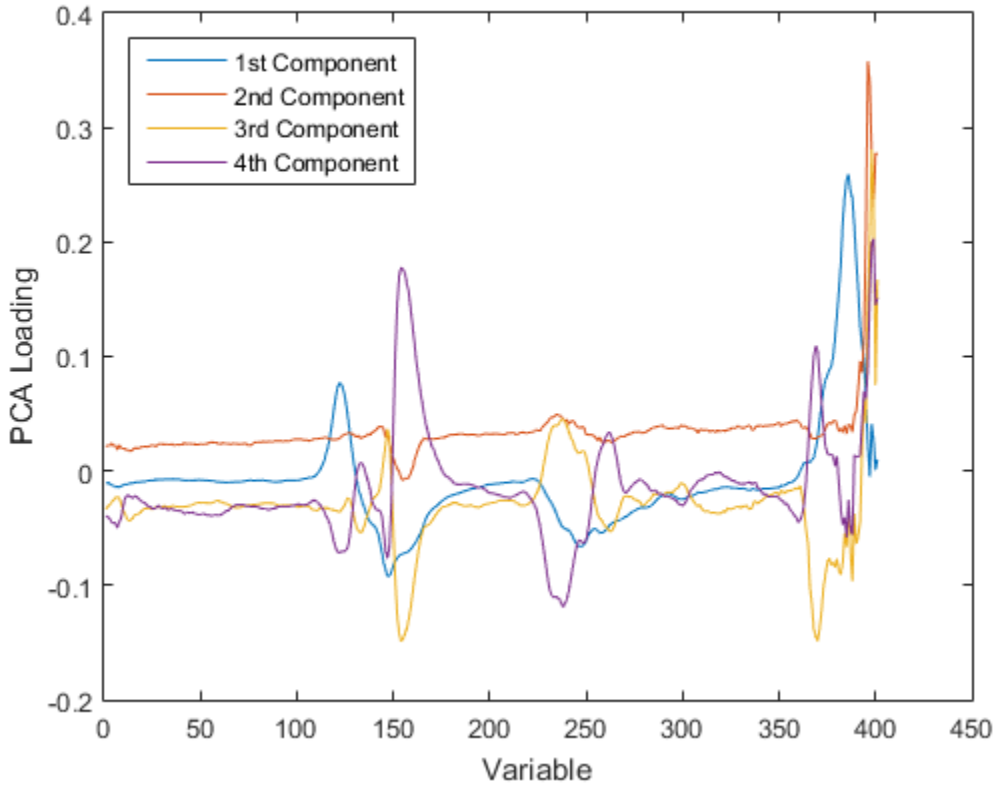
The PLS weights are the linear combinations of the original variables that define the PLS components, i.e., they describe how strongly each component in the PLSR depends on the original variables, and in what direction.

```
[Xl,Yl,Xs,Ys,beta,pctVar,mse,stats] = plsregress(X,y,3);
plot(1:401,stats.W,'-');
xlabel('Variable');
ylabel('PLS Weight');
legend({'1st Component' '2nd Component' '3rd Component'},  ...
 'location','NW');
```



Similarly, the PCA loadings describe how strongly each component in the PCR depends on the original variables.

```
plot(1:401,PCALoadings(:,1:4),'-');
xlabel('Variable');
ylabel('PCA Loading');
legend({'1st Component' '2nd Component' '3rd Component'  ...
 '4th Component'},'location','NW');
```



For either PLSR or PCR, it may be that each component can be given a physically meaningful interpretation by inspecting which variables it weights most heavily. For instance, with these spectral data it may be possible to interpret intensity peaks in terms of compounds present in the gasoline, and then to observe that weights for a particular component pick out a small number of those compounds. From that perspective, fewer components are simpler to interpret, and because PLSR often requires fewer components to predict the response adequately, it leads to more parsimonious models.

On the other hand, both PLSR and PCR result in one regression coefficient for each of the original predictor variables, plus an intercept. In that sense, neither is more parsimonious, because regardless of how many components are used, both models depend on all predictors. More concretely, for these data, both models need 401 spectral intensity values in order to make a prediction.

However, the ultimate goal may to reduce the original set of variables to a smaller subset still able to predict the response accurately. For example, it may be possible to use the PLS weights or the PCA loadings to select only those variables that contribute most to each component. As shown earlier, some components from a PCR model fit may serve primarily to describe the variation in the predictor variables, and may include large weights for variables that are not strongly correlated with the response. Thus, PCR can lead to retaining variables that are unnecessary for prediction.

For the data used in this example, the difference in the number of components needed by PLSR and PCR for accurate prediction is not great, and the PLS weights and PCA loadings seem to pick out the same variables. That may not be true for other data.

Cluster Analysis

Introduction to Cluster Analysis

Cluster analysis, also called *segmentation analysis* or *taxonomy analysis*, creates groups, or *clusters*, of data. Clusters are formed in such a way that objects in the same cluster are very similar and objects in different clusters are very distinct. Measures of similarity depend on the application.

"Hierarchical Clustering" on page 14-3 groups data over a variety of scales by creating a cluster tree or *dendrogram*. The tree is not a single set of clusters, but rather a multilevel hierarchy, where clusters at one level are joined as clusters at the next level. This allows you to decide the level or scale of clustering that is most appropriate for your application. The Statistics and Machine Learning Toolbox function `clusterdata` performs all of the necessary steps for you. It incorporates the `pdist`, `linkage`, and `cluster` functions, which may be used separately for more detailed analysis. The `dendrogram` function plots the cluster tree.

"*k*-Means Clustering" on page 14-21 is a partitioning method. The function `kmeans` partitions data into *k* mutually exclusive clusters, and returns the index of the cluster to which it has assigned each observation. Unlike hierarchical clustering, *k*-means clustering operates on actual observations (rather than the larger set of dissimilarity measures), and creates a single level of clusters. The distinctions mean that *k*-means clustering is often more suitable than hierarchical clustering for large amounts of data.

"Clustering Using Gaussian Mixture Models" on page 14-29 form clusters by representing the probability density function of observed variables as a mixture of multivariate normal densities. Mixture models of the `gmdistribution` class use an expectation maximization (EM) algorithm to fit data, which assigns posterior probabilities to each component density with respect to each observation. Clusters are assigned by selecting the component that maximizes the posterior probability. Clustering using Gaussian mixture models is sometimes considered a soft clustering method. The posterior probabilities for each point indicate that each data point has some probability of belonging to each cluster. Like *k*-means clustering, Gaussian mixture modeling uses an iterative algorithm that converges to a local optimum. Gaussian mixture modeling may be more appropriate than *k*-means clustering when clusters have different sizes and correlation within them.

Hierarchical Clustering

In this section...

Introduction to Hierarchical Clustering

Hierarchical clustering groups data over a variety of scales by creating a cluster tree or *dendrogram*. The tree is not a single set of clusters, but rather a multilevel hierarchy, where clusters at one level are joined as clusters at the next level. This allows you to decide the level or scale of clustering that is most appropriate for your application. The Statistics and Machine Learning Toolbox function `clusterdata` supports agglomerative clustering and performs all of the necessary steps for you. It incorporates the `pdist`, `linkage`, and `cluster` functions, which you can use separately for more detailed analysis. The `dendrogram` function plots the cluster tree.

Algorithm Description

To perform agglomerative hierarchical cluster analysis on a data set using Statistics and Machine Learning Toolbox functions, follow this procedure:

1. **Find the similarity or dissimilarity between every pair of objects in the data set.** In this step, you calculate the *distance* between objects using the `pdist` function. The `pdist` function supports many different ways to compute this measurement. See "Similarity Measures" on page 14-4 for more information.
2. **Group the objects into a binary, hierarchical cluster tree.** In this step, you link pairs of objects that are in close proximity using the `linkage` function. The `linkage` function uses the distance information generated in step 1 to determine the proximity of objects to each other. As objects are paired into binary clusters, the

newly formed clusters are grouped into larger clusters until a hierarchical tree is formed. See "Linkages" on page 14-6 for more information.

3 **Determine where to cut the hierarchical tree into clusters.** In this step, you use the `cluster` function to prune branches off the bottom of the hierarchical tree, and assign all the objects below each cut to a single cluster. This creates a partition of the data. The `cluster` function can create these clusters by detecting natural groupings in the hierarchical tree or by cutting off the hierarchical tree at an arbitrary point.

The following sections provide more information about each of these steps.

Note The Statistics and Machine Learning Toolbox function `clusterdata` performs all of the necessary steps for you. You do not need to execute the `pdist`, `linkage`, or `cluster` functions separately.

Similarity Measures

You use the `pdist` function to calculate the distance between every pair of objects in a data set. For a data set made up of m objects, there are $m*(m-1)/2$ pairs in the data set. The result of this computation is commonly known as a distance or dissimilarity matrix.

There are many ways to calculate this distance information. By default, the `pdist` function calculates the Euclidean distance between objects; however, you can specify one of several other options. See `pdist` for more information.

Note You can optionally normalize the values in the data set before calculating the distance information. In a real world data set, variables can be measured against different scales. For example, one variable can measure Intelligence Quotient (IQ) test scores and another variable can measure head circumference. These discrepancies can distort the proximity calculations. Using the `zscore` function, you can convert all the values in the data set to use the same proportional scale. See `zscore` for more information.

For example, consider a data set, `X`, made up of five objects where each object is a set of *x,y* coordinates.

- **Object 1**: 1, 2

- **Object 2**: 2.5, 4.5
- **Object 3**: 2, 2
- **Object 4**: 4, 1.5
- **Object 5**: 4, 2.5

You can define this data set as a matrix

```
rng default;  % For reproducibility
X = [1 2;2.5 4.5;2 2;4 1.5;...
    4 2.5];
```

and pass it to `pdist`. The `pdist` function calculates the distance between object 1 and object 2, object 1 and object 3, and so on until the distances between all the pairs have been calculated. The following figure plots these objects in a graph. The Euclidean distance between object 2 and object 3 is shown to illustrate one interpretation of distance.

Distance Information

The `pdist` function returns this distance information in a vector, `Y`, where each element contains the distance between a pair of objects.

```
Y = pdist(X)
```

```
Y =
```

```
  Columns 1 through 7

    2.9155    1.0000    3.0414    3.0414    2.5495    3.3541    2.5000

  Columns 8 through 10

    2.0616    2.0616    1.0000
```

To make it easier to see the relationship between the distance information generated by `pdist` and the objects in the original data set, you can reformat the distance vector into a matrix using the `squareform` function. In this matrix, element *i,j* corresponds to the distance between object *i* and object *j* in the original data set. In the following example, element 1,1 represents the distance between object 1 and itself (which is zero). Element 1,2 represents the distance between object 1 and object 2, and so on.

```
squareform(Y)
```

```
ans =

         0    2.9155    1.0000    3.0414    3.0414
    2.9155         0    2.5495    3.3541    2.5000
    1.0000    2.5495         0    2.0616    2.0616
    3.0414    3.3541    2.0616         0    1.0000
    3.0414    2.5000    2.0616    1.0000         0
```

Linkages

Once the proximity between objects in the data set has been computed, you can determine how objects in the data set should be grouped into clusters, using the `linkage` function. The `linkage` function takes the distance information generated by `pdist` and links pairs of objects that are close together into binary clusters (clusters made up of two objects). The `linkage` function then links these newly formed clusters to each other and to other objects to create bigger clusters until all the objects in the original data set are linked together in a hierarchical tree.

For example, given the distance vector `Y` generated by `pdist` from the sample data set of *x*- and *y*-coordinates, the `linkage` function generates a hierarchical cluster tree, returning the linkage information in a matrix, `Z`.

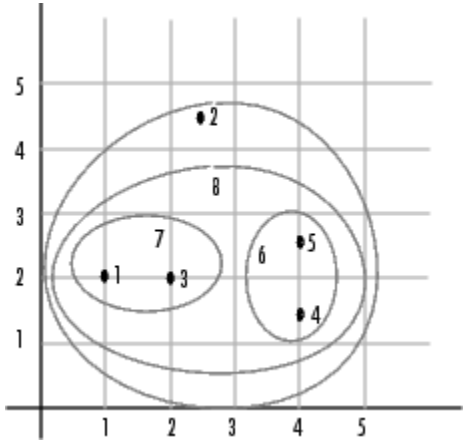
```
Z = linkage(Y)

Z =

    4.0000    5.0000    1.0000
    1.0000    3.0000    1.0000
    6.0000    7.0000    2.0616
    2.0000    8.0000    2.5000
```

In this output, each row identifies a link between objects or clusters. The first two columns identify the objects that have been linked. The third column contains the distance between these objects. For the sample data set of x- and y-coordinates, the `linkage` function begins by grouping objects 4 and 5, which have the closest proximity (distance value = 1.0000). The `linkage` function continues by grouping objects 1 and 3, which also have a distance value of 1.0000.

The third row indicates that the `linkage` function grouped objects 6 and 7. If the original sample data set contained only five objects, what are objects 6 and 7? Object 6 is the newly formed binary cluster created by the grouping of objects 4 and 5. When the `linkage` function groups two objects into a new cluster, it must assign the cluster a unique index value, starting with the value $m + 1$, where m is the number of objects in the original data set. (Values 1 through m are already used by the original data set.) Similarly, object 7 is the cluster formed by grouping objects 1 and 3.

`linkage` uses distances to determine the order in which it clusters objects. The distance vector `Y` contains the distances between the original objects 1 through 5. But linkage must also be able to determine distances involving clusters that it creates, such as objects 6 and 7. By default, `linkage` uses a method known as single linkage. However, there are a number of different methods available. See the `linkage` reference page for more information.

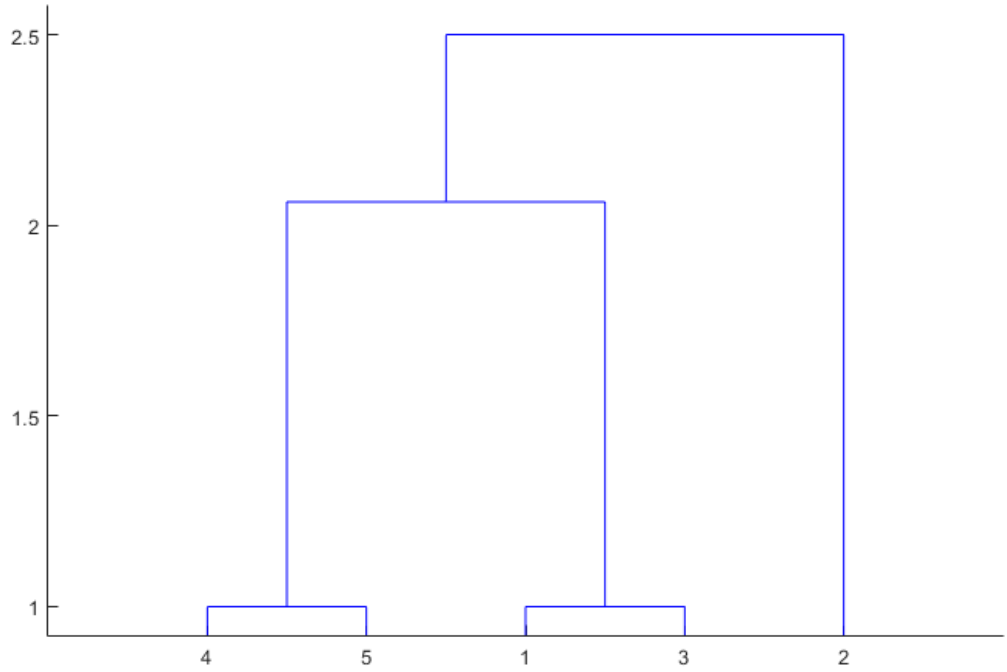
As the final cluster, the `linkage` function grouped object 8, the newly formed cluster made up of objects 6 and 7, with object 2 from the original data set. The following figure graphically illustrates the way `linkage` groups the objects into a hierarchy of clusters.



Dendrograms

The hierarchical, binary cluster tree created by the `linkage` function is most easily understood when viewed graphically. The Statistics and Machine Learning Toolbox function `dendrogram` plots the tree as follows.

```
dendrogram(Z)
```



In the figure, the numbers along the horizontal axis represent the indices of the objects in the original data set. The links between objects are represented as upside-down U-shaped lines. The height of the U indicates the distance between the objects. For example, the link representing the cluster containing objects 1 and 3 has a height of 1. The link representing the cluster that groups object 2 together with objects 1, 3, 4, and 5, (which are already clustered as object 8) has a height of 2.5. The height represents the distance `linkage` computes between objects 2 and 8. For more information about creating a dendrogram diagram, see the `dendrogram` reference page.

Verify the Cluster Tree

After linking the objects in a data set into a hierarchical cluster tree, you might want to verify that the distances (that is, heights) in the tree reflect the original distances accurately. In addition, you might want to investigate natural divisions that exist among

links between objects. Statistics and Machine Learning Toolbox functions are available for both of these tasks, as described in the following sections.

Verify Dissimilarity

In a hierarchical cluster tree, any two objects in the original data set are eventually linked together at some level. The height of the link represents the distance between the two clusters that contain those two objects. This height is known as the *cophenetic distance* between the two objects. One way to measure how well the cluster tree generated by the `linkage` function reflects your data is to compare the cophenetic distances with the original distance data generated by the `pdist` function. If the clustering is valid, the linking of objects in the cluster tree should have a strong correlation with the distances between objects in the distance vector. The `cophenet` function compares these two sets of values and computes their correlation, returning a value called the *cophenetic correlation coefficient*. The closer the value of the cophenetic correlation coefficient is to 1, the more accurately the clustering solution reflects your data.

You can use the cophenetic correlation coefficient to compare the results of clustering the same data set using different distance calculation methods or clustering algorithms. For example, you can use the `cophenet` function to evaluate the clusters created for the sample data set.

```
c = cophenet(Z,Y)
```

```
c =

    0.8615
```

`Z` is the matrix output by the `linkage` function and `Y` is the distance vector output by the `pdist` function.

Execute `pdist` again on the same data set, this time specifying the city block metric. After running the `linkage` function on this new `pdist` output using the average linkage method, call `cophenet` to evaluate the clustering solution.

```
Y = pdist(X,'cityblock');
```

```
Z = linkage(Y,'average');
c = cophenet(Z,Y)


c =

    0.9047
```

The cophenetic correlation coefficient shows that using a different distance and linkage method creates a tree that represents the original distances slightly better.

Verify Consistency

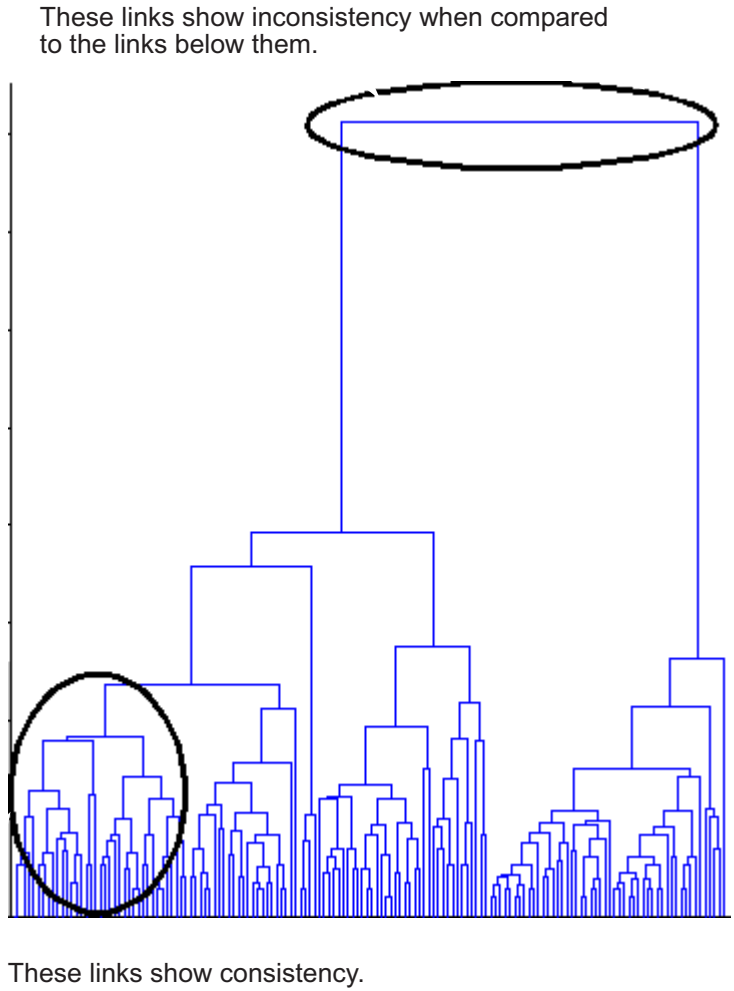
One way to determine the natural cluster divisions in a data set is to compare the height of each link in a cluster tree with the heights of neighboring links below it in the tree.

A link that is approximately the same height as the links below it indicates that there are no distinct divisions between the objects joined at this level of the hierarchy. These links are said to exhibit a high level of consistency, because the distance between the objects being joined is approximately the same as the distances between the objects they contain.

On the other hand, a link whose height differs noticeably from the height of the links below it indicates that the objects joined at this level in the cluster tree are much farther apart from each other than their components were when they were joined. This link is said to be inconsistent with the links below it.

In cluster analysis, inconsistent links can indicate the border of a natural division in a data set. The `cluster` function uses a quantitative measure of inconsistency to determine where to partition your data set into clusters.

The following dendrogram illustrates inconsistent links. Note how the objects in the dendrogram fall into two groups that are connected by links at a much higher level in the tree. These links are inconsistent when compared with the links below them in the hierarchy.



The relative consistency of each link in a hierarchical cluster tree can be quantified and expressed as the *inconsistency coefficient*. This value compares the height of a link in a cluster hierarchy with the average height of links below it. Links that join distinct clusters have a high inconsistency coefficient; links that join indistinct clusters have a low inconsistency coefficient.

To generate a listing of the inconsistency coefficient for each link in the cluster tree, use the `inconsistent` function. By default, the `inconsistent` function compares each

link in the cluster hierarchy with adjacent links that are less than two levels below it in the cluster hierarchy. This is called the *depth* of the comparison. You can also specify other depths. The objects at the bottom of the cluster tree, called leaf nodes, that have no further objects below them, have an inconsistency coefficient of zero. Clusters that join two leaves also have a zero inconsistency coefficient.

For example, you can use the `inconsistent` function to calculate the inconsistency values for the links created by the `linkage` function in "Linkages" on page 14-6.

First, recompute the distance and linkage values using the default settings.

```
Y = pdist(X);
Z = linkage(Y);
```

Next, use `inconsistent` to calculate the inconsistency values.

```
I = inconsistent(Z)
```

```
I =

    1.0000         0    1.0000         0
    1.0000         0    1.0000         0
    1.3539    0.6129    3.0000    1.1547
    2.2808    0.3100    2.0000    0.7071
```

The `inconsistent` function returns data about the links in an (m-1)-by-4 matrix, whose columns are described in the following table.

Column	Description
1	Mean of the heights of all the links included in the calculation
2	Standard deviation of all the links included in the calculation
3	Number of links included in the calculation
4	Inconsistency coefficient

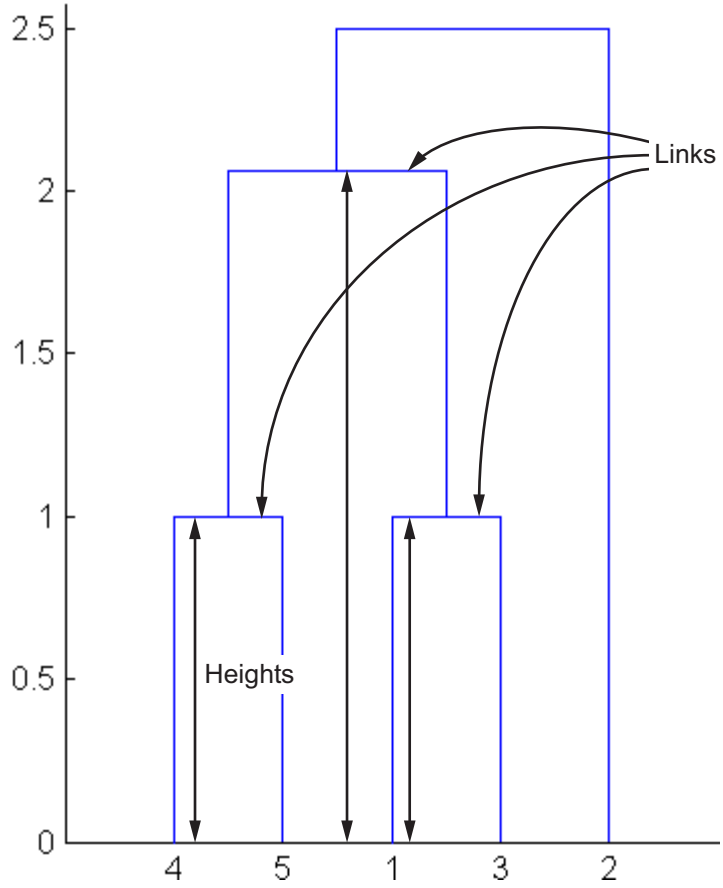
In the sample output, the first row represents the link between objects 4 and 5. This cluster is assigned the index 6 by the `linkage` function. Because both 4 and 5 are leaf nodes, the inconsistency coefficient for the cluster is zero. The second row represents the link between objects 1 and 3, both of which are also leaf nodes. This cluster is assigned the index 7 by the linkage function.

The third row evaluates the link that connects these two clusters, objects 6 and 7. (This new cluster is assigned index 8 in the `linkage` output). Column 3 indicates that three links are considered in the calculation: the link itself and the two links directly below it in the hierarchy. Column 1 represents the mean of the heights of these links. The `inconsistent` function uses the height information output by the `linkage` function to calculate the mean. Column 2 represents the standard deviation between the links. The last column contains the inconsistency value for these links, 1.1547. It is the difference between the current link height and the mean, normalized by the standard deviation.

```
(2.0616 - 1.3539) / .6129
```

```
ans =

    1.1547
```

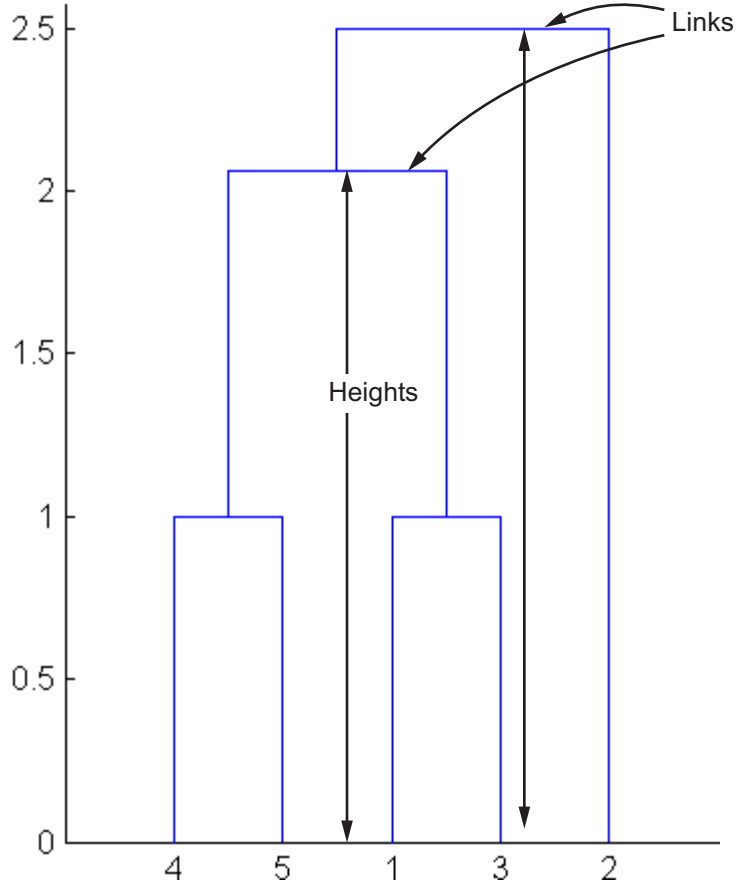
The following figure illustrates the links and heights included in this calculation.



Note In the preceding figure, the lower limit on the *y*-axis is set to `0` to show the heights of the links. To set the lower limit to `0`, select `Axes Properties` from the **Edit** menu, click the **Y Axis** tab, and enter `0` in the field immediately to the right of **Y Limits**.

Row 4 in the output matrix describes the link between object 8 and object 2. Column 3 indicates that two links are included in this calculation: the link itself and the link directly below it in the hierarchy. The inconsistency coefficient for this link is 0.7071.

The following figure illustrates the links and heights included in this calculation.



Create Clusters

After you create the hierarchical tree of binary clusters, you can prune the tree to partition your data into clusters using the `cluster` function. The `cluster` function lets you create clusters in two ways, as discussed in the following sections:

- "Find Natural Divisions in Data" on page 14-17
- "Specify Arbitrary Clusters" on page 14-18

Find Natural Divisions in Data

The hierarchical cluster tree may naturally divide the data into distinct, well-separated clusters. This can be particularly evident in a dendrogram diagram created from data where groups of objects are densely packed in certain areas and not in others. The inconsistency coefficient of the links in the cluster tree can identify these divisions where the similarities between objects change abruptly. (See “Verify the Cluster Tree” on page 14-9 for more information about the inconsistency coefficient.) You can use this value to determine where the `cluster` function creates cluster boundaries.

For example, if you use the `cluster` function to group the sample data set into clusters, specifying an inconsistency coefficient threshold of `1.2` as the value of the `cutoff` argument, the `cluster` function groups all the objects in the sample data set into one cluster. In this case, none of the links in the cluster hierarchy had an inconsistency coefficient greater than `1.2`.

```
T = cluster(Z,'cutoff',1.2)
```

```
T =

     1
     1
     1
     1
     1
```

The `cluster` function outputs a vector, `T`, that is the same size as the original data set. Each element in this vector contains the number of the cluster into which the corresponding object from the original data set was placed.

If you lower the inconsistency coefficient threshold to `0.8`, the `cluster` function divides the sample data set into three separate clusters.

```
T = cluster(Z,'cutoff',0.8)
```

```
T =

     3
     2
     3
```

```
     1
     1
```

This output indicates that objects 1 and 3 are in one cluster, objects 4 and 5 are in another cluster, and object 2 is in its own cluster.

When clusters are formed in this way, the cutoff value is applied to the inconsistency coefficient. These clusters may, but do not necessarily, correspond to a horizontal slice across the dendrogram at a certain height. If you want clusters corresponding to a horizontal slice of the dendrogram, you can either use the `criterion` option to specify that the cutoff should be based on distance rather than inconsistency, or you can specify the number of clusters directly as described in the following section.

Specify Arbitrary Clusters

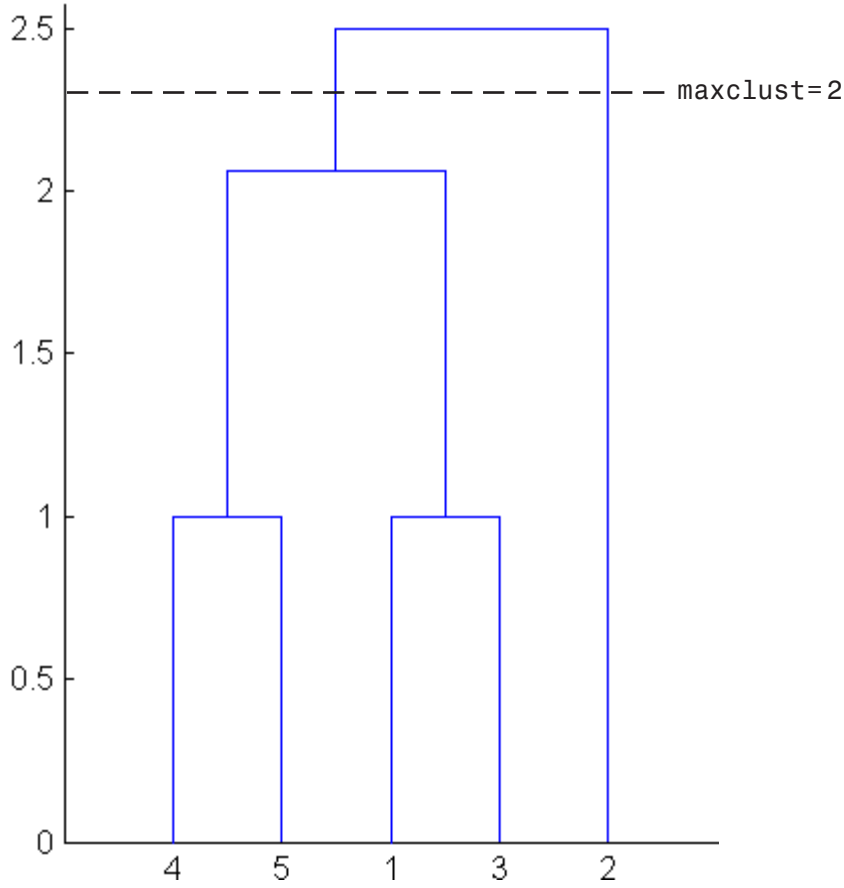
Instead of letting the `cluster` function create clusters determined by the natural divisions in the data set, you can specify the number of clusters you want created.

For example, you can specify that you want the `cluster` function to partition the sample data set into two clusters. In this case, the `cluster` function creates one cluster containing objects 1, 3, 4, and 5 and another cluster containing object 2.

```
T = cluster(Z,'maxclust',2)
```

```
T =

     2
     1
     2
     2
     2
```

To help you visualize how the `cluster` function determines these clusters, the following figure shows the dendrogram of the hierarchical cluster tree. The horizontal dashed line intersects two lines of the dendrogram, corresponding to setting `'maxclust'` to `2`. These two lines partition the objects into two clusters: the objects below the left-hand line, namely 1, 3, 4, and 5, belong to one cluster, while the object below the right-hand line, namely 2, belongs to the other cluster.



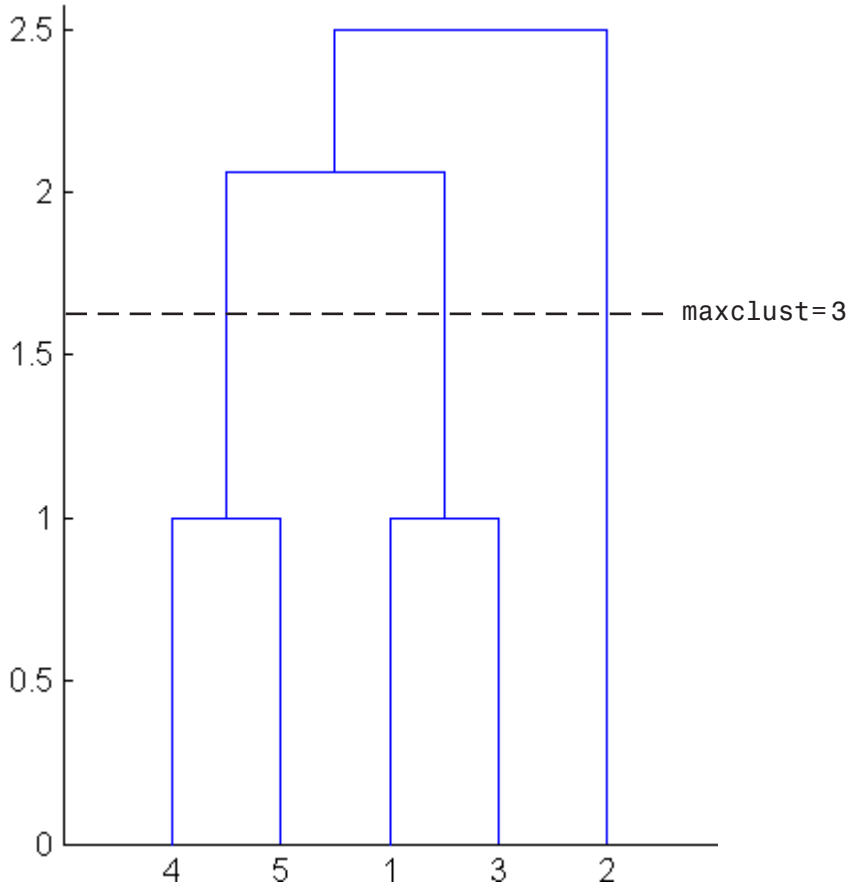
On the other hand, if you set `'maxclust'` to `3`, the cluster function groups objects 4 and 5 in one cluster, objects 1 and 3 in a second cluster, and object 2 in a third cluster. The following command illustrates this.

```
T = cluster(Z,'maxclust',3)
```

```
T =

     2
     3
     2
     1
```

```
     1
```

This time, the `cluster` function cuts off the hierarchy at a lower point, corresponding to the horizontal line that intersects three lines of the dendrogram in the following figure.



k-Means Clustering

In this section...

Introduction to *k*-Means Clustering

k-means clustering is a partitioning method. The function `kmeans` partitions data into *k* mutually exclusive clusters, and returns the index of the cluster to which it has assigned each observation. Unlike hierarchical clustering, *k*-means clustering operates on actual observations (rather than the larger set of dissimilarity measures), and creates a single level of clusters. The distinctions mean that *k*-means clustering is often more suitable than hierarchical clustering for large amounts of data.

`kmeans` treats each observation in your data as an object having a location in space. It finds a partition in which objects within each cluster are as close to each other as possible, and as far from objects in other clusters as possible. You can choose from five different distance measures, depending on the kind of data you are clustering.

Each cluster in the partition is defined by its member objects and by its centroid, or center. The centroid for each cluster is the point to which the sum of distances from all objects in that cluster is minimized. `kmeans` computes cluster centroids differently for each distance measure, to minimize the sum with respect to the measure that you specify.

`kmeans` uses an iterative algorithm that minimizes the sum of distances from each object to its cluster centroid, over all clusters. This algorithm moves objects between clusters until the sum cannot be decreased further. The result is a set of clusters that are as compact and well-separated as possible. You can control the details of the minimization using several optional input parameters to `kmeans`, including ones for the initial values of the cluster centroids, and for the maximum number of iterations. By default, `kmeans` uses the *k*-means++ algorithm for cluster center initialization and the squared Euclidean metric to determine distances.

Create Clusters and Determine Separation

The following example explores possible clustering in four-dimensional data by analyzing the results of partitioning the points into three, four, and five clusters.

Note Because each part of this example generates random numbers sequentially, i.e., without setting a new state, you must perform all steps in sequence to duplicate the results shown. If you perform the steps out of sequence, the answers will be essentially the same, but the intermediate results, number of iterations, or ordering of the silhouette plots may differ.

First, load some data.

```
rng default;  % For reproducibility
load kmeansdata;
size(X)
```

```
ans =

   560     4
```

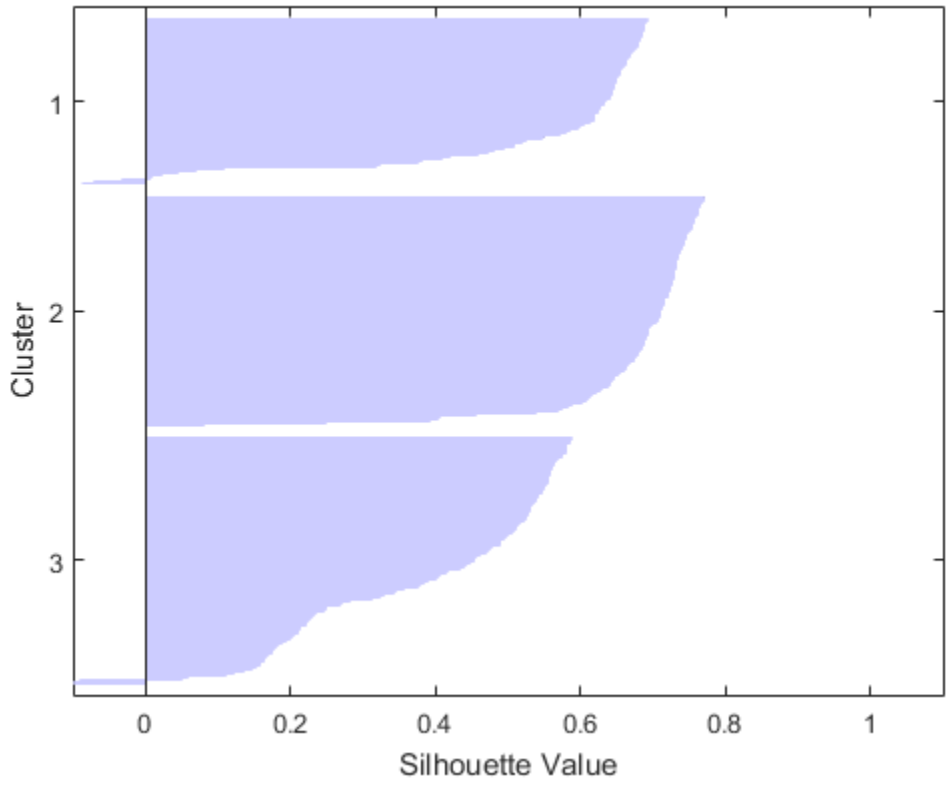
Even though these data are four-dimensional, and cannot be easily visualized, `kmeans` enables you to investigate whether a group structure exists in them. Call `kmeans` with `k`, the desired number of clusters, equal to `3`. For this example, specify the city block distance measure, and use the default *k*-means++ algorithm for cluster center initialization.

```
idx3 = kmeans(X,3,'Distance','cityblock');
```

To get an idea of how well-separated the resulting clusters are, you can make a silhouette plot using the cluster indices output from `kmeans`. The silhouette plot displays a measure of how close each point in one cluster is to points in the neighboring clusters. This measure ranges from +1, indicating points that are very distant from neighboring clusters, through 0, indicating points that are not distinctly in one cluster or another, to -1, indicating points that are probably assigned to the wrong cluster. `silhouette` returns these values in its first output.

```
figure;
```

```
[silh3,h] = silhouette(X,idx3,'cityblock');
h = gca;
h.Children.EdgeColor = [.8 .8 1];
xlabel 'Silhouette Value';
ylabel 'Cluster';
```



From the silhouette plot, you can see that most points in the second cluster have a large silhouette value, greater than 0.6, indicating that the cluster is somewhat separated from neighboring clusters. However, the third cluster contains many points with low silhouette values, and the first contains a few points with negative values, indicating that those two clusters are not well separated.

Determine the Correct Number of Clusters

Increase the number of clusters to see if `kmeans` can find a better grouping of the data. This time, use the `'Display'` name-value pair argument to print information about each iteration.

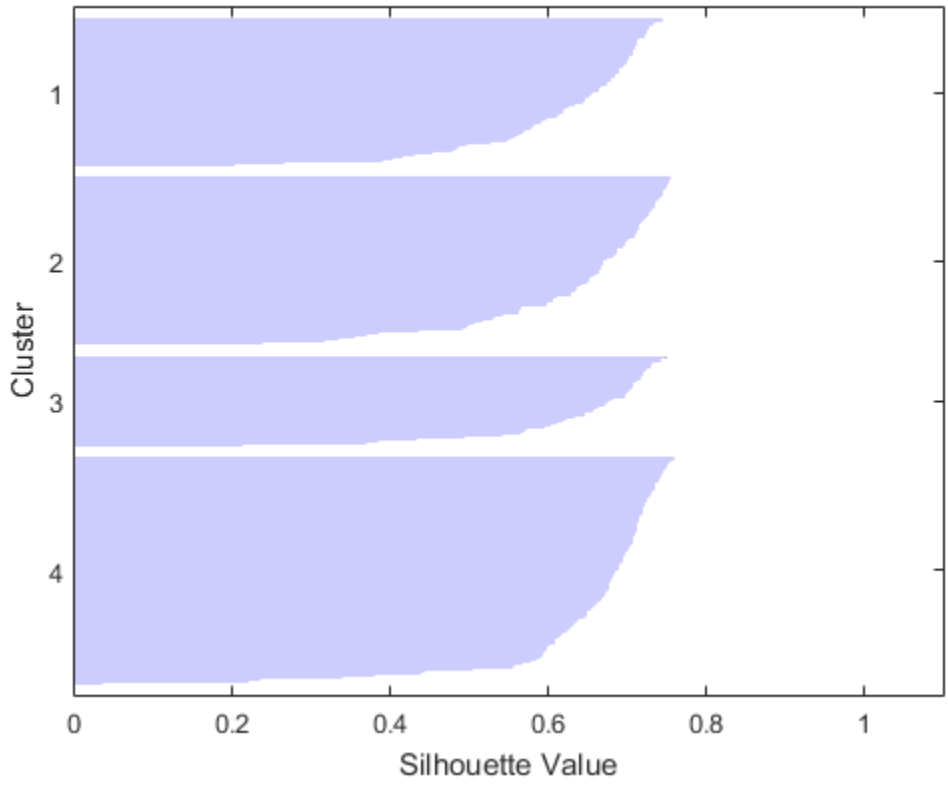
```
idx4 = kmeans(X,4, 'Distance','cityblock','Display','iter');
```

```
  iter  phase      num          sum
     1      1      560      1792.72
     2      1        6       1771.1
     3      2        0       1771.1
Best total sum of distances = 1771.1
```

Notice that the total sum of distances decreases at each iteration as `kmeans` reassigns points between clusters and recomputes cluster centroids. In this case, the second phase of the algorithm did not make any reassignments, indicating that the first phase reached a minimum after five iterations. In some problems, the first phase might not reach a minimum, but the second phase always will.

A silhouette plot for this solution indicates that these four clusters are better separated than the three in the previous solution.

```
figure;
[silh4,h] = silhouette(X,idx4,'cityblock');
h = gca;
h.Children.EdgeColor = [.8 .8 1];
xlabel 'Silhouette Value';
ylabel 'Cluster';
```



A more quantitative way to compare the two solutions is to look at the average silhouette values for the two cases.

```
cluster3 = mean(silh3)
cluster4 = mean(silh4)
```

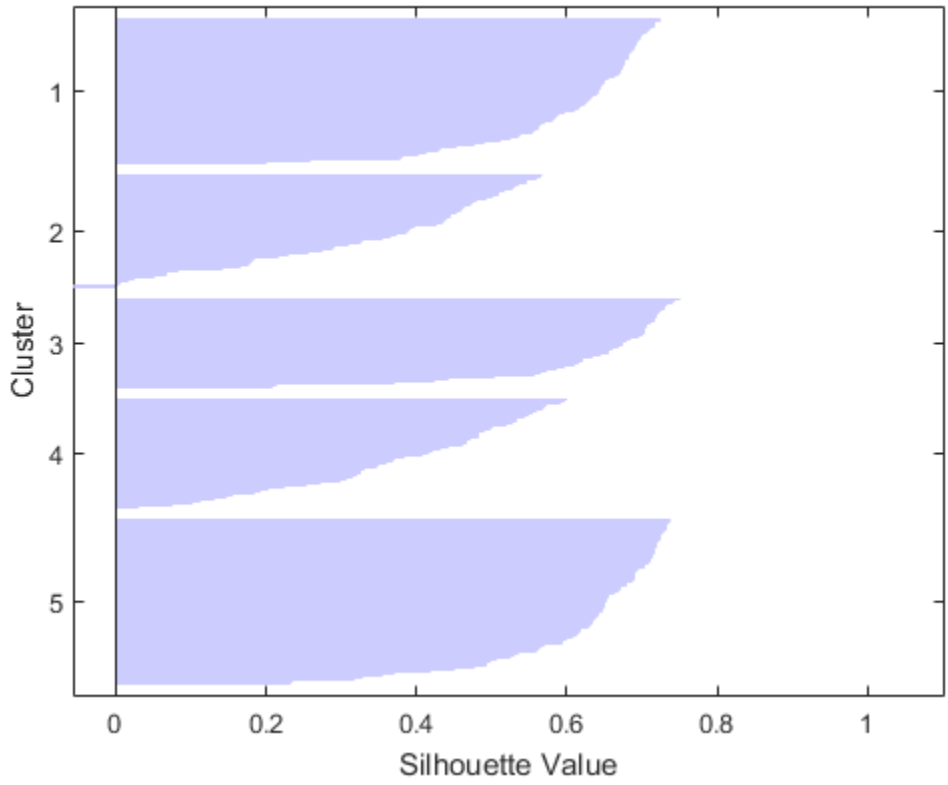
```
cluster3 =

    0.5352


cluster4 =
```

```
    0.6400
```

Finally, try clustering the data using five clusters.

```
idx5 = kmeans(X,5,'Distance','cityblock','Replicates',5);
figure;
[silh5,h] = silhouette(X,idx5,'city');
h = gca;
h.Children.EdgeColor = [.8 .8 1];
xlabel 'Silhouette Value';
ylabel 'Cluster';
mean(silh5)
```

```
ans =

    0.5266
```



This silhouette plot indicates that this is probably not the right number of clusters, since two of the clusters contain points with mostly low silhouette values. Without some knowledge of how many clusters are really in the data, it is a good idea to experiment with a range of values for `k`.

Avoid Local Minima

Like many other types of numerical minimizations, the solution that `kmeans` reaches often depends on the starting points. It is possible for `kmeans` to reach a local minimum, where reassigning any one point to a new cluster would increase the total sum of point-to-centroid distances, but where a better solution does exist. However, you can use the `'Replicates'` name-value pair argument to overcome that problem.

For four clusters, specify five replicates, and use the `'Display'` name-value pair argument to print out the final sum of distances for each of the solutions.

```
[idx4,cent4,sumdist] = kmeans(X,4,'Distance','cityblock',...
                       'Display','final','Replicates',5);
```

```
Replicate 1, 5 iterations, total sum of distances = 1771.1.
Replicate 2, 3 iterations, total sum of distances = 1771.1.
Replicate 3, 7 iterations, total sum of distances = 2303.36.
Replicate 4, 6 iterations, total sum of distances = 2303.36.
Replicate 5, 7 iterations, total sum of distances = 1771.1.
Best total sum of distances = 1771.1
```

In this example, `kmeans` found the same minimum in all five replications. However, even for relatively simple problems, nonglobal minima do exist. Each of these five replicates began from a different randomly selected set of initial centroids, so sometimes `kmeans` finds more than one local minimum. However, the final solution that `kmeans` returns is the one with the lowest total sum of distances, over all replicates.

```
sum(sumdist)
```

```
ans =

   1.7711e+03
```

Clustering Using Gaussian Mixture Models

In this section...

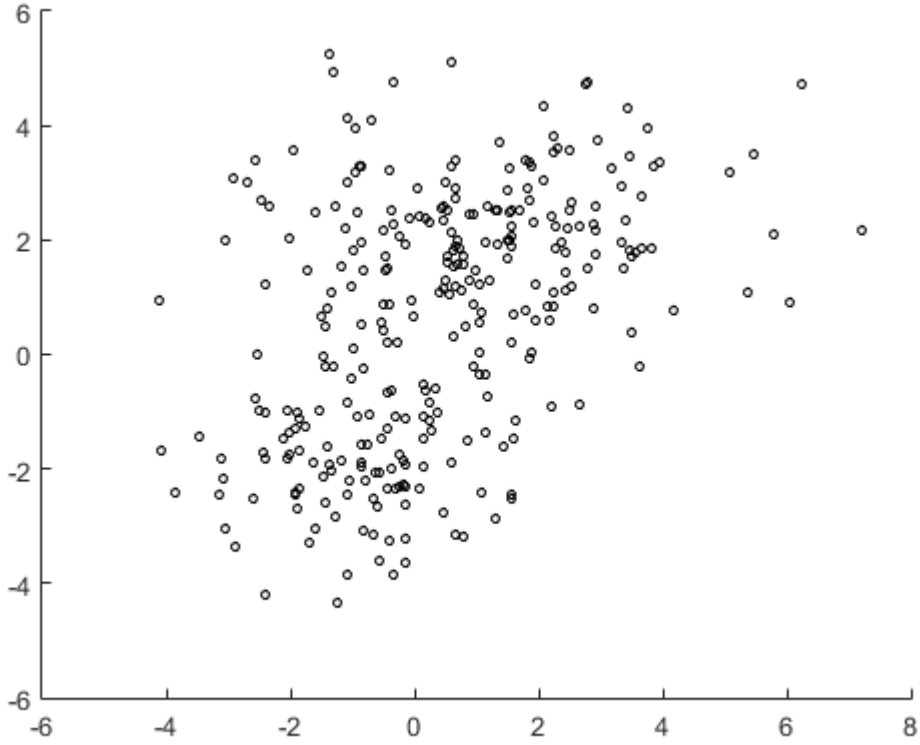
Gaussian mixture models are often used for data clustering. Clusters are assigned by selecting the component that maximizes the posterior probability. Like *k*-means clustering, Gaussian mixture modeling uses an iterative algorithm that converges to a local optimum. Gaussian mixture modeling may be more appropriate than *k*-means clustering when clusters have different sizes and correlation within them. Clustering using Gaussian mixture models is sometimes considered a soft clustering method. The posterior probabilities for each point indicate that each data point has some probability of belonging to each cluster.

Clustering Using Gaussian Mixture Distributions

Gaussian mixture distributions can be used for clustering data, by realizing that the multivariate normal components of the fitted model can represent clusters.

1 To demonstrate the process, first generate some simulated data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function.

```
rng default;  % For reproducibility
mu1 = [1 2];
sigma1 = [3 .2; .2 2];
mu2 = [-1 -2];
sigma2 = [2 0; 0 1];
X = [mvnrnd(mu1,sigma1,200);mvnrnd(mu2,sigma2,100)];

scatter(X(:,1),X(:,2),10,'ko')
```



2 Fit a two-component Gaussian mixture distribution. Here, you know the correct number of components to use. In practice, with real data, this decision would require comparing models with different numbers of components.

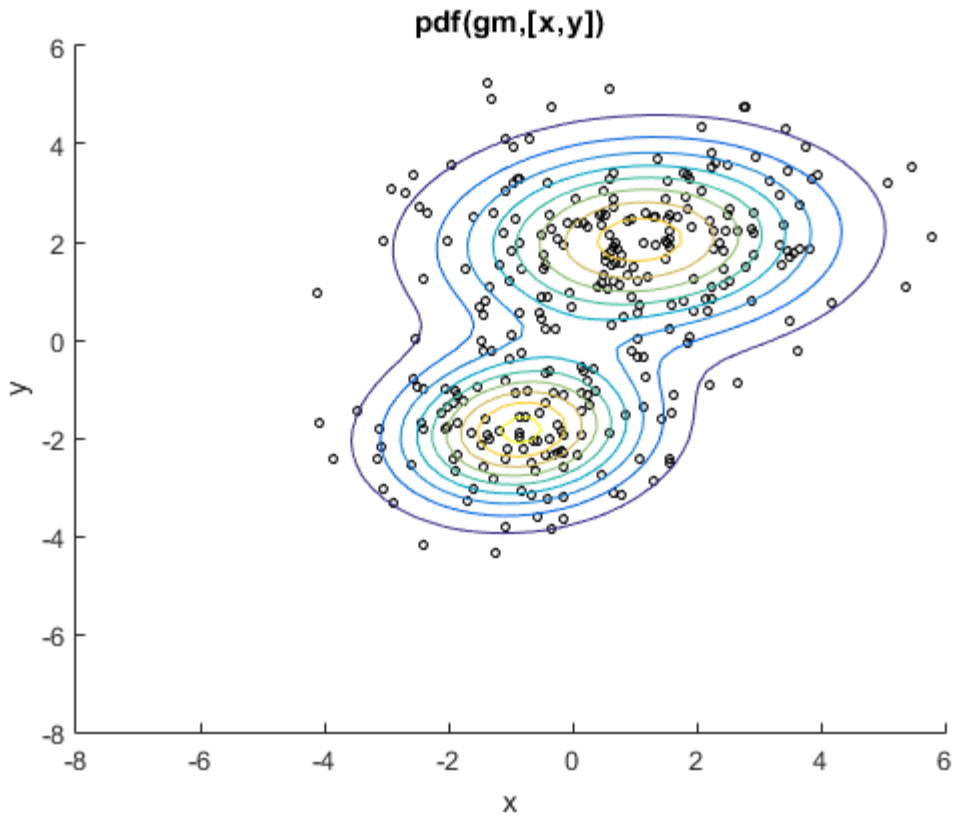
```
options = statset('Display','final');
gm = fitgmdist(X,2,'Options',options);
```

```
33 iterations, log-likelihood = -1210.59
```

3 Plot the estimated probability density contours for the two-component mixture distribution. The two bivariate normal components overlap, but their peaks are distinct. This suggests that the data could reasonably be divided into two clusters.

```
hold on
```

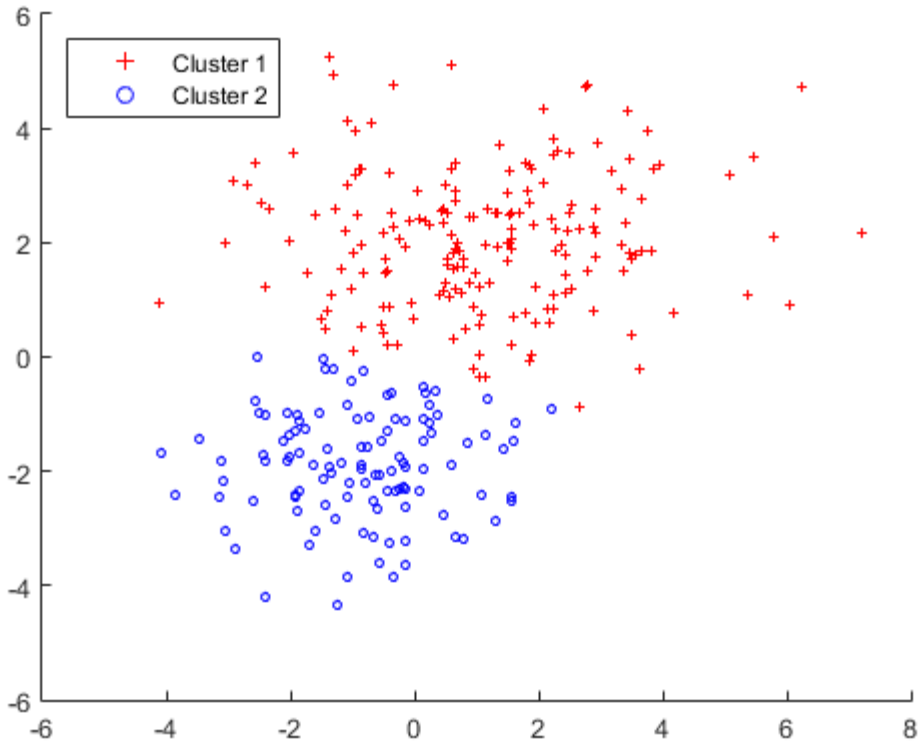
```
ezcontour(@(x,y)pdf(gm,[x y]),[-8 6],[-8 6]);
hold off
```



4 Partition the data into clusters using the `cluster` method for the fitted mixture distribution. The `cluster` method assigns each point to one of the two components in the mixture distribution.

```
idx = cluster(gm,X);
cluster1 = (idx == 1);
cluster2 = (idx == 2);

scatter(X(cluster1,1),X(cluster1,2),10,'r+');
hold on
scatter(X(cluster2,1),X(cluster2,2),10,'bo');
```

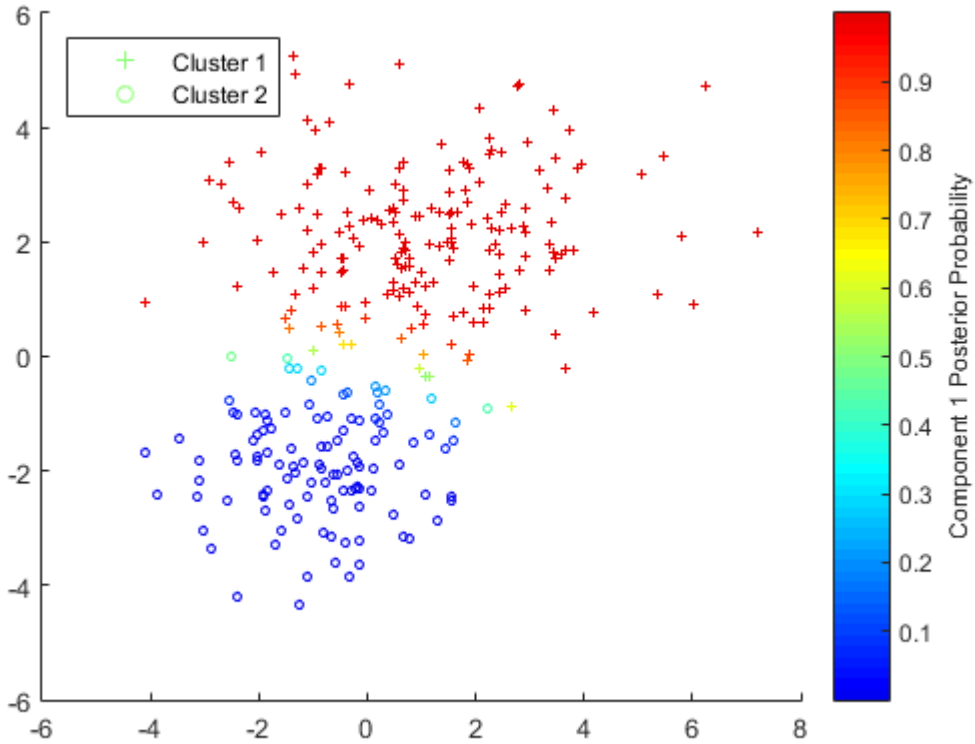
```
hold off
legend('Cluster 1','Cluster 2','Location','NW')
```



Each cluster corresponds to one of the bivariate normal components in the mixture distribution. `cluster` assigns points to clusters based on the estimated posterior probability that a point came from a component; each point is assigned to the cluster corresponding to the highest posterior probability. The posterior method returns those `posterior` probabilities. For example, plot the posterior probability of the first component for each point.

```
P = posterior(gm,X);

scatter(X(cluster1,1),X(cluster1,2),10,P(cluster1,1),'+')
```

```
hold on
scatter(X(cluster2,1),X(cluster2,2),10,P(cluster2,1),'o')
hold off
legend('Cluster 1','Cluster 2','Location','NW')
clrmap = jet(80); colormap(clrmap(9:72,:))
ylabel(colorbar,'Component 1 Posterior Probability')
```

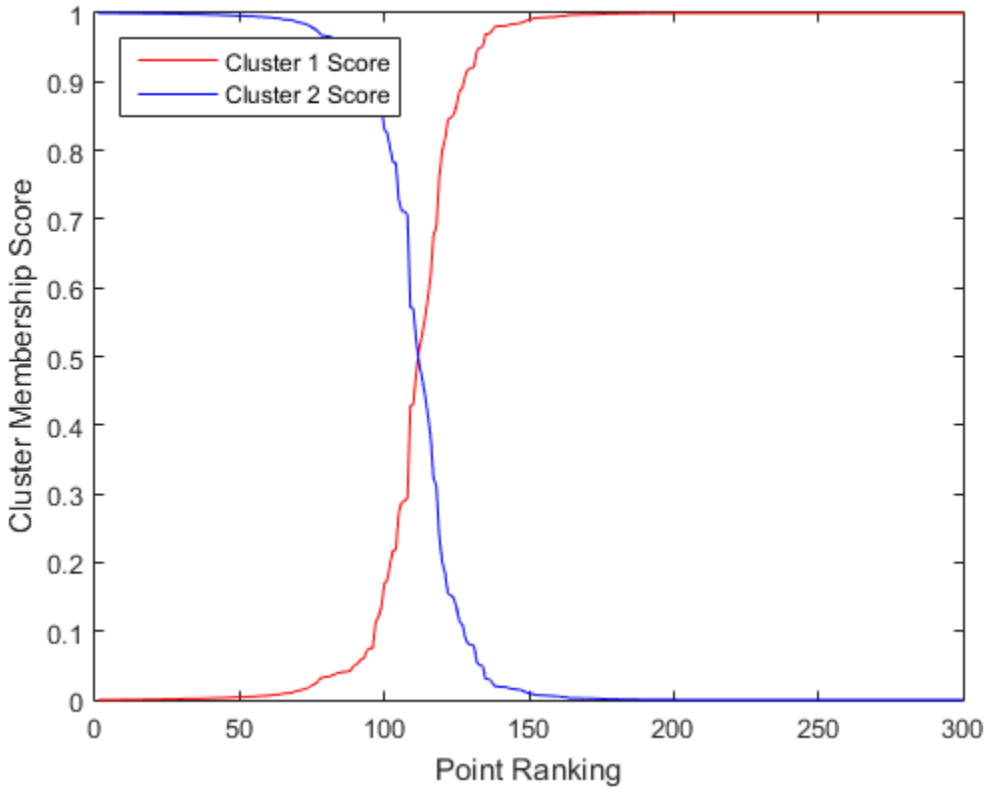


Soft Clustering Using Gaussian Mixture Distributions

An alternative to the previous example is to use the posterior probabilities for "soft clustering". Each point is assigned a membership score to each cluster. Membership scores are simply the posterior probabilities, and describe how similar each point is to

each cluster's archetype, i.e., the mean of the corresponding component. The points can be ranked by their membership score in a given cluster.

```
[~,order] = sort(P(:,1));
plot(1:size(X,1),P(order,1),'r-',1:size(X,1),P(order,2),'b-');
legend({'Cluster 1 Score' 'Cluster 2 Score'},'location','NW');
ylabel('Cluster Membership Score');
xlabel('Point Ranking');
```



Although a clear separation of the data is hard to see in a scatter plot of the data, plotting the membership scores indicates that the fitted distribution does a good job of separating the data into groups. Very few points have scores close to 0.5.

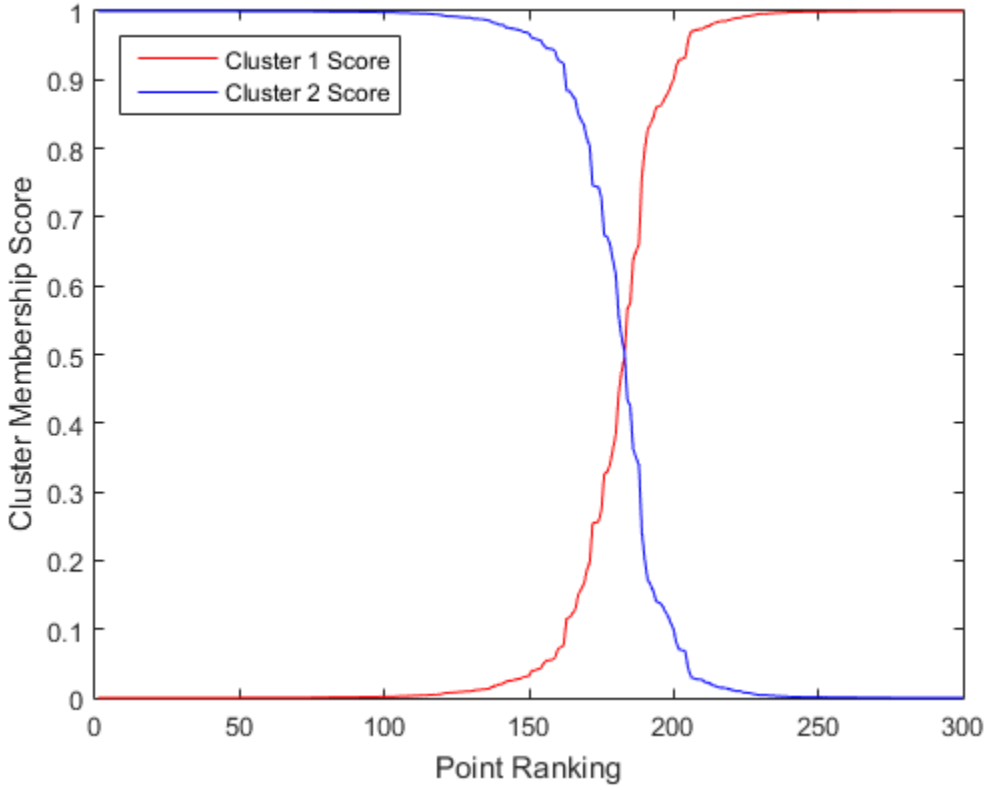
Soft clustering using a Gaussian mixture distribution is similar to fuzzy *k*-means clustering, which also assigns each point to each cluster with a membership score. The fuzzy *k*-means algorithm assumes that clusters are roughly spherical in shape, and all of roughly equal size. This is comparable to a Gaussian mixture distribution with a single covariance matrix that is shared across all components, and is a multiple of the identity matrix. In contrast, `gmdistribution` allows you to specify different covariance options. The default is to estimate a separate, unconstrained covariance matrix for each component. A more restricted option, closer to *k*-means, would be to estimate a shared, diagonal covariance matrix.

```
gm2 = fitgmdist(X,2,'CovType','Diagonal',...
  'SharedCov',true);
```

This covariance option is similar to fuzzy *k*-means clustering, but provides more flexibility by allowing unequal variances for different variables.

You can compute the soft cluster membership scores without computing hard cluster assignments, using `posterior`, or as part of hard clustering, as the third output from `cluster`.

```
P2 = posterior(gm2,X); % equivalently [idx,~,P2] = cluster(gm2,X)
[~,order] = sort(P2(:,1));
plot(1:size(X,1),P2(order,1),'r-',1:size(X,1),P2(order,2),'b-');
legend({'Cluster 1 Score' 'Cluster 2 Score'},'location','NW');
ylabel('Cluster Membership Score');
xlabel('Point Ranking');
```



Assign New Data to Clusters

In the previous example, fitting the mixture distribution to data using `fitgmdist`, and clustering those data using `cluster`, are separate steps. However, the same data are used in both steps. You can also use the `cluster` method to assign new data points to the clusters (mixture components) found in the original data.

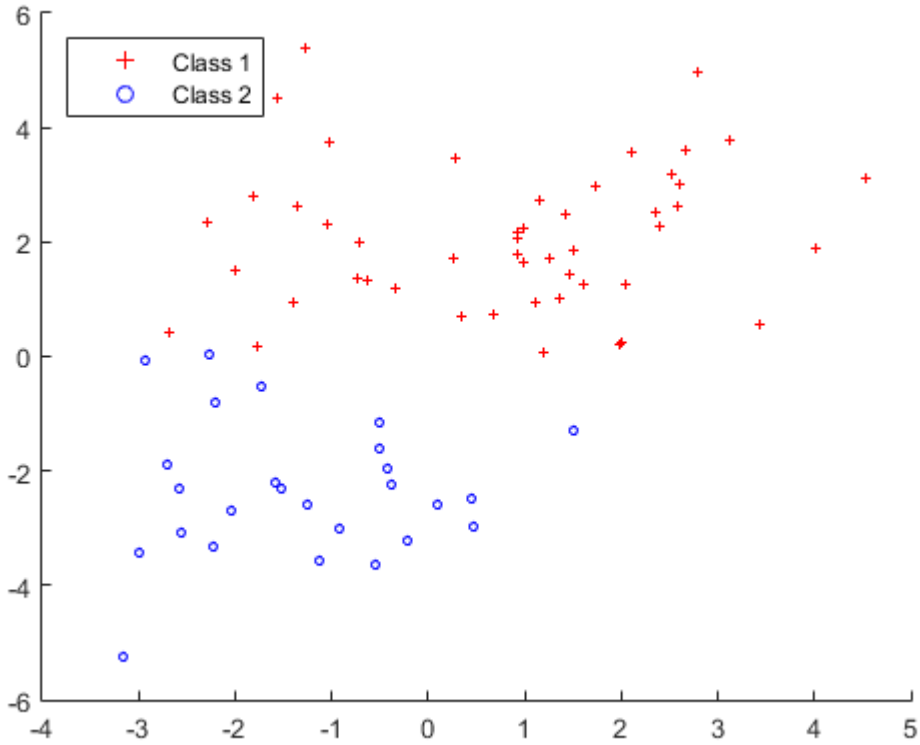
1. Given a data set `X`, first fit a Gaussian mixture distribution. The previous code has already done that.

   ```
   gm
   ```

```
gm =

Gaussian mixture distribution with 2 components in 2 dimensions
Component 1:
Mixing proportion: 0.629379
Mean:    1.0758    2.0426

Component 2:
Mixing proportion: 0.370621
Mean:   -0.8292   -1.8482
```

2 You can then use `cluster` to assign each point in a new data set, `Y`, to one of the clusters defined for the original data.

```
Y = [mvnrnd(mu1,sigma1,50);mvnrnd(mu2,sigma2,25)];

idx = cluster(gm,Y);
cluster1 = (idx == 1);
cluster2 = (idx == 2);

scatter(Y(cluster1,1),Y(cluster1,2),10,'r+');
hold on
scatter(Y(cluster2,1),Y(cluster2,2),10,'bo');
hold off
legend('Class 1','Class 2','Location','NW')
```



As with the previous example, the posterior probabilities for each point can be treated as membership scores rather than determining "hard" cluster assignments.

For `cluster` to provide meaningful results with new data, `Y` should come from the same population as `X`, the original data used to create the mixture distribution. In particular, the estimated mixing probabilities for the Gaussian mixture distribution fitted to `X` are used when computing the posterior probabilities for `Y`.

15

Parametric Classification

Parametric Classification

Models of data with a categorical response are called *classifiers*. A classifier is built from *training data*, for which classifications are known. The classifier assigns new *test data* to one of the categorical levels of the response.

Parametric methods, like “Discriminant Analysis” on page 15-3, fit a parametric model to the training data and interpolate to classify test data.

Nonparametric methods, like classification and regression trees, use other means to determine classifications.

Discriminant Analysis

In this section...

What Is Discriminant Analysis?

Discriminant analysis is a classification method. It assumes that different classes generate data based on different Gaussian distributions.

- To train (create) a classifier, the fitting function estimates the parameters of a Gaussian distribution for each class (see "Creating a Classifier Using fitcdiscr" on page 15-4).
- To predict the classes of new data, the trained classifier finds the class with the smallest misclassification cost (see "How the predict Method Classifies" on page 15-6).

Linear discriminant analysis is also known as the Fisher discriminant, named for its inventor, Sir R. A. Fisher [2].

Create Discriminant Analysis Classifiers

To create the basic types of discriminant analysis classifiers for the Fisher iris data:

1 Load the data:

```
load fisheriris;
```

2 Create a default (linear) discriminant analysis classifier:

```
linclass = fitcdiscr(meas,species);
```

To visualize the classification boundaries of a 2-D linear classification of the data, see “Create and Visualize Discriminant Analysis Classifier” on page 15-9.

3 Classify an iris with average measurements:

```
meanmeas = mean(meas);
meanclass = predict(linclass,meanmeas)

meanclass =
    'versicolor'
```

4 Create a quadratic classifier:

```
quadclass = fitcdiscr(meas,species,...
    'discrimType','quadratic');
```

To visualize the classification boundaries of a 2-D quadratic classification of the data, see “Create and Visualize Discriminant Analysis Classifier” on page 15-9.

5 Classify an iris with average measurements using the quadratic classifier:

```
meanclass2 = predict(quadclass,meanmeas)

meanclass2 =
    'versicolor'
```

Creating a Classifier Using fitcdiscr

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. In other words, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class; only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

Under this modeling assumption, `fitcdiscr` infers the mean and covariance parameters of each class.

- For linear discriminant analysis, it computes the sample mean of each class. Then it computes the sample covariance by first subtracting the sample mean of each class from the observations of that class, and taking the empirical covariance matrix of the result.
- For quadratic discriminant analysis, it computes the sample mean of each class. Then it computes the sample covariances by first subtracting the sample mean of each class from the observations of that class, and taking the empirical covariance matrix of each class.

The `fit` method does not use prior probabilities or costs for fitting.

Weighted Observations

The `fit` method constructs weighted classifiers using the following scheme. Suppose M is an N-by-K class membership matrix:
$M_{nk} = 1$ if observation n is from class k
$M_{nk} = 0$ otherwise.

The estimate of the class mean for unweighted data is

$$\hat{\mu}_k = \frac{\sum_{n=1}^{N} M_{nk} x_n}{\sum_{n=1}^{N} M_{nk}}.$$

For weighted data with positive weights w_n, the natural generalization is

$$\hat{\mu}_k = \frac{\sum_{n=1}^{N} M_{nk} w_n x_n}{\sum_{n=1}^{N} M_{nk} w_n}.$$

The unbiased estimate of the pooled-in covariance matrix for unweighted data is

$$\hat{\Sigma} = \frac{\sum_{n=1}^{N} \sum_{k=1}^{K} M_{nk} \left(x_n - \hat{\mu}_k\right)\left(x_n - \hat{\mu}_k\right)^T}{N - K}.$$

For quadratic discriminant analysis, the `fit` method uses $K = 1$.

For weighted data, assuming the weights sum to 1, the unbiased estimate of the pooled-in covariance matrix is

$$\hat{\Sigma} = \frac{\sum_{n=1}^{N}\sum_{k=1}^{K} M_{nk} w_n (x_n - \hat{\mu}_k)(x_n - \hat{\mu}_k)^T}{1 - \sum_{k=1}^{K} \frac{W_k^{(2)}}{W_k}},$$

where

- $W_k = \sum_{n=1}^{N} M_{nk} w_n$ is the sum of the weights for class k.
- $W_k^{(2)} = \sum_{n=1}^{N} M_{nk} w_n^2$ is the sum of squared weights per class.

How the predict Method Classifies

There are three elements in the `predict` classification algorithm:

- "Posterior Probability" on page 15-7
- "Prior Probability" on page 15-7
- "Cost" on page 15-8

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.

- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

The space of `X` values divides into regions where a classification `Y` is a particular value. The regions are separated by straight lines for linear discriminant analysis, and by conic sections (ellipses, hyperbolas, or parabolas) for quadratic discriminant analysis. For a visualization of these regions, see "Create and Visualize Discriminant Analysis Classifier" on page 15-9.

Posterior Probability

The posterior probability that a point x belongs to class k is the product of the prior probability and the multivariate normal density. The density function of the multivariate normal with mean μ_k and covariance Σ_k at a point x is

$$P(x \mid k) = \frac{1}{\left(2\pi|\Sigma_k|\right)^{1/2}} \exp\left(-\frac{1}{2}(x-\mu_k)^T \Sigma_k^{-1}(x-\mu_k) \right),$$

where $|\Sigma_k|$ is the determinant of Σ_k, and Σ_k^{-1} is the inverse matrix.

Let $P(k)$ represent the prior probability of class k. Then the posterior probability that an observation x is of class k is

$$\hat{P}(k \mid x) = \frac{P(x \mid k)P(k)}{P(x)},$$

where $P(x)$ is a normalization constant, namely, the sum over k of $P(x \mid k)P(k)$.

Prior Probability

The prior probability is one of three choices:

- `'uniform'` — The prior probability of class `k` is 1 over the total number of classes.
- `'empirical'` — The prior probability of class `k` is the number of training samples of class `k` divided by the total number of training samples.

- A numeric vector — The prior probability of class `k` is the `j`th element of the `Prior` vector. See `fitcdiscr`.

After creating a classifier `obj`, you can set the prior using dot notation:

```
obj.Prior = v;
```

where `v` is a vector of positive elements representing the frequency with which each element occurs. You do not need to retrain the classifier when you set a new prior.

Cost

There are two costs associated with discriminant analysis classification: the true misclassification cost per class, and the expected misclassification cost per observation.

True Misclassification Cost per Class

`Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

You can set any cost matrix you like when creating a classifier. Pass the cost matrix in the `Cost` name-value pair in `fitcdiscr`.

After you create a classifier `obj`, you can set a custom cost using dot notation:

```
obj.Cost = B;
```

`B` is a square matrix of size `K`-by-`K` when there are `K` classes. You do not need to retrain the classifier when you set a new cost.

Expected Misclassification Cost per Observation

Suppose you have `Nobs` observations that you want to classify with a trained discriminant analysis classifier `obj`. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row. The command

```
[label,score,cost] = predict(obj,Xnew)
```

returns, among other outputs, a cost matrix of size `Nobs`-by-`K`. Each row of the cost matrix contains the expected (average) cost of classifying the observation into each of the `K` classes. `cost(n,k)` is

$$\sum_{i=1}^{K} \hat{P}(i \mid Xnew(n))C(k \mid i),$$

where

- K is the number of classes.
- $\hat{P}(i \mid Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.
- $C(k \mid i)$ is the cost of classifying an observation as k when its true class is i.

Create and Visualize Discriminant Analysis Classifier

This example shows how to perform linear and quadratic classification of Fisher iris data.

Load the sample data.

```
load fisheriris
```

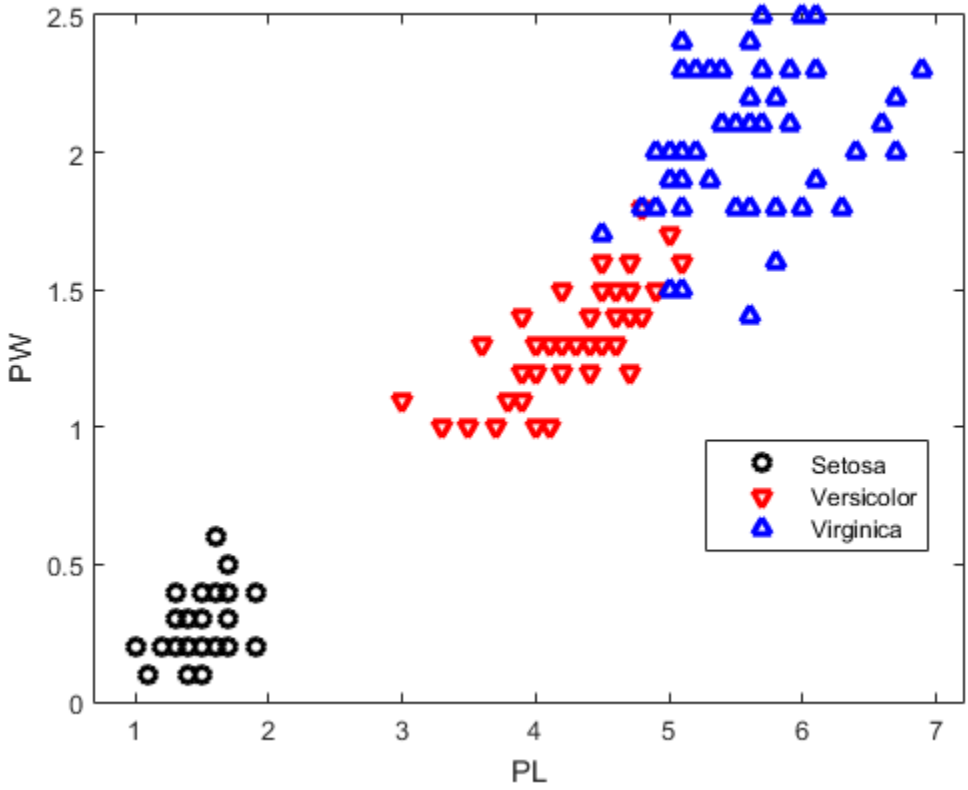
The column vector, `species` , consists of iris flowers of three different species, setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers, the length and width of sepals and petals in centimeters, respectively.

Use petal length (third column in `meas`) and petal width (fourth column in `meas`) measurements. Save these as variables PL and PW, respectively.

```
PL = meas(:,3);
PW = meas(:,4);
```

Plot the data, showing the classification, that is, create a scatter plot of the measurements, grouped by species.

```
h1 = gscatter(PL,PW,species,'krb','ov^',[],'off');
h1(1).LineWidth = 2;
h1(2).LineWidth = 2;
h1(3).LineWidth = 2;
legend('Setosa','Versicolor','Virginica','Location','best')
hold on
```



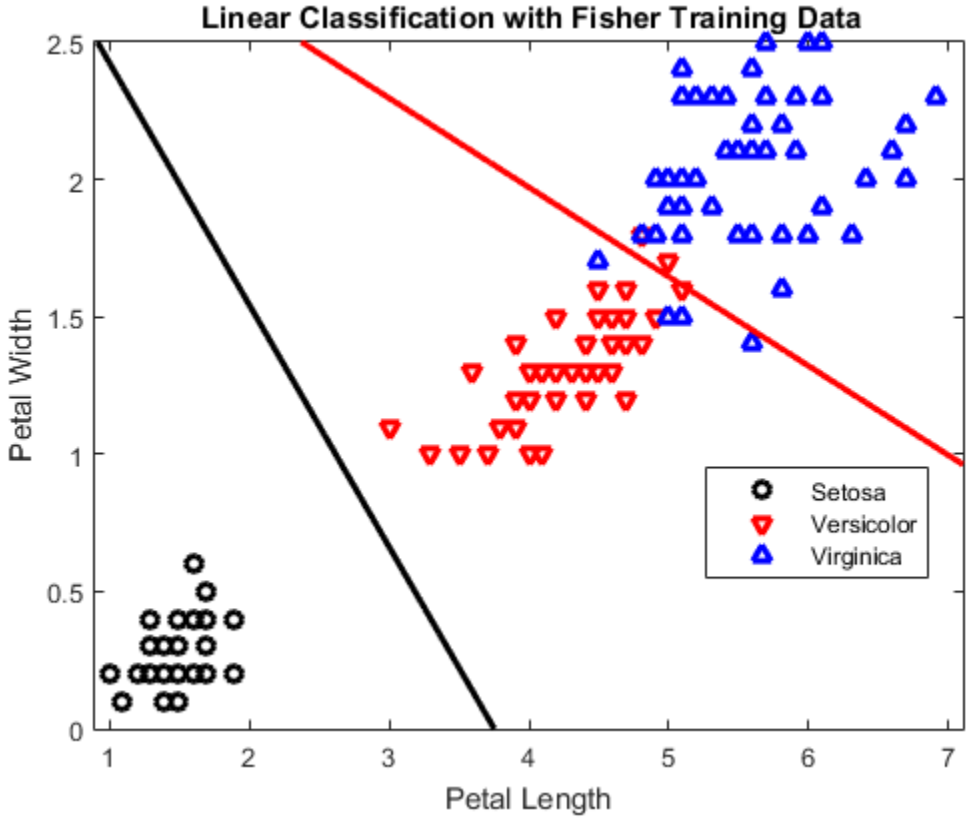
Create a linear classifier.

```
X = [PL,PW];
cls = fitcdiscr(X,species);
```

Plot the classification boundaries.

```
K = cls.Coeffs(2,3).Const; % First retrieve the coefficients for the linear
L = cls.Coeffs(2,3).Linear;% boundary between the second and third classes
                           % (versicolor and virginica).

% Plot the curve K + [x,y]*L  = 0.
f = @(x1,x2) K + L(1)*x1 + L(2)*x2;
h2 = ezplot(f,[.9 7.1 0 2.5]);
h2.Color = 'r';
```

```
h2.LineWidth = 2;

% Now, retrieve the coefficients for the linear boundary between the first
% and second classes (setosa and versicolor).
K = cls.Coeffs(1,2).Const;
L = cls.Coeffs(1,2).Linear;

% Plot the curve K + [x1,x2]*L  = 0:
f = @(x1,x2) K + L(1)*x1 + L(2)*x2;
h3 = ezplot(f,[.9 7.1 0 2.5]);
h3.Color = 'k';
h3.LineWidth = 2;
axis([.9 7.1 0 2.5])
xlabel('Petal Length')
ylabel('Petal Width')
title('{\bf Linear Classification with Fisher Training Data}')
```



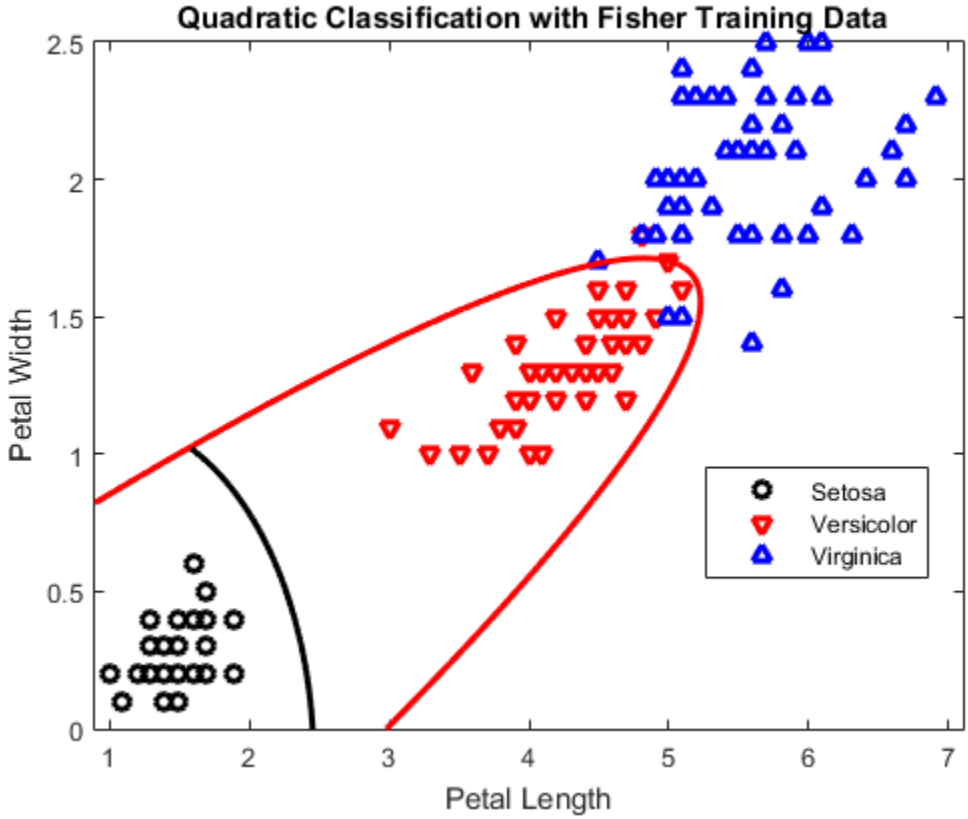
Create a quadratic discriminant classifier.

```
cqs = fitcdiscr(X,species,...
    'DiscrimType','quadratic');
```

Plot the classification boundaries similarly.

```
delete(h2); delete(h3) % First, remove the linear boundaries from the plot.

% Now, retrieve the coefficients for the quadratic boundary between the
% second and third classes (versicolor and virginica).
K = cqs.Coeffs(2,3).Const;
L = cqs.Coeffs(2,3).Linear;
Q = cqs.Coeffs(2,3).Quadratic;
```

```
% Plot the curve K + [x1,x2]*L + [x1,x2]*Q*[x1,x2]' = 0.
f = @(x1,x2) K + L(1)*x1 + L(2)*x2 + Q(1,1)*x1.^2 + ...
    (Q(1,2)+Q(2,1))*x1.*x2 + Q(2,2)*x2.^2;
h2 = ezplot(f,[.9 7.1 0 2.5]);
h2.Color = 'r';
h2.LineWidth = 2;

% Now, retrieve the coefficients for the quadratic boundary between the
% first and second classes (setosa and versicolor).
K = cqs.Coeffs(1,2).Const;
L = cqs.Coeffs(1,2).Linear;
Q = cqs.Coeffs(1,2).Quadratic;

% Plot the curve K + [x1,x2]*L + [x1,x2]*Q*[x1,x2]'=0:
f = @(x1,x2) K + L(1)*x1 + L(2)*x2 + Q(1,1)*x1.^2 + ...
    (Q(1,2)+Q(2,1))*x1.*x2 + Q(2,2)*x2.^2;
h3 = ezplot(f,[.9 7.1 0 1.02]); % Plot the relevant portion of the curve.
h3.Color = 'k';
h3.LineWidth = 2;
axis([.9 7.1 0 2.5])
xlabel('Petal Length')
ylabel('Petal Width')
title('{\bf Quadratic Classification with Fisher Training Data}')
hold off
```



Improve a Discriminant Analysis Classifier

Deal with Singular Data

Discriminant analysis needs data sufficient to fit Gaussian models with invertible covariance matrices. If your data is not sufficient to fit such a model uniquely, `fitcdiscr` fails. This section shows methods for handling failures.

Tip To obtain a discriminant analysis classifier without failure, set the `DiscrimType` name-value pair to `'pseudoLinear'` or `'pseudoQuadratic'` in `fitcdiscr`.

"Pseudo" discriminants never fail, because they use the pseudoinverse of the covariance matrix Σ_k (see `pinv`).

Example: Singular Covariance Matrix

When the covariance matrix of the fitted classifier is singular, `fitcdiscr` can fail:

```
load popcorn
X = popcorn(:,[1 2]);
X(:,3) = 0; % a zero-variance column
Y = popcorn(:,3);
ppcrn = fitcdicr(X,Y);

Error using ClassificationDiscriminant (line 635)
Predictor x3 has zero variance. Either exclude this predictor or set 'discrimType' to
'pseudoLinear' or 'diagLinear'.

Error in classreg.learning.FitTemplate/fit (line 243)
            obj = this.MakeFitObject(X,Y,W,this.ModelParameters,fitArgs{:});

Error in fitcdiscr (line 296)
            this = fit(temp,X,Y);
```

To proceed with linear discriminant analysis, use a `pseudoLinear` or `diagLinear` discriminant type:

```
ppcrn = fitcdiscr(X,Y,...
    'discrimType','pseudoLinear');
meanpredict = predict(ppcrn,mean(X))

meanpredict =
    3.5000
```

Choose a Discriminant Type

There are six types of discriminant analysis classifiers: linear and quadratic, with *diagonal* and *pseudo* variants of each type.

Tip To see if your covariance matrix is singular, set `discrimType` to `'linear'` or `'quadratic'`. If the matrix is singular, the `fitcdiscr` method fails for `'quadratic'`, and the `Gamma` property is nonzero for `'linear'`.

To obtain a quadratic classifier even when your covariance matrix is singular, set `discrimType` to `'pseudoQuadratic'` or `'diagQuadratic'`.

```
obj = fitcdiscr(X,Y,...
    'discrimType','pseudoQuadratic') % or 'diagQuadratic'
```

Choose a classifier type by setting the `discrimType` name-value pair to one of:

- `'linear'` (default) — Estimate one covariance matrix for all classes.
- `'quadratic'` — Estimate one covariance matrix for each class.
- `'diagLinear'` — Use the diagonal of the `'linear'` covariance matrix, and use its pseudoinverse if necessary.
- `'diagQuadratic'` — Use the diagonals of the `'quadratic'` covariance matrices, and use their pseudoinverses if necessary.
- `'pseudoLinear'` — Use the pseudoinverse of the `'linear'` covariance matrix if necessary.
- `'pseudoQuadratic'` — Use the pseudoinverses of the `'quadratic'` covariance matrices if necessary.

`fitcdiscr` can fail for the `'linear'` and `'quadratic'` classifiers. When it fails, it returns an explanation, as shown in "Deal with Singular Data" on page 15-15.

`fitcdiscr` always succeeds with the diagonal and pseudo variants. For information about pseudoinverses, see `pinv`.

You can set the discriminant type using dot notation after constructing a classifier:

```
obj.DiscrimType = 'discrimType'
```

You can change between linear types or between quadratic types, but cannot change between a linear and a quadratic type.

Examine the Resubstitution Error and Confusion Matrix

The *resubstitution error* is the difference between the response training data and the predictions the classifier makes of the response based on the input training data. If the

resubstitution error is high, you cannot expect the predictions of the classifier to be good. However, having low resubstitution error does not guarantee good predictions for new data. Resubstitution error is often an overly optimistic estimate of the predictive error on new data.

The *confusion matrix* shows how many errors, and which types, arise in resubstitution. When there are `K` classes, the confusion matrix `R` is a `K`-by-`K` matrix with `R(i,j)` = the number of observations of class `i` that the classifier predicts to be of class `j`.

Example: Resubstitution Error of a Discriminant Analysis Classifier

Examine the resubstitution error of the default discriminant analysis classifier for the Fisher iris data:

```
load fisheriris
obj = fitcdiscr(meas,species);
resuberror = resubLoss(obj)

resuberror =
    0.0200
```

The resubstitution error is very low, meaning `obj` classifies nearly all the Fisher iris data correctly. The total number of misclassifications is:

```
resuberror * obj.NumObservations

ans =
    3.0000
```

To see the details of the three misclassifications, examine the confusion matrix:

```
R = confusionmat(obj.Y,resubPredict(obj))

R =
    50     0     0
     0    48     2
     0     1    49

obj.ClassNames

ans =
    'setosa'
    'versicolor'
```

```
    'virginica'
```

- `R(1,:) = [50 0 0]` means `obj` classifies all 50 setosa irises correctly.
- `R(2,:) = [0 48 2]` means `obj` classifies 48 versicolor irises correctly, and misclassifies two versicolor irises as virginica.
- `R(3,:) = [0 1 49]` means `obj` classifies 49 virginica irises correctly, and misclassifies one virginica iris as versicolor.

Cross Validation

Typically, discriminant analysis classifiers are robust and do not exhibit overtraining when the number of predictors is much less than the number of observations. Nevertheless, it is good practice to cross validate your classifier to ensure its stability.

Cross Validating a Discriminant Analysis Classifier

This example shows how to perform five-fold cross validation of a quadratic discriminant analysis classifier.

Load the sample data.

```
load fisheriris
```

Create a quadratic discriminant analysis classifier for the data.

```
quadisc = fitcdiscr(meas,species,'DiscrimType','quadratic');
```

Find the resubstitution error of the classifier.

```
qerror = resubLoss(quadisc)
```

```
qerror =

    0.0200
```

The classifier does an excellent job. Nevertheless, resubstitution error can be an optimistic estimate of the error when classifying new data. So proceed to cross validation.

Create a cross-validation model.

```
cvmodel = crossval(quadisc,'kfold',5);
```

Find the cross-validation loss for the model, meaning the error of the out-of-fold observations.

```
cverror = kfoldLoss(cvmodel)
```

```
cverror =

    0.0200
```

The cross-validated loss is as low as the original resubstitution loss. Therefore, you can have confidence that the classifier is reasonably accurate.

Change Costs and Priors

Sometimes you want to avoid certain misclassification errors more than others. For example, it might be better to have oversensitive cancer detection instead of undersensitive cancer detection. Oversensitive detection gives more false positives (unnecessary testing or treatment). Undersensitive detection gives more false negatives (preventable illnesses or deaths). The consequences of underdetection can be high. Therefore, you might want to set costs to reflect the consequences.

Similarly, the training data `Y` can have a distribution of classes that does not represent their true frequency. If you have a better estimate of the true frequency, you can include this knowledge in the classification `Prior` property.

Example: Setting Custom Misclassification Costs

Consider the Fisher iris data. Suppose that the cost of classifying a versicolor iris as virginica is 10 times as large as making any other classification error. Create a classifier from the data, then incorporate this cost and then view the resulting classifier.

1. Load the Fisher iris data and create a default (linear) classifier as in "Example: Resubstitution Error of a Discriminant Analysis Classifier" on page 15-17:

   ```
   load fisheriris
   obj = fitcdiscr(meas,species);
   resuberror = resubLoss(obj)

   resuberror =
       0.0200

   R = confusionmat(obj.Y,resubPredict(obj))
   ```

```
R =
    50     0     0
     0    48     2
     0     1    49

obj.ClassNames

ans =
    'setosa'
    'versicolor'
    'virginica'
```

`R(2,:) = [0 48 2]` means `obj` classifies 48 versicolor irises correctly, and misclassifies two versicolor irises as virginica.

2 Change the cost matrix to make fewer mistakes in classifying versicolor irises as virginica:

```
obj.Cost(2,3) = 10;
R2 = confusionmat(obj.Y,resubPredict(obj))

R2 =
    50     0     0
     0    50     0
     0     7    43
```

`obj` now classifies all versicolor irises correctly, at the expense of increasing the number of misclassifications of virginica irises from 1 to 7.

Example: Setting Alternative Priors

Consider the Fisher iris data. There are 50 irises of each kind in the data. Suppose that, in a particular region, you have historical data that shows virginica are five times as prevalent as the other kinds. Create a classifier that incorporates this information.

1 Load the Fisher iris data and make a default (linear) classifier as in "Example: Resubstitution Error of a Discriminant Analysis Classifier" on page 15-17:

```
load fisheriris
obj = fitcdiscr(meas,species);
resuberror = resubLoss(obj)

resuberror =
    0.0200
```

```
R = confusionmat(obj.Y,resubPredict(obj))

R =
    50     0     0
     0    48     2
     0     1    49

obj.ClassNames

ans =
    'setosa'
    'versicolor'
    'virginica'
```

`R(3,:) = [0 1 49]` means `obj` classifies 49 virginica irises correctly, and misclassifies one virginica iris as versicolor.

2 Change the prior to match your historical data, and examine the confusion matrix of the new classifier:

```
obj.Prior = [1 1 5];
R2 = confusionmat(obj.Y,resubPredict(obj))

R2 =
    50     0     0
     0    46     4
     0     0    50
```

The new classifier classifies all virginica irises correctly, at the expense of increasing the number of misclassifications of versicolor irises from 2 to 4.

Regularize a Discriminant Analysis Classifier

This example shows how to make a more robust and simpler model by trying to remove predictors without hurting the predictive power of the model. This is especially important when you have many predictors in your data. Linear discriminant analysis uses the two regularization parameters, `Gamma` and `Delta`, to identify and remove redundant predictors. The `cvshrink` method helps identify appropriate settings for these parameters.

Load data and create a classifier.

Create a linear discriminant analysis classifier for the `ovariancancer` data. Set the `SaveMemory` and `FillCoeffs` name-value pair arguments to keep the resulting model

reasonably small. For computational ease, this example uses a random subset of half of the predictors to train the classifier.

```
load ovariancancer
rng(1); % For reproducibility
numPred = size(obs,2);
obs = obs(:,randsample(numPred,numPred/2));
Mdl = fitcdiscr(obs,grp,...
    'SaveMemory','on','FillCoeffs','off');
```

Cross validate the classifier.

Use 30 levels of `Gamma` and 30 levels of `Delta` to search for good parameters. This search is time consuming. Set `Verbose` to `1` to view the progress.

```
[err,gamma,delta,numpred] = cvshrink(Mdl,...
    'NumGamma',29,'NumDelta',29,'Verbose',1);
```

Examine the quality of the regularized classifiers.

Plot the number of predictors against the error.

```
figure;
plot(err,numpred,'k.')
xlabel('Error rate');
ylabel('Number of predictors');
```

Examine the lower-left part of the plot more closely.

```
axis([0 .1 0 1000])
```

There is a clear tradeoff between lower number of predictors and lower error.

Choose an optimal tradeoff between model size and accuracy.

Multiple pairs of `Gamma` and `Delta` values produce about the same minimal error. Display the indices of these pairs and their values.

```
minerr = min(min(err))
[p q] = find(err < minerr + 1e-4); % Subscripts of err producing minimal error
numel(p)
idx = sub2ind(size(delta),p,q); % Convert from subscripts to linear indices
[gamma(p) delta(idx)]
```

These points have as few as a quarter of the total predictors that have nonzero coefficients in the model.

```
numpred(idx)
```

To further lower the number of predictors, you must accept larger error rates. For example, to choose the `Gamma` and `Delta` that give the lowest error rate with 250 or fewer predictors.

```
low250 = min(min(err(numpred <= 250)));
lownum = min(min(numpred(err == low250)));
[low250 lownum]
```

You need 216 predictors to achieve an error rate of 0.0185, and this is the lowest error rate among those that have 250 predictors or fewer.

Display the `Gamma` and `Delta` that achieve this error/number of predictors.

```
[r,s] = find((err == low250) & (numpred == lownum));
[gamma(r); delta(r,s)]
```

Set the regularization parameters.

To set the classifier with these values of `Gamma` and `Delta`, use dot notation.

```
Mdl.Gamma = gamma(r);
Mdl.Delta = delta(r,s);
```

Heat map plot

To compare the `cvshrink` calculation to that in Guo, Hastie, and Tibshirani [3], plot heat maps of error and number of predictors against `Gamma` and the index of the `Delta` parameter. (The `Delta` parameter range depends on the value of the `Gamma` parameter. So to get a rectangular plot, use the `Delta` index, not the parameter itself.)

```
% Create the Delta index matrix
indx = repmat(1:size(delta,2),size(delta,1),1);
figure
subplot(1,2,1)
imagesc(err);
colorbar;
colormap('jet')
title 'Classification error';
xlabel 'Delta index';
ylabel 'Gamma index';

subplot(1,2,2)
```

```
imagesc(numpred);
colorbar;
title 'Number of predictors in the model';
xlabel 'Delta index' ;
ylabel 'Gamma index' ;
```

You see the best classification error when `Delta` is small, but fewest predictors when `Delta` is large.

Examine the Gaussian Mixture Assumption

Discriminant analysis assumes that the data comes from a Gaussian mixture model (see "Creating a Classifier Using fitcdiscr" on page 15-4). If the data appears to come from a Gaussian mixture model, you can expect discriminant analysis to be a good classifier. Furthermore, the default linear discriminant analysis assumes that all class covariance matrices are equal. This section shows methods to check these assumptions:

- "Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis" on page 15-24
- "Q-Q Plot" on page 15-26
- "Mardia Kurtosis Test of Multivariate Normality" on page 15-29

Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis

The Bartlett test (see Box [1]) checks equality of the covariance matrices of the various classes. If the covariance matrices are equal, the test indicates that linear discriminant analysis is appropriate. If not, consider using quadratic discriminant analysis, setting the `DiscrimType` name-value pair to `'quadratic'` in `fitcdiscr`.

The Bartlett test assumes normal (Gaussian) samples, where neither the means nor covariance matrices are known. To determine whether the covariances are equal, compute the following quantities:

- Sample covariance matrices per class σ_i, $1 \le i \le k$, where k is the number of classes.
- Pooled-in covariance matrix σ.
- Test statistic V:

$$V = (n-k)\log(|\Sigma|) - \sum_{i=1}^{k}(n_i - 1)\log(|\Sigma_i|)$$

where n is the total number of observations, and n_i is the number of observations in class i, and $|\Sigma|$ means the determinant of the matrix Σ.

- Asymptotically, as the number of observations in each class n_i become large, V is distributed approximately χ^2 with $kd(d+1)/2$ degrees of freedom, where d is the number of predictors (number of dimensions in the data).

The Bartlett test is to check whether V exceeds a given percentile of the χ^2 distribution with $kd(d+1)/2$ degrees of freedom. If it does, then reject the hypothesis that the covariances are equal.

Example: Bartlett Test for Equal Covariance Matrices

Check whether the Fisher iris data is well modeled by a single Gaussian covariance, or whether it would be better to model it as a Gaussian mixture.

```
load fisheriris;
prednames = {'SepalLength','SepalWidth','PetalLength','PetalWidth'};
L = fitcdiscr(meas,species,'PredictorNames',prednames);
Q = fitcdiscr(meas,species,'PredictorNames',prednames,'DiscrimType','quadratic');
D = 4; % Number of dimensions of X
Nclass = [50 50 50];
N = L.NumObservations;
K = numel(L.ClassNames);
SigmaQ = Q.Sigma;
SigmaL = L.Sigma;
logV = (N-K)*log(det(SigmaL));
for k=1:K
    logV = logV - (Nclass(k)-1)*log(det(SigmaQ(:,:,k)));
end
nu = (K-1)*D*(D+1)/2;
pval = 1 - chi2cdf(logV,nu)


pval =

     0
```

The Bartlett test emphatically rejects the hypothesis of equal covariance matrices. If `pval` had been greater than `0.05`, the test would not have rejected the hypothesis. The result indicates to use quadratic discriminant analysis, as opposed to linear discriminant analysis.

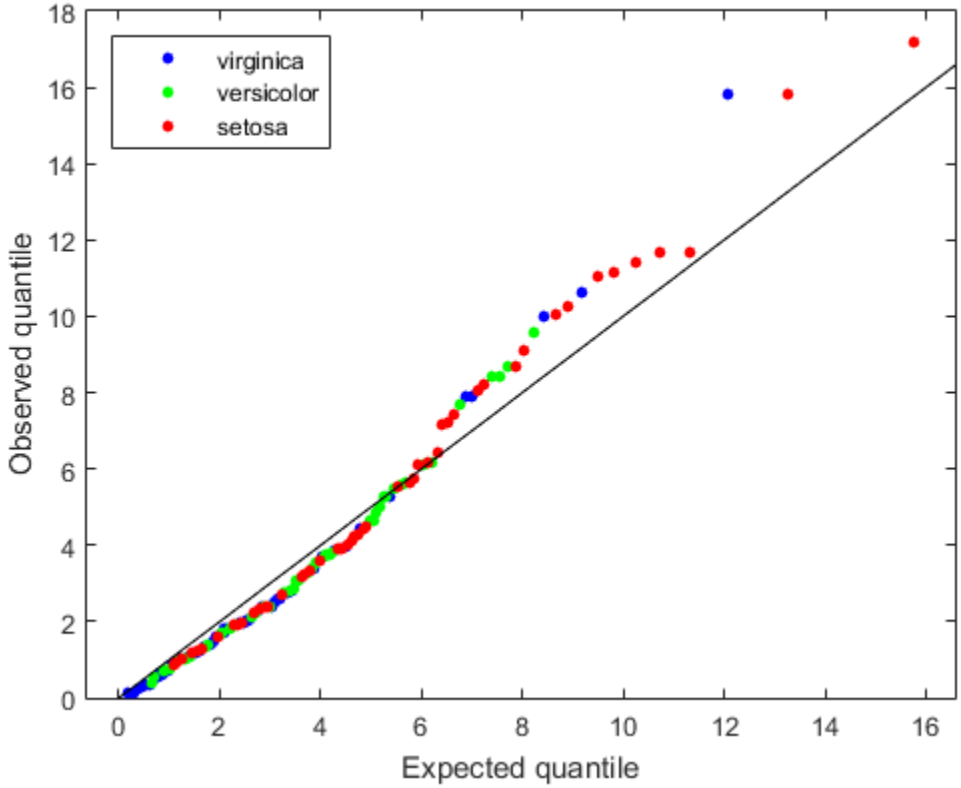
Q-Q Plot

A Q-Q plot graphically shows whether an empirical distribution is close to a theoretical distribution. If the two are equal, the Q-Q plot lies on a 45° line. If not, the Q-Q plot strays from the 45° line.

Check Q-Q Plots for Linear and Quadratic Discriminants

For linear discriminant analysis, use a single covariance matrix for all classes.

```
load fisheriris;
prednames = {'SepalLength','SepalWidth','PetalLength','PetalWidth'};
L = fitcdiscr(meas,species,'PredictorNames',prednames);
N = L.NumObservations;
K = numel(L.ClassNames);
mahL = mahal(L,L.X,'ClassLabels',L.Y);
D = 4;
expQ = chi2inv(((1:N)-0.5)/N,D); % expected quantiles
[mahL,sorted] = sort(mahL); % sorted obbserved quantiles
figure;
gscatter(expQ,mahL,L.Y(sorted),'bgr',[],[],'off');
legend('virginica','versicolor','setosa','Location','NW');
xlabel('Expected quantile');
ylabel('Observed quantile');
line([0 20],[0 20],'color','k');
```

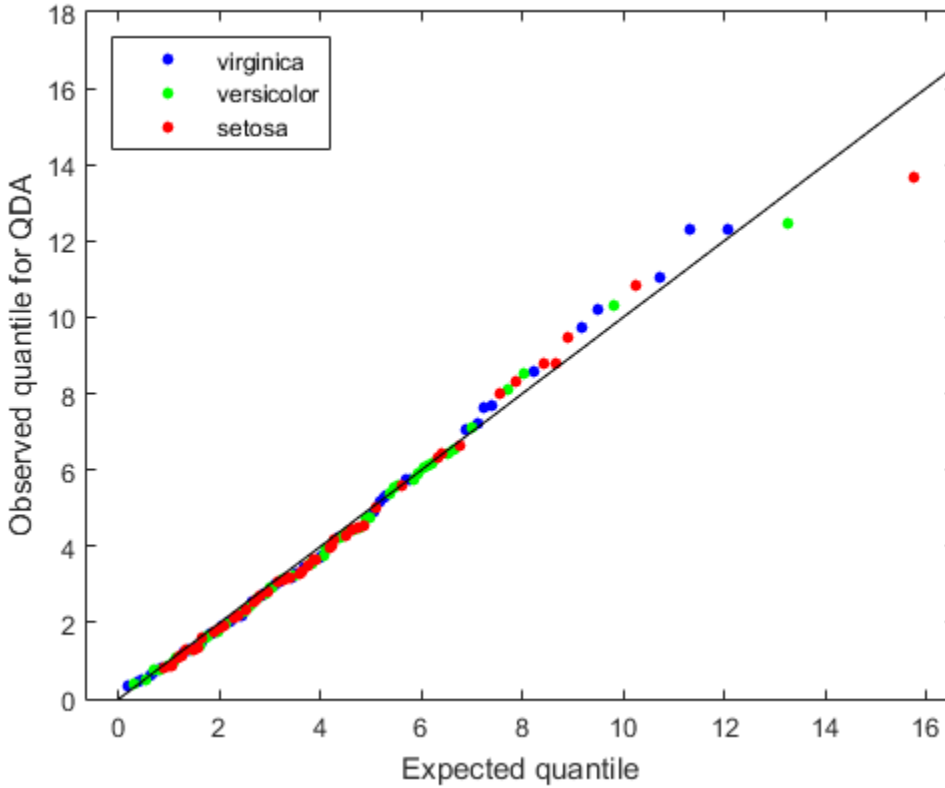


Overall, the agreement between the expected and observed quantiles is good. Look at the right half of the plot. The deviation of the plot from the 45° line upward indicates that the data has tails heavier than a normal distribution. There are three possible outliers on the right: two observations from class `'setosa'` and one observation from class `'virginica'`.

As shown in "Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis" on page 15-24, the data does not match a single covariance matrix. Redo the calculations for a quadratic discriminant.

```
load fisheriris;
prednames = {'SepalLength','SepalWidth','PetalLength','PetalWidth'};
Q = fitcdiscr(meas,species,'PredictorNames',prednames,'DiscrimType','quadratic');
Nclass = [50 50 50];
```

```
N = L.NumObservations;
K = numel(L.ClassNames);
mahQ = mahal(Q,Q.X,'ClassLabels',Q.Y);
expQ = chi2inv(((1:N)-0.5)/N,D);
[mahQ,sorted] = sort(mahQ);
figure;
gscatter(expQ,mahQ,Q.Y(sorted),'bgr',[],[],'off');
legend('virginica','versicolor','setosa','Location','NW');
xlabel('Expected quantile');
ylabel('Observed quantile for QDA');
line([0 20],[0 20],'color','k');
```



The Q-Q plot shows a better agreement between the observed and expected quantiles. There is only one outlier candidate, from class `'setosa'`.

Mardia Kurtosis Test of Multivariate Normality

The Mardia kurtosis test (see Mardia [4]) is an alternative to examining a Q-Q plot. It gives a numeric approach to deciding if data matches a Gaussian mixture model.

In the Mardia kurtosis test you compute M, the mean of the fourth power of the Mahalanobis distance of the data from the class means. If the data is normally distributed with constant covariance matrix (and is thus suitable for linear discriminant analysis), M is asymptotically distributed as normal with mean $d(d + 2)$ and variance $8d(d + 2)/n$, where

- d is the number of predictors (number of dimensions in the data).
- n is the total number of observations.

The Mardia test is two sided: check whether M is close enough to $d(d + 2)$ with respect to a normal distribution of variance $8d(d + 2)/n$.

Example: Mardia Kurtosis Test for Linear and Quadratic Discriminants

Check whether the Fisher iris data is approximately normally distributed for both linear and quadratic discriminant analysis. According to “Bartlett Test of Equal Covariance Matrices for Linear Discriminant Analysis” on page 15-24, the data is not normal for linear discriminant analysis (the covariance matrices are different). “Check Q-Q Plots for Linear and Quadratic Discriminants” on page 15-26 indicates that the data is well modeled by a Gaussian mixture model with different covariances per class. Check these conclusions with the Mardia kurtosis test:

```
load fisheriris;
prednames = {'SepalLength','SepalWidth','PetalLength','PetalWidth'};
L = fitcdiscr(meas,species,'PredictorNames',prednames);
mahL = mahal(L,L.X,'ClassLabels',L.Y);
D = 4;
N = L.NumObservations;
obsKurt = mean(mahL.^2);
expKurt = D*(D+2);
varKurt = 8*D*(D+2)/N;
[~,pval] = ztest(obsKurt,expKurt,sqrt(varKurt))
```

```
pval =

    0.0208
```

The Mardia test indicates to reject the hypothesis that the data is normally distributed.

Continuing the example with quadratic discriminant analysis:

```
Q = fitcdiscr(meas,species,'PredictorNames',prednames,'DiscrimType','quadratic');
mahQ = mahal(Q,Q.X,'ClassLabels',Q.Y);
obsKurt = mean(mahQ.^2);
[~,pval] = ztest(obsKurt,expKurt,sqrt(varKurt))
```

```
pval =

    0.7230
```

Because `pval` is high, you conclude the data are consistent with the multivariate normal distribution.

Bibliography

[1] Box, G. E. P. *A General Distribution Theory for a Class of Likelihood Criteria.* Biometrika 36(3), pp. 317–346, 1949.

[2] Fisher, R. A. *The Use of Multiple Measurements in Taxonomic Problems.* Annals of Eugenics, Vol. 7, pp. 179–188, 1936. Available at http://digital.library.adelaide.edu.au/dspace/handle/2440/15227.

[3] Guo, Y., T. Hastie, and R. Tibshirani. *Regularized Discriminant Analysis and Its Application in Microarray.* Biostatistics, Vol. 8, No. 1, pp. 86–100, 2007.

[4] Mardia, K. V. *Measures of multivariate skewness and kurtosis with applications.* Biometrika 57 (3), pp. 519–530, 1970.

Naive Bayes Classification

The naive Bayes classifier is designed for use when predictors are independent of one another within each class, but it appears to work well in practice even when that independence assumption is not valid. It classifies data in two steps:

1. Training step: Using the training data, the method estimates the parameters of a probability distribution, assuming predictors are conditionally independent given the class.
2. Prediction step: For any unseen test data, the method computes the posterior probability of that sample belonging to each class. The method then classifies the test data according the largest posterior probability.

The class-conditional independence assumption greatly simplifies the training step since you can estimate the one-dimensional class-conditional density for each predictor individually. While the class-conditional independence between predictors is not true in general, research shows that this optimistic assumption works well in practice. This assumption of class-conditional independence of the predictors allows the naive Bayes classifier to estimate the parameters required for accurate classification while using less training data than many other classifiers. This makes it particularly effective for data sets containing many predictors.

Supported Distributions

The training step in naive Bayes classification is based on estimating $P(X|Y)$, the probability or probability density of predictors `X` given class `Y`. The naive Bayes classification model `ClassificationNaiveBayes` and training function `fitcnb` provide support for normal (Gaussian), kernel, multinomial, and multivariate, multinomial predictor conditional distributions. To specify distributions for the predictors, use the `DistributionNames` name-value pair argument of `fitcnb`. You can specify one type of distribution for all predictors by supplying the string corresponding to the distribution name, or specify different distributions for the predictors by supplying a length D cell array of strings, where D is the number of predictors (that is, the number of columns of X).

Normal (Gaussian) Distribution

The `'normal'` distribution (specify using `'normal'`) is appropriate for predictors that have normal distributions in each class. For each predictor you model with a normal

distribution, the naive Bayes classifier estimates a separate normal distribution for each class by computing the mean and standard deviation of the training data in that class.

Kernel Distribution

The `'kernel'` distribution (specify using `'kernel'`) is appropriate for predictors that have a continuous distribution. It does not require a strong assumption such as a normal distribution and you can use it in cases where the distribution of a predictor may be skewed or have multiple peaks or modes. It requires more computing time and more memory than the normal distribution. For each predictor you model with a kernel distribution, the naive Bayes classifier computes a separate kernel density estimate for each class based on the training data for that class. By default the kernel is the normal kernel, and the classifier selects a width automatically for each class and predictor. The software supports specifying different kernels for each predictor, and different widths for each predictor or class.

Multivariate Multinomial Distribution

The multivariate, multinomial distribution (specify using `'mvmn'`) is appropriate for a predictor whose observations are categorical. Naive Bayes classifier construction using a multivariate multinomial predictor is described below. To illustrate the steps, consider an example where observations are labeled 0, 1, or 2, and a predictor the weather when the sample was conducted.

1. Record the distinct categories represented in the observations of the entire predictor. For example, the distinct categories (or predictor levels) might include sunny, rain, snow, and cloudy.
2. Separate the observations by response class. For example, segregate observations labeled 0 from observations labeled 1 and 2, and observations labeled 1 from observations labeled 2.
3. For each response class, fit a multinomial model using the category relative frequencies and total number of observations. For example, for observations labeled 0, the estimated probability it was sunny is $p_{sunny|0}$ = (number of sunny observations with label 0)/(number of observations with label 0), and similar for the other categories and response labels.

The class-conditional, multinomial random variables comprise a multivariate multinomial random variable.

Here are some other properties of naive Bayes classifiers that use multivariate multinomial.

- For each predictor you model with a multivariate multinomial distribution, the naive Bayes classifier:
  - Records a separate set of distinct predictor levels for each predictor
  - Computes a separate set of probabilities for the set of predictor levels for each class.
- The software supports modeling continuous predictors as mutlivariate multinomial. In this case, the predictor levels are the distinct occurrences of a measurement. This can lead a predictor having many predictor levels. It is good practice to discretize such predictors.

If an *observation* is a set of successes for various categories (represented by all of the predictors) out of a fixed number of independent trials, then specify that the predictors comprise a multinomial distribution. For details, see "Multinomial Distribution" on page 15-33.

Multinomial Distribution

The multinomial distribution (specify using `'DistributionNames','mn'`) is appropriate when, given the class, each *observation* is a multinomial random variable. That is, observation, or row, j of the predictor data X represents D categories, where x_{jd} is the number of successes for category (i.e., predictor) d in $n_j = \sum_{d=1}^{D} x_{jd}$ independent trials.

The steps to train a naive Bayes classifier are outlined next.

1. For each class, fit a multinomial distribution for the predictors given the class by:
   a. Aggregating the weighted, category counts over all observations. Additionally, the software implements additive smoothing [1].
   b. Estimating the D category probabilities within each class using the aggregated category counts. These category probabilities compose the probability parameters of the multinomial distribution.
2. Let a new observation have a total count of m. Then, the naive Bayes classifier:
   a. Sets the total count parameter of each multinomial distribution to m
   b. For each class, estimates the class posterior probability using the estimated multinomial distributions
   c. Predicts the observation into the class corresponding to the highest posterior probability

Consider the so-called the bag-of-tokens model, where there is a bag containing a number of tokens of various types and proportions. Each predictor represents a distinct type of token in the bag, an observation is n independent draws (i.e., with replacement) of tokens from the bag, and the data is a vector of counts, where element d is the number of times token d appears.

A machine-learning application is the construction of an email spam classifier, where each predictor represents a word, character, or phrase (i.e., token), an observation is an email, and the data are counts of the tokens in the email. One predictor might count the number of exclamation points, another might count the number of times the word "money" appears, and another might count the number of times the recipient's name appears. This is a naive Bayes model under the further assumption that the total number of tokens (or the total document length) is independent of response class.

Other properties of naive Bayes classifiers that use multinomial observations include:

- Classification is based on the relative frequencies of the categories. If $n_j = 0$ for observation j, then classification is not possible for that observation.
- The predictors are not conditionally independent since they must sum to n_j.
- Naive Bayes is not appropriate when n_j provides information about the class. That is, this classifier requires that n_j is independent of the class.
- If you specify that the predictors are conditionally multinomial, then the software applies this specification to all predictors. In other words, you cannot include `'mn'` in a cell array when specifying `'DistributionNames'`.

If a *predictor* is categorical, i.e., is multinomial within a response class, then specify that it is multivariate multinomial. For details, see “Multivariate Multinomial Distribution” on page 15-32.

References

[1] Manning, C. D., P. Raghavan, and M. Schütze. *Introduction to Information Retrieval*, NY: Cambridge University Press, 2008.

See Also

`ClassificationNaiveBayes` | `fitcnb` | `predict`

Related Examples

- “Classification”

Performance Curves

In this section...

Introduction to Performance Curves

After a classification algorithm such as `NaiveBayes` or `TreeBagger` has trained on data, you may want to examine the performance of the algorithm on a specific test dataset. One common way of doing this would be to compute a gross measure of performance such as quadratic loss or accuracy, averaged over the entire test dataset.

What are ROC Curves?

You may want to inspect the classifier performance more closely, for example, by plotting a Receiver Operating Characteristic (ROC) curve. By definition, a ROC curve [1,2] shows true positive rate versus false positive rate (equivalently, sensitivity versus 1–specificity) for different thresholds of the classifier output. You can use it, for example, to find the threshold that maximizes the classification accuracy or to assess, in more broad terms, how the classifier performs in the regions of high sensitivity and high specificity.

Evaluate Classifier Performance Using perfcurve

`perfcurve` computes measures for a plot of classifier performance. You can use this utility to evaluate classifier performance on test data after you train the classifier. Various measures such as mean squared error, classification error, or exponential loss can summarize the predictive power of a classifier in a single number. However, a performance curve offers more information as it lets you explore the classifier performance across a range of thresholds on its output.

You can use `perfcurve` with any classifier or, more broadly, with any method that returns a numeric score for an instance of input data. By convention adopted here,

- A high score returned by a classifier for any given instance signifies that the instance is likely from the positive class.

- A low score signifies that the instance is likely from the negative classes.

For some classifiers, you can interpret the score as the posterior probability of observing an instance of the positive class at point `X`. An example of such a score is the fraction of positive observations in a leaf of a decision tree. In this case, scores fall into the range from 0 to 1 and scores from positive and negative classes add up to unity. Other methods can return scores ranging between minus and plus infinity, without any obvious mapping from the score to the posterior class probability.

`perfcurve` does not impose any requirements on the input score range. Because of this lack of normalization, you can use `perfcurve` to process scores returned by any classification, regression, or fit method. `perfcurve` does not make any assumptions about the nature of input scores or relationships between the scores for different classes. As an example, consider a problem with three classes, `A`, `B`, and `C`, and assume that the scores returned by some classifier for two instances are as follows:

	`A`	`B`	`C`
instance 1	0.4	0.5	0.1
instance 2	0.4	0.1	0.5

If you want to compute a performance curve for separation of classes `A` and `B`, with `C` ignored, you need to address the ambiguity in selecting `A` over `B`. You could opt to use the score ratio, `s(A)/s(B)`, or score difference, `s(A)-s(B)`; this choice could depend on the nature of these scores and their normalization. `perfcurve` always takes one score per instance. If you only supply scores for class `A`, `perfcurve` does not distinguish between observations 1 and 2. The performance curve in this case may not be optimal.

`perfcurve` is intended for use with classifiers that return scores, not those that return only predicted classes. As a counter-example, consider a decision tree that returns only hard classification labels, 0 or 1, for data with two classes. In this case, the performance curve reduces to a single point because classified instances can be split into positive and negative categories in one way only.

For input, `perfcurve` takes true class labels for some data and scores assigned by a classifier to these data. By default, this utility computes a Receiver Operating Characteristic (ROC) curve and returns values of 1–specificity, or false positive rate, for `X` and sensitivity, or true positive rate, for `Y`. You can choose other criteria for `X` and `Y` by selecting one out of several provided criteria or specifying an arbitrary criterion through an anonymous function. You can display the computed performance curve using `plot(X,Y)`.

`perfcurve` can compute values for various criteria to plot either on the x- or the y-axis. All such criteria are described by a 2-by-2 confusion matrix, a 2-by-2 cost matrix, and a 2-by-1 vector of scales applied to class counts.

The `confusion` matrix, `C`, is defined as

$$\begin{pmatrix} TP & FN \\ FP & TN \end{pmatrix}$$

where

- P stands for "positive".
- N stands for "negative".
- T stands for "true".
- F stands for "false".

For example, the first row of the confusion matrix defines how the classifier identifies instances of the positive class: `C(1,1)` is the count of correctly identified positive instances and `C(1,2)` is the count of positive instances misidentified as negative.

The cost matrix defines the cost of misclassification for each category:

$$\begin{pmatrix} Cost(P \mid P) & Cost(N \mid P) \\ Cost(P \mid N) & Cost(N \mid N) \end{pmatrix}$$

where `Cost(I|J)` is the cost of assigning an instance of class `J` to class `I`. Usually `Cost(I|J)=0` for `I=J`. For flexibility, `perfcurve` allows you to specify nonzero costs for correct classification as well.

The two scales include prior information about class probabilities. `perfcurve` computes these scales by taking `scale(P)=prior(P)*N` and `scale(N)=prior(N)*P` and normalizing the sum `scale(P)+scale(N)` to 1. `P=TP+FN` and `N=TN+FP` are the total instance counts in the positive and negative class, respectively. The function then applies the scales as multiplicative factors to the counts from the corresponding class: `perfcurve` multiplies counts from the positive class by `scale(P)` and counts from the negative class by `scale(N)`. Consider, for example, computation of positive predictive value, `PPV = TP/(TP+FP)`. `TP` counts come from the positive class and `FP` counts come from the negative class. Therefore, you need to scale `TP` by `scale(P)` and `FP` by

`scale(N)`, and the modified formula for `PPV` with prior probabilities taken into account is now:

$$PPV = \frac{scale(P) * TP}{scale(P) * TP + scale(N) * FP}$$

If all scores in the data are above a certain threshold, `perfcurve` classifies all instances as `'positive'`. This means that `TP` is the total number of instances in the positive class and `FP` is the total number of instances in the negative class. In this case, `PPV` is simply given by the prior:

$$PPV = \frac{prior(P)}{prior(P) + prior(N)}$$

The `perfcurve` function returns two vectors, `X` and `Y`, of performance measures. Each measure is some function of `confusion`, `cost`, and `scale` values. You can request specific measures by name or provide a function handle to compute a custom measure. The function you provide should take `confusion`, `cost`, and `scale` as its three inputs and return a vector of output values.

The criterion for `X` must be a monotone function of the positive classification count, or equivalently, threshold for the supplied scores. If `perfcurve` cannot perform a one-to-one mapping between values of the `X` criterion and score thresholds, it exits with an error message.

By default, `perfcurve` computes values of the `X` and `Y` criteria for all possible score thresholds. Alternatively, it can compute a reduced number of specific `X` values supplied as an input argument. In either case, for `M` requested values, `perfcurve` computes `M+1` values for `X` and `Y`. The first value out of these `M+1` values is special. `perfcurve` computes it by setting the `TP` instance count to zero and setting `TN` to the total count in the negative class. This value corresponds to the `'reject all'` threshold. On a standard ROC curve, this translates into an extra point placed at `(0,0)`.

If there are `NaN` values among input scores, `perfcurve` can process them in either of two ways:

- It can discard rows with `NaN` scores.
- It can add them to false classification counts in the respective class.

That is, for any threshold, instances with NaN scores from the positive class are counted as false negative (FN), and instances with NaN scores from the negative class are counted as false positive (FP). In this case, the first value of X or Y is computed by setting TP to zero and setting TN to the total count minus the NaN count in the negative class. For illustration, consider an example with two rows in the positive and two rows in the negative class, each pair having a NaN score:

Class	Score
Negative	0.2
Negative	NaN
Positive	0.7
Positive	NaN

If you discard rows with NaN scores, then as the score cutoff varies, perfcurve computes performance measures as in the following table. For example, a cutoff of 0.5 corresponds to the middle row where rows 1 and 3 are classified correctly, and rows 2 and 4 are omitted.

TP	FN	FP	TN
0	1	0	1
1	0	0	1
1	0	1	0

If you add rows with NaN scores to the false category in their respective classes, perfcurve computes performance measures as in the following table. For example, a cutoff of 0.5 corresponds to the middle row where now rows 2 and 4 are counted as incorrectly classified. Notice that only the FN and FP columns differ between these two tables.

TP	FN	FP	TN
0	2	1	1
1	1	1	1
1	1	2	0

For data with three or more classes, perfcurve takes one positive class and a list of negative classes for input. The function computes the X and Y values using counts in the positive class to estimate TP and FN, and using counts in all negative classes to

estimate TN and FP. perfcurve can optionally compute Y values for each negative class separately and, in addition to Y, return a matrix of size M-by-C, where M is the number of elements in X or Y and C is the number of negative classes. You can use this functionality to monitor components of the negative class contribution. For example, you can plot TP counts on the X-axis and FP counts on the Y-axis. In this case, the returned matrix shows how the FP component is split across negative classes.

You can also use perfcurve to estimate confidence intervals. perfcurve computes confidence bounds using either cross-validation or bootstrap. If you supply cell arrays for labels and scores, perfcurve uses cross-validation and treats elements in the cell arrays as cross-validation folds. If you set input parameter NBoot to a positive integer, perfcurve generates nboot bootstrap replicas to compute pointwise confidence bounds.

perfcurve estimates the confidence bounds using one of two methods:

- Vertical averaging (VA) — estimate confidence bounds on Y and T at fixed values of X. Use the XVals input parameter to use this method for computing confidence bounds.
- Threshold averaging (TA) — estimate confidence bounds for X and Y at fixed thresholds for the positive class score. Use the TVals input parameter to use this method for computing confidence bounds.

To use observation weights instead of observation counts, you can use the 'Weights' parameter in your call to perfcurve. When you use this parameter, to compute X, Y and T or to compute confidence bounds by cross-validation, perfcurve uses your supplied observation weights instead of observation counts. To compute confidence bounds by bootstrap, perfcurve samples N out of N with replacement using your weights as multinomial sampling probabilities.

16

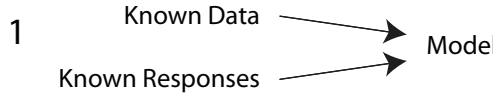
Nonparametric Supervised Learning

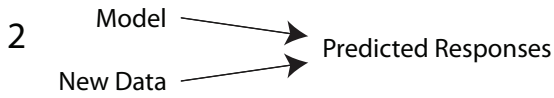
Supervised Learning Workflow and Algorithms

In this section...

Steps in Supervised Learning

Supervised learning (machine learning) takes a known set of input data and known responses to the data, and seeks to build a predictor model that generates reasonable predictions for the response to new data.





Suppose you want to predict if someone will have a heart attack within a year. You have a set of data on previous , including age, weight, height, blood pressure, etc. You know if the previous had heart attacks within a year of their data measurements. So the problem is combining all the existing data into a model that can predict whether a new person will have a heart attack within a year.

Supervised learning splits into two broad categories:

- Classification for responses that can have just a few known values, such as `'true'` or `'false'`. Classification algorithms apply to nominal, not ordinal response values.
- Regression for responses that are a real number, such as miles per gallon for a particular car.

You can have trouble deciding whether you have a classification problem or a regression problem. In that case, create a regression model first, because they are often more computationally efficient.

While there are many Statistics and Machine Learning Toolbox algorithms for supervised learning, most use the same basic workflow for obtaining a predictor model. (Detailed instruction on the steps for ensemble learning is in "Framework for Ensemble Learning" on page 16-68.) The steps for supervised learning are:

1. "Prepare Data" on page 16-3
2. "Choose an Algorithm" on page 16-3
3. "Fit a Model" on page 16-4
4. "Choose a Validation Method" on page 16-4
5. "Examine Fit and Update Until Satisfied" on page 16-5
6. "Use Fitted Model for Predictions" on page 16-6

Prepare Data

All supervised learning methods start with an input data matrix, usually called `X` here. Each row of `X` represents one observation. Each column of `X` represents one variable, or predictor. Represent missing entries with `NaN` values in `X`. Statistics and Machine Learning Toolbox supervised learning algorithms can handle `NaN` values, either by ignoring them or by ignoring any row with a `NaN` value.

You can use various data types for response data `Y`. Each element in `Y` represents the response to the corresponding row of `X`. Observations with missing `Y` data are ignored.

- For regression, `Y` must be a numeric vector with the same number of elements as the number of rows of `X`.
- For classification, `Y` can be any of these data types. This table also contains the method of including missing entries.

Data Type	Missing Entry
Numeric vector	`NaN`
Categorical vector	`<undefined>`
Character array	Row of spaces
Cell array of strings	`''`
Logical vector	(Cannot represent)

Choose an Algorithm

There are tradeoffs between several characteristics of algorithms, such as:

- Speed of training
- Memory usage
- Predictive accuracy on new data
- Transparency or interpretability, meaning how easily you can understand the reasons an algorithm makes its predictions

Details of the algorithms appear in "Characteristics of Classification Algorithms" on page 16-6. More detail about ensemble algorithms is in "Choose an Applicable Ensemble Method" on page 16-70.

Fit a Model

The fitting function you use depends on the algorithm you choose.

Algorithm	Fitting Function
Classification Trees	`fitctree`
Regression Trees	`fitrtree`
Discriminant Analysis (classification)	`fitcdiscr`
k-Nearest Neighbors (classification)	`fitcknn`
Naive Bayes (classification)	`fitcnb`
Support Vector Machines (SVM)	`fitcsvm`
Mutliclass models for SVM or other classifiers	`fitcecoc`
Classification or Regression Ensembles	`fitensemble`
Classification or Regression Ensembles in Parallel	`TreeBagger`

Choose a Validation Method

The three main methods to examine the accuracy of the resulting fitted model are:

- Examine the resubstitution error. For examples, see:
  - "Example: Resubstitution Error of a Classification Tree" on page 16-44
  - "Cross Validate a Regression Tree" on page 16-45

  - "Test Ensemble Quality" on page 16-79
  - "Example: Resubstitution Error of a Discriminant Analysis Classifier" on page 15-17
- Examine the cross-validation error. For examples, see:
  - "Cross Validate a Regression Tree" on page 16-45
  - "Test Ensemble Quality" on page 16-79
  - "Classification with Many Categorical Levels" on page 16-96
  - "Cross Validating a Discriminant Analysis Classifier" on page 15-18
- Examine the out-of-bag error for bagged decision trees. For examples, see:
  - "Test Ensemble Quality" on page 16-79
  - "Regression of Insurance Risk Rating for Car Imports Using TreeBagger" on page 16-129
  - "Classifying Radar Returns for Ionosphere Data Using TreeBagger" on page 16-141

Examine Fit and Update Until Satisfied

After validating the model, you might want to change it for better accuracy, better speed, or to use less memory.

- Change fitting parameters to try to get a more accurate model. For examples, see:
  - "Tune RobustBoost" on page 16-121
  - "Example: Unequal Classification Costs" on page 16-91
  - "Improve a Discriminant Analysis Classifier" on page 15-14
- Change fitting parameters to try to get a smaller model. This sometimes gives a model with more accuracy. For examples, see:
  - "Select Appropriate Tree Depth" on page 16-46
  - "Prune a Classification Tree" on page 16-51
  - "Surrogate Splits" on page 16-100
  - "Regularize a Regression Ensemble" on page 16-110
  - "Regression of Insurance Risk Rating for Car Imports Using TreeBagger" on page 16-129

- "Classifying Radar Returns for Ionosphere Data Using TreeBagger" on page 16-141

- Try a different algorithm. For applicable choices, see:
  - "Characteristics of Classification Algorithms" on page 16-6
  - "Choose an Applicable Ensemble Method" on page 16-70

When satisfied with a model of some types, you can trim it using the appropriate `compact` method (`compact` for classification trees, `compact` for classification ensembles, `compact` for regression trees, `compact` for regression ensembles, `compact` for discriminant analysis). `compact` removes training data and pruning information, so the model uses less memory.

Use Fitted Model for Predictions

To predict classification or regression response for most fitted models, use the `predict` method:

```
Ypredicted = predict(obj,Xnew)
```

- `obj` is the fitted model object.
- `Xnew` is the new input data.
- `Ypredicted` is the predicted response, either classification or regression.

Characteristics of Classification Algorithms

This table shows typical characteristics of the various supervised learning algorithms. The characteristics in any particular case can vary from the listed ones. Use the table as a guide for your initial choice of algorithms, but be aware that the table can be inaccurate for some problems.

Algorithm	Predictive Accuracy	Fitting Speed	Prediction Speed	Memory Usage	Easy to Interpret	Handles Categorical Predictors
Trees	Medium	Fast	Fast	Low	Yes	Yes
SVM	High	Medium	*	*	*	No
Naive Bayes	Medium	**	**	**	Yes	Yes
Nearest Neighbor	***	Fast***	Medium	High	No	Yes***

Algorithm	Predictive Accuracy	Fitting Speed	Prediction Speed	Memory Usage	Easy to Interpret	Handles Categorical Predictors
Discriminant Analysis	****	Fast	Fast	Low	Yes	No
Ensembles	See "Suggestions for Choosing an Appropriate Ensemble Algorithm" on page 16-72 and "General Characteristics of Ensemble Algorithms" on page 16-73					

* — SVM prediction speed and memory usage are good if there are few support vectors, but can be poor if there are many support vectors. When you use a kernel function, it can be difficult to interpret how SVM classifies data, though the default linear scheme is easy to interpret.

** — Naive Bayes speed and memory usage are good for simple distributions, but can be poor for kernel distributions and large data sets.

*** — Nearest Neighbor usually has good predictions in low dimensions, but can have poor predictions in high dimensions. For linear search, Nearest Neighbor does not perform any fitting. For *k*d-trees, Nearest Neighbor does perform fitting. Nearest Neighbor can have either continuous or categorical predictors, but not both.

**** — Discriminant Analysis is accurate when the modeling assumptions are satisfied (multivariate normal by class). Otherwise, the predictive accuracy varies.

Classification Using Nearest Neighbors

In this section...

Pairwise Distance Metrics

Categorizing query points based on their distance to points in a training dataset can be a simple yet effective way of classifying new points. You can use various metrics to determine the distance, described next. Use `pdist2` to find the distance between a set of data and query points.

Distance Metrics

Given an *mx*-by-*n* data matrix `X`, which is treated as *mx* (1-by-*n*) row vectors $\mathtt{x}_1$, $\mathtt{x}_2$, ..., $\mathtt{x}_{mx}$, and *my*-by-*n* data matrix `Y`, which is treated as *my* (1-by-*n*) row vectors $\mathtt{y}_1$, $\mathtt{y}_2$, ...,$\mathtt{y}_{my}$, the various distances between the vector $\mathtt{x}_s$ and $\mathtt{y}_t$ are defined as follows:

- Euclidean distance

  $$d_{st}^2 = (x_s - y_t)(x_s - y_t)'$$

  The Euclidean distance is a special case of the Minkowski metric, where `p` = 2.
- Standardized Euclidean distance

  $$d_{st}^2 = (x_s - y_t)V^{-1}(x_s - y_t)'$$

where V is the n-by-n diagonal matrix whose jth diagonal element is $S(j)^2$, where S is the vector containing the inverse weights.

- Mahalanobis distance

$$d_{st}^2 = (x_s - y_t)C^{-1}(x_s - y_t)'$$

where C is the covariance matrix.

- City block metric

$$d_{st} = \sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|$$

The city block distance is a special case of the Minkowski metric, where p = 1.

- Minkowski metric

$$d_{st} = \sqrt[p]{\sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|^p}$$

For the special case of p = 1, the Minkowski metric gives the city block metric, for the special case of p = 2, the Minkowski metric gives the Euclidean distance, and for the special case of p = ∞, the Minkowski metric gives the Chebychev distance.

- Chebychev distance

$$d_{st} = \max_j \left\{ \left| x_{sj} - y_{tj} \right| \right\}$$

The Chebychev distance is a special case of the Minkowski metric, where p = ∞.

- Cosine distance

$$d_{st} = \left(1 - \frac{x_s y_t'}{\sqrt{(x_s x_s')(y_t y_t')}} \right)$$

- Correlation distance

$$d_{st} = 1 - \frac{(x_s - \bar{x}_s)(y_t - \bar{y}_t)'}{\sqrt{(x_s - \bar{x}_s)(x_s - \bar{x}_s)'}\sqrt{(y_t - \bar{y}_t)(y_t - \bar{y}_t)'}}$$

where

$$\bar{x}_s = \frac{1}{n}\sum_j x_{sj}$$

and

$$\bar{y}_t = \frac{1}{n}\sum_j y_{tj}$$

- Hamming distance

$$d_{st} = (\#(x_{sj} \neq y_{tj}) / n)$$

- Jaccard distance

$$d_{st} = \frac{\#\left[\left(x_{sj} \neq y_{tj}\right) \cap \left(\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right)\right]}{\#\left[\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right]}$$

- Spearman distance

$$d_{st} = 1 - \frac{(r_s - \bar{r}_s)(r_t - \bar{r}_t)'}{\sqrt{(r_s - \bar{r}_s)(r_s - \bar{r}_s)'}\sqrt{(r_t - \bar{r}_t)(r_t - \bar{r}_t)'}}$$

where

  - r_{sj} is the rank of x_{sj} taken over x_{1j}, x_{2j}, ...$x_{mx,j}$, as computed by `tiedrank`.
  - r_{tj} is the rank of y_{tj} taken over y_{1j}, y_{2j}, ...$y_{my,j}$, as computed by `tiedrank`.
  - r_s and r_t are the coordinate-wise rank vectors of x_s and y_t, i.e., $r_s = (r_{s1}, r_{s2}, \ldots r_{sn})$ and $r_t = (r_{t1}, r_{t2}, \ldots r_{tn})$.

- $\bar{r}_s = \frac{1}{n}\sum_j r_{sj} = \frac{(n+1)}{2}$.
- $\bar{r}_t = \frac{1}{n}\sum_j r_{tj} = \frac{(n+1)}{2}$.

k-Nearest Neighbor Search and Radius Search

Given a set X of n points and a distance function, k-nearest neighbor (kNN) search lets you find the k closest points in X to a query point or set of points `Y`. The kNN search technique and kNN-based algorithms are widely used as benchmark learning rules. The relative simplicity of the kNN search technique makes it easy to compare the results from other classification techniques to kNN results. The technique has been used in various areas such as:

- bioinformatics
- image processing and data compression
- document retrieval
- computer vision
- multimedia database
- marketing data analysis

You can use kNN search for other machine learning algorithms, such as:

- kNN classification
- local weighted regression
- missing data imputation and interpolation
- density estimation

You can also use kNN search with many distance-based learning functions, such as K-means clustering.

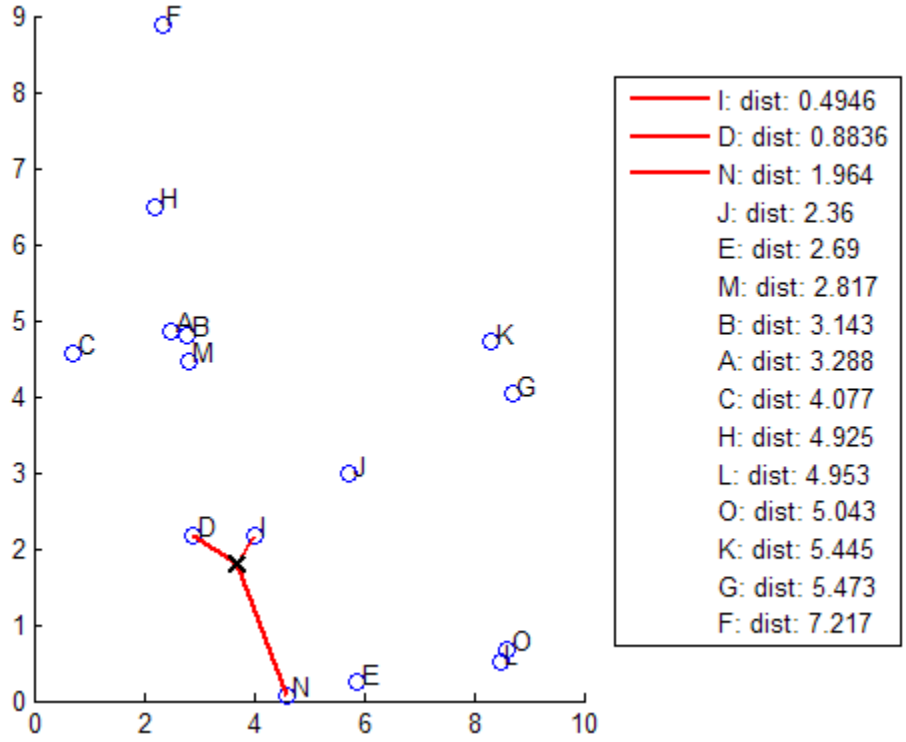
In contrast, for a positive real value `r`, `rangesearch` finds all points in `X` that are within a distance `r` of each point in `Y`. This fixed-radius search is closely related to kNN search, as it supports the same distance metrics and search classes, and uses the same search algorithms.

k-Nearest Neighbor Search Using Exhaustive Search

When your input data meets any of the following criteria, `knnsearch` uses the exhaustive search method by default to find the *k*-nearest neighbors:

- The number of columns of `X` is more than 10.
- `X` is sparse.
- The distance measure is either:
  - `'seuclidean'`
  - `'mahalanobis'`
  - `'cosine'`
  - `'correlation'`
  - `'spearman'`
  - `'hamming'`
  - `'jaccard'`
  - A custom distance function

`knnsearch` also uses the exhaustive search method if your search object is an `ExhaustiveSearcher` model object. The exhaustive search method finds the distance from each query point to every point in `X`, ranks them in ascending order, and returns the *k* points with the smallest distances. For example, this diagram shows the $k = 3$ nearest neighbors.



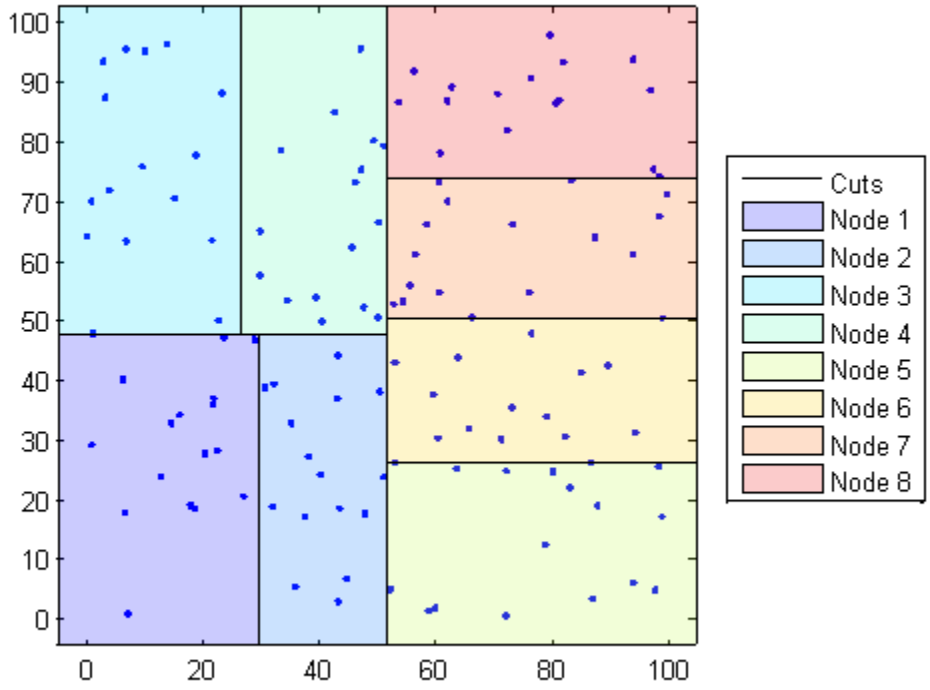
k-Nearest Neighbor Search Using a *K*d-Tree

When your input data meets all of the following criteria, `knnsearch` creates a *K*d-tree by default to find the *k*-nearest neighbors:

- The number of columns of `X` is less than 10.
- `X` is not sparse.
- The distance measure is either:
  - `'euclidean'` (default)
  - `'cityblock'`
  - `'minkowski'`
  - `'chebychev'`

`knnsearch` also uses a *K*d-tree if your search object is a `KDTreeSearcher` model object.

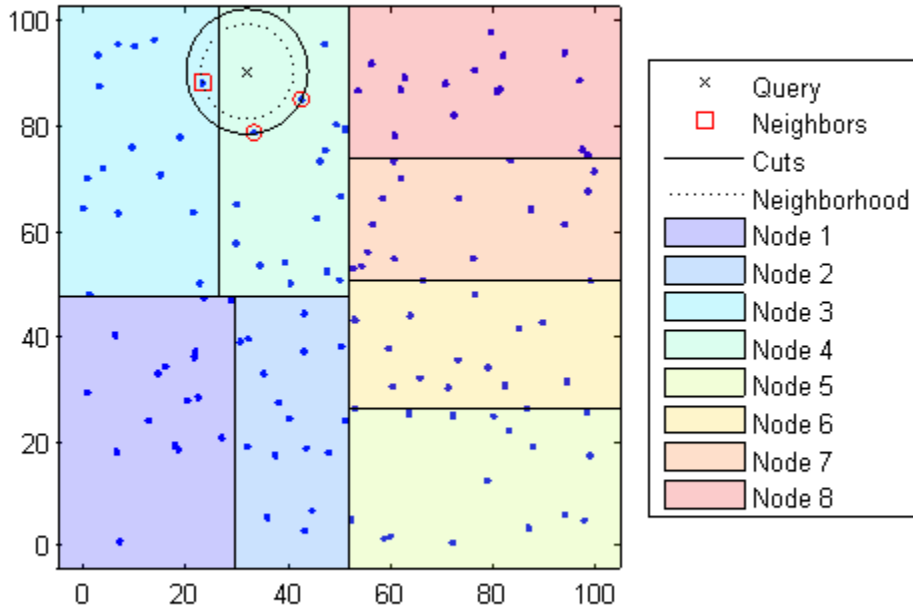
*K*d-trees divide your data into nodes with at most `BucketSize` (default is 50) points per node, based on coordinates (as opposed to categories). The following diagrams illustrate this concept using `patch` objects to color code the different "buckets."



When you want to find the *k*-nearest neighbors to a given query point, `knnsearch` does the following:

1. Determines the node to which the query point belongs. In the following example, the query point (32,90) belongs to Node 4.
2. Finds the closest *k* points within that node and its distance to the query point. In the following example, the points in red circles are equidistant from the query point, and are the closest points to the query point within Node 4.

3. Chooses all other nodes having any area that is within the same distance, in any direction, from the query point to the *k*th closest point. In this example, only Node 3 overlaps the solid black circle centered at the query point with radius equal to the distance to the closest points within Node 4.
4. Searches nodes within that range for any points closer to the query point. In the following example, the point in a red square is slightly closer to the query point than those within Node 4.



Using a *K*d-tree for large data sets with fewer than 10 dimensions (columns) can be much more efficient than using the exhaustive search method, as `knnsearch` needs to calculate only a subset of the distances. To maximize the efficiency of *K*d-trees, use a `KDTreeSearcher` model.

What Are Search Model Objects?

Basically, model objects are a convenient way of storing information. Related models have the same properties with values and types relevant to a specified search method. In addition to storing information within models, you can perform certain actions on models.

You can efficiently perform a k-nearest neighbors search on your search model using `knnsearch`. Or, you can search for all neighbors within a specified radius using your search model and `rangesearch`. In addition, there are a generic `knnsearch` and `rangesearch` functions that search without creating or using a model.

To determine which type of model and search method is best for your data, consider the following:

- Does your data have many columns, say more than 10? The `ExhaustiveSearcher` model may perform better.
- Is your data sparse? Use the `ExhaustiveSearcher` model.
- Do you want to use one of these distance measures to find the nearest neighbors? Use the `ExhaustiveSearcher` model.
  - `'seuclidean'`
  - `'mahalanobis'`
  - `'cosine'`
  - `'correlation'`
  - `'spearman'`
  - `'hamming'`
  - `'jaccard'`
  - A custom distance function
- Is your data set huge (but with fewer than 10 columns)? Use the `KDTreeSearcher` model.
- Are you searching for the nearest neighbors for a large number of query points? Use the `KDTreeSearcher` model.

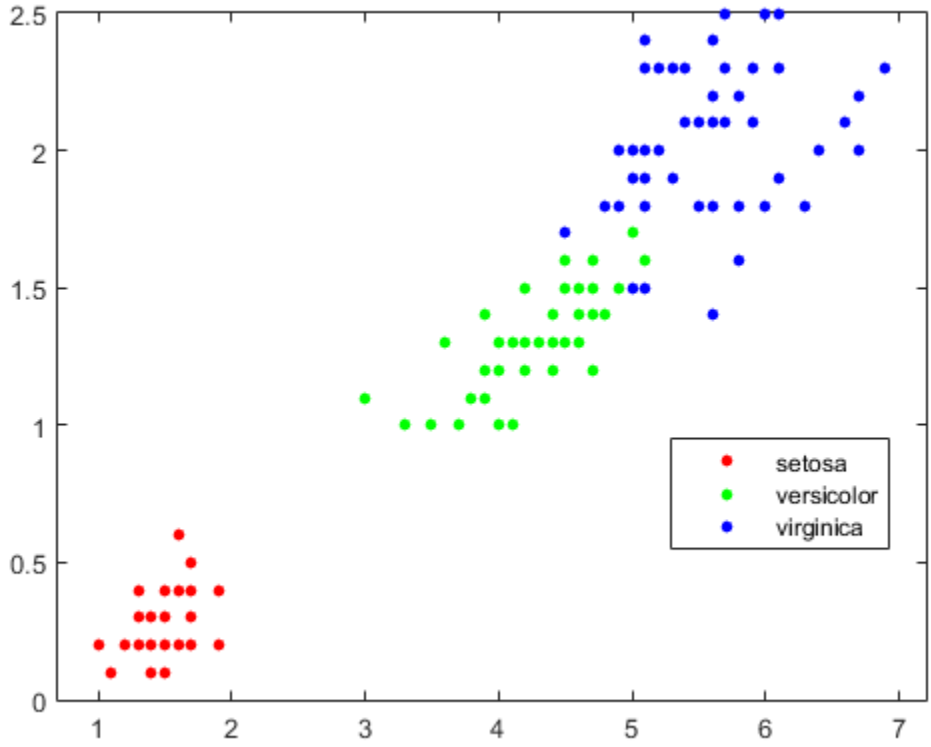
Classify Query Data

This example shows how to classify query data by:

1. Growing a K d-tree
2. Conducting a k nearest neighbors search using the grown tree.
3. Assigning each query point the class with the highest representation among their respective nearest neighbors.

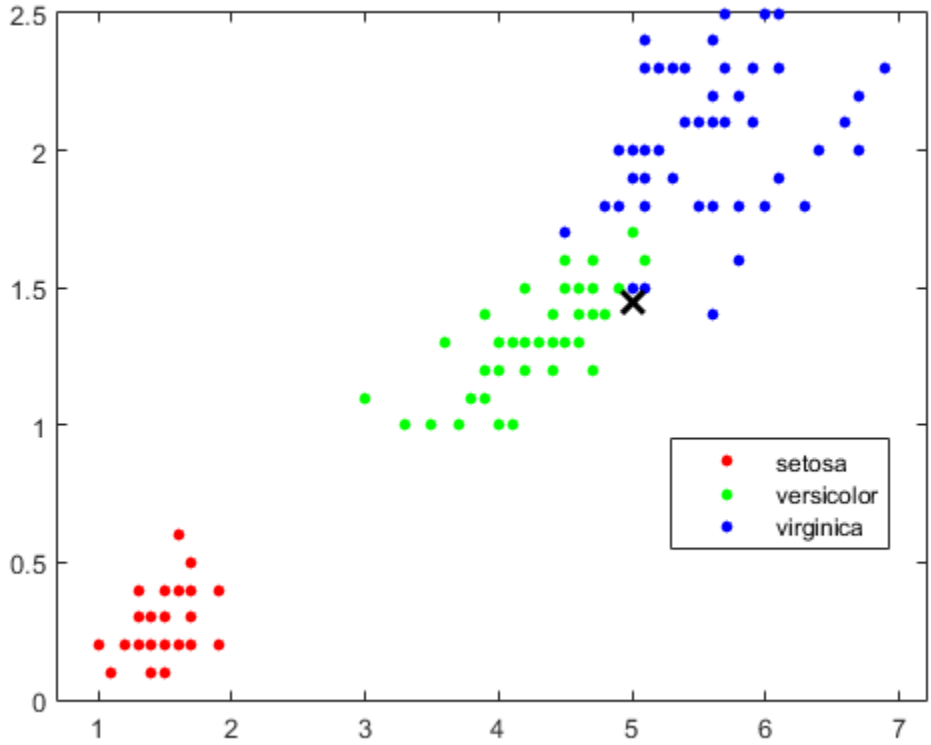
Classify a new point based on the last two columns of the Fisher iris data. Using only the last two columns makes it easier to plot.

```
load fisheriris
x = meas(:,3:4);
gscatter(x(:,1),x(:,2),species)
legend('Location','best')
```



Plot the new point.

```
newpoint = [5 1.45];
line(newpoint(1),newpoint(2),'marker','x','color','k',...
   'markersize',10,'linewidth',2)
```



Prepare a K d-tree neighbor searcher model.

```
Mdl = KDTreeSearcher(x)
```

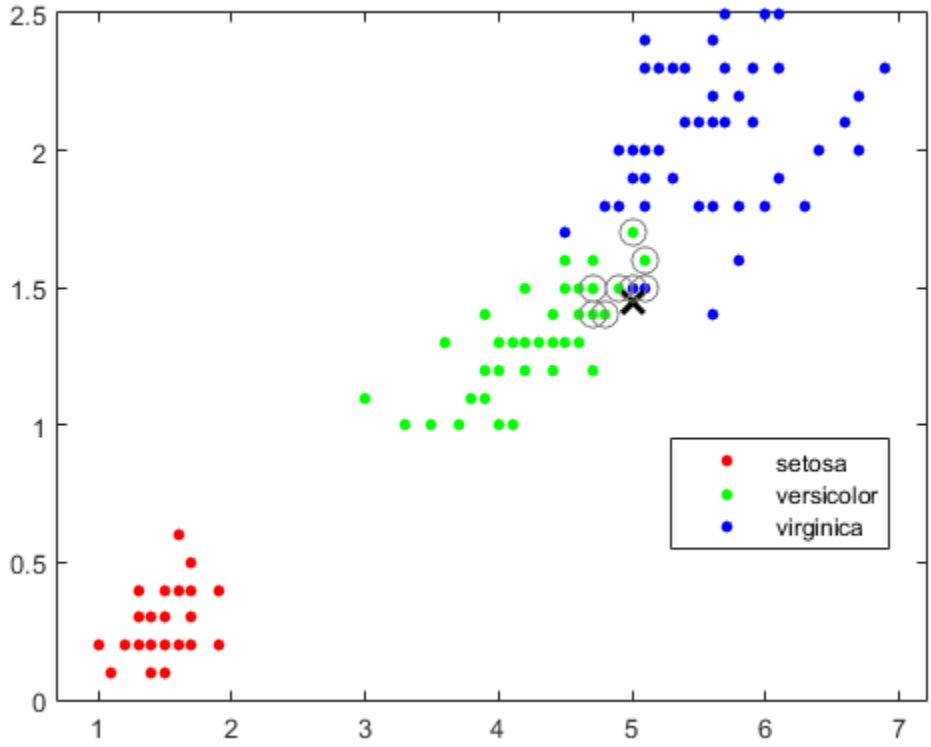
```
Mdl =

  KDTreeSearcher with properties:
```

```
    BucketSize: 50
      Distance: 'euclidean'
DistParameter: []
             X: [150x2 double]
```

`Mdl` is a `KDTreeSearcher` model. By default, the distance metric it uses to search for neighbors is Euclidean distance.

Find the 10 sample points closest to the new point.

```
[n,d] = knnsearch(Mdl,newpoint,'k',10);
line(x(n,1),x(n,2),'color',[.5 .5 .5],'marker','o',...
    'linestyle','none','markersize',10)
```



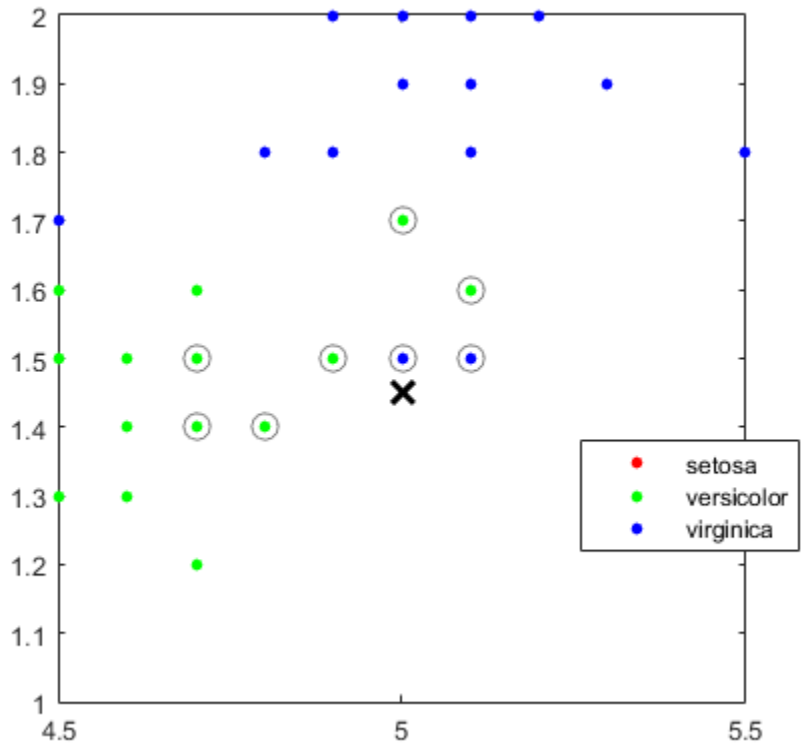
It appears that `knnsearch` has found only the nearest eight neighbors. In fact, this particular dataset contains duplicate values.

```
x(n,:)
```

```
ans =

    5.0000    1.5000
    4.9000    1.5000
    4.9000    1.5000
    5.1000    1.5000
    5.1000    1.6000
    4.8000    1.4000
    5.0000    1.7000
    4.7000    1.4000
    4.7000    1.4000
    4.7000    1.5000
```

Make the axes equal so the calculated distances correspond to the apparent distances on the plot axis equal and zoom in to see the neighbors better.

```
xlim([4.5 5.5]);
ylim([1 2]);
axis square
```



Find the species of the 10 neighbors.

```
tabulate(species(n))
```

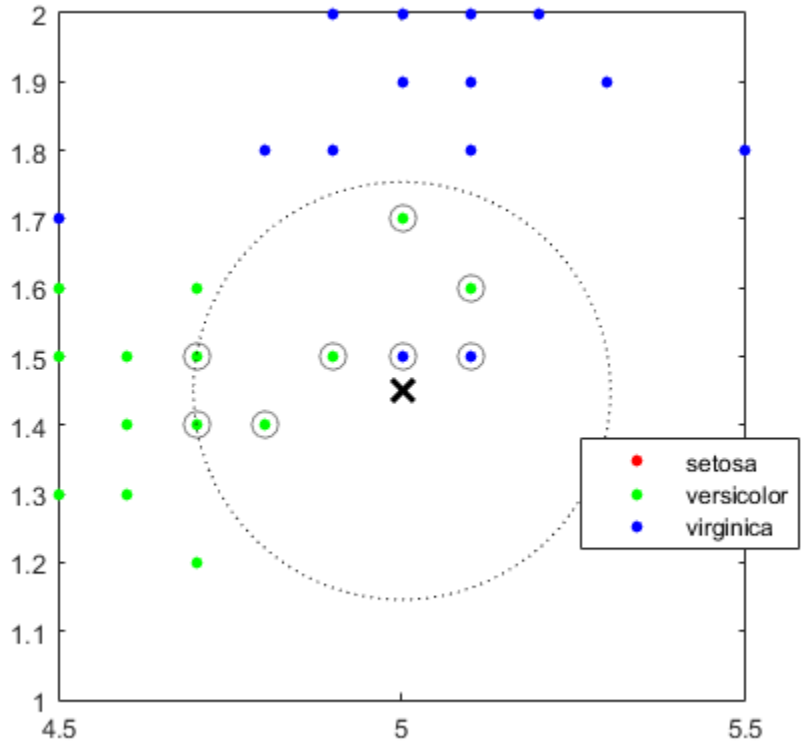
```
       Value    Count   Percent
   virginica        2     20.00%
  versicolor        8     80.00%
```

Using a rule based on the majority vote of the 10 nearest neighbors, you can classify this new point as a versicolor.

Visually identify the neighbors by drawing a circle around the group of them. Define the center and diameter of a circle, based on the location of the new point.

```
ctr = newpoint - d(end);
```

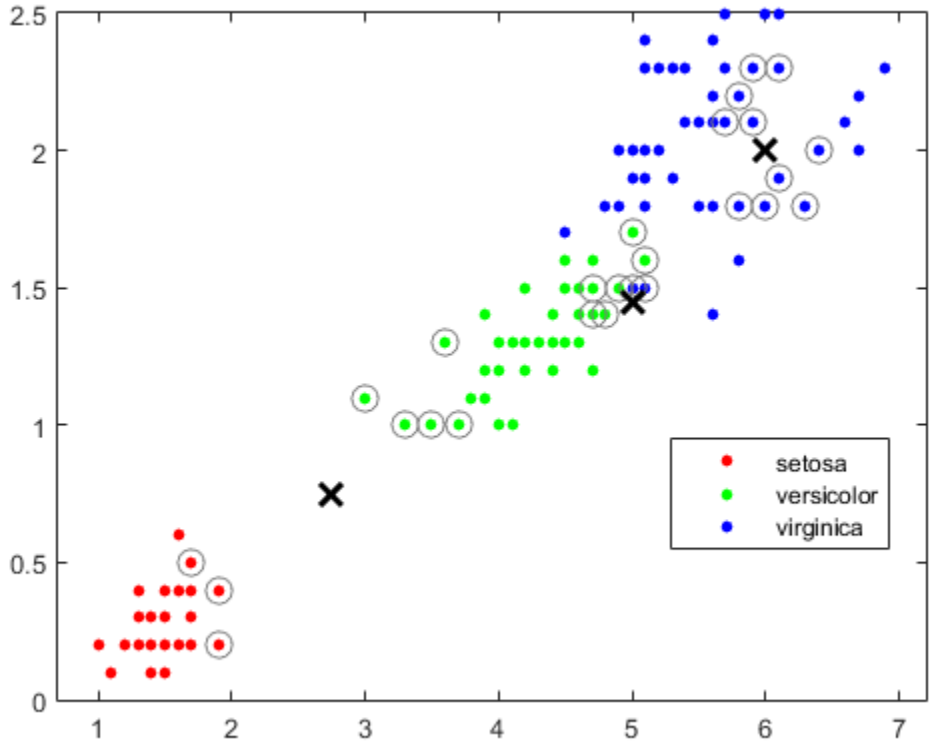
```
diameter = 2*d(end);
% Draw a circle around the 10 nearest neighbors.
h = rectangle('position',[ctr,diameter,diameter],...
    'curvature',[1 1]);
h.LineStyle = ':';
```



Using the same dataset, find the 10 nearest neighbors to three new points.

```
figure
newpoint2 = [5 1.45;6 2;2.75 .75];
gscatter(x(:,1),x(:,2),species)
legend('location','best')
[n2,d2] = knnsearch(Mdl,newpoint2,'k',10);
line(x(n2,1),x(n2,2),'color',[.5 .5 .5],'marker','o',...
```

```
    'linestyle','none','markersize',10)
line(newpoint2(:,1),newpoint2(:,2),'marker','x','color','k',...
    'markersize',10,'linewidth',2,'linestyle','none')
```



Find the species of the 10 nearest neighbors for each new point.

```
tabulate(species(n2(1,:)))
```

```
       Value     Count   Percent
   virginica         2     20.00%
  versicolor         8     80.00%
```

```
tabulate(species(n2(2,:)))
```

```
      Value     Count   Percent
```

```
  virginica       10    100.00%

tabulate(species(n2(3,:)))

      Value    Count   Percent
  versicolor       7     70.00%
      setosa       3     30.00%
```

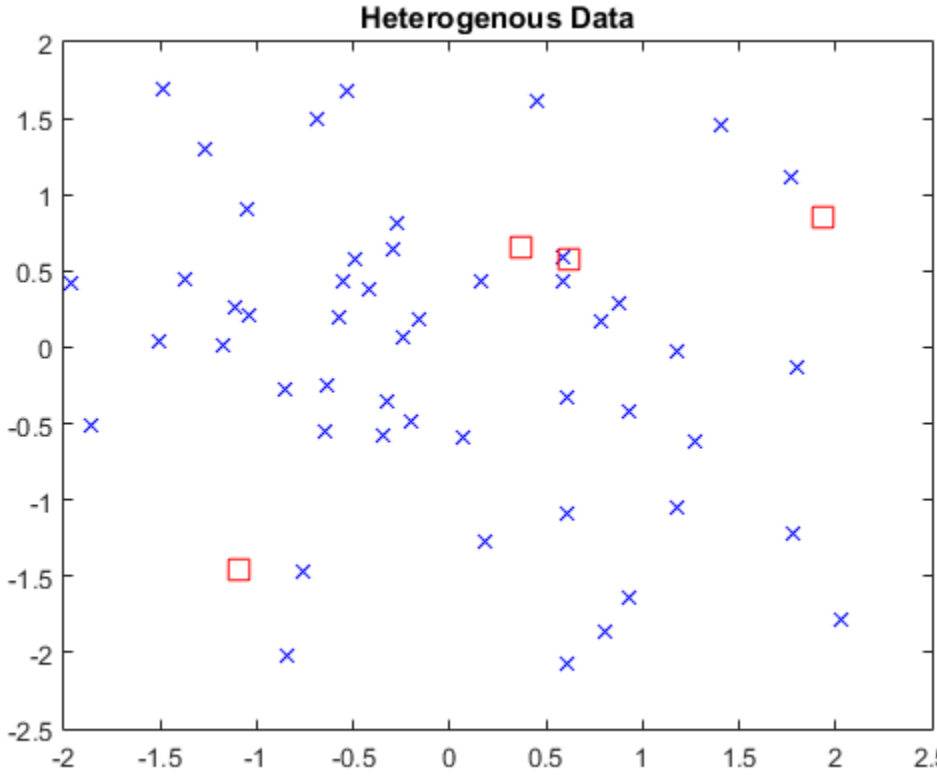
For more examples using `knnsearch` methods and function, see the individual reference pages.

Find Nearest Neighbors Using a Custom Distance Metric

This example shows how to find the indices of the three nearest observations in `X` to each observation in `Y` with respect to the chi-square distance. This distance metric is used in correspondence analysis, particularly in ecological applications.

Randomly generate normally distributed data into two matrices. The number of rows can vary, but the number of columns must be equal. This example uses 2-D data for plotting.

```
rng(1); % For reproducibility
X = randn(50,2);
Y = randn(4,2);

h = zeros(3,1);
figure;
h(1) = plot(X(:,1),X(:,2),'bx');
hold on;
h(2) = plot(Y(:,1),Y(:,2),'rs','MarkerSize',10);
title('Heterogenous Data')
```



The rows of X and Y correspond to observations, and the columns are, in general, dimensions (for example, predictors).

The chi-square distance between j-dimensional points x and z is

$$\chi(x,z) = \sqrt{\sum_{j=1}^{J} w_j (x_j - z_j)^2},$$

where w_j is the weight associated with dimension j.

Choose weights for each dimension, and specify the chi-square distance function. The distance function must:

- Take as input arguments one row of X, e.g., x, and the matrix Z.
- Compare x to each row of Z.
- Return a vector D of length n_z, where n_z is the number of rows of Z. Each element of D is the distance between the observation corresponding to x and the observations corresponding to each row of Z.

```
w = [0.4; 0.6];
chiSqrDist = @(x,Z)sqrt((bsxfun(@minus,x,Z).^2)*w);
```

This example uses arbitrary weights for illustration.

Find the indices of the three nearest observations in X to each observation in Y.

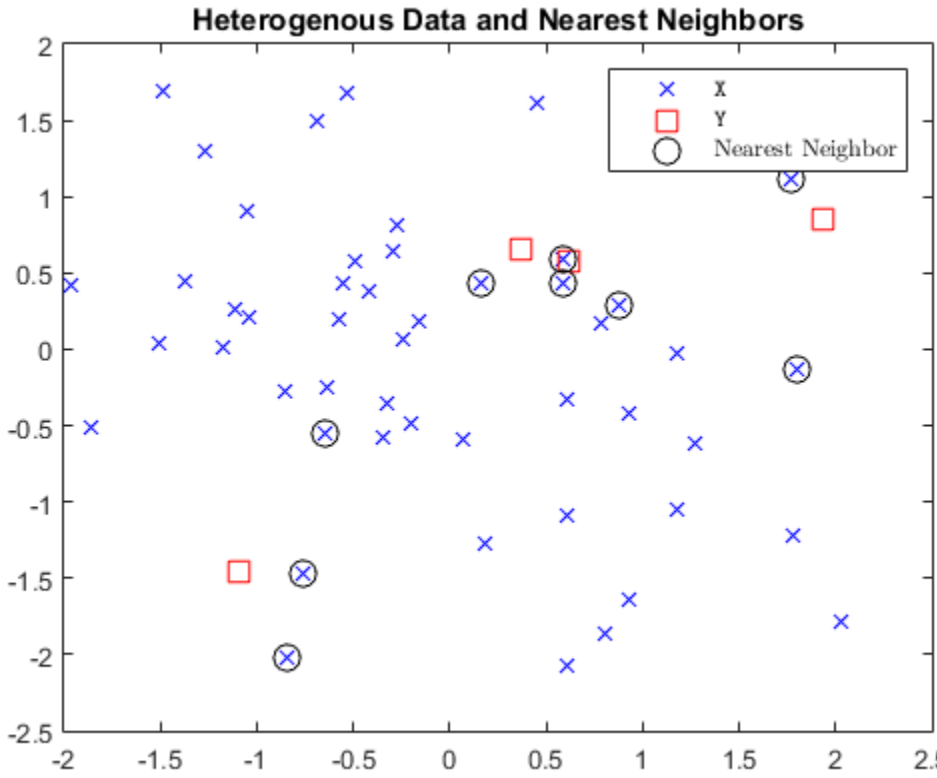
```
k = 3;
[Idx,D] = knnsearch(X,Y,'Distance',chiSqrDist,'k',k);
```

idx and D are 4-by-3 matrices.

- idx(j,1) is the row index of the closest observation in X to observation *j* of Y, and D(j,1) is their distance.
- idx(j,2) is the row index of the next closest observation in X to observation *j* of Y, and D(j,2) is their distance.
- And so on.

Identify the nearest observations in the plot.

```
for j = 1:k;
    h(3) = plot(X(Idx(:,j),1),X(Idx(:,j),2),'ko','MarkerSize',10);
end
legend(h,{'\texttt{X}','\texttt{Y}','Nearest Neighbor'},'Interpreter','latex');
title('Heterogenous Data and Nearest Neighbors')
hold off;
```



Several observations of Y share nearest neighbors.

Verify that the chi-square distance metric is equivalent to the Euclidean distance metric, but with an optional scaling parameter.

```
[IdxE,DE] = knnsearch(X,Y,'Distance','seuclidean','k',k,...
    'Scale',1./(sqrt(w)));
AreDiffIdx = sum(sum(Idx ~= IdxE))
AreDiffDist = sum(sum(abs(D - DE) > eps))
```

```
AreDiffIdx =

     0
```

```
AreDiffDist =

     0
```

The indices and distances between the two implementations of three nearest neighbors are practically equivalent.

K-Nearest Neighbor Classification for Supervised Learning

The `ClassificationKNN` class lets you:

- "Construct a KNN Classifier" on page 16-28
- "Examine the Quality of a KNN Classifier" on page 16-29
- "Predict Classification Based on a KNN Classifier" on page 16-30
- "Modify a KNN Classifier" on page 16-30

Work with the classifier as you would with `ClassificationTree` or `ClassificationDiscriminant`. In particular, prepare your data for classification according to the procedure in "Steps in Supervised Learning" on page 16-2. Then construct the classifier using `fitcknn`.

Construct a KNN Classifier

This example shows how to construct a *k*-nearest neighbor classifier for the Fisher iris data.

Load the Fisher iris data.

```
load fisheriris
X = meas; % use all data for fitting
Y = species; % response data
```

Construct the classifier using `fitcknn`.

```
mdl = fitcknn(X,Y)
```

```
mdl =
```

```
  ClassificationKNN
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
     NumObservations: 150
          Distance: 'euclidean'
      NumNeighbors: 1


  Properties, Methods
```

A default *k*-nearest neighbor classifier uses just the single nearest neighbor. Often, a classifier is more robust with more neighbors than that. Change the neighborhood size of `mdl` to `4`, meaning `mdl` classifies using the four nearest neighbors:

```
mdl.NumNeighbors = 4;
```

Examine the Quality of a KNN Classifier

This example shows how to examine the quality of a *k*-nearest neighbor classifier using resubstitution and cross validation.

Construct a KNN classifier for the Fisher iris data as in "Construct a KNN Classifier" on page 16-28.

```
load fisheriris
X = meas; % use all data for fitting
Y = species; % response data
mdl = fitcknn(X,Y,'NumNeighbors',4);
```

Examine the resubstitution loss, which, by default, is the fraction of misclassifications from the predictions of `mdl`. (For nondefault cost, weights, or priors, see `ClassificationKNN.loss`.)

```
rloss = resubLoss(mdl)
```

```
rloss =

    0.0400
```

The classifier predicts incorrectly for 4% of the training data.

Construct a cross-validated classifier from the model.

```
cvmdl = crossval(mdl);
```

Examine the cross-validation loss, which is the average loss of each cross-validation model when predicting on data that is not used for training.

```
kloss = kfoldLoss(cvmdl)
```

```
kloss =

    0.0600
```

The cross-validated classification accuracy resembles the resubstitution accuracy. Therefore, you can expect `mdl` to misclassify approximately 5% of new data, assuming that the new data has about the same distribution as the training data.

Predict Classification Based on a KNN Classifier

This example shows how to predict classification for a *k*-nearest neighbor classifier.

Construct a default KNN classifier for the Fisher iris data as in "Construct a KNN Classifier" on page 16-28.

```
load fisheriris
X = meas; % use all data for fitting
Y = species; % response data
mdl = fitcknn(X,Y);
```

Predict the classification of an average flower.

```
flwr = mean(X); % an average flower
flwrClass = predict(mdl,flwr)
```

```
flwrClass =

    'versicolor'
```

Modify a KNN Classifier

This example shows how to modify a *k*-nearest neighbor classifier.

Construct a default KNN classifier for the Fisher iris data as in "Construct a KNN Classifier" on page 16-28.

```
load fisheriris
X = meas; % use all data for fitting
Y = species; % response data
mdl = fitcknn(X,Y);
```

Modify the model to use the three nearest neighbors, rather than the default one nearest neighbor.

```
mdl.NumNeighbors = 3;
```

Compare the resubstitution predictions and cross-validation loss with the new number of neighbors.

```
rloss = resubLoss(mdl)
```

```
rloss =

    0.0400
```

```
rng('default')
cvmdl = crossval(mdl,'kfold',5);
kloss = kfoldLoss(cvmdl)
```

```
kloss =

    0.0333
```

The model with three neighbors has lower cross-validated loss than a model with four neighbors (see “Examine the Quality of a KNN Classifier” on page 16-29).

Modify the model to use cosine distance instead of the default, and examine the loss. To use cosine distance, you must recreate the model using the exhaustive search method.

```
cmdl = fitcknn(X,Y,'NSMethod','exhaustive',...
    'Distance','cosine');
cmdl.NumNeighbors = 3;
closs = resubLoss(cmdl)
```

```
closs =

    0.0200
```

The classifier now has lower resubstitution error than before.

Check the quality of a cross-validated version of the new model.

```
cvcmdl = crossval(cmdl);
kcloss = kfoldLoss(cvcmdl)
```

```
kcloss =

    0.0333
```

The cross-validated loss is the same as before. The lesson is that improving the resubstitution error does not necessarily produce a model with better predictions.

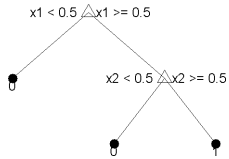
Classification Trees and Regression Trees

In this section...

What Are Classification Trees and Regression Trees?

Classification trees and regression trees predict responses to data. To predict a response, follow the decisions in the tree from the root (beginning) node down to a leaf node. The leaf node contains the response. Classification trees give responses that are nominal, such as `'true'` or `'false'`. Regression trees give numeric responses.

Statistics and Machine Learning Toolbox trees are binary. Each step in a prediction involves checking the value of one predictor (variable). For example, here is a simple classification tree:



This tree predicts classifications based on two predictors, `x1` and `x2`. To predict, start at the top node, represented by a triangle (Δ). The first decision is whether `x1` is smaller than `0.5`. If so, follow the left branch, and see that the tree classifies the data as type `0`.

If, however, `x1` exceeds `0.5`, then follow the right branch to the lower-right triangle node. Here the tree asks if `x2` is smaller than `0.5`. If so, then follow the left branch to see that the tree classifies the data as type `0`. If not, then follow the right branch to see that the that the tree classifies the data as type `1`.

To learn how to prepare your data for classification or regression using decision trees, see “Steps in Supervised Learning” on page 16-2.

Creating a Classification Tree

To create a classification tree for the `ionosphere` data:

```
load ionosphere % contains X and Y variables
ctree = fitctree(X,Y)

ctree =

  ClassificationTree
           PredictorNames: {1x34 cell}
             ResponseName: 'Y'
                ClassNames: {'b'  'g'}
           ScoreTransform: 'none'
    CategoricalPredictors: []
            NumObservations: 351


  Properties, Methods
```

Creating a Regression Tree

To create a regression tree for the `carsmall` data based on the `Horsepower` and `Weight` vectors for data, and `MPG` vector for response:

```
load carsmall % contains Horsepower, Weight, MPG
X = [Horsepower Weight];
rtree = fitrtree(X,MPG)

rtree =

  RegressionTree
           PredictorNames: {'x1'  'x2'}
             ResponseName: 'Y'
        ResponseTransform: 'none'
    CategoricalPredictors: []
            NumObservations: 94


  Properties, Methods
```

Viewing a Classification or Regression Tree

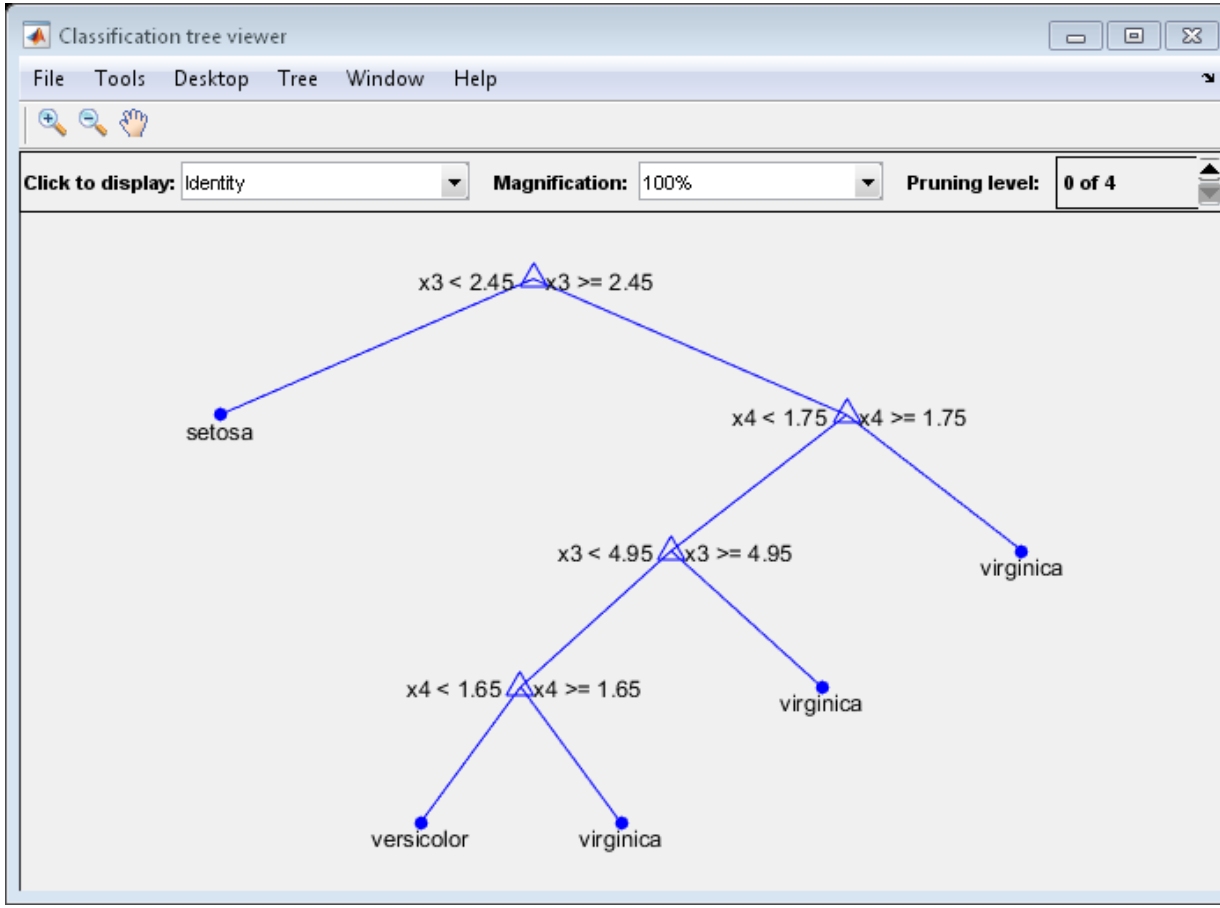
This example shows how to view a classification or a regression tree. There are two ways to view a tree: `view(tree)` returns a text description and `view(tree,'mode','graph')` returns a graphic description of the tree.

Create and view a classification tree.

```
load fisheriris % load the sample data
ctree = fitctree(meas,species); % create classification tree
view(ctree) % text description
```

```
Decision tree for classification
1  if x3<2.45 then node 2 elseif x3>=2.45 then node 3 else setosa
2  class = setosa
3  if x4<1.75 then node 4 elseif x4>=1.75 then node 5 else versicolor
4  if x3<4.95 then node 6 elseif x3>=4.95 then node 7 else versicolor
5  class = virginica
6  if x4<1.65 then node 8 elseif x4>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica
```

```
view(ctree,'mode','graph') % graphic description
```



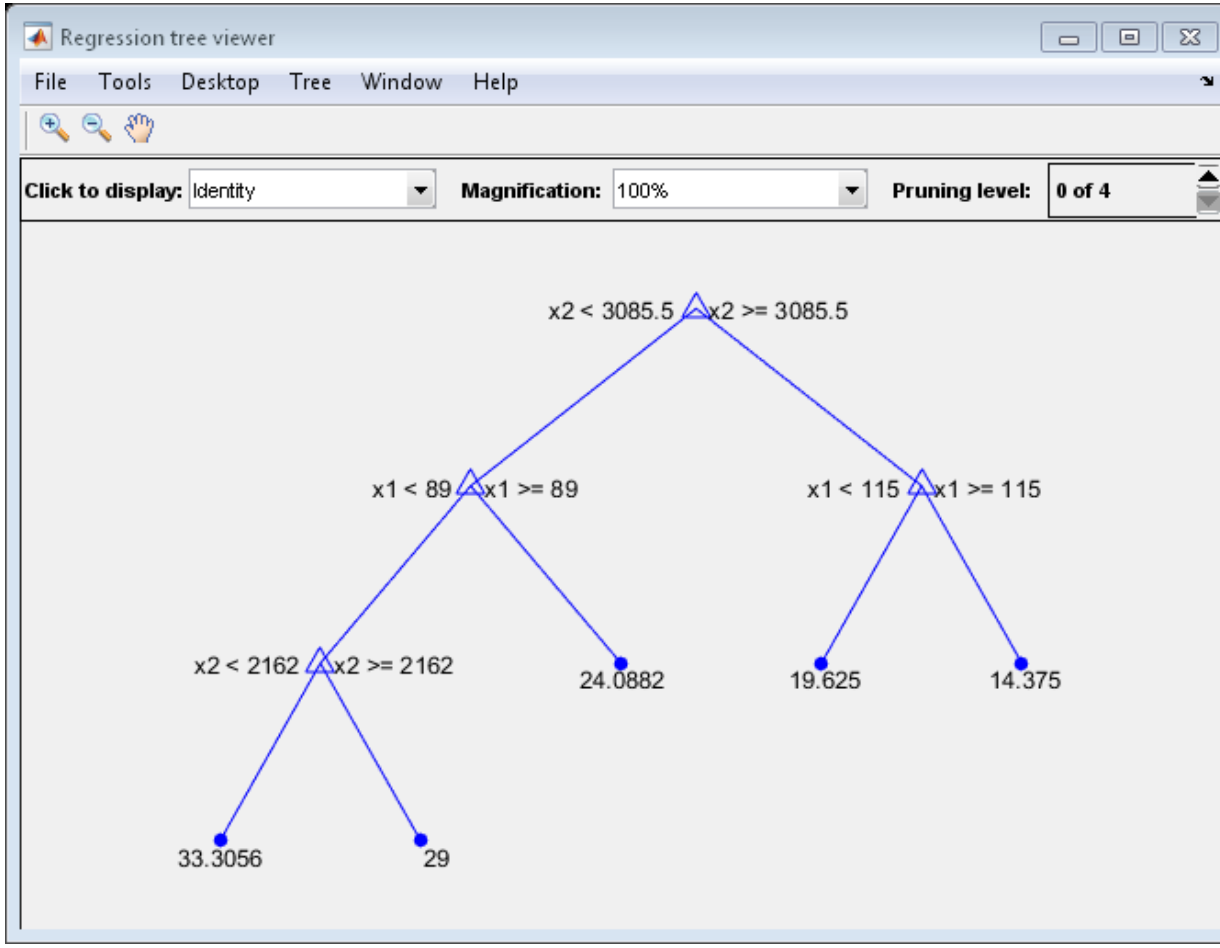
Now, create and view a regression tree.

```
load carsmall % load the sample data, contains Horsepower, Weight, MPG
X = [Horsepower Weight];
rtree = fitrtree(X,MPG,'MinParent',30); % create classification tree
view(rtree) % text description
```

```
Decision tree for regression
1  if x2<3085.5 then node 2 elseif x2>=3085.5 then node 3 else 23.7181
2  if x1<89 then node 4 elseif x1>=89 then node 5 else 28.7931
3  if x1<115 then node 6 elseif x1>=115 then node 7 else 15.5417
```

```
4  if x2<2162 then node 8 elseif x2>=2162 then node 9 else 30.9375
5  fit = 24.0882
6  fit = 19.625
7  fit = 14.375
8  fit = 33.3056
9  fit = 29
```

```
view(rtree,'mode','graph') % graphic description
```



How the Fit Methods Create Trees

The `fitctree` and `fitrtree` methods perform the following steps to create decision trees:

1. Start with all input data, and examine all possible binary splits on every predictor.
2. Select a split with best optimization criterion.

    - If the split leads to a child node having too few observations (less than the `MinLeafSize` parameter), select a split with the best optimization criterion subject to the `MinLeafSize` constraint.

3. Impose the split.
4. Repeat recursively for the two child nodes.

The explanation requires two more items: description of the optimization criterion, and stopping rule.

Stopping rule: Stop splitting when any of the following hold:

- The node is *pure*.
    - For classification, a node is pure if it contains only observations of one class.
    - For regression, a node is pure if the mean squared error (MSE) for the observed response in this node drops below the MSE for the observed response in the entire data multiplied by the tolerance on quadratic error per node (`QuadraticErrorTolerance` parameter).
- There are fewer than `MinParentSize` observations in this node.
- Any split imposed on this node produces children with fewer than `MinLeafSize` observations.
- The algorithm splits `MaxNumSplits` nodes.

Optimization criterion:

- Regression: mean-squared error (MSE). Choose a split to minimize the MSE of predictions compared to the training data.
- Classification: One of three measures, depending on the setting of the `SplitCriterion` name-value pair:
    - `'gdi'` (Gini's diversity index, the default)
    - `'twoing'`
    - `'deviance'`

    For details, see `ClassificationTree` "Definitions" on page 22-443.

For a continuous predictor, a tree can split halfway between any two adjacent unique values found for this predictor. For a categorical predictor with L levels, a classification

tree needs to consider $2^{L-1}-1$ splits to find the optimal split. Alternatively, you can choose a heuristic algorithm to find a good split, as described in "Splitting Categorical Predictors" on page 16-65.

For dual-core systems and above, `fitctree` and `fitrtree` parallelize training decision trees using Intel® Threading Building Blocks (TBB). For details on Intel TBB, see https://software.intel.com/en-us/intel-tbb.

Predicting Responses With Classification and Regression Trees

After creating a tree, you can easily predict responses for new data. Suppose `Xnew` is new data that has the same number of columns as the original data `X`. To predict the classification or regression based on the tree and the new data, enter

```
Ynew = predict(tree,Xnew);
```

For each row of data in `Xnew`, `predict` runs through the decisions in `tree` and gives the resulting prediction in the corresponding element of `Ynew`. For more information for classification, see the classification `predict` reference page; for regression, see the regression `predict` reference page.

For example, to find the predicted classification of a point at the mean of the `ionosphere` data:

```
load ionosphere % contains X and Y variables
ctree = fitctree(X,Y);
Ynew = predict(ctree,mean(X))
```

```
Ynew =

    'g'
```

To find the predicted `MPG` of a point at the mean of the `carsmall` data:

```
load carsmall % contains Horsepower, Weight, MPG
X = [Horsepower Weight];
rtree = fitrtree(X,MPG);
Ynew = predict(rtree,mean(X))
```

```
Ynew =

   28.7931
```

Predict Out-of-Sample Responses of Subtrees

This example hows how to predict out-of-sample responses of regression trees, and then plot the results.

Load the `carsmall` data set. Consider `Weight` as a predictor of the response `MPG`.

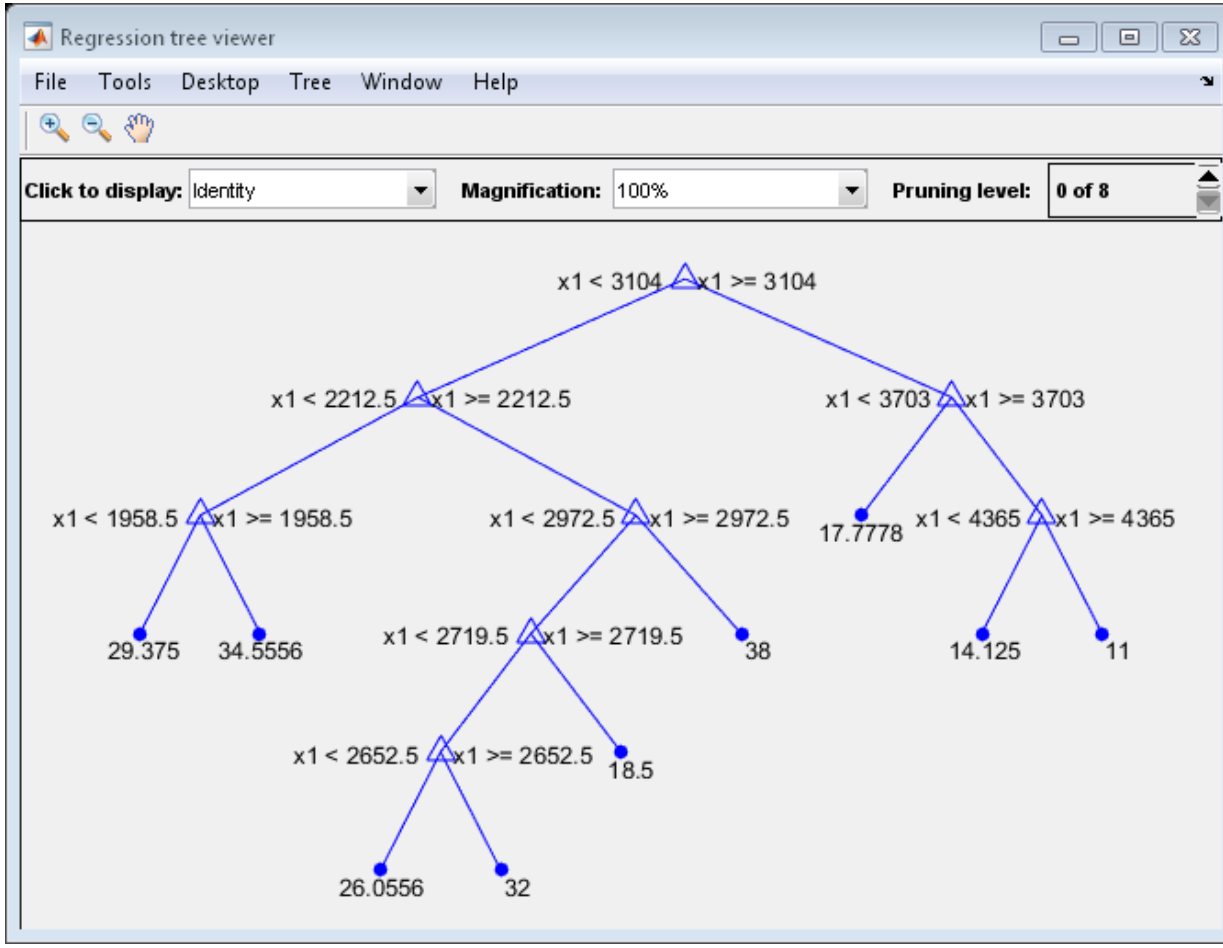
```
load carsmall
idxNaN = isnan(MPG + Weight);
X = Weight(~idxNaN);
Y = MPG(~idxNaN);
n = numel(X);
```

Partition the data into training (50%) and validation (50%) sets.

```
rng(1) % For reproducibility
idxTrn = false(n,1);
idxTrn(randsample(n,round(0.5*n))) = true; % Training set logical indices
idxVal = idxTrn == false;                  % Validation set logical indices
```

Grow a regression tree using the training observations.

```
Mdl = fitrtree(X(idxTrn),Y(idxTrn));
view(Mdl,'Mode','graph')
```



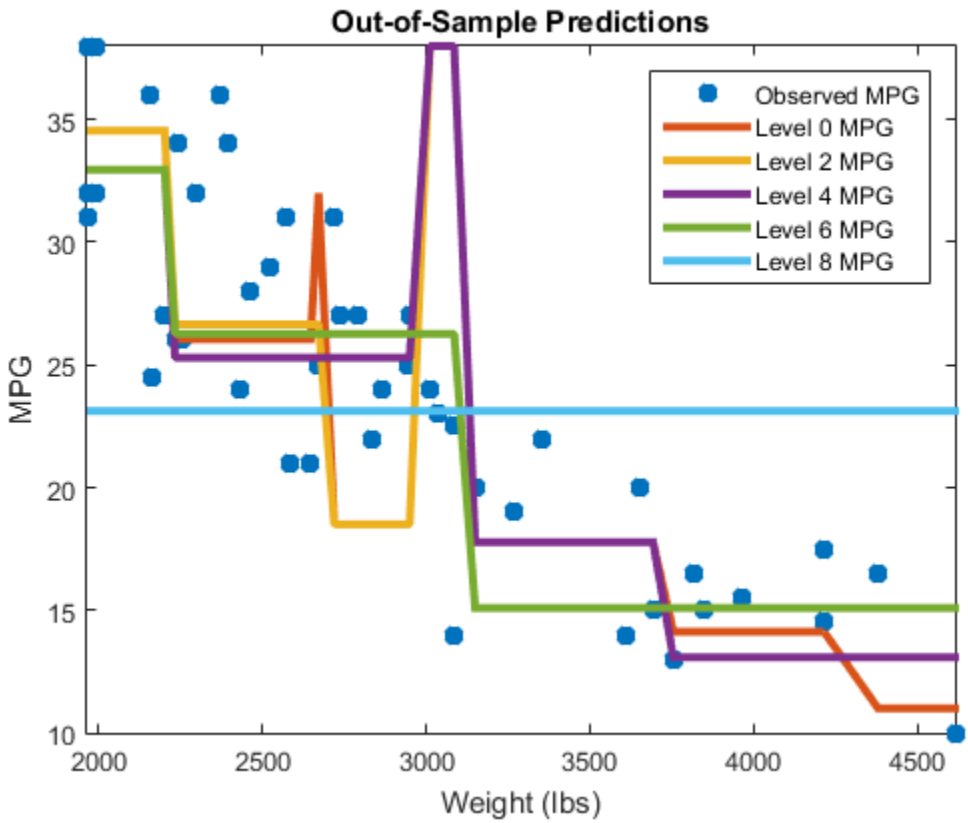
Compute fitted values of the validation observations for each of several subtrees.

```
m = max(Mdl.PruneList);
pruneLevels = 0:2:m; % Pruning levels to consider
z = numel(pruneLevels);
Yfit = predict(Mdl,X(idxVal),'SubTrees',pruneLevels);
```

`Yfit` is an `n`-by-`z` matrix of fitted values in which the rows correspond to observations and the columns correspond to a subtree.

Plot `Yfit` and `Y` against `X`.

```
figure;
sortDat = sortrows([X(idxVal) Y(idxVal) Yfit],1); % Sort all data with respect to X
plot(sortDat(:,1),sortDat(:,2),'*');
hold on;
plot(repmat(sortDat(:,1),1,size(Yfit,2)),sortDat(:,3:end));
lev = cellstr(num2str((pruneLevels)','Level %d MPG'));
legend(['Observed MPG'; lev])
title 'Out-of-Sample Predictions'
xlabel 'Weight (lbs)';
ylabel 'MPG';
h = findobj(gcf);
axis tight;
set(h(4:end),'LineWidth',3) % Widen all lines
```



The values of `Yfit` for lower pruning levels tend to follow the data more closely than higher levels. Higher pruning levels tend to be flat for large `X` intervals.

Improving Classification Trees and Regression Trees

You can tune trees by setting name-value pairs in `fitctree` and `fitrtree`. The remainder of this section describes how to determine the quality of a tree, how to decide which name-value pairs to set, and how to control the size of a tree:

Examining Resubstitution Error

Resubstitution error is the difference between the response training data and the predictions the tree makes of the response based on the input training data. If the resubstitution error is high, you cannot expect the predictions of the tree to be good. However, having low resubstitution error does not guarantee good predictions for new data. Resubstitution error is often an overly optimistic estimate of the predictive error on new data.

Example: Resubstitution Error of a Classification Tree

Examine the resubstitution error of a default classification tree for the Fisher iris data:

```
load fisheriris
ctree = fitctree(meas,species);
resuberror = resubLoss(ctree)
```

```
resuberror =

    0.0200
```

The tree classifies nearly all the Fisher iris data correctly.

Cross Validation

To get a better sense of the predictive accuracy of your tree for new data, cross validate the tree. By default, cross validation splits the training data into 10 parts at random. It

trains 10 new trees, each one on nine parts of the data. It then examines the predictive accuracy of each new tree on the data not included in training that tree. This method gives a good estimate of the predictive accuracy of the resulting tree, since it tests the new trees on new data.

Cross Validate a Regression Tree

This example shows how to examine the resubstitution and cross-validation accuracy of a regression tree for predicting mileage based on the `carsmall` data.

Load the `carsmall` data set. Consider acceleration, displacement, horsepower, and weight as predictors of MPG.

```
load carsmall
X = [Acceleration Displacement Horsepower Weight];
```

Grow a regression tree using all of the observations.

```
rtree = fitrtree(X,MPG);
```

Compute the in-sample error.

```
resuberror = resubLoss(rtree)
```

```
resuberror =

    4.7188
```

The resubstitution loss for a regression tree is the mean-squared error. The resulting value indicates that a typical predictive error for the tree is about the square root of 4.7, or a bit over 2.

Estimate the cross-validation MSE.

```
rng 'default';
cvrtree = crossval(rtree);
cvloss = kfoldLoss(cvrtree)
```

```
cvloss =

   23.8065
```

The cross-validated loss is almost 25, meaning a typical predictive error for the tree on new data is about 5. This demonstrates that cross-validated loss is usually higher than simple resubstitution loss.

Control Depth or "Leafiness"

When you grow a decision tree, consider its simplicity and predictive power. A deep tree with many leaves is usually highly accurate on the training data. However, the tree is not guaranteed to show a comparable accuracy on an independent test set. A leafy tree tends to overtrain (or overfit), and its test accuracy is often far less than its training (resubstitution) accuracy. In contrast, a shallow tree does not attain high training accuracy. But a shallow tree can be more robust — its training accuracy could be close to that of a representative test set. Also, a shallow tree is easy to interpret. If you do not have enough data for training and test, estimate tree accuracy by cross validation.

`fitctree` and `fitrtree` have three name-value pair arguments that control the depth of resulting decision trees:

- `MaxNumSplits` — The maximal number of branch node splits is `MaxNumSplits` per tree. Set a large value for `MaxNumSplits` to get a deep tree. The default is `size(X,1) - 1`.
- `MinLeafSize` — Each leaf has at least `MinLeafSize` observations. Set small values of `MinLeafSize` to get deep trees. The default is `1`.
- `MinParentSize` — Each branch node in the tree has at least `MinParentSize` observations. Set small values of `MinParentSize` to get deep trees. The default is `10`.

If you specify `MinParentSize` and `MinLeafSize`, the learner uses the setting that yields trees with larger leaves (i.e., shallower trees):
`MinParent = max(MinParentSize,2*MinLeafSize)`

If you supply `MaxNumSplits`, the software splits a tree until one of the three splitting criteria is satisfied.

For an alternative method of controlling the tree depth, see "Pruning" on page 16-51.

Select Appropriate Tree Depth

This example shows how to control the depth of a decision tree, and how to choose an appropriate depth.

Load the `ionosphere` data:

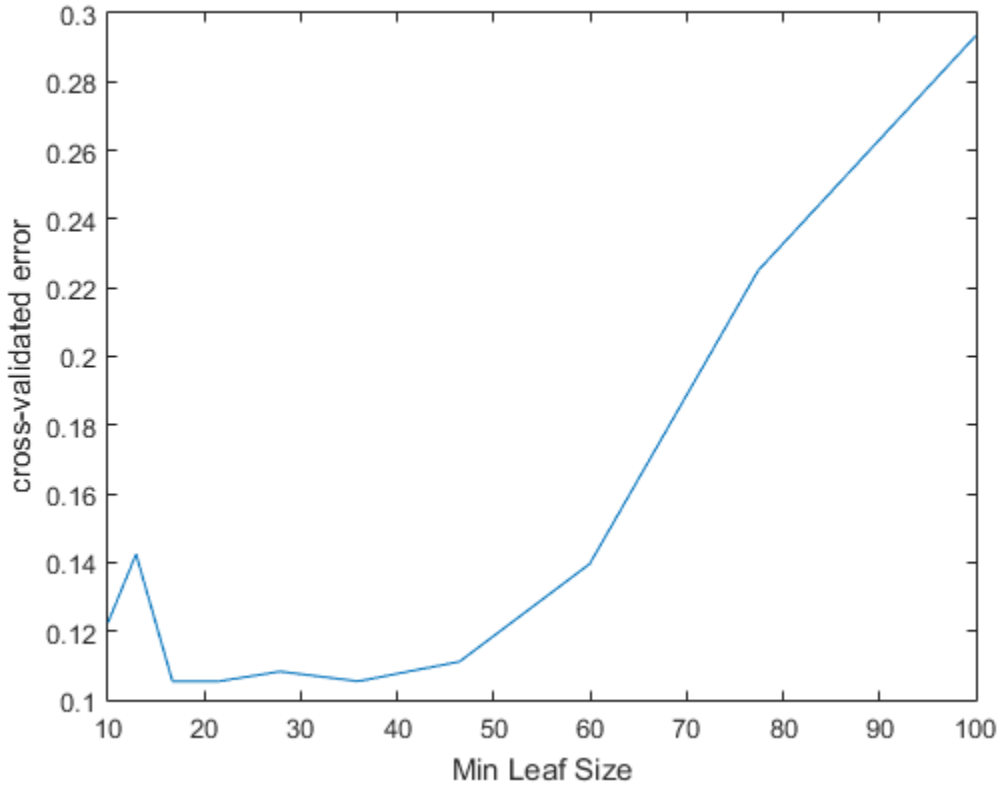
```
load ionosphere
```

Generate minimum leaf occupancies for classification trees from `10` to `100`, spaced exponentially apart:

```
leafs = logspace(1,2,10);
```

Create cross validated classification trees for the `ionosphere` data with minimum leaf occupancies from `leafs`:

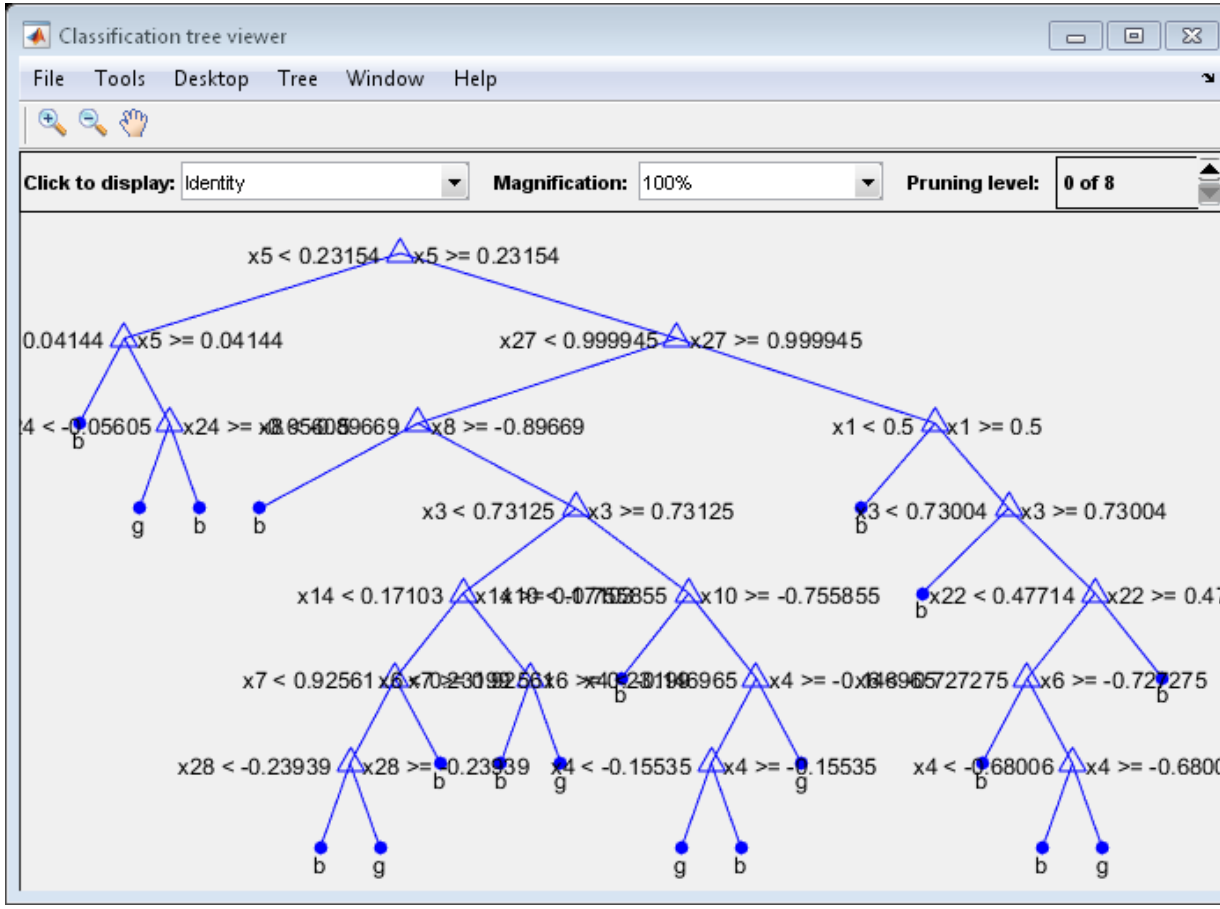
```
rng('default')
N = numel(leafs);
err = zeros(N,1);
for n=1:N
    t = fitctree(X,Y,'CrossVal','On',...
        'MinLeaf',leafs(n));
    err(n) = kfoldLoss(t);
end
plot(leafs,err);
xlabel('Min Leaf Size');
ylabel('cross-validated error');
```

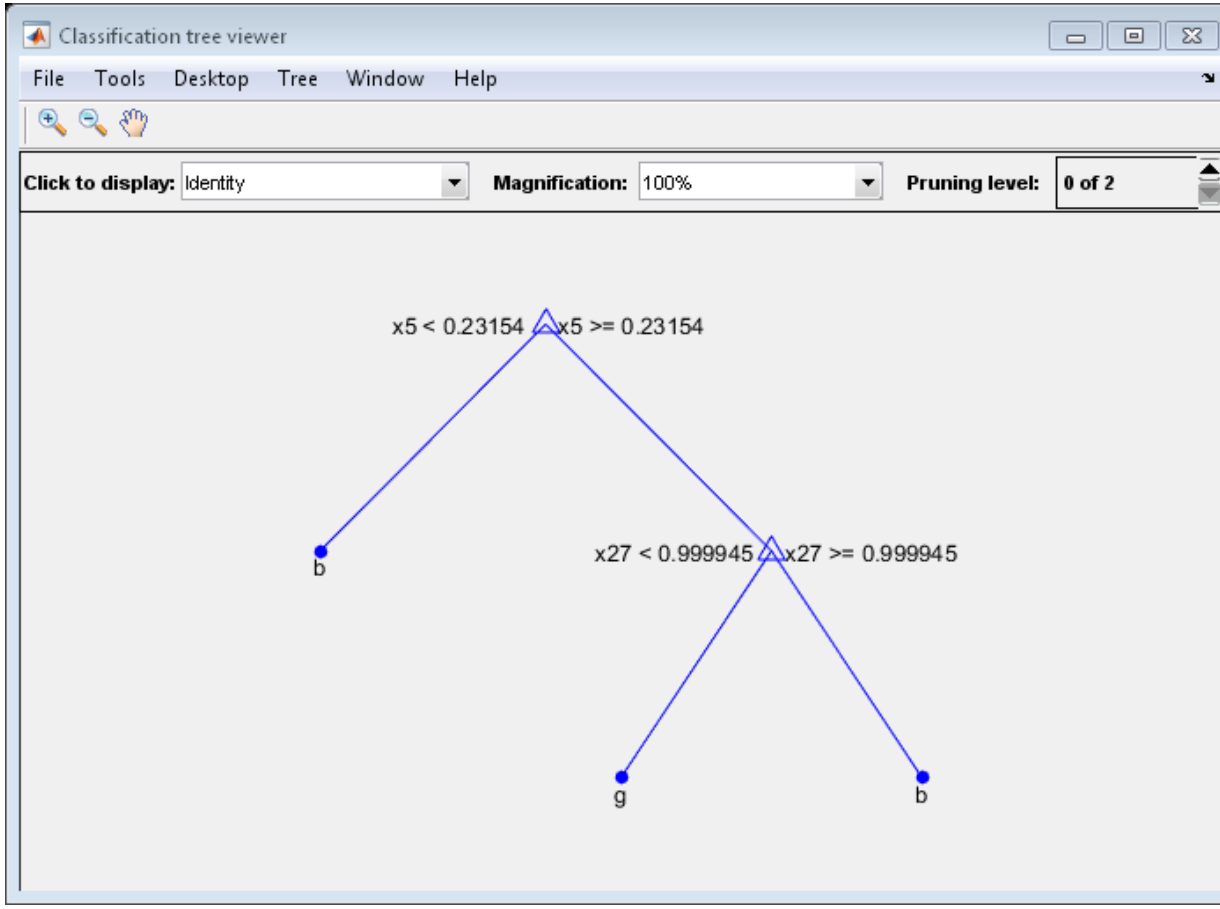


The best leaf size is between about 20 and 50 observations per leaf.

Compare the near-optimal tree with at least 40 observations per leaf with the default tree, which uses 10 observations per parent node and 1 observation per leaf.

```
DefaultTree = fitctree(X,Y);
view(DefaultTree,'Mode','Graph')

OptimalTree = fitctree(X,Y,'minleaf',40);
view(OptimalTree,'mode','graph')
```


Classification tree viewer
File Tools Desktop Tree Window Help
Click to display: Identity
Magnification: 100%
Pruning level: 0 of 8
x5 < 0.23154
x5 >= 0.23154
0.04144
x5 >= 0.04144
x27 < 0.999945
x27 >= 0.999945
x8 >= -0.89669
x1 < 0.5
x1 >= 0.5
x3 < 0.73125
x3 >= 0.73125
x3 < 0.73004
x3 >= 0.73004
x14 < 0.17103
x10 >= -0.755855
x22 < 0.47714
x7 < 0.92561
x4 >= -0.15535
x6 >= -0.727275
x28 < -0.23939
x4 < -0.15535
x4 >= -0.15535
x4 >= -0.6800




```
resubOpt = resubLoss(OptimalTree);
lossOpt = kfoldLoss(crossval(OptimalTree));
resubDefault = resubLoss(DefaultTree);
lossDefault = kfoldLoss(crossval(DefaultTree));
resubOpt,resubDefault,lossOpt,lossDefault
```

```
resubOpt =

    0.0883
```

```
resubDefault =

    0.0114


lossOpt =

    0.1054


lossDefault =

    0.1111
```

The near-optimal tree is much smaller and gives a much higher resubstitution error. Yet it gives similar accuracy for cross-validated data.

Pruning

Pruning optimizes tree depth (leafiness) is by merging leaves on the same tree branch. “Control Depth or “Leafiness”” on page 16-46 describes one method for selecting the optimal depth for a tree. Unlike in that section, you do not need to grow a new tree for every node size. Instead, grow a deep tree, and prune it to the level you choose.

Prune a tree at the command line using the `prune` method (classification) or `prune` method (regression). Alternatively, prune a tree interactively with the tree viewer:

```
view(tree,'mode','graph')
```

To prune a tree, the tree must contain a pruning sequence. By default, both `fitctree` and `fitrtree` calculate a pruning sequence for a tree during construction. If you construct a tree with the `'Prune'` name-value pair set to `'off'`, or if you prune a tree to a smaller level, the tree does not contain the full pruning sequence. Generate the full pruning sequence with the `prune` method (classification) or `prune` method (regression).

Prune a Classification Tree

This example creates a classification tree for the `ionosphere` data, and prunes it to a good level.

Load the `ionosphere` data:

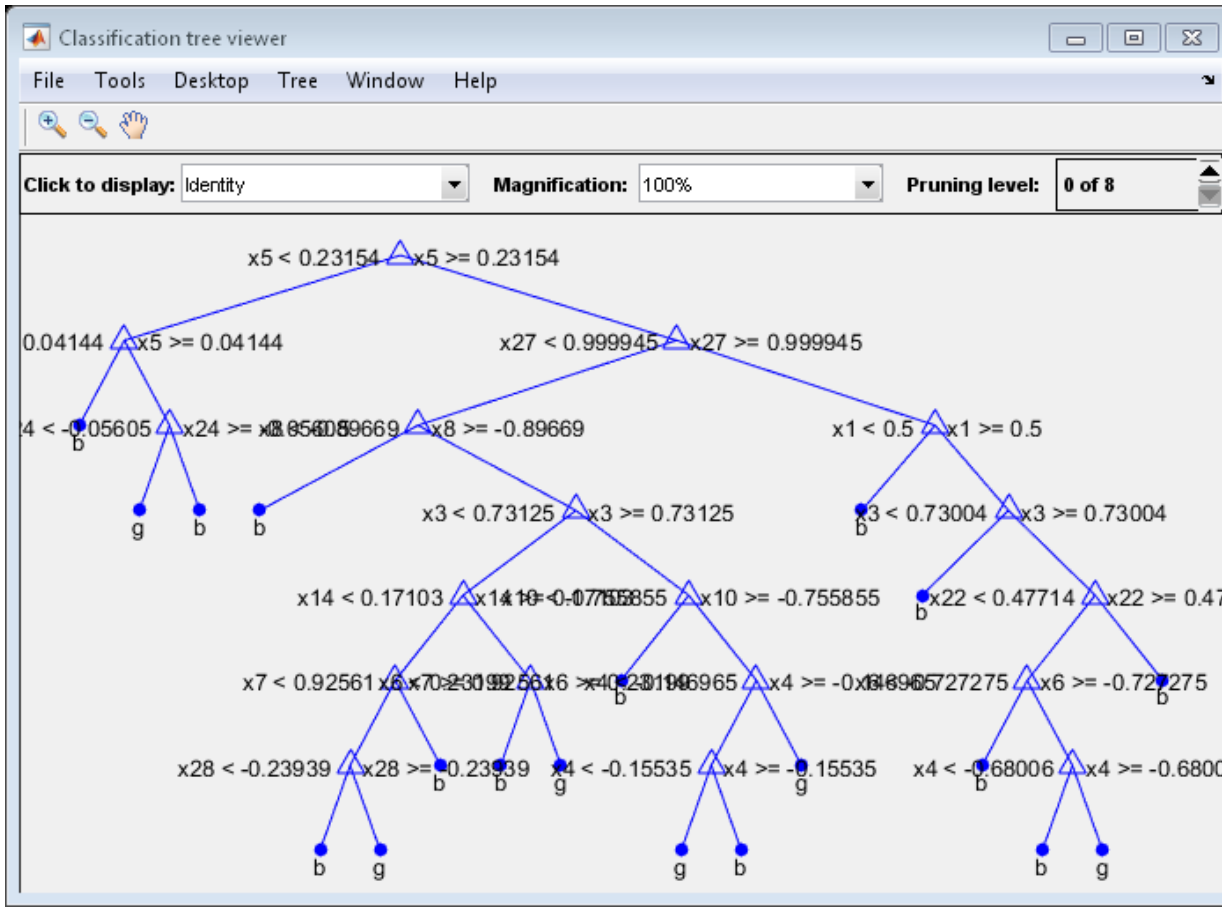
```
load ionosphere
```

Construct a default classification tree for the data:

```
tree = fitctree(X,Y);
```

View the tree in the interactive viewer:

```
view(tree,'Mode','Graph')
```



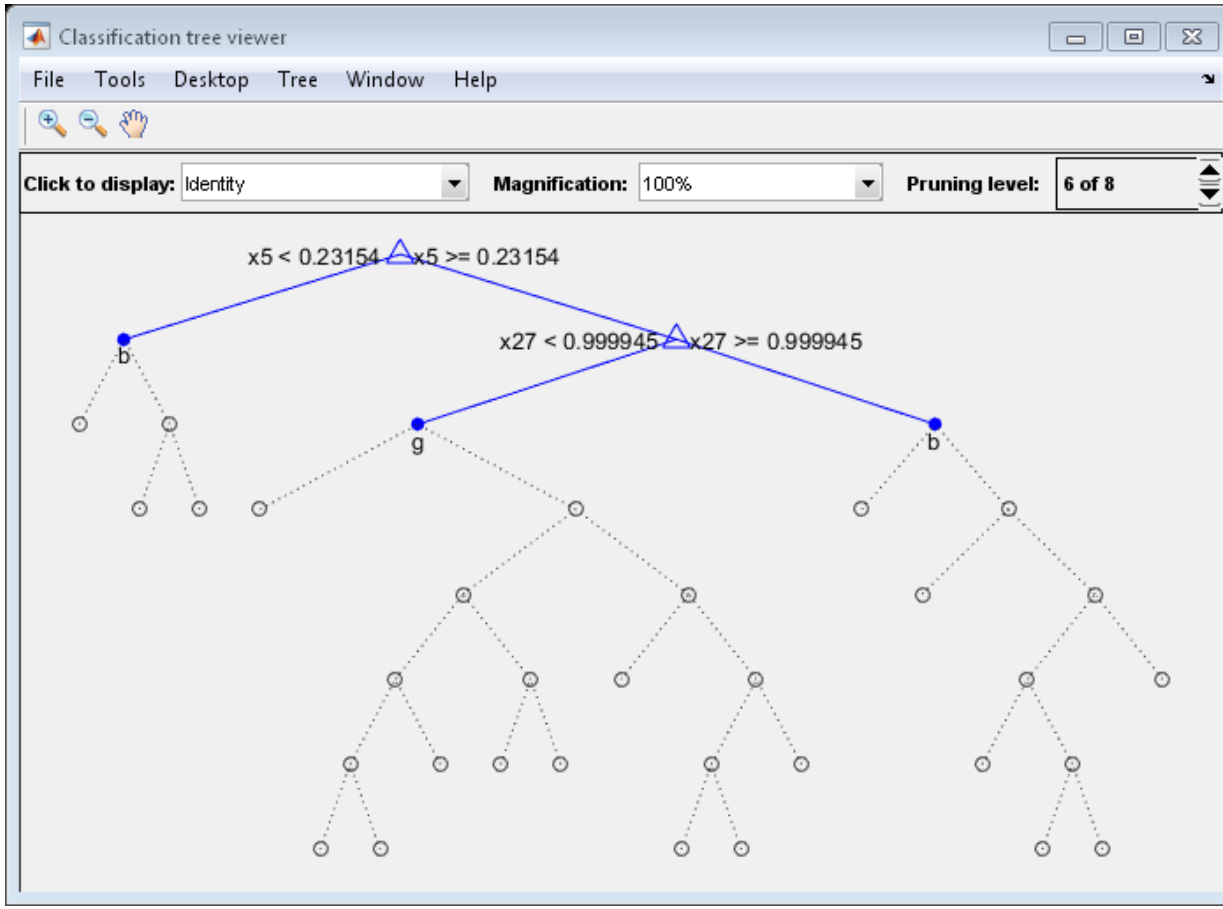
Find the optimal pruning level by minimizing cross-validated loss:

```
[~,~,~,bestlevel] = cvLoss(tree,...
```

```
    'SubTrees','All','TreeSize','min')

bestlevel =

     6
```

Prune the tree to level 6:

```
view(tree,'Mode','Graph','Prune',6)
```



Alternatively, use the interactive window to prune the tree.

The pruned tree is the same as the near-optimal tree in the "Select Appropriate Tree Depth" example.

Set `'TreeSize'` to `'SE'` (default) to find the maximal pruning level for which the tree error does not exceed the error from the best level plus one standard deviation:

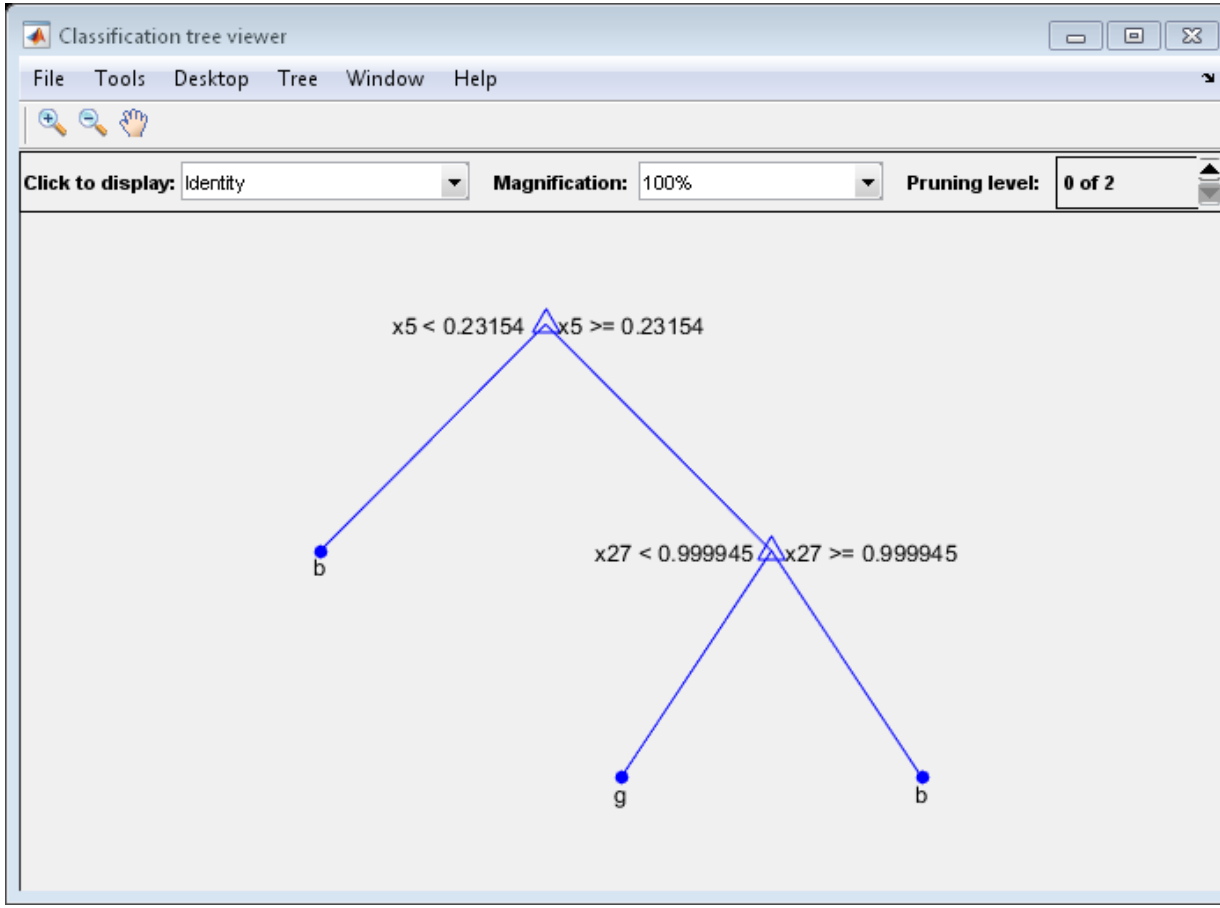
```
[~,~,~,bestlevel] = cvLoss(tree,'SubTrees','All')
```

```
bestlevel =

     6
```

In this case the level is the same for either setting of `'TreeSize'`.

Prune the tree to use it for other purposes:

```
tree = prune(tree,'Level',6);
view(tree,'Mode','Graph')
```



Alternative: classregtree

The `ClassificationTree` and `RegressionTree` classes were released in MATLAB R2011a. Previously, you represented both classification trees and regression trees with a `classregtree` object. The new classes provide all the functionality of the `classregtree` class, and are more convenient when used with "Ensemble Methods" on page 16-68.

Statistics and Machine Learning Toolbox software maintains `classregtree` and its predecessors `treefit`, `treedisp`, `treeval`, `treeprune`, and `treetest` for backward compatibility. These functions will be removed in a future release.

Train Classification Trees Using classregtree

This example uses Fisher's iris data in `fisheriris.mat` to create a classification tree for predicting species using measurements of sepal length, sepal width, petal length, and petal width as predictors. Here, the predictors are continuous and the response is categorical.

Load the data and use the `classregtree` constructor of the `classregtree` class to create the classification tree.

```
load fisheriris

t = classregtree(meas,species,...
                 'Names',{'SL' 'SW' 'PL' 'PW'})
```

```
t =

Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica
```

`t` is a `classregtree` object and can be operated on with any class method.

Use the `type` method of the `classregtree` class to show the type of the tree.

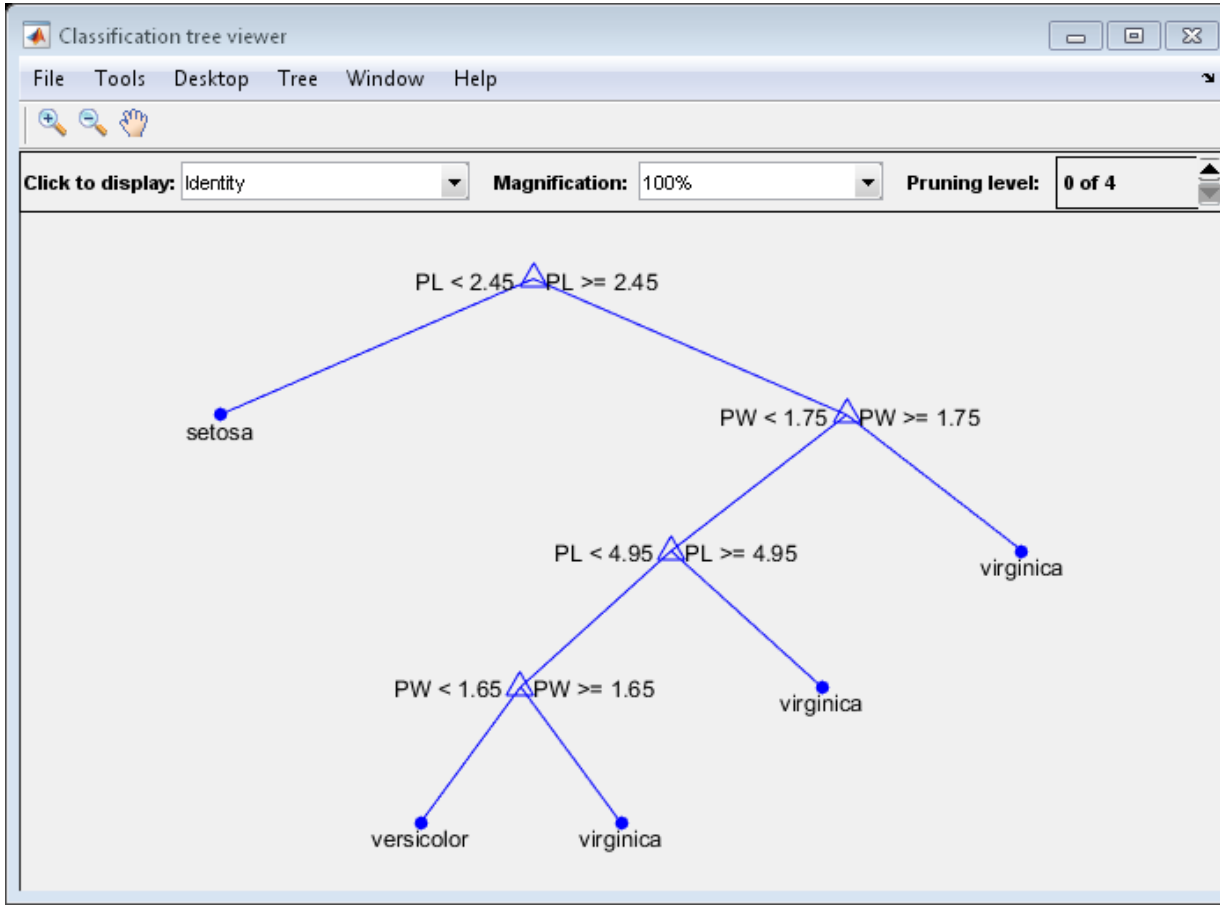
```
treetype = type(t)
```

```
treetype =

classification
```

`classregtree` creates a classification tree because `species` is a cell array of strings, and the response is assumed to be categorical.

To view the tree, use the `view` method of the `classregtree` class.

```
view(t)
```



The tree predicts the response values at the circular leaf nodes based on a series of questions about the iris at the triangular branching nodes. A `true` answer to any question follows the branch to the left. A `false` follows the branch to the right.

The tree does not use sepal measurements for predicting species. These can go unmeasured in new data, and you can enter them as `NaN` values for predictions. For example, use the tree to predict the species of an iris with petal length `4.8` and petal width `1.6`.

```
predicted = t([NaN NaN 4.8 1.6])
```

```
predicted =

    'versicolor'
```

The object allows for functional evaluation, of the form `t(X)`. This is a shorthand way of calling the `eval` method of the `classregtree` class. The predicted species is the left leaf node at the bottom of the tree in the previous view.

You can use a variety of methods of the `classregtree` class, such as `cutvar` and `cuttype` to get more information about the split at node `6` that makes the final distinction between `versicolor` and `virginica`.

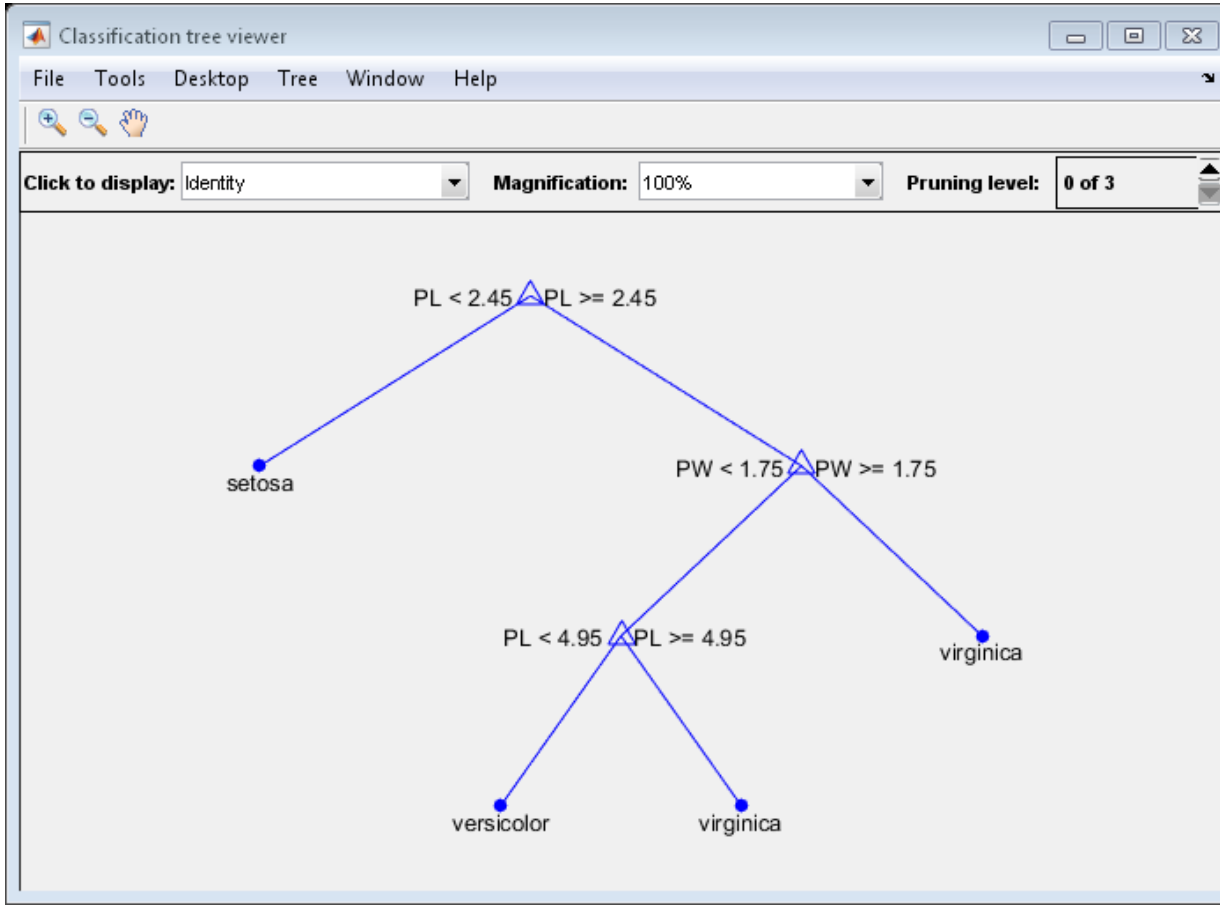
```
var6 = cutvar(t,6) % What variable determines the split?
type6 = cuttype(t,6) % What type of split is it?
```

```
var6 =

    'PW'


type6 =

    'continuous'
```

Classification trees fit the original (training) data well, but can do a poor job of classifying new values. Lower branches, especially, can be strongly affected by outliers. A simpler tree often avoids overfitting. You can use the `prune` method of the `classregtree` class to find the next largest tree from an optimal pruning sequence.

```
pruned = prune(t,'Level',1)
view(pruned)
```

```
pruned =

Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  class = versicolor
7  class = virginica
```



To find the best classification tree, employing the techniques of resubstitution and cross validation, use the `test` method of the `classregtree` class.

Train Regression Trees Using classregtree

This example uses the data on cars in `carsmall.mat` to create a regression tree for predicting mileage using measurements of weight and the number of cylinders as predictors. Here, one predictor (weight) is continuous and the other (cylinders) is categorical. The response (mileage) is continuous.

Load the data and use the `classregtree` constructor of the `classregtree` class to create the regression tree:

```
load carsmall

t = classregtree([Weight, Cylinders],MPG,...
                 'Categorical',2,'MinParent',20,...
                 'Names',{'W','C'})


t =

Decision tree for regression
 1  if W<3085.5 then node 2 elseif W>=3085.5 then node 3 else 23.7181
 2  if W<2371 then node 4 elseif W>=2371 then node 5 else 28.7931
 3  if C=8 then node 6 elseif C in {4 6} then node 7 else 15.5417
 4  if W<2162 then node 8 elseif W>=2162 then node 9 else 32.0741
 5  if C=6 then node 10 elseif C=4 then node 11 else 25.9355
 6  if W<4381 then node 12 elseif W>=4381 then node 13 else 14.2963
 7  fit = 19.2778
 8  fit = 33.3056
 9  fit = 29.6111
10  fit = 23.25
11  if W<2827.5 then node 14 elseif W>=2827.5 then node 15 else 27.2143
12  if W<3533.5 then node 16 elseif W>=3533.5 then node 17 else 14.8696
13  fit = 11
14  fit = 27.6389
15  fit = 24.6667
16  fit = 16.6
17  fit = 14.3889
```

`t` is a `classregtree` object and can be operated on with any of the methods of the class.

Use the `type` method of the `classregtree` class to show the type of the tree:

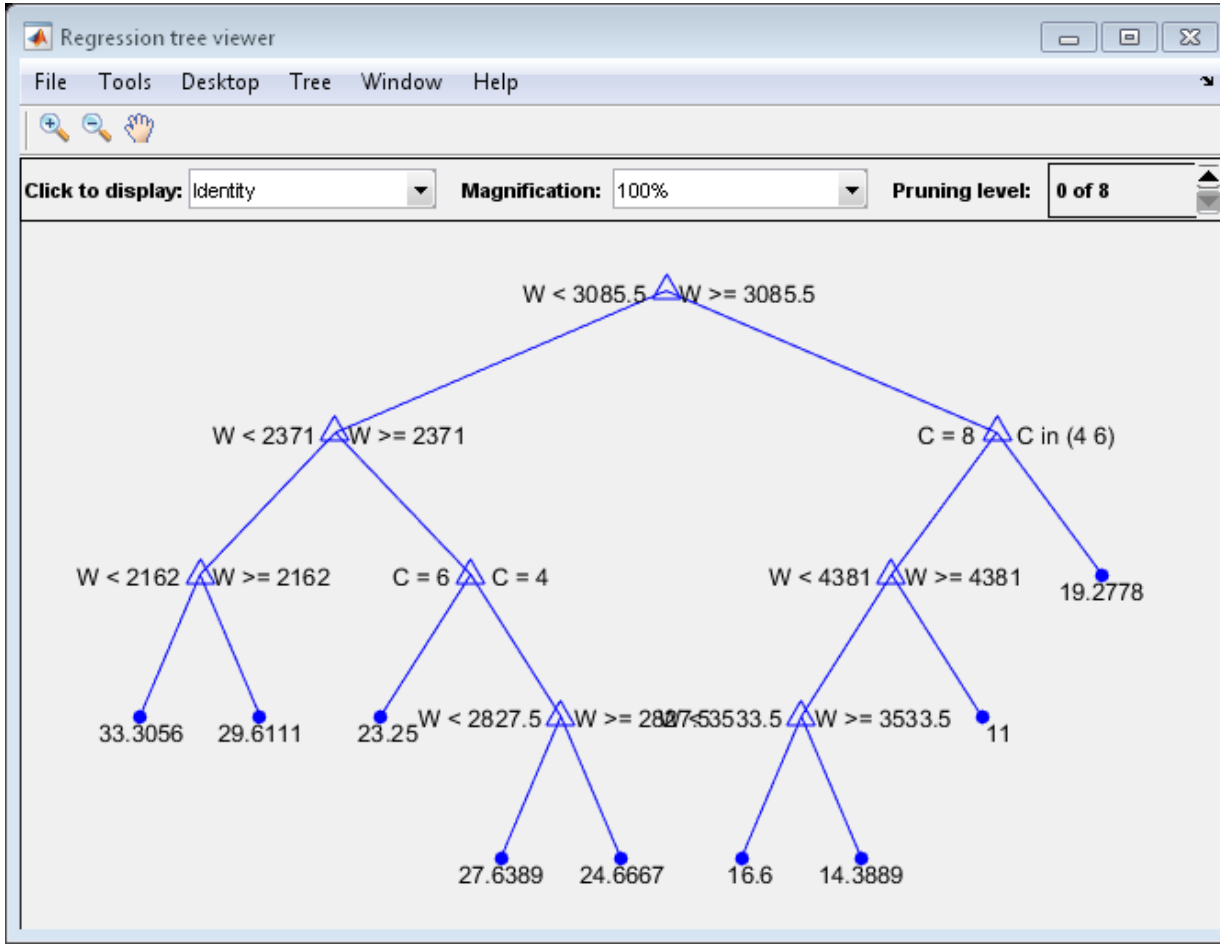
```
treetype = type(t)
```

```
treetype =

regression
```

`classregtree` creates a regression tree because MPG is a numerical vector, and the response is assumed to be continuous.

To view the tree, use the `view` method of the `classregtree` class:

```
view(t)
```



The tree predicts the response values at the circular leaf nodes based on a series of questions about the car at the triangular branching nodes. A `true` answer to any question follows the branch to the left; a `false` follows the branch to the right.

Use the tree to predict the mileage for a 2000-pound car with either 4, 6, or 8 cylinders:

```
mileage2K = t([2000 4; 2000 6; 2000 8])
```

```
mileage2K =
```

```
   33.3056
   33.3056
   33.3056
```

The object allows for functional evaluation, of the form `t(X)`. This is a shorthand way of calling the `eval` method of the `classregtree` class.

5.The predicted responses computed above are all the same. This is because they follow a series of splits in the tree that depend only on weight, terminating at the leftmost leaf node in the view above. A 4000-pound car, following the right branch from the top of the tree, leads to different predicted responses:

```
mileage4K = t([4000 4; 4000 6; 4000 8])
```

```
mileage4K =

   19.2778
   19.2778
   14.3889
```

You can use a variety of other methods of the `classregtree` class, such as `cutvar`, `cuttype`, and `cutcategories`, to get more information about the split at node 3 that distinguishes the 8-cylinder car:

```
var3 = cutvar(t,3)      % What variable determines the split?
type3 = cuttype(t,3)    % What type of split is it?
c = cutcategories(t,3); % Which classes are sent to the left
                        % child node, and which to the right?
leftChildNode = c{1}
rightChildNode = c{2}
```

```
var3 =

    'C'


type3 =

    'categorical'
```

```
leftChildNode =

     8


rightChildNode =

     4     6
```

Regression trees fit the original (training) data well, but may do a poor job of predicting new values. Lower branches, especially, may be strongly affected by outliers. A simpler tree often avoids overfitting. To find the best regression tree, employing the techniques of resubstitution and cross validation, use the `test` method of the `classregtree` class.

Splitting Categorical Predictors

In this section...

Challenges in Splitting Multilevel Predictors

When growing a classification tree, finding an optimal binary split for a categorical predictor with many levels is significantly more computationally challenging than finding a split for a continuous predictor. For a continuous predictor, a tree can split halfway between any two adjacent unique values of this predictor.

In contrast, to find an exact optimal binary split for a categorical predictor with L levels, a classification tree needs to consider $2^{L-1}-1$ splits. To obtain this formula, observe that you can assign L distinct values to the left and right nodes in 2^L ways. Two out of these 2^L configurations leave either the left or right node empty, and therefore should be discarded. Now, divide by 2 because left and right can be swapped.

For regression and binary classification problems, with $K = 2$ response classes, there is a computational shortcut [1]. The tree can order the categories by mean response (for regression) or class probability for one of the classes (for classification). Then, the optimal split is one of the $L - 1$ splits for the ordered list. When $K = 2$, `fitctree` always uses an exact search.

Therefore, computational challenges really only arise when growing classification trees for data with $K \geq 3$ classes. To reduce computation, there are several heuristic algorithms for finding a good split. When using `fitctree` to grow a classification tree, you can choose an algorithm for splitting categorical predictors using the `AlgorithmForCategorical` name-value pair argument. You can also set this algorithm when creating a classification `template`.

If you do not specify an algorithm, `fitctree` splits categorical predictors using the exact search algorithm, provided the predictor has at most `MaxNumCategories` levels (the default is 10 levels, and, depending on your platform, you cannot perform an exact search

on categorical predictors with more than 32 or 64 levels). Otherwise, `fitctree` chooses a good inexact search algorithm based on the number of classes and levels.

The available heuristic algorithms are: pull left by purity, a principal component-based partitioning, and one versus all by class.

Pull Left By Purity

This algorithm starts with all L categorical levels on the right branch. Inspect the K categories that have the largest class probabilities for each class. Move the category with the maximum value of the split criterion to the left branch. Continue moving categories from right to left, recording the split criterion at each move, until the right child has only one category remaining. Out of this sequence, the chosen split is the one that maximizes the split criterion.

Select this pull left by purity algorithm by using the `'AlgorithmForCategorial','PullLeft'` name-value pair in `fitctree`.

Principal Component-Based Partitioning

This algorithm was developed by Coppersmith, Hong, and Hosking [2]. It finds a close-to-optimal binary partition of the L predictor levels by searching for a separating hyperplane that is perpendicular to the first principal component of the weighted covariance matrix of the centered class probability matrix.

The algorithm assigns a score to each of the L categories, computed as the inner product between the found principal component and the vector of class probabilities for that category. Then, the chosen split is the one of the $L - 1$ splits of the scores that maximizes the split criterion.

Select this principal component-based partitioning by using the `'AlgorithmForCategorical','PCA'` name-value pair in `fitctree`.

One Versus All By Class

This algorithm starts with all L categorical levels on the right branch. For each of the K classes, order the categories based on their probability for that class.

For the first class, move each category to the left branch in order, recording the split criterion at each move. Repeat for the remaining classes. Out of this sequence, the chosen split is the one that maximizes the split criterion.

Select this one versus all by class algorithm by using the `'AlgorithmForCategorial','OVAbyClass'` name-value pair in `fitctree`.

References

[1] Breiman, L., J. H. Friedman, R. A. Olshen, and C. J. Stone. *Classification and Regression Trees*. Chapman & Hall, Boca Raton, 1993.

[2] Coppersmith, D., S. J. Hong, and J. R. M. Hosking. "Partitioning Nominal Attributes in Decision Trees." *Data Mining and Knowledge Discovery*, Vol. 3, 1999, pp. 197–217.

See Also

`fitctree` | `fitrtree` | `template`

Related Examples

- "How the Fit Methods Create Trees" on page 16-38

More About

- "What Are Classification Trees and Regression Trees?" on page 16-33

Ensemble Methods

In this section...

Framework for Ensemble Learning

You have several methods for melding results from many weak learners into one high-quality ensemble predictor. These methods closely follow the same syntax, so you can try different methods with minor changes in your commands.

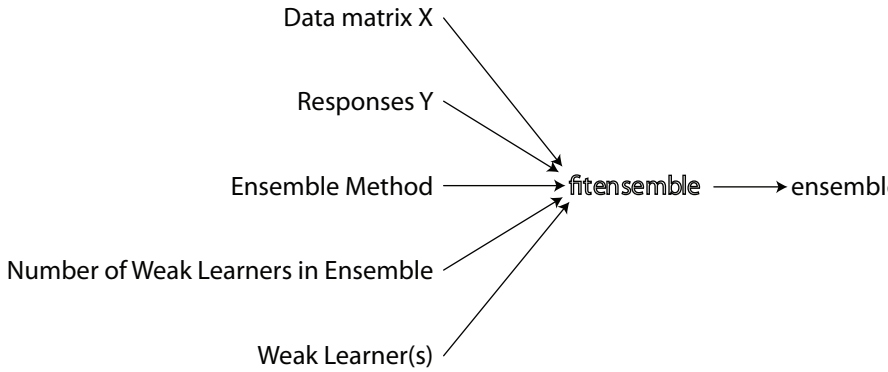
Create an ensemble with the `fitensemble` function. Its syntax is

```
ens = fitensemble(X,Y,model,numberens,learners)
```

- `X` is the matrix of data. Each row contains one observation, and each column contains one predictor variable.
- `Y` is the vector of responses, with the same number of observations as the rows in `X`.
- `model` is a string naming the type of ensemble.
- `numberens` is the number of weak learners in `ens` from each element of `learners`. So the number of elements in `ens` is `numberens` times the number of elements in `learners`.

- `learners` is either a string naming a weak learner, a weak learner template, or a cell array of such templates.

Pictorially, here is the information you need to create an ensemble:



For all classification or nonlinear regression problems, follow these steps to create an ensemble:

1. "Put Predictor Data in a Matrix" on page 16-69
2. "Prepare the Response Data" on page 16-69
3. "Choose an Applicable Ensemble Method" on page 16-70
4. "Set the Number of Ensemble Members" on page 16-73
5. "Prepare the Weak Learners" on page 16-74
6. "Call fitensemble" on page 16-75

Put Predictor Data in a Matrix

All supervised learning methods start with a data matrix, usually called `X` in this documentation. Each row of `X` represents one observation. Each column of `X` represents one variable, or predictor.

Prepare the Response Data

You can use a wide variety of data types for response data.

- For regression ensembles, `Y` must be a numeric vector with the same number of elements as the number of rows of `X`.
- For classification ensembles, `Y` can be any of the following data types. This table also contains the method of including missing entries.

Data Type	Missing Entry
Numeric vector	`NaN`
Categorical vector	`<undefined>`
Character array	Row of spaces
Cell array of strings	`''`
Logical vector	(not possible to represent)

`fitensemble` ignores missing values in `Y` when creating an ensemble.

For example, suppose your response data consists of three observations in the following order: `true`, `false`, `true`. You could express `Y` as:

- `[1;0;1]` (numeric vector)
- `nominal({'true','false','true'})` (categorical vector)
- `[true;false;true]` (logical vector)
- `['true ';'false';'true ']` (character array, padded with spaces so each row has the same length)
- `{'true','false','true'}` (cell array of strings)

Use whichever data type is most convenient. Because you cannot represent missing values with logical entries, do not use logical entries when you have missing values in `Y`.

Choose an Applicable Ensemble Method

`fitensemble` uses one of these algorithms to create an ensemble.

- For classification with two classes:
  - `'AdaBoostM1'`
  - `'LogitBoost'`
  - `'GentleBoost'`
  - `'RobustBoost'` (requires an Optimization Toolbox license)
  - `'LPBoost'` (requires an Optimization Toolbox license)
  - `'TotalBoost'` (requires an Optimization Toolbox license)
  - `'RUSBoost'`

  - `'Subspace'`
  - `'Bag'`
- For classification with three or more classes:
  - `'AdaBoostM2'`
  - `'LPBoost'` (requires an Optimization Toolbox license)
  - `'TotalBoost'` (requires an Optimization Toolbox license)
  - `'RUSBoost'`
  - `'Subspace'`
  - `'Bag'`
- For regression:
  - `'LSBoost'`
  - `'Bag'`

`'Bag'` applies to all methods. When using `'Bag'`, indicate whether you want a classifier or regressor with the `type` name-value pair set to `'classification'` or `'regression'`.

For descriptions of the various algorithms, see “Ensemble Algorithms” on page 16-155.

See “Suggestions for Choosing an Appropriate Ensemble Algorithm” on page 16-72.

This table lists characteristics of the various algorithms. In the table titles:

- `Regress.` — Regression
- `Classif.` — Classification
- `Preds.` — Predictors
- `Imbalance` — Good for imbalanced data (one class has many more observations than the other)
- `Stop` — Algorithm self-terminates
- `Sparse` — Requires fewer weak learners than other ensemble algorithms

Algorithm	Regress.	Binary Classif.	Binary Classif. Multi- Level Preds.	Classif. 3+ Classes	Class Imbalance	Stop	Sparse
`Bag`	×	×		×			
`AdaBoostM1`		×					
`AdaBoostM2`				×			
`LogitBoost`		×	×				
`GentleBoost`		×	×				
`RobustBoost`		×					
`LPBoost`		×		×		×	×
`TotalBoost`		×		×		×	×
`RUSBoost`		×		×	×		
`LSBoost`	×						
`Subspace`		×		×			

`RobustBoost`, `LPBoost`, and `TotalBoost` require an Optimization Toolbox license. Try `TotalBoost` before `LPBoost`, as `TotalBoost` can be more robust.

Suggestions for Choosing an Appropriate Ensemble Algorithm

- **Regression** — Your choices are `LSBoost` or `Bag`. See "General Characteristics of Ensemble Algorithms" on page 16-73 for the main differences between boosting and bagging.
- **Binary Classification** — Try `AdaBoostM1` first, with these modifications:

Data Characteristic	Recommended Algorithm
Many predictors	`Subspace`
Skewed data (many more observations of one class)	`RUSBoost`
Categorical predictors with over 31 levels	`LogitBoost` or `GentleBoost`
Label noise (some training data has the wrong class)	`RobustBoost`
Many observations	Avoid `LPBoost`, `TotalBoost`, and `Bag`

- **Multiclass Classification** — Try `AdaBoostM2` first, with these modifications:

Data Characteristic	Recommended Algorithm
Many predictors	`Subspace`
Skewed data (many more observations of one class)	`RUSBoost`
Many observations	Avoid `LPBoost`, `TotalBoost`, and `Bag`

For details of the algorithms, see "Ensemble Algorithms" on page 16-155.

General Characteristics of Ensemble Algorithms

- `Bag` generally constructs deep trees. This construction is both time consuming and memory-intensive. This also leads to relatively slow predictions.
- `Boost` algorithms generally use very shallow trees. This construction uses relatively little time or memory. However, for effective predictions, boosted trees might need more ensemble members than bagged trees. Therefore it is not always clear which class of algorithms is superior.
- `Bag` can estimate the generalization error without additional cross validation. See `oobLoss`.
- Except for `Subspace`, all boosting and bagging algorithms are based on tree learners. `Subspace` can use either discriminant analysis or *k*-nearest neighbor learners.

For details of the characteristics of individual ensemble members, see "Characteristics of Classification Algorithms" on page 16-6.

Set the Number of Ensemble Members

Choosing the size of an ensemble involves balancing speed and accuracy.

- Larger ensembles take longer to train and to generate predictions.
- Some ensemble algorithms can become overtrained (inaccurate) when too large.

To set an appropriate size, consider starting with several dozen to several hundred members in an ensemble, training the ensemble, and then checking the ensemble quality, as in "Test Ensemble Quality" on page 16-79. If it appears that you need more members, add them using the `resume` method (classification) or the `resume` method (regression). Repeat until adding more members does not improve ensemble quality.

Tip For classification, the `LPBoost` and `TotalBoost` algorithms are self-terminating, meaning you do not have to investigate the appropriate ensemble size. Try setting `numberens` to `500`. The algorithms usually terminate with fewer members.

Prepare the Weak Learners

Currently the weak learner types are:

- `'Discriminant'` (recommended for `Subspace` ensemble)
- `'KNN'` (only for `Subspace` ensemble)
- `'Tree'` (for any ensemble except `Subspace`)

There are two ways to set the weak learner type in the ensemble.

- To create an ensemble with default weak learner options, pass in the string as the weak learner. For example:

  ```
  ens = fitensemble(X,Y,'AdaBoostM2',50,'Tree');
  % or
  ens = fitensemble(X,Y,'Subspace',50,'KNN');
  ```

- To create an ensemble with nondefault weak learner options, create a nondefault weak learner using the appropriate `template` method. For example, if you have missing data, and want to use trees with surrogate splits for better accuracy:

  ```
  templ = templateTree('Surrogate','all');
  ens = fitensemble(X,Y,'AdaBoostM2',50,templ);
  ```

  To grow trees with leaves containing a number of observations that is at least 10% of the sample size:

  ```
  templ = templateTree('MinLeafSize',size(X,1)/10);
  ens = fitensemble(X,Y,'AdaBoostM2',50,templ);
  ```

  Alternatively, choose the maximal number of splits per tree:

  ```
  templ = templateTree('MaxNumSplits',4);
  ens = fitensemble(X,Y,'AdaBoostM2',50,templ);
  ```

While you can give `fitensemble` a cell array of learner templates, the most common usage is to give just one weak learner template.

For examples using a template, see “Example: Unequal Classification Costs” on page 16-91 and “Surrogate Splits” on page 16-100.

Decision trees can handle `NaN` values in `X`. Such values are called “missing”. If you have some missing values in a row of `X`, a decision tree finds optimal splits using nonmissing values only. If an entire row consists of `NaN`, `fitensemble` ignores that row. If you have data with a large fraction of missing values in `X`, use surrogate decision splits. For examples of surrogate splits, see “Example: Unequal Classification Costs” on page 16-91 and “Surrogate Splits” on page 16-100.

Common Settings for Tree Weak Learners

- The depth of a weak learner tree makes a difference for training time, memory usage, and predictive accuracy. You control the depth these parameters:
  - `MaxNumSplits` — The maximal number of branch node splits is `MaxNumSplits` per tree. Set large values of `MaxNumSplits` to get deep trees. The default for bagging is `size(X,1) - 1`. The default for boosting is `1`.
  - `MinLeafSize` — Each leaf has at least `MinLeafSize` observations. Set small values of `MinLeafSize` to get deep trees. The default for classification is `1` and `5` for regression.
  - `MinParentSize` — Each branch node in the tree has at least `MinParentSize` observations. Set small values of `MinParentSize` to get deep trees. The default for classification is `2` and `10` for regression.

  If you supply both `MinParentSize` and `MinLeafSize`, the learner uses the setting that gives larger leaves (shallower trees):
  `MinParent = max(MinParent,2*MinLeaf)`

  If you additionally supply `MaxNumSplits`, then the software splits a tree until one of the three splitting criteria is satisfied.
- `Surrogate` — Grow decision trees with surrogate splits when `Surrogate` is `'on'`. Use surrogate splits when your data has missing values.

  Note: Surrogate splits cause slower training and use more memory.

Call fitensemble

The syntax of `fitensemble` is:

```
ens = fitensemble(X,Y,model,numberens,learners)
```

- `X` is the matrix of data. Each row contains one observation, and each column contains one predictor variable.
- `Y` is the responses, with the same number of observations as rows in `X`.
- `model` is a string naming the type of ensemble.
- `numberens` is the number of weak learners in `ens` from each element of `learners`. The number of elements in `ens` is `numberens` times the number of elements in `learners`.
- `learners` is a string naming a weak learner, a weak learner template, or a cell array of such strings and templates.

The result of `fitensemble` is an ensemble object, suitable for making predictions on new data. For a basic example of creating a classification ensemble, see "Train a Classification Ensemble" on page 16-76. For a basic example of creating a regression ensemble, see "Train a Regression Ensemble" on page 16-78.

Where to Set Name-Value Pairs

There are several name-value pairs you can pass to `fitensemble`, and several that apply to the weak learners (`templateDiscriminant`, `templateKNN`, and `templateTree`). To determine which name-value pair argument is appropriate, the ensemble or the weak learner:

- Use template name-value pairs to control the characteristics of the weak learners.
- Use `fitensemble` name-value pair arguments to control the ensemble as a whole, either for algorithms or for structure.

For example, for an ensemble of boosted classification trees with each tree deeper than the default, set the `templateTree` name-value pair arguments `MinLeafSize` and `MinParentSize` to smaller values than the defaults. Or, `MaxNumSplits` to a larger value than the defaults. The trees are then leafier (deeper).

To name the predictors in the ensemble (part of the structure of the ensemble), use the `PredictorNames` name-value pair in `fitensemble`.

Basic Ensemble Examples

Train a Classification Ensemble

This example shows how to create a classification tree ensemble for the Fisher iris data, and use it to predict the classification of a flower with average measurements.

Load Fisher's iris data set.

```
load fisheriris
```

The predictor data is the `meas` matrix and the response data is in the `species` cell array of strings.

For classification trees with three or more classes, "Suggestions for Choosing an Appropriate Ensemble Algorithm" suggests using the `AdaBoostM2` algorithm.

For this example, arbitrarily choose an ensemble of 100 trees, and use the default tree options.

Train an ensemble of classification trees.

```
Mdl = fitensemble(meas,species,'AdaBoostM2',100,'Tree')
```

```
Mdl =

  classreg.learning.classif.ClassificationEnsemble
         PredictorNames: {'x1'  'x2'  'x3'  'x4'}
           ResponseName: 'Y'
             ClassNames: {'setosa'  'versicolor'  'virginica'}
         ScoreTransform: 'none'
        NumObservations: 150
             NumTrained: 100
                 Method: 'AdaBoostM2'
           LearnerNames: {'Tree'}
    ReasonForTermination: 'Terminated normally after completing the reques...'
                FitInfo: [100x1 double]
     FitInfoDescription: {2x1 cell}
```

`Mdl` is a `ClassificationEnsemble` model.

Predict the classification of a flower with average measurements.

```
flower = predict(Mdl,mean(meas))
```

```
flower =
```

```
    'versicolor'
```

Train a Regression Ensemble

This example shows how to create a regression ensemble to predict mileage of cars based on their horsepower and weight, trained on the `carsmall` data.

Load the `carsmall` data set.

```
load carsmall
```

Prepare the predictor data.

```
X = [Horsepower Weight];
```

The response data is `MPG`. The only available boosted regression ensemble type is `LSBoost`. For this example, arbitrarily choose an ensemble of 100 trees, and use the default tree options.

Train an ensemble of regression trees.

```
Mdl = fitensemble(X,MPG,'LSBoost',100,'Tree')
```

```
Mdl =

  classreg.learning.regr.RegressionEnsemble
         PredictorNames: {'x1'  'x2'}
           ResponseName: 'Y'
      ResponseTransform: 'none'
        NumObservations: 94
             NumTrained: 100
                 Method: 'LSBoost'
          LearnerNames: {'Tree'}
    ReasonForTermination: 'Terminated normally after completing the reques...'
                FitInfo: [100x1 double]
      FitInfoDescription: {2x1 cell}
          Regularization: []
```

Predict the mileage of a car with 150 horsepower weighing 2750 lbs.

```
mileage = predict(Mdl,[150 2750])

mileage =

   22.4236
```

Test Ensemble Quality

Usually you cannot evaluate the predictive quality of an ensemble based on its performance on training data. Ensembles tend to "overtrain," meaning they produce overly optimistic estimates of their predictive power. This means the result of `resubLoss` for classification (`resubLoss` for regression) usually indicates lower error than you get on new data.

To obtain a better idea of the quality of an ensemble, use one of these methods:

- Evaluate the ensemble on an independent test set (useful when you have a lot of training data).
- Evaluate the ensemble by cross validation (useful when you don't have a lot of training data).
- Evaluate the ensemble on out-of-bag data (useful when you create a bagged ensemble with `fitensemble`).

Test Ensemble Quality

This example uses a bagged ensemble so it can use all three methods of evaluating ensemble quality.

Generate an artificial dataset with 20 predictors. Each entry is a random number from 0 to 1. The initial classification is $Y = 1$ if $X_1 + X_2 + X_3 + X_4 + X_5 > 2.5$ and $Y = 0$ otherwise.

```
rng(1,'twister') % for reproducibility
X = rand(2000,20);
Y = sum(X(:,1:5),2) > 2.5;
```

In addition, to add noise to the results, randomly switch 10% of the classifications:

```
idx = randsample(2000,200);
```

```
Y(idx) = ~Y(idx);
```

Independent Test Set

Create independent training and test sets of data. Use 70% of the data for a training set by calling `cvpartition` using the `holdout` option:

```
cvpart = cvpartition(Y,'holdout',0.3);
Xtrain = X(training(cvpart),:);
Ytrain = Y(training(cvpart),:);
Xtest = X(test(cvpart),:);
Ytest = Y(test(cvpart),:);
```

Create a bagged classification ensemble of 200 trees from the training data:

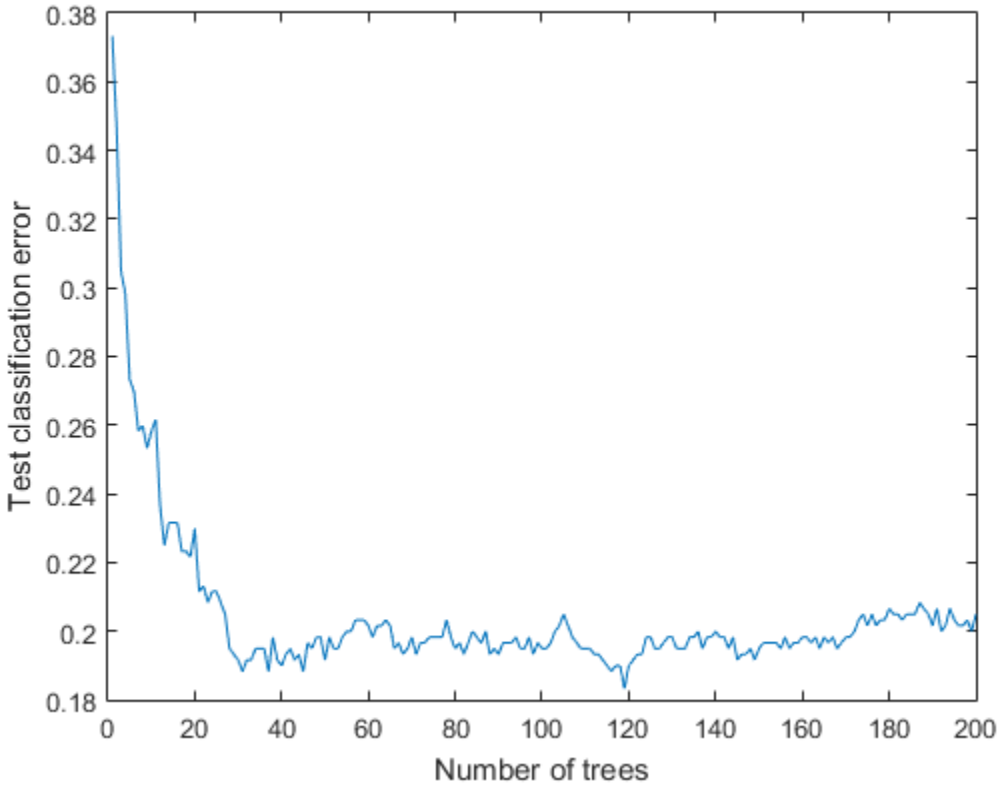
```
bag = fitensemble(Xtrain,Ytrain,'Bag',200,'Tree',...
    'Type','Classification')
```

```
bag =

  classreg.learning.classif.ClassificationBaggedEnsemble
         PredictorNames: {1x20 cell}
           ResponseName: 'Y'
             ClassNames: [0 1]
         ScoreTransform: 'none'
        NumObservations: 1400
             NumTrained: 200
                 Method: 'Bag'
           LearnerNames: {'Tree'}
   ReasonForTermination: 'Terminated normally after completing the reques...'
               FitInfo: []
     FitInfoDescription: 'None'
              FResample: 1
                Replace: 1
       UseObsForLearner: [1400x200 logical]
```

Plot the loss (misclassification) of the test data as a function of the number of trained trees in the ensemble:

```
figure;
plot(loss(bag,Xtest,Ytest,'mode','cumulative'));
```

```
xlabel('Number of trees');
ylabel('Test classification error');
```



Cross Validation

Generate a five-fold cross-validated bagged ensemble:

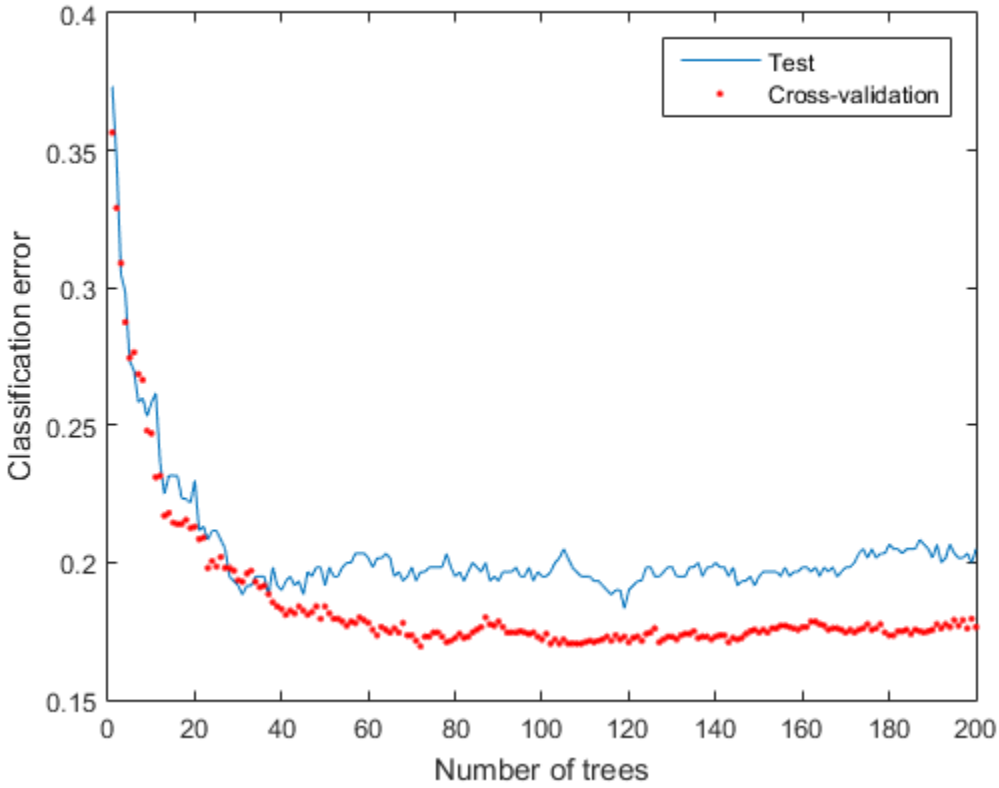
```
cv = fitensemble(X,Y,'Bag',200,'Tree',...
     'type','classification','kfold',5)
```

```
cv =
```

```
  classreg.learning.partition.ClassificationPartitionedEnsemble
    CrossValidatedModel: 'Bag'
         PredictorNames: {1x20 cell}
           ResponseName: 'Y'
        NumObservations: 2000
                  KFold: 5
              Partition: [1x1 cvpartition]
    NumTrainedPerFold: [200 200 200 200 200]
             ClassNames: [0 1]
         ScoreTransform: 'none'
```

Examine the cross-validation loss as a function of the number of trees in the ensemble:

```
figure;
plot(loss(bag,Xtest,Ytest,'mode','cumulative'));
hold on;
plot(kfoldLoss(cv,'mode','cumulative'),'r.');
hold off;
xlabel('Number of trees');
ylabel('Classification error');
legend('Test','Cross-validation','Location','NE');
```



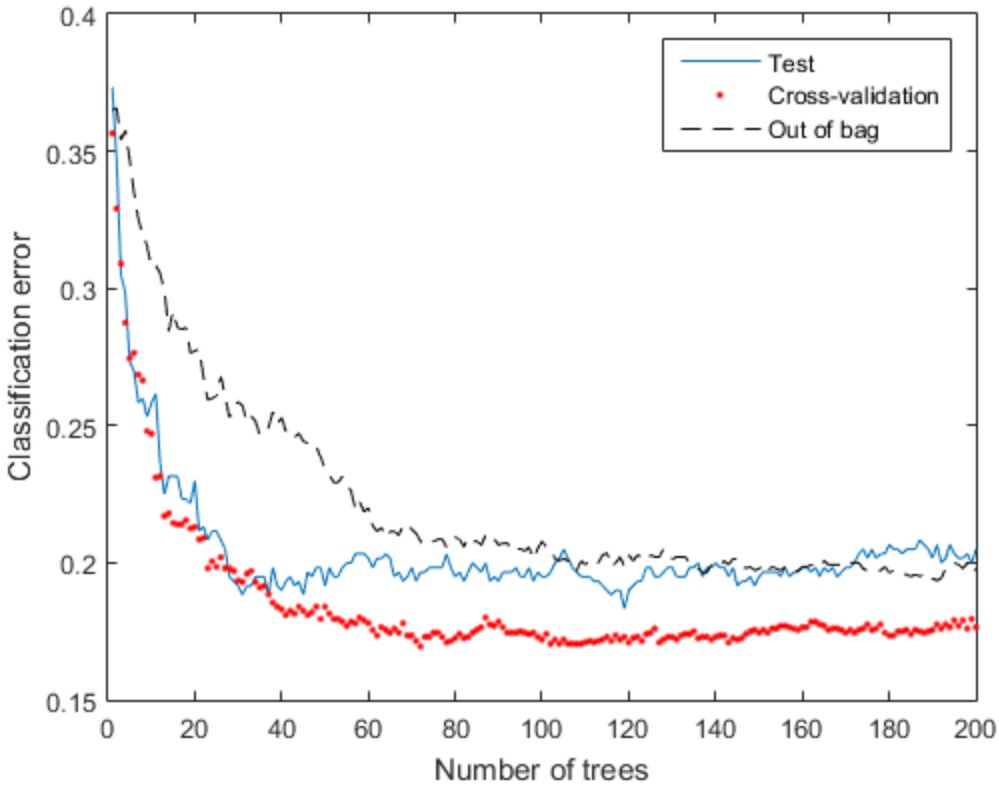
Cross validating gives comparable estimates to those of the independent set.

Out-of-Bag Estimates

Generate the loss curve for out-of-bag estimates, and plot it along with the other curves:

```
figure;
plot(loss(bag,Xtest,Ytest,'mode','cumulative'));
hold on;
plot(kfoldLoss(cv,'mode','cumulative'),'r.');
plot(oobLoss(bag,'mode','cumulative'),'k--');
hold off;
xlabel('Number of trees');
ylabel('Classification error');
```

```
legend('Test','Cross-validation','Out of bag','Location','NE');
```



The out-of-bag estimates are again comparable to those of the other methods.

Classification with Imbalanced Data

This example shows how to classify when one class has many more observations than another. Try the `RUSBoost` algorithm first, because it is designed to handle this case.

This example uses the "Cover type" data from the UCI machine learning archive, described in http://archive.ics.uci.edu/ml/datasets/Covertype. The data classifies types of forest (ground cover), based on predictors such as elevation, soil type, and distance to

water. The data has over 500,000 observations and over 50 predictors, so training and using a classifier is time consuming.

Blackard and Dean [3] describe a neural net classification of this data. They quote a 70.6% classification accuracy. `RUSBoost` obtains over 76% classification accuracy; see steps 6 and 7.

Step 1. Obtain the data.

```
urlwrite('http://archive.ics.uci.edu/ml/machine-learning-databases/covtype/covtype.data
```

Then, extract the data from the `forestcover.gz` file. The data is in the `covtype.data` file.

Step 2. Import the data and prepare it for classification.

Import the data into your workspace. Extract the last data column into a variable named `Y`.

```
load covtype.data
Y = covtype(:,end);
covtype(:,end) = [];
```

Step 3. Examine the response data.

```
tabulate(Y)
```

```
  Value    Count   Percent
      1   211840     36.46%
      2   283301     48.76%
      3    35754      6.15%
      4     2747      0.47%
      5     9493      1.63%
      6    17367      2.99%
      7    20510      3.53%
```

There are hundreds of thousands of data points. Those of class `4` are less than 0.5% of the total. This imbalance indicates that `RUSBoost` is an appropriate algorithm.

Step 4. Partition the data for quality assessment.

Use half the data to fit a classifier, and half to examine the quality of the resulting classifier.

```
part = cvpartition(Y,'holdout',0.5);
istrain = training(part); % data for fitting
```

```
istest = test(part); % data for quality assessment
tabulate(Y(istrain))
```

```
  Value    Count   Percent
      1   105920     36.46%
      2   141651     48.76%
      3    17877      6.15%
      4     1374      0.47%
      5     4746      1.63%
      6     8683      2.99%
      7    10255      3.53%
```

Step 5. Create the ensemble.

Use deep trees for higher ensemble accuracy. To do so, set the trees to have minimal leaf size of `5`. Set `LearnRate` to `0.1` in order to achieve higher accuracy as well. The data is large, and, with deep trees, creating the ensemble is time consuming.

```
t = templateTree('MinLeafSize',5);
tic
rusTree = fitensemble(covtype(istrain,:),Y(istrain),'RUSBoost',1000,t,...
    'LearnRate',0.1,'nprint',100);
toc
```

```
Training RUSBoost...
Grown weak learners: 100
Grown weak learners: 200
Grown weak learners: 300
Grown weak learners: 400
Grown weak learners: 500
Grown weak learners: 600
Grown weak learners: 700
Grown weak learners: 800
Grown weak learners: 900
Grown weak learners: 1000
Elapsed time is 918.258401 seconds.
```

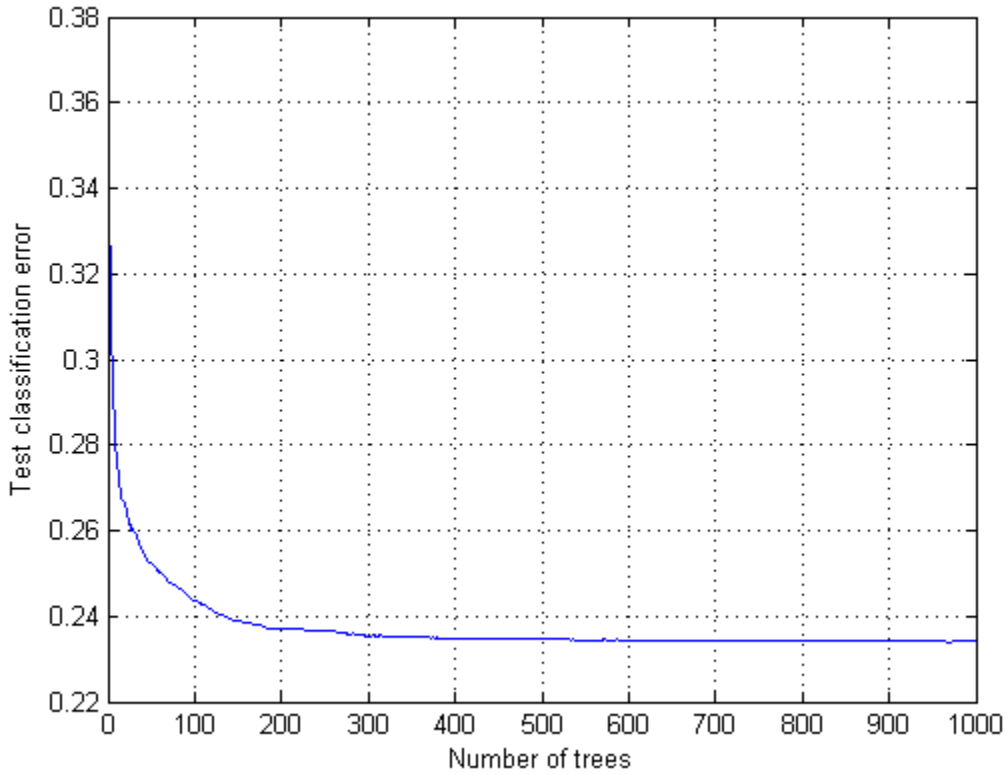
Step 6. Inspect the classification error.

Plot the classification error against the number of members in the ensemble.

```
figure;
tic
plot(loss(rusTree,covtype(istest,:),Y(istest),'mode','cumulative'));
toc
grid on;
```

```
xlabel('Number of trees');
ylabel('Test classification error');
```

```
Elapsed time is 775.646935 seconds.
```



The ensemble achieves a classification error of under 24% using 150 or more trees. It achieves the lowest error for 400 or more trees.

Examine the confusion matrix for each class as a percentage of the true class.

```
tic
Yfit = predict(rusTree,covtype(istest,:));
toc
tab = tabulate(Y(istest));
bsxfun(@rdivide,confusionmat(Y(istest),Yfit),tab(:,2))*100
```

```
Elapsed time is 427.293168 seconds.

ans =

  Columns 1 through 6

   83.3771    7.4056    0.0736         0    1.7051    0.2681
   18.3156   66.4652    2.1193    0.0162    9.3435    2.8239
         0    0.0839   90.8038    2.3885    0.6545    6.0693
         0         0    2.4763   95.8485         0    1.6752
         0    0.2739    0.6530         0   98.6518    0.4213
         0    0.1036    3.8346    1.1400    0.4030   94.5187
    0.2340         0         0         0    0.0195         0

  Column 7

    7.1705
    0.9163
         0
         0
         0
         0
   99.7465
```

All classes except class 2 have over 80% classification accuracy, and classes 3 through 7 have over 90% accuracy. But class 2 makes up close to half the data, so the overall accuracy is not that high.

Step 7. Compact the ensemble.

The ensemble is large. Remove the data using the `compact` method.

```
cmpctRus = compact(rusTree);

sz(1) = whos('rusTree');
sz(2) = whos('cmpctRus');
[sz(1).bytes sz(2).bytes]

ans =

   1.0e+09 *

    1.6947    0.9790
```

The compacted ensemble is about half the size of the original.

Remove half the trees from `cmpctRus`. This action is likely to have minimal effect on the predictive performance, based on the observation that 400 out of 1000 trees give nearly optimal accuracy.

```
cmpctRus = removeLearners(cmpctRus,[500:1000]);

sz(3) = whos('cmpctRus');
sz(3).bytes
```

```
ans =

   475495669
```

The reduced compact ensemble takes about a quarter the memory of the full ensemble. Its overall loss rate is under 24%:

```
L = loss(cmpctRus,covtype(istest,:),Y(istest))
```

```
L =

    0.2326
```

The predictive accuracy on new data might differ, because the ensemble accuracy might be biased. The bias arises because the same data used for assessing the ensemble was used for reducing the ensemble size. To obtain an unbiased estimate of requisite ensemble size, you should use cross validation. However, that procedure is time consuming.

Classification: Imbalanced Data or Unequal Misclassification Costs

In many real-world applications, you might prefer to treat classes in your data asymmetrically. For example, you might have data with many more observations of one class than of any other. Or you might work on a problem in which misclassifying observations of one class has more severe consequences than misclassifying observations of another class. In such situations, you can use two optional parameters for `fitensemble`: `prior` and `cost`.

By using `prior`, you set prior class probabilities (that is, class probabilities used for training). Use this option if some classes are under- or overrepresented in your training set. For example, you might obtain your training data by simulation. Because simulating class `A` is more expensive than class `B`, you opt to generate fewer observations of class `A` and more observations of class `B`. You expect, however, that class `A` and class `B` are mixed in a different proportion in the real world. In this case, set prior probabilities

for class `A` and `B` approximately to the values you expect to observe in the real world. `fitensemble` normalizes prior probabilities to make them add up to `1`; multiplying all prior probabilities by the same positive factor does not affect the result of classification.

If classes are adequately represented in the training data but you want to treat them asymmetrically, use the `cost` parameter. Suppose you want to classify benign and malignant tumors in cancer patients. Failure to identify a malignant tumor (false negative) has far more severe consequences than misidentifying benign as malignant (false positive). You should assign high cost to misidentifying malignant as benign and low cost to misidentifying benign as malignant.

You must pass misclassification costs as a square matrix with nonnegative elements. Element `C(i,j)` of this matrix is the cost of classifying an observation into class `j` if the true class is `i`. The diagonal elements `C(i,i)` of the cost matrix must be `0`. For the previous example, you can choose malignant tumor to be class 1 and benign tumor to be class 2. Then you can set the cost matrix to

$$\begin{bmatrix} 0 & c \\ 1 & 0 \end{bmatrix}$$

where $c > 1$ is the cost of misidentifying a malignant tumor as benign. Costs are relative—multiplying all costs by the same positive factor does not affect the result of classification.

If you have only two classes, `fitensemble` adjusts their prior probabilities using $\tilde{P}_i = C_{ij}P_i$ for class $i = 1,2$ and $j \neq i$. P_i are prior probabilities either passed into `fitensemble` or computed from class frequencies in the training data, and $\tilde{P}_i$ are adjusted prior probabilities. Then `fitensemble` uses the default cost matrix

$$\begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}$$

and these adjusted probabilities for training its weak learners. Manipulating the cost matrix is thus equivalent to manipulating the prior probabilities.

If you have three or more classes, `fitensemble` also converts input costs into adjusted prior probabilities. This conversion is more complex. First, `fitensemble` attempts to solve a matrix equation described in Zhou and Liu [31]. If it fails to find a solution,

`fitensemble` applies the "average cost" adjustment described in Breiman et al. [10]. For more information, see Zadrozny, Langford, and Abe [30].

Example: Unequal Classification Costs

This example uses data on patients with hepatitis to see if they live or die as a result of the disease. The data set is described at http://archive.ics.uci.edu/ml/datasets/Hepatitis.

1. Read the hepatitis data set from the UCI repository as a character array. Then convert the result to a cell array of strings using `textscan`. Specify a cell array of strings containing the variable names.

```
hepatitis = textscan(urlread(['http://archive.ics.uci.edu/ml/' ...
    'machine-learning-databases/hepatitis/hepatitis.data']),...
    '%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f%f','TreatAsEmpty','?',...
    'Delimiter',',');
size(hepatitis)
VarNames = {'dieOrLive' 'age' 'sex' 'steroid' 'antivirals' 'fatigue' ...
    'malaise' 'anorexia' 'liverBig' 'liverFirm' 'spleen' ...
    'spiders' 'ascites' 'varices' 'bilirubin' 'alkPhosphate' 'sgot' ...
    'albumin' 'protime' 'histology'};
```

```
ans =

     1    20
```

   `hepatitis` is a 1-by-20 cell array of strings. The cells correspond to the response (`liveOrDie`) and 19 heterogeneous predictors.

2. Specify a numeric matrix containing the predictors and a cell vector containing the strings `'Die'` and `'Live'`, which are response categories. The response contains two values: 1 indicates that a patient died, and 2 indicates that a patient lived. Specify a cell vector of strings for the response using the response categories. The first variable in `hepatitis` contains the response.

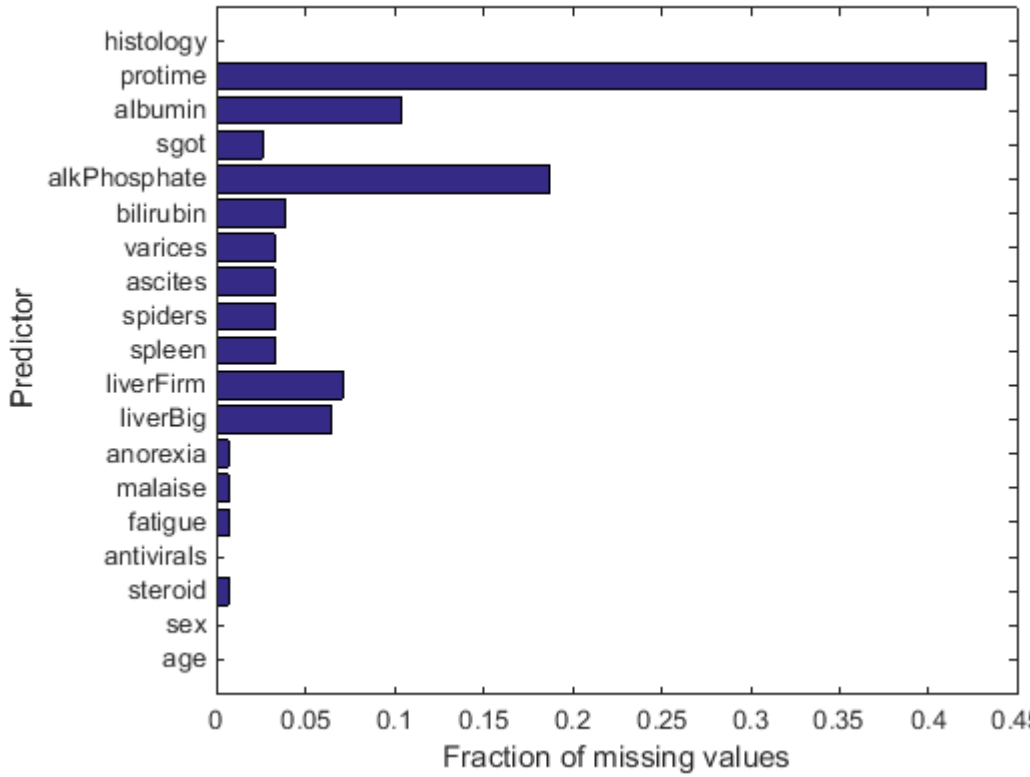
```
X = cell2mat(hepatitis(2:end));
ClassNames = {'Die' 'Live'};
Y = ClassNames(hepatitis{:,1});
```

   `X` is a numeric matrix containing the 19 predictors. `Y` is a cell array of strings containing the response.

3. Inspect the data for missing values.

```
figure;
barh(sum(isnan(X),1)/size(X,1));
```

```
h = gca;
h.YTick = 1:numel(VarNames) - 1;
h.YTickLabel = VarNames(2:end);
ylabel 'Predictor';
xlabel 'Fraction of missing values';
```



Most predictors have missing values, and one has nearly 45% of the missing values. Therefore, use decision trees with surrogate splits for better accuracy. Because the data set is small, training time with surrogate splits should be tolerable.

4 Create a classification tree template that uses surrogate splits.

```
rng(0,'twister') % for reproducibility
t = templateTree('surrogate','all');
```

5 Examine the data or the description of the data to see which predictors are categorical.

```
X(1:5,:)

ans =

  Columns 1 through 6

   30.0000    2.0000    1.0000    2.0000    2.0000    2.0000
   50.0000    1.0000    1.0000    2.0000    1.0000    2.0000
   78.0000    1.0000    2.0000    2.0000    1.0000    2.0000
   31.0000    1.0000       NaN    1.0000    2.0000    2.0000
   34.0000    1.0000    2.0000    2.0000    2.0000    2.0000

  Columns 7 through 12

    2.0000    1.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    1.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    2.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    2.0000    2.0000    2.0000    2.0000    2.0000
    2.0000    2.0000    2.0000    2.0000    2.0000    2.0000

  Columns 13 through 18

    2.0000    1.0000   85.0000   18.0000    4.0000       NaN
    2.0000    0.9000  135.0000   42.0000    3.5000       NaN
    2.0000    0.7000   96.0000   32.0000    4.0000       NaN
    2.0000    0.7000   46.0000   52.0000    4.0000   80.0000
    2.0000    1.0000       NaN  200.0000    4.0000       NaN

  Column 19

    1.0000
    1.0000
    1.0000
    1.0000
    1.0000
```

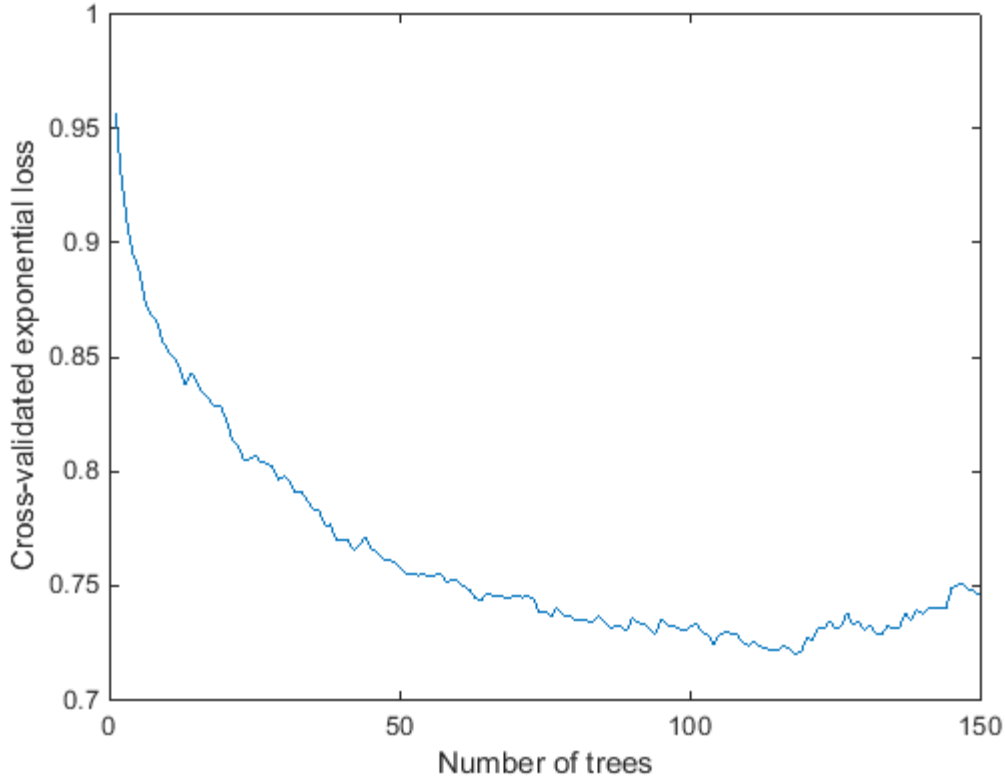
It appears that predictors 2 through 13 are categorical, as well as predictor 19. You can confirm this inference using the data set description at http://archive.ics.uci.edu/ml/datasets/Hepatitis.

6 List the categorical variables.

```
catIdx = [2:13,19];
```

7 Create a cross-validated ensemble using 150 learners and the `GentleBoost` algorithm.

```
Ensemble = fitensemble(X,Y,'GentleBoost',150,t,...
  'PredictorNames',VarNames(2:end),'LearnRate',0.1,...
  'CategoricalPredictors',catIdx,'KFold',5);
figure;
plot(kfoldLoss(Ensemble,'Mode','cumulative','LossFun','exponential'));
xlabel('Number of trees');
ylabel('Cross-validated exponential loss');
```



8 Inspect the confusion matrix to see which patients the ensemble predicts correctly.

```
[yFit,sFit] = kfoldPredict(Ensemble);
confusionmat(Y,yFit,'Order',ClassNames)

ans =

    18    14
    11   112
```

Of the 123 patient who live, the ensemble predicts correctly that 112 will live. But for the 32 patients who die of hepatitis, the ensemble only predicts correctly that about half will die of hepatitis.

9 There are two types of error in the predictions of the ensemble:

- Predicting that the patient lives, but the patient dies
- Predicting that the patient dies, but the patient lives

Suppose you believe that the first error is five times worse than the second. Create a new classification cost matrix that reflects this belief.

```
cost.ClassNames = ClassNames;
cost.ClassificationCosts = [0 5; 1 0];
```

10 Create a new cross-validated ensemble using `cost` as the misclassification cost, and inspect the resulting confusion matrix.

```
EnsembleCost = fitensemble(X,Y,'GentleBoost',150,t,...
  'PredictorNames',VarNames(2:end),'LearnRate',0.1,...
  'CategoricalPredictors',catIdx,'KFold',5,...
  'Cost',cost);
[yFitCost,sFitCost] = kfoldPredict(EnsembleCost);
confusionmat(Y,yFitCost,'Order',ClassNames)

ans =

    19    13
     8   115
```

As expected, the new ensemble does a better job classifying the who die. Somewhat surprisingly, the new ensemble also does a better job classifying the who live, though the result is not statistically significantly better. The results of the cross validation are random, so this result is simply a statistical fluctuation. The result seems to indicate that the classification of who live is not very sensitive to the cost.

Classification with Many Categorical Levels

Generally, you cannot use classification with more than 31 levels in any categorical predictor. However, two boosting algorithms can classify data with many categorical predictor levels and binary responses: `LogitBoost` and `GentleBoost`. For details, see "LogitBoost" on page 16-162 and "GentleBoost" on page 16-161.

This example uses demographic data from the U.S. Census Bureau, available at http://archive.ics.uci.edu/ml/machine-learning-databases/adult/. The objective of the researchers who posted the data is predicting whether an individual makes over $50,000 a year, based on a set of characteristics. You can see details of the data, including predictor names, in the `adult.names` file at the site.

1. Load the `'adult.data'` file from the UCI Machine Learning Repository. Specify a cell array of strings containing the variable names.

```
adult = urlread(['http://archive.ics.uci.edu/ml/'...
    'machine-learning-databases/adult/adult.data']);
VarNames = {'age' 'workclass' 'fnlwgt' 'education' 'educationNum'...
    'maritalStatus' 'occupation' 'relationship' 'race'...
    'sex' 'capitalGain' 'capitalLoss'...
    'hoursPerWeek' 'nativeCountry' 'income'};
```

2. `adult.data` represents missing data as `'?'`. Replace instances of missing data with an empty string. Use `textscan` to put the data into a cell array of strings.

```
adult = strrep(adult,'?','');
adult = textscan(adult,'%f%s%f%s%f%s%s%s%s%s%f%f%f%s%s',...
    'Delimiter',',','TreatAsEmpty','');
```

   The name-value pair argument `TreatAsEmpty` converts all observations corresponding to numeric variables to `NaN` if the observation is an empty string.

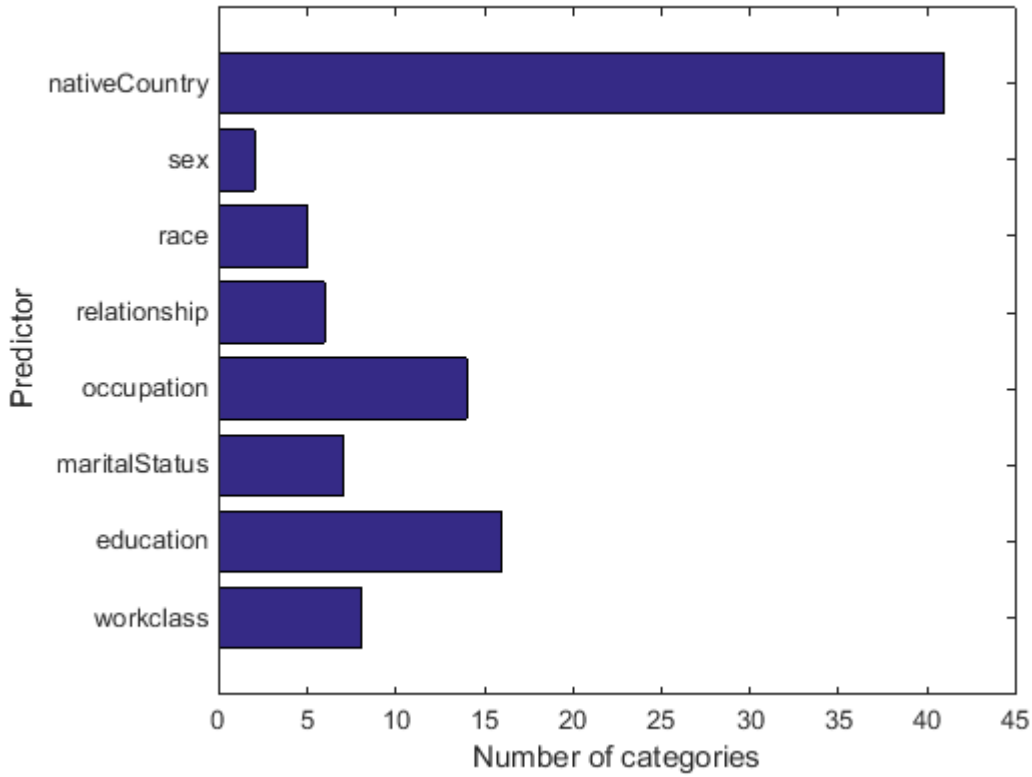
3. Since the variables are heterogeneous, put the set into a MATLAB table.

```
adult = table(adult{:},'VariableNames',VarNames);
```

4. Some categorical variables have many levels. Plot the number of levels of each categorical predictor.

```
cat = varfun(@iscellstr,adult(:,1:end - 1),...
    'OutputFormat','uniform'); % Logical flag for categorical variables
catVars = find(cat);           % Indices of categorical variables

countCats = @(var)numel(categories(nominal(var)));
numCat = varfun(@(var)countCats(var),adult(:,catVars),...
```

```
    'OutputFormat','uniform');

figure;
barh(numCat);
h = gca;
h.YTickLabel = VarNames(catVars);
ylabel 'Predictor';
xlabel 'Number of categories';
```



The anonymous function `countCats` converts a predictor to a nominal array, then counts the unique, nonempty categories of the predictor. Predictor 14 (`'nativeCountry'`) has more than 40 categorical levels. For binary classification, `fitctree` uses a computational shortcut to find an optimal split for categorical

predictors with many categories. For classification with more than two classes, you can choose a heuristic algorithm to find a good split. For details, see “Splitting Categorical Predictors” on page 16-65.

5 Specify the predictor matrix using `classreg.regr.modelutils.predictormatrix` and the response vector.

```
X = classreg.regr.modelutils.predictormatrix(adult,'ResponseVar',...
    size(adult,2));
Y = nominal(adult.income);
```

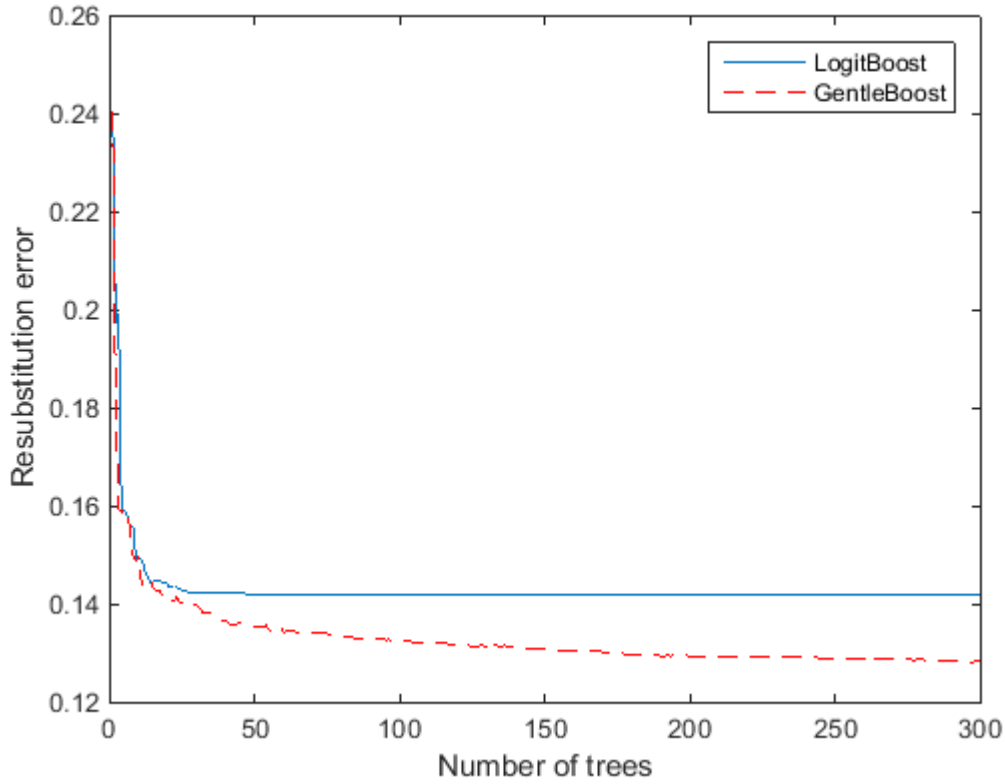
`X` is a numeric matrix; `predictormatrix` converts all categorical variables into group indices. The name-value pair argument `ResponseVar` indicates that the last column is the response variable, and excludes it from the predictor matrix. `Y` is a nominal, categorical array.

6 Train classification ensembles using both `LogitBoost` and `GentleBoost`.

```
rng(1); % For reproducibility
LBEnsemble = fitensemble(X,Y,'LogitBoost',300,'Tree',...
    'CategoricalPredictors',cat,'PredictorNames',VarNames(1:end-1),...
    'ResponseName','income');
GBEnsemble = fitensemble(X,Y,'GentleBoost',300,'Tree',...
    'CategoricalPredictors',cat,'PredictorNames',VarNames(1:end-1),...
    'ResponseName','income');
```

7 Examine the resubstitution error for both ensembles.

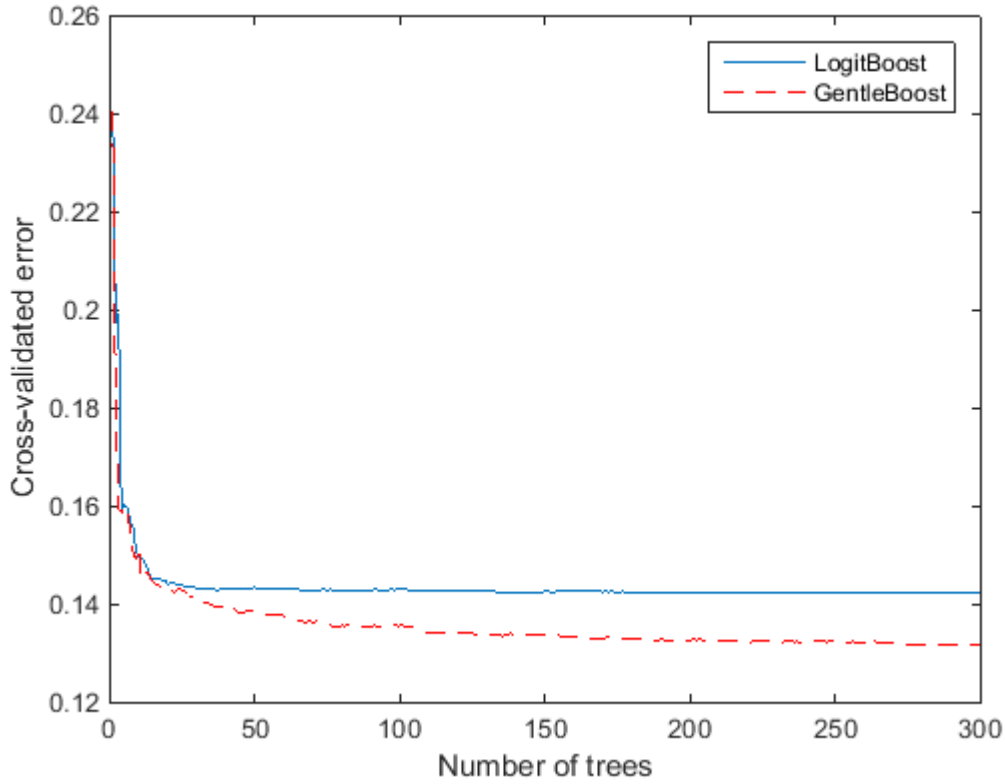
```
figure;
plot(resubLoss(LBEnsemble,'Mode','cumulative'));
hold on
plot(resubLoss(GBEnsemble,'Mode','cumulative'),'r--');
hold off
xlabel('Number of trees');
ylabel('Resubstitution error');
legend('LogitBoost','GentleBoost','Location','NE');
```



The `GentleBoost` algorithm has a slightly smaller resubstitution error.

8 Estimate the generalization error for both algorithms by cross validation.

```
CVLBEnsemble = crossval(LBEnsemble,'KFold',5);
CVGBEnsemble = crossval(GBEnsemble,'KFold',5);
figure;
plot(kfoldLoss(CVLBEnsemble,'Mode','cumulative'));
hold on
plot(kfoldLoss(CVGBEnsemble,'Mode','cumulative'),'r--');
hold off
xlabel('Number of trees');
ylabel('Cross-validated error');
legend('LogitBoost','GentleBoost','Location','NE');
```



The cross-validated loss is nearly the same as the resubstitution error.

Surrogate Splits

When you have missing data, trees and ensembles of trees give better predictions when they include surrogate splits. Furthermore, estimates of predictor importance are often different with surrogate splits. Eliminating unimportant predictors can save time and memory for predictions, and can make predictions easier to understand.

This example shows the effects of surrogate splits for predictions for data containing missing entries in the test set.

Load sample data. Partition it into a training and test set.

```
load ionosphere;

rng(10) % for reproducibility
cv = cvpartition(Y,'Holdout',0.3);
Xtrain = X(training(cv),:);
Ytrain = Y(training(cv));
Xtest = X(test(cv),:);
Ytest = Y(test(cv));
```

Bag decision trees with and without surrogate splits.

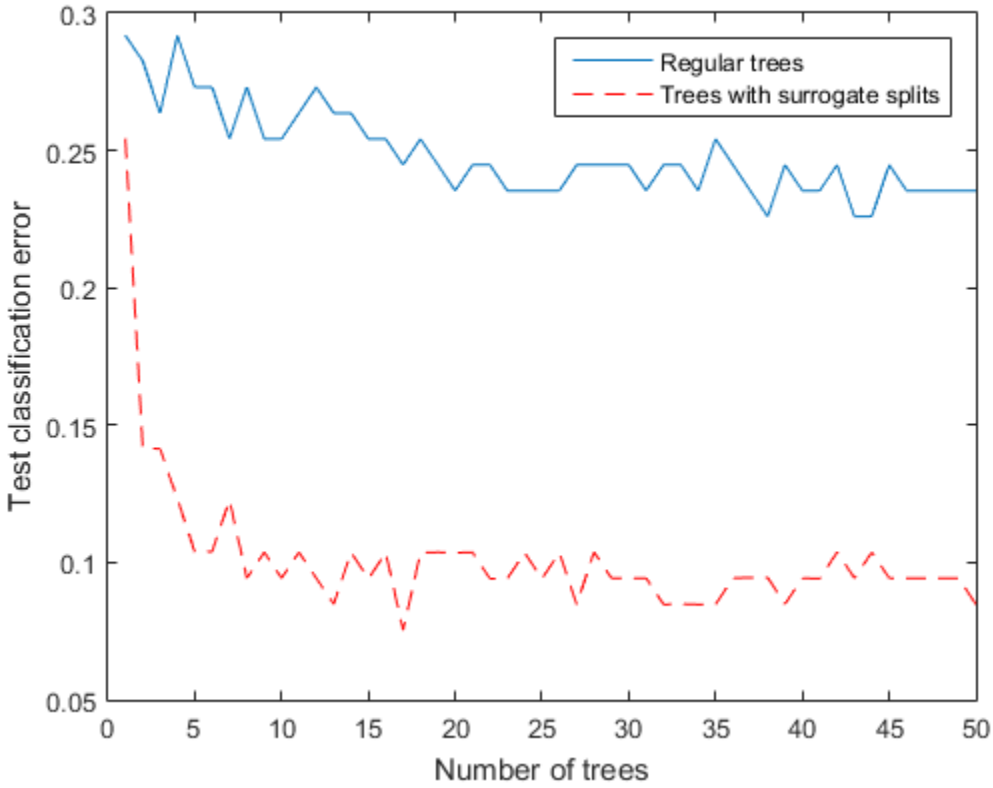
```
b = fitensemble(Xtrain,Ytrain,'Bag',50,'Tree',...
     'Type','Class');

templS = templateTree('Surrogate','On');
bs = fitensemble(Xtrain,Ytrain,'Bag',50,templS,...
    'Type','Class');
```

Suppose half of the values in the test set are missing.

```
Xtest(rand(size(Xtest))>0.5) = NaN;
```

Test accuracy with and without surrogate splits.

```
figure;
plot(loss(b,Xtest,Ytest,'Mode','Cumulative'));
hold on;
plot(loss(bs,Xtest,Ytest,'Mode','Cumulative'),'r--');
legend('Regular trees','Trees with surrogate splits');
xlabel('Number of trees');
ylabel('Test classification error');
```



Check the statistical significance of the difference in results with the McNemar test. Convert the labels to a `nominal` data type to make it easier to check for equality.

```
Yfit = nominal(predict(b,Xtest));
YfitS = nominal(predict(bs,Xtest));
N10 = sum(Yfit==nominal(Ytest) & YfitS~=nominal(Ytest));
N01 = sum(Yfit~=nominal(Ytest) & YfitS==nominal(Ytest));
mcnemar = (abs(N10-N01) - 1)^2/(N10+N01);
pval = 1 - chi2cdf(mcnemar,1)
```

```
pval =

   1.7683e-04
```

The extremely low *p*-value indicates that the ensemble with surrogate splits is better in a statistically significant manner.

LPBoost and TotalBoost for Small Ensembles

This example shows how to obtain the benefits of the `LPBoost` and `TotalBoost` algorithms. These algorithms share two beneficial characteristics:

They are self-terminating, so you don't have to guess how many members to include.

They produce ensembles with some very small weights, so you can safely remove ensemble members.

Note that the algorithms in this example require an Optimization Toolbox™ license.

Load the data

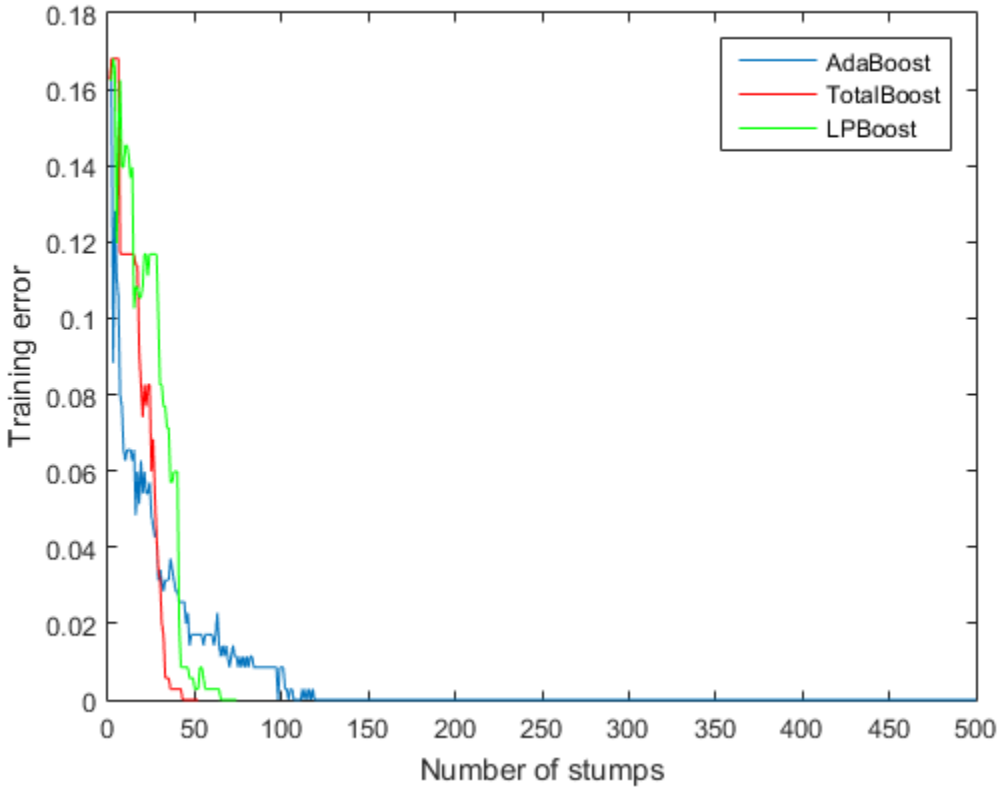
Load the `ionosphere` data set.

```
load ionosphere
```

Create the classification ensembles

Create ensembles for classifying the `ionosphere` data using the `LPBoost`, `TotalBoost`, and, for comparison, `AdaBoostM1` algorithms. It is hard to know how many members to include in an ensemble. For `LPBoost` and `TotalBoost`, try using `500`. For comparison, also use `500` for `AdaBoostM1`.

```
rng default % For reproducibility
T = 500;
adaStump = fitensemble(X,Y,'AdaBoostM1',T,'Tree');
totalStump = fitensemble(X,Y,'TotalBoost',T,'Tree');
lpStump = fitensemble(X,Y,'LPBoost',T,'Tree');
figure;
plot(resubLoss(adaStump,'Mode','Cumulative'));
hold on
plot(resubLoss(totalStump,'Mode','Cumulative'),'r');
plot(resubLoss(lpStump,'Mode','Cumulative'),'g');
hold off
xlabel('Number of stumps');
ylabel('Training error');
legend('AdaBoost','TotalBoost','LPBoost','Location','NE');
```



All three algorithms achieve perfect prediction on the training data after a while.

Examine the number of members in all three ensembles.

```
[adaStump.NTrained totalStump.NTrained lpStump.NTrained]
```

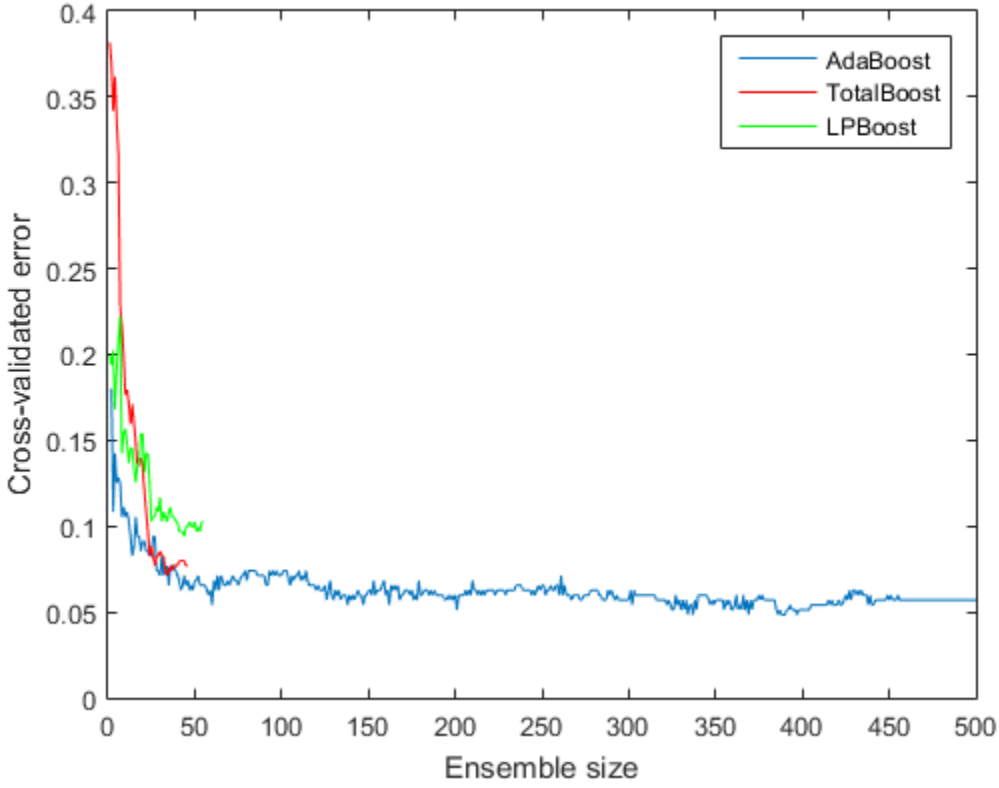
```
ans =

   500     52     74
```

`AdaBoostM1` trained all `500` members. The other two algorithms stopped training early.

Cross validate the ensembles

Cross validate the ensembles to better determine ensemble accuracy.

```
cvlp = crossval(lpStump,'KFold',5);
cvtotal = crossval(totalStump,'KFold',5);
cvada = crossval(adaStump,'KFold',5);

figure;
plot(kfoldLoss(cvada,'Mode','Cumulative'));
hold on
plot(kfoldLoss(cvtotal,'Mode','Cumulative'),'r');
plot(kfoldLoss(cvlp,'Mode','Cumulative'),'g');
hold off
xlabel('Ensemble size');
ylabel('Cross-validated error');
legend('AdaBoost','TotalBoost','LPBoost','Location','NE');
```



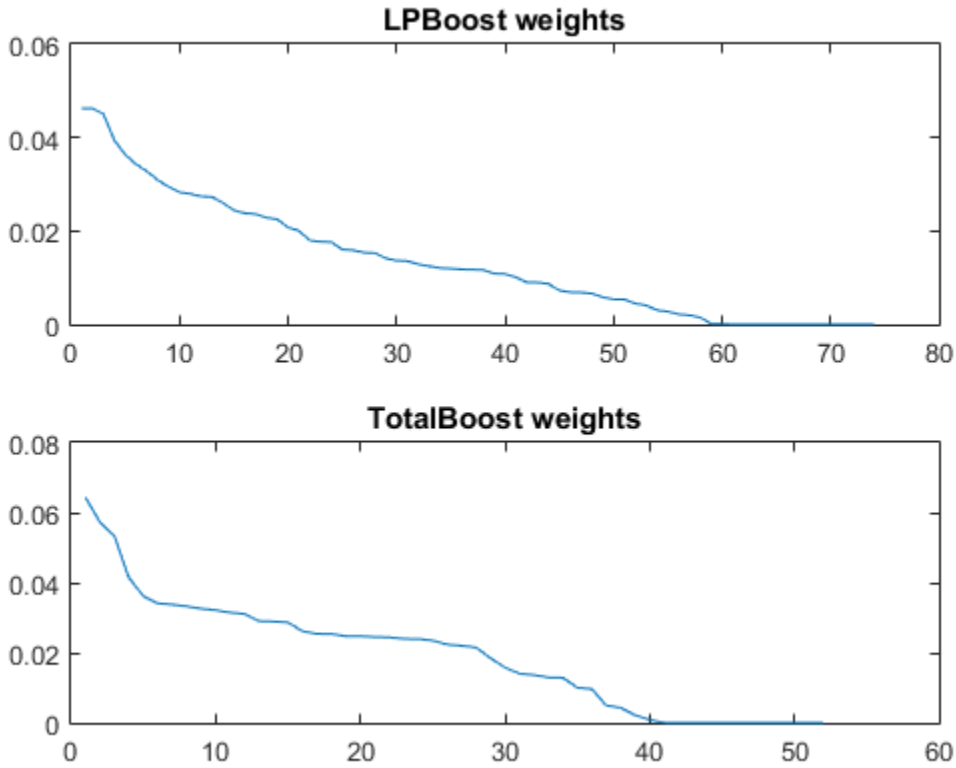
It appears that each boosting algorithms achieves 10% or lower loss with 50 ensemble members, and `AdaBoostM1` achieves near 6% error with 150 or more ensemble members.

Compact and remove ensemble members

To reduce the ensemble sizes, compact them, and then use `removeLearners`. The question is, how many learners should you remove? The cross-validated loss curves give you one measure. For another, examine the learner weights for `LPBoost` and `TotalBoost` after compacting.

```
cada = compact(adaStump);
clp = compact(lpStump);
ctotal = compact(totalStump);
```

```
figure
subplot(2,1,1)
plot(clp.TrainedWeights)
title('LPBoost weights')
subplot(2,1,2)
plot(ctotal.TrainedWeights)
title('TotalBoost weights')
```



Both `LPBoost` and `TotalBoost` show clear points where the ensemble member weights become negligible.

Remove the unimportant ensemble members.

```
cada = removeLearners(cada,150:cada.NTrained);
```

```
clp = removeLearners(clp,60:clp.NTrained);
ctotal = removeLearners(ctotal,40:ctotal.NTrained);
```

Check that removing these learners does not affect ensemble accuracy on the training data.

```
[loss(cada,X,Y) loss(clp,X,Y) loss(ctotal,X,Y)]
```

```
ans =

     0     0     0
```

Check the resulting compact ensemble sizes.

```
s(1) = whos('cada');
s(2) = whos('clp');
s(3) = whos('ctotal');
s.bytes
```

```
ans =

      543067


ans =

      216603


ans =

      144063
```

The sizes of the compact ensembles are approximately proportional to the number of members in each.

Ensemble Regularization

Regularization is a process of choosing fewer weak learners for an ensemble in a way that does not diminish predictive performance. Currently you can regularize regression

ensembles. (You can also regularize a discriminant analysis classifier in a non-ensemble context; see “Regularize a Discriminant Analysis Classifier” on page 15-21.)

The `regularize` method finds an optimal set of learner weights a_t that minimize

$$\sum_{n=1}^{N} w_n g\left(\left(\sum_{t=1}^{T}\alpha_t h_t(x_n)\right), y_n\right) + \lambda\sum_{t=1}^{T}|\alpha_t|.$$

Here

- $\lambda \geq 0$ is a parameter you provide, called the lasso parameter.
- h_t is a weak learner in the ensemble trained on N observations with predictors x_n, responses y_n, and weights w_n.
- $g(f,y) = (f-y)^2$ is the squared error.

The ensemble is regularized on the same (x_n,y_n,w_n) data used for training, so

$$\sum_{n=1}^{N} w_n g\left(\left(\sum_{t=1}^{T}\alpha_t h_t(x_n)\right), y_n\right)$$

is the ensemble resubstitution error. The error is measured by mean squared error (MSE).

If you use $\lambda = 0$, `regularize` finds the weak learner weights by minimizing the resubstitution MSE. Ensembles tend to overtrain. In other words, the resubstitution error is typically smaller than the true generalization error. By making the resubstitution error even smaller, you are likely to make the ensemble accuracy worse instead of improving it. On the other hand, positive values of λ push the magnitude of the a_t coefficients to 0. This often improves the generalization error. Of course, if you choose λ too large, all the optimal coefficients are 0, and the ensemble does not have any accuracy. Usually you can find an optimal range for λ in which the accuracy of the regularized ensemble is better or comparable to that of the full ensemble without regularization.

A nice feature of lasso regularization is its ability to drive the optimized coefficients precisely to 0. If a learner's weight a_t is 0, this learner can be excluded from the

regularized ensemble. In the end, you get an ensemble with improved accuracy and fewer learners.

Regularize a Regression Ensemble

This example uses data for predicting the insurance risk of a car based on its many attributes.

Load the `imports-85` data into the MATLAB workspace:

```
load imports-85;
```

Look at a description of the data to find the categorical variables and predictor names:

```
Description
```

```
Description =

1985 Auto Imports Database from the UCI repository
http://archive.ics.uci.edu/ml/machine-learning-databases/autos/imports-85.names
Variables have been reordered to place variables with numeric values (referred
to as "continuous" on the UCI site) to the left and categorical values to the
right. Specifically, variables 1:16 are: symboling, normalized-losses,
wheel-base, length, width, height, curb-weight, engine-size, bore, stroke,
compression-ratio, horsepower, peak-rpm, city-mpg, highway-mpg, and price.
Variables 17:26 are: make, fuel-type, aspiration, num-of-doors, body-style,
drive-wheels, engine-location, engine-type, num-of-cylinders, and fuel-system.
```

The objective of this process is to predict the "symboling," the first variable in the data, from the other predictors. "symboling" is an integer from `-3` (good insurance risk) to `3` (poor insurance risk). You could use a classification ensemble to predict this risk instead of a regression ensemble. When you have a choice between regression and classification, you should try regression first.

Prepare the data for ensemble fitting:

```
Y = X(:,1);
X(:,1) = [];
VarNames = {'normalized-losses' 'wheel-base' 'length' 'width' 'height' ...
  'curb-weight' 'engine-size' 'bore' 'stroke' 'compression-ratio' ...
  'horsepower' 'peak-rpm' 'city-mpg' 'highway-mpg' 'price' 'make' ...
```

```
  'fuel-type' 'aspiration' 'num-of-doors' 'body-style' 'drive-wheels' ...
  'engine-location' 'engine-type' 'num-of-cylinders' 'fuel-system'};
catidx = 16:25; % indices of categorical predictors
```

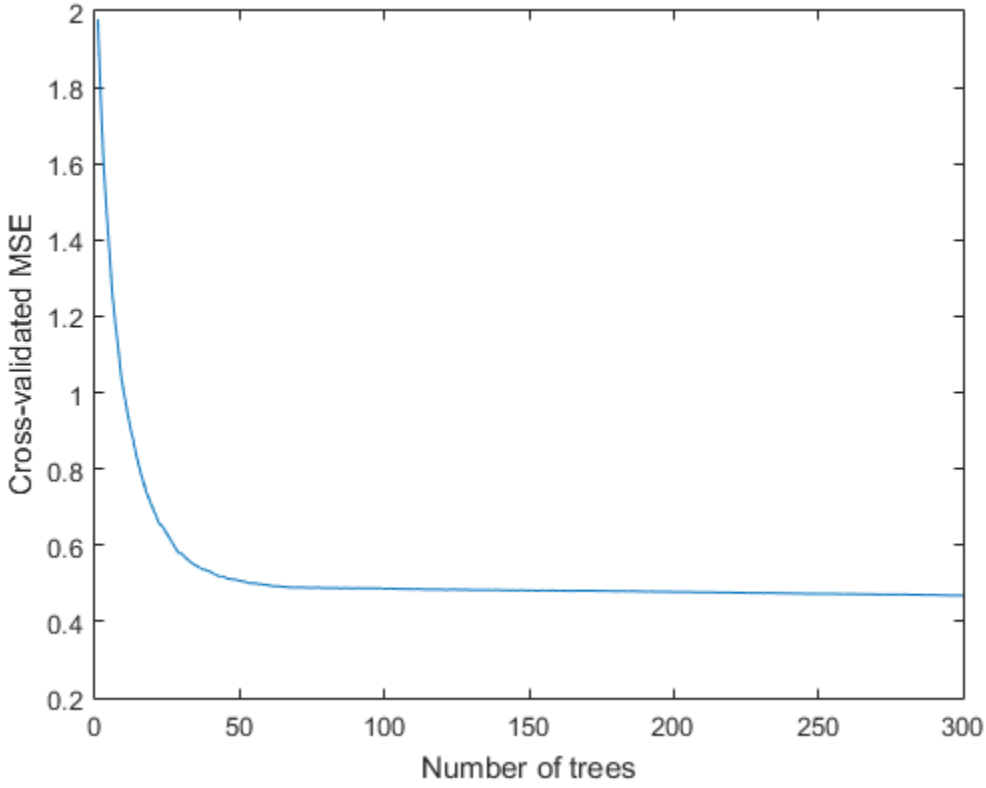
Create a regression ensemble from the data using 300 default trees:

```
ls = fitensemble(X,Y,'LSBoost',300,'Tree','LearnRate',0.1,...
    'PredictorNames',VarNames,'ResponseName','Symboling',...
    'CategoricalPredictors',catidx)
```

```
ls =

  classreg.learning.regr.RegressionEnsemble
         PredictorNames: {1x25 cell}
           ResponseName: 'Symboling'
      ResponseTransform: 'none'
        NumObservations: 205
             NumTrained: 300
                 Method: 'LSBoost'
          LearnerNames: {'Tree'}
    ReasonForTermination: 'Terminated normally after completing the reques...'
                FitInfo: [300x1 double]
     FitInfoDescription: {2x1 cell}
         Regularization: []
```

The final line, `Regularization`, is empty ([]). To regularize the ensemble, you have to use the `regularize` method.

```
cv = crossval(ls,'KFold',5);
figure;
plot(kfoldLoss(cv,'Mode','Cumulative'));
xlabel('Number of trees');
ylabel('Cross-validated MSE');
ylim([0.2,2])
```



It appears you might obtain satisfactory performance from a smaller ensemble, perhaps one containing from 50 to 100 trees.

6.Call the `regularize` method to try to find trees that you can remove from the ensemble. By default, `regularize` examines 10 values of the lasso (`Lambda`) parameter spaced exponentially.

```
ls = regularize(ls)
```

```
ls =

  classreg.learning.regr.RegressionEnsemble
         PredictorNames: {1x25 cell}
```

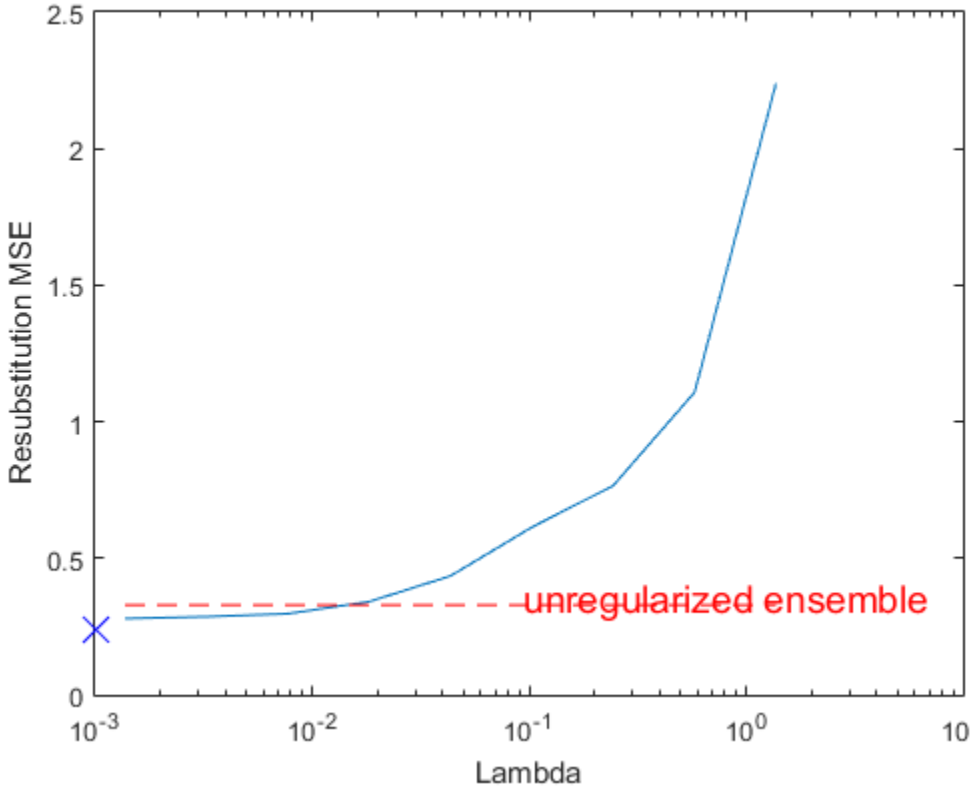
```
             ResponseName: 'Symboling'
        ResponseTransform: 'none'
          NumObservations: 205
               NumTrained: 300
                   Method: 'LSBoost'
             LearnerNames: {'Tree'}
    ReasonForTermination: 'Terminated normally after completing the reques...'
                 FitInfo: [300x1 double]
      FitInfoDescription: {2x1 cell}
          Regularization: [1x1 struct]
```

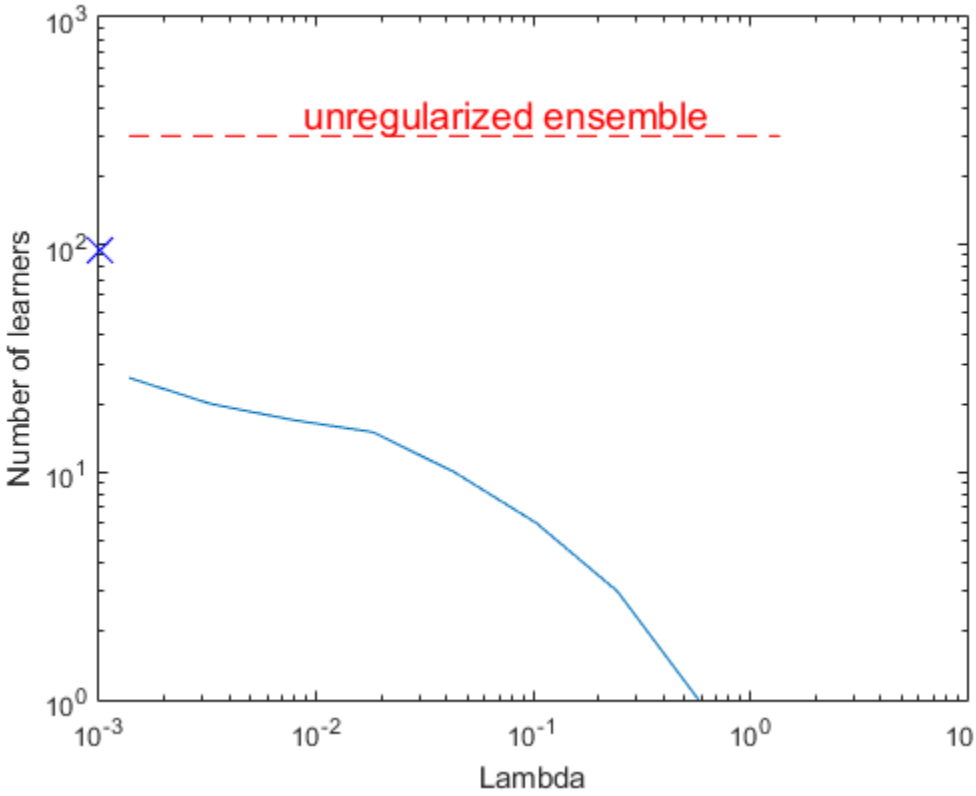
The `Regularization` property is no longer empty.

Plot the resubstitution mean-squared error (MSE) and number of learners with nonzero weights against the lasso parameter. Separately plot the value at `Lambda = 0`. Use a logarithmic scale because the values of `Lambda` are exponentially spaced.

```
figure;
semilogx(ls.Regularization.Lambda,ls.Regularization.ResubstitutionMSE);
line([1e-3 1e-3],[ls.Regularization.ResubstitutionMSE(1) ...
     ls.Regularization.ResubstitutionMSE(1)],...
    'Marker','x','Markersize',12,'Color','b');
r0 = resubLoss(ls);
line([ls.Regularization.Lambda(2) ls.Regularization.Lambda(end)],...
     [r0 r0],'Color','r','LineStyle','--');
xlabel('Lambda');
ylabel('Resubstitution MSE');
annotation('textbox',[0.5 0.22 0.5 0.05],'String','unregularized ensemble',...
    'Color','r','FontSize',14,'LineStyle','none');

figure;
loglog(ls.Regularization.Lambda,sum(ls.Regularization.TrainedWeights>0,1));
line([1e-3 1e-3],...
    [sum(ls.Regularization.TrainedWeights(:,1)>0) ...
    sum(ls.Regularization.TrainedWeights(:,1)>0)],...
    'marker','x','markersize',12,'color','b');
line([ls.Regularization.Lambda(2) ls.Regularization.Lambda(end)],...
    [ls.NTrained ls.NTrained],...
    'color','r','LineStyle','--');
xlabel('Lambda');
ylabel('Number of learners');
annotation('textbox',[0.3 0.8 0.5 0.05],'String','unregularized ensemble',...
```

```
'color','r','FontSize',14,'LineStyle','none');
```



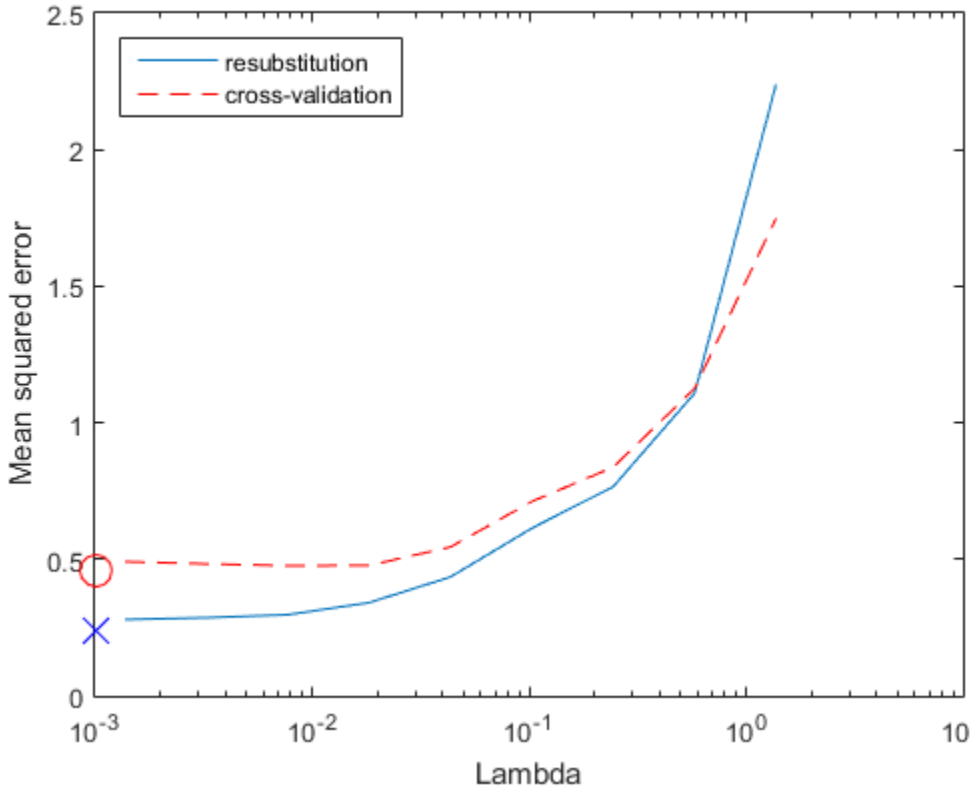


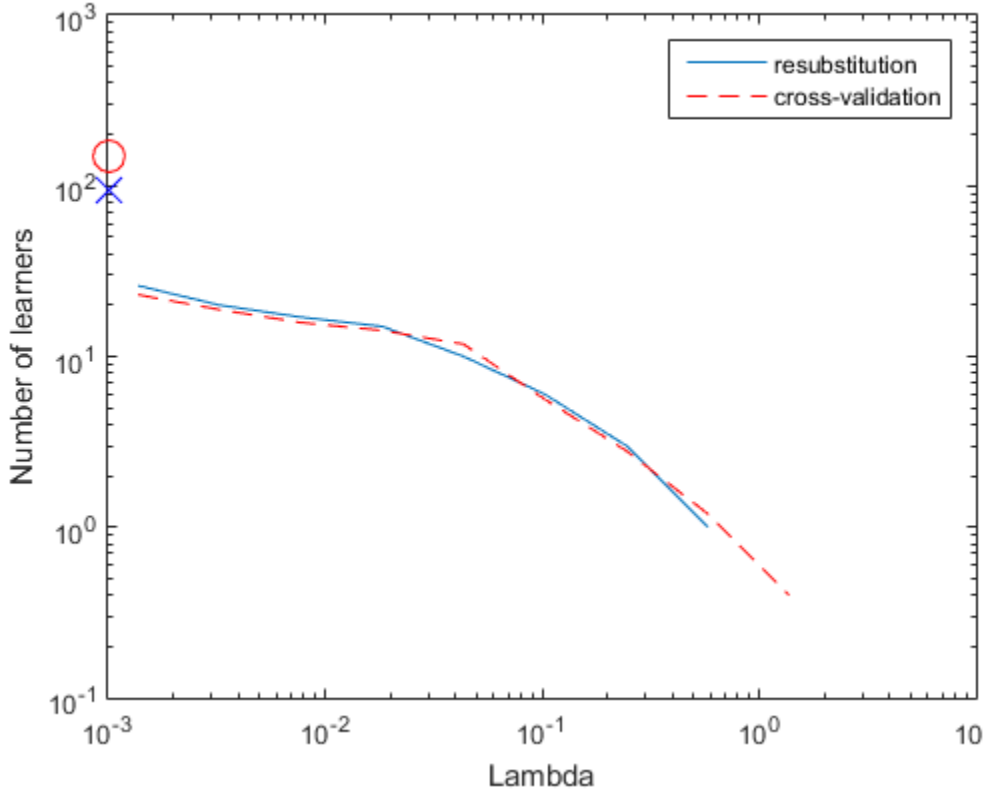
The resubstitution MSE values are likely to be overly optimistic. To obtain more reliable estimates of the error associated with various values of `Lambda`, cross validate the ensemble using `cvshrink`. Plot the resulting cross-validation loss (MSE) and number of learners against `Lambda`.

```
rng(0,'Twister') % for reproducibility
[mse,nlearn] = cvshrink(ls,'Lambda',ls.Regularization.Lambda,'KFold',5);

figure;
semilogx(ls.Regularization.Lambda,ls.Regularization.ResubstitutionMSE);
hold;
semilogx(ls.Regularization.Lambda,mse,'r--');
hold off;
xlabel('Lambda');
```

```
ylabel('Mean squared error');
legend('resubstitution','cross-validation','Location','NW');
line([1e-3 1e-3],[ls.Regularization.ResubstitutionMSE(1) ...
     ls.Regularization.ResubstitutionMSE(1)],...
    'Marker','x','Markersize',12,'Color','b');
line([1e-3 1e-3],[mse(1) mse(1)],'Marker','o',...
    'Markersize',12,'Color','r','LineStyle','--');

figure;
loglog(ls.Regularization.Lambda,sum(ls.Regularization.TrainedWeights>0,1));
hold;
loglog(ls.Regularization.Lambda,nlearn,'r--');
hold off;
xlabel('Lambda');
ylabel('Number of learners');
legend('resubstitution','cross-validation','Location','NE');
line([1e-3 1e-3],...
    [sum(ls.Regularization.TrainedWeights(:,1)>0) ...
    sum(ls.Regularization.TrainedWeights(:,1)>0)],...
    'Marker','x','Markersize',12,'Color','b');
line([1e-3 1e-3],[nlearn(1) nlearn(1)],'marker','o',...
    'Markersize',12,'Color','r','LineStyle','--');
```

```
Warning: Some folds do not have any trained weak learners.
Warning: Some folds do not have any trained weak learners.
Warning: Some folds do not have any trained weak learners.
Current plot held
Current plot held
```


resubstitution
cross-validation
Mean squared error
Lambda
2.5
2
1.5
1
0.5
0
10^-3
10^-2
10^-1
10^0
10^1



Examining the cross-validated error shows that the cross-validation MSE is almost flat for `Lambda` up to a bit over `1e-2`.

Examine `ls.Regularization.Lambda` to find the highest value that gives MSE in the flat region (up to a bit over `1e-2`):

```
jj = 1:length(ls.Regularization.Lambda);
[jj;ls.Regularization.Lambda]
```

```
ans =

  Columns 1 through 7
```

```
    1.0000    2.0000    3.0000    4.0000    5.0000    6.0000    7.0000
         0    0.0014    0.0033    0.0077    0.0183    0.0435    0.1031

  Columns 8 through 10

    8.0000    9.0000   10.0000
    0.2446    0.5800    1.3754
```

Element `5` of `ls.Regularization.Lambda` has value `0.0183`, the largest in the flat range.

Reduce the ensemble size using the `shrink` method. `shrink` returns a compact ensemble with no training data. The generalization error for the new compact ensemble was already estimated by cross validation in `mse(5)`.

```
cmp = shrink(ls,'weightcolumn',5)
```

```
cmp =

  classreg.learning.regr.CompactRegressionEnsemble
       PredictorNames: {1x25 cell}
         ResponseName: 'Symboling'
    ResponseTransform: 'none'
           NumTrained: 15
```

There are only 15 trees in the new ensemble, notably reduced from the 300 in `ls`.

Compare the sizes of the ensembles:

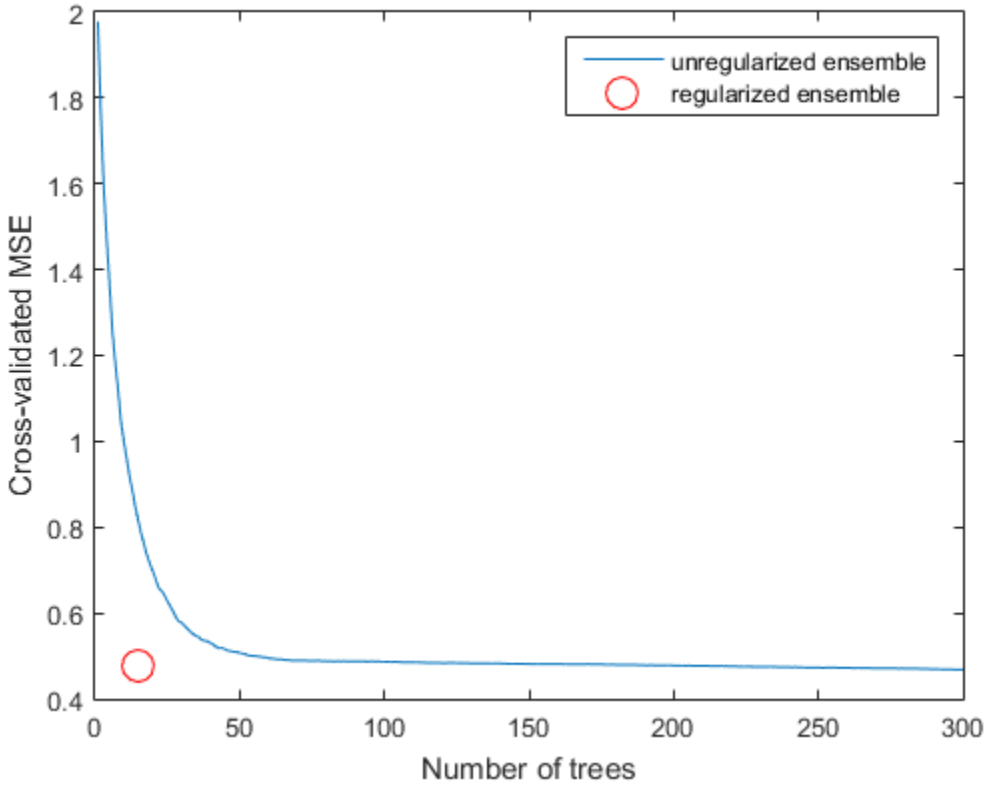
```
sz(1) = whos('cmp'); sz(2) = whos('ls');
[sz(1).bytes sz(2).bytes]
```

```
ans =

       84544     1775699
```

The reduced ensemble is about 5% the size of the original.

Compare the MSE of the reduced ensemble to that of the original ensemble:

```
figure;
plot(kfoldLoss(cv,'mode','cumulative'));
hold on
plot(cmp.NTrained,mse(5),'ro','MarkerSize',12);
xlabel('Number of trees');
ylabel('Cross-validated MSE');
legend('unregularized ensemble','regularized ensemble',...
    'Location','NE');
hold off
```



The reduced ensemble gives low loss while using many fewer trees.

Tune RobustBoost

The `RobustBoost` algorithm can make good classification predictions even when the training data has noise. However, the default `RobustBoost` parameters can produce an ensemble that does not predict well. This example shows one way of tuning the parameters for better predictive accuracy.

Note that `RobustBoost` requires an Optimization Toolbox™ license.

Generate data with label noise. This example has twenty uniform random numbers per observation, and classifies the observation as `1` if the sum of the first five numbers exceeds 2.5 (so is larger than average), and `0` otherwise:

```
rng(0,'twister') % for reproducibility
Xtrain = rand(2000,20);
Ytrain = sum(Xtrain(:,1:5),2) > 2.5;
```

To add noise, randomly switch 10% of the classifications:

```
idx = randsample(2000,200);
Ytrain(idx) = ~Ytrain(idx);
```

Create an ensemble with `AdaBoostM1` for comparison purposes:

```
ada = fitensemble(Xtrain,Ytrain,'AdaBoostM1',...
    300,'Tree','LearnRate',0.1);
```

Create an ensemble with `RobustBoost`. Because the data has 10% incorrect classification, perhaps an error goal of 15% is reasonable.

```
rb1 = fitensemble(Xtrain,Ytrain,'RobustBoost',300,...
   'Tree','RobustErrorGoal',0.15,'RobustMaxMargin',1);
```

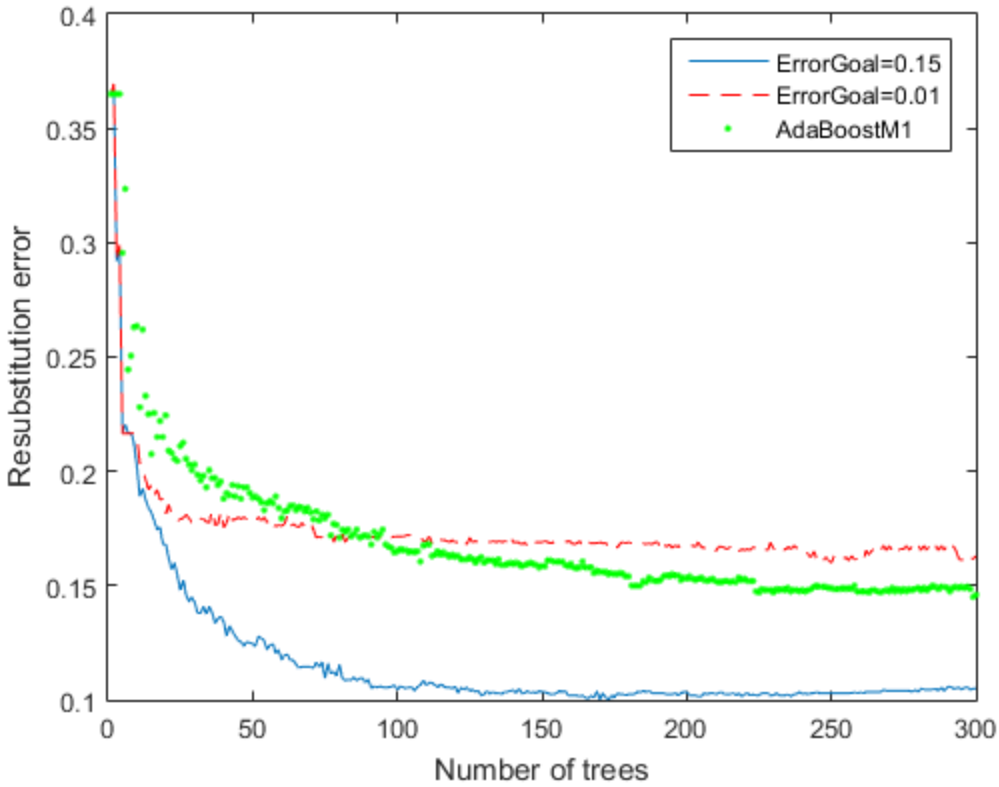
Note that if you set the error goal to a high enough value, then the software returns an error.

Create an ensemble with very optimistic error goal, `0.01`:

```
rb2 = fitensemble(Xtrain,Ytrain,'RobustBoost',300,...
   'Tree','RobustErrorGoal',0.01);
```

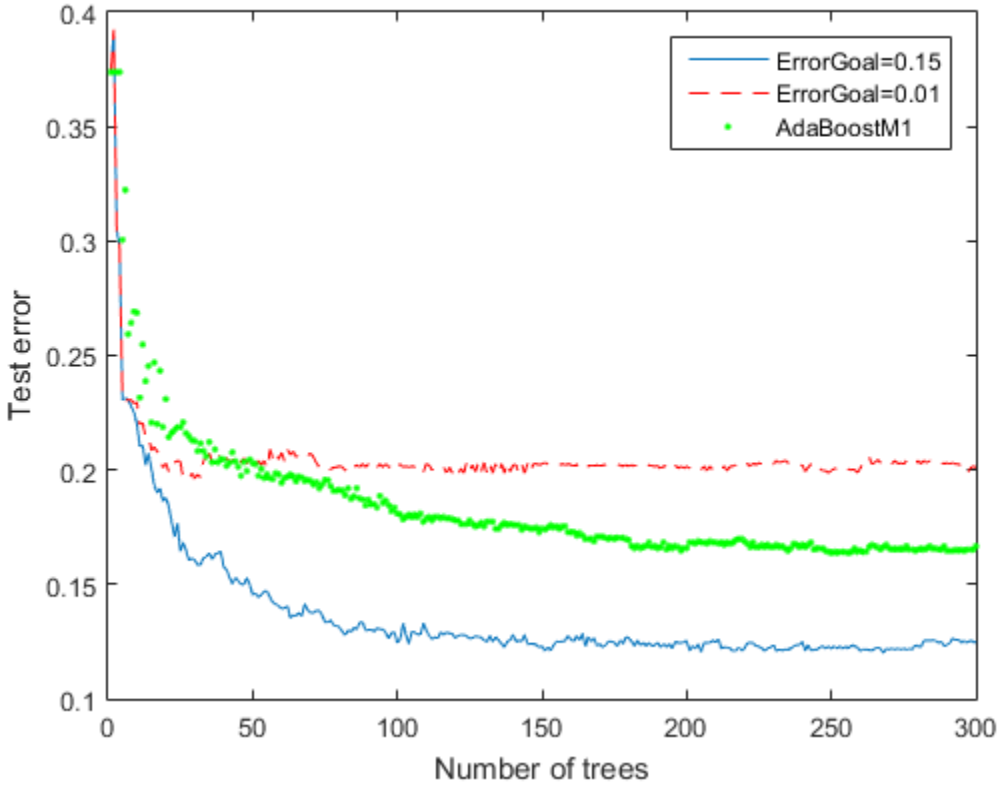
Compare the resubstitution error of the four ensembles:

```
figure
plot(resubLoss(rb1,'Mode','Cumulative'));
hold on
plot(resubLoss(rb2,'Mode','Cumulative'),'r--');
plot(resubLoss(ada,'Mode','Cumulative'),'g.');
hold off;
xlabel('Number of trees');
ylabel('Resubstitution error');
legend('ErrorGoal=0.15','ErrorGoal=0.01',...
    'AdaBoostM1','Location','NE');
```



All the `RobustBoost` curves show lower resubstitution error than the `AdaBoostM1` curve. The error goal of `0.15` curve shows the lowest resubstitution error over most of the range.

```
Xtest = rand(2000,20);
Ytest = sum(Xtest(:,1:5),2) > 2.5;
idx = randsample(2000,200);
Ytest(idx) = ~Ytest(idx);
figure;
plot(loss(rb1,Xtest,Ytest,'Mode','Cumulative'));
hold on
plot(loss(rb2,Xtest,Ytest,'Mode','Cumulative'),'r--');
plot(loss(ada,Xtest,Ytest,'Mode','Cumulative'),'g.');
hold off;
xlabel('Number of trees');
ylabel('Test error');
legend('ErrorGoal=0.15','ErrorGoal=0.01',...
    'AdaBoostM1','Location','NE');
```



The error curve for error goal 0.15 is lowest (best) in the plotted range. `AdaBoostM1` has higher error than the curve for error goal 0.15. The curve for the too-optimistic error goal 0.01 remains substantially higher (worse) than the other algorithms for most of the plotted range.

Random Subspace Classification

This example shows how to use a random subspace ensemble to increase the accuracy of classification. It also shows how to use cross validation to determine good parameters for both the weak learner template and the ensemble.

Load the data

Load the `ionosphere` data. This data has 351 binary responses to 34 predictors.

```
load ionosphere;
[N,D] = size(X)
resp = unique(Y)
```

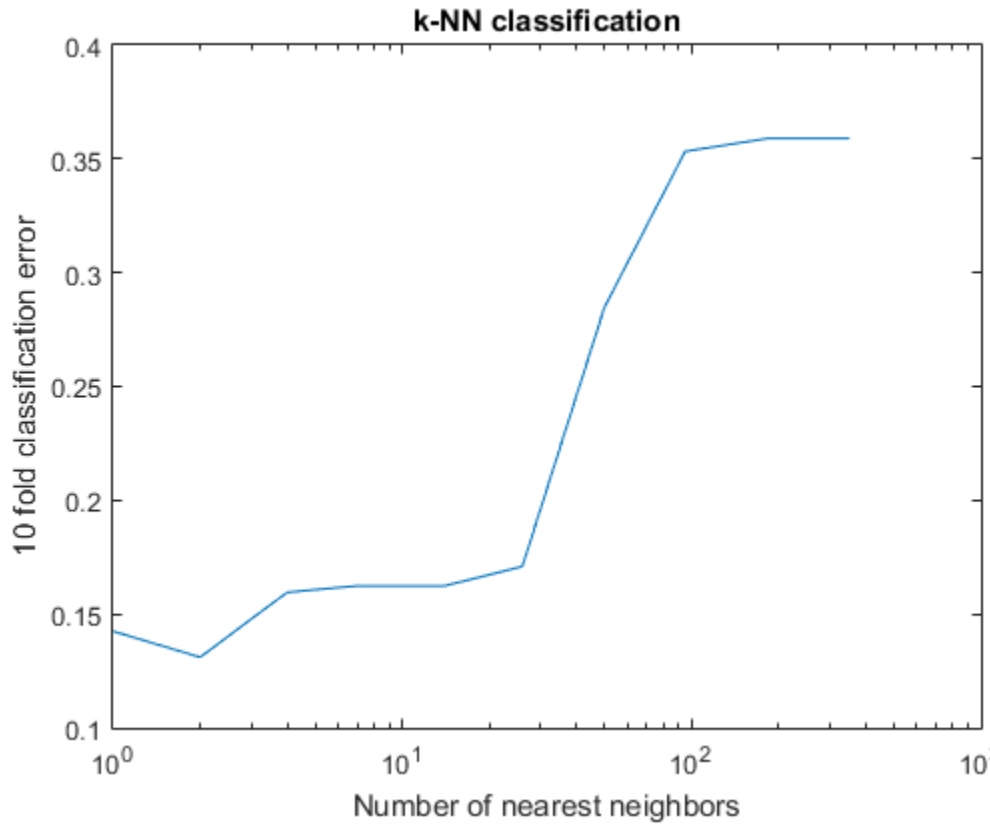
```
N =

   351


D =

    34


resp =

    'b'
    'g'
```

Choose the number of nearest neighbors

Find a good choice for `k`, the number of nearest neighbors in the classifier, by cross validation. Choose the number of neighbors approximately evenly spaced on a logarithmic scale.

```
rng(8000,'twister') % for reproducibility
```

```
K = round(logspace(0,log10(N),10)); % number of neighbors
cvloss = zeros(numel(K),1);
for k=1:numel(K)
    knn = fitcknn(X,Y,...
        'NumNeighbors',K(k),'CrossVal','On');
    cvloss(k) = kfoldLoss(knn);
end
figure; % Plot the accuracy versus k
semilogx(K,cvloss);
xlabel('Number of nearest neighbors');
ylabel('10 fold classification error');
title('k-NN classification');
```



The lowest cross-validation error occurs for `k = 2`.

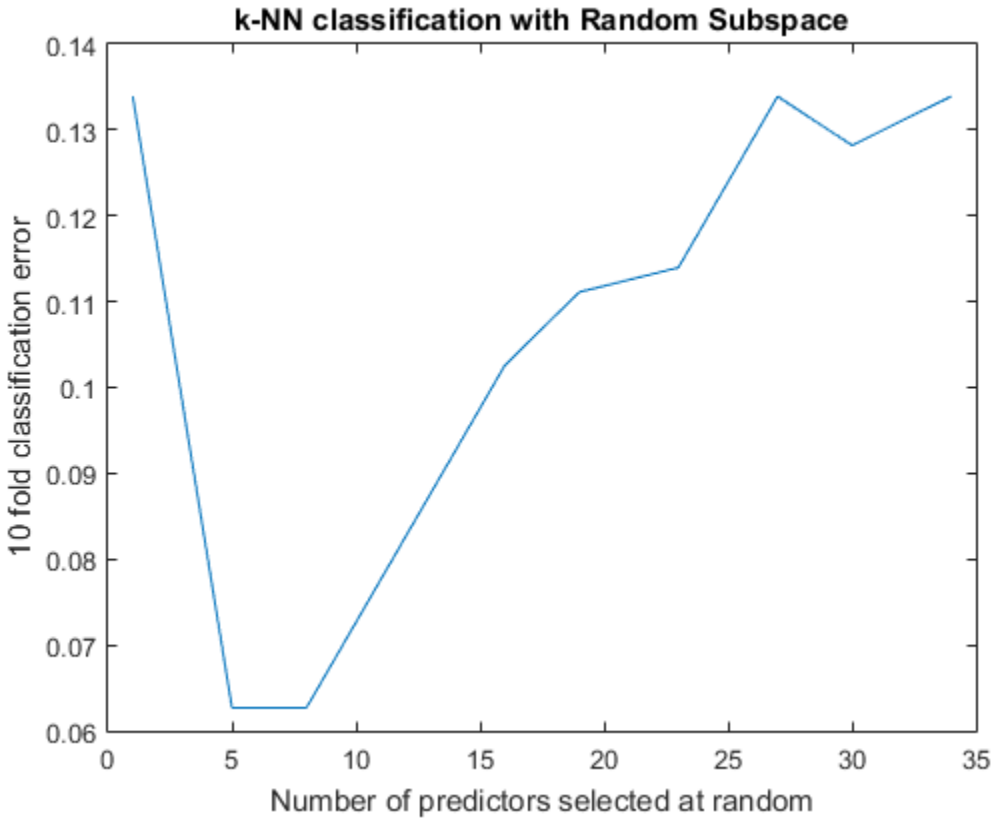
Create the ensembles

Create ensembles for 2-nearest neighbor classification with various numbers of dimensions, and examine the cross-validated loss of the resulting ensembles.

This step takes a long time. To keep track of the progress, print a message as each dimension finishes.

```
NPredToSample = round(linspace(1,D,10)); % linear spacing of dimensions
cvloss = zeros(numel(NPredToSample),1);
learner = templateKNN('NumNeighbors',2);
for npred=1:numel(NPredToSample)
   subspace = fitensemble(X,Y,'Subspace',100,learner,...
       'NPredToSample',NPredToSample(npred),'CrossVal','On');
   cvloss(npred) = kfoldLoss(subspace);
   fprintf('Random Subspace %i done.\n',npred);
end
figure; % plot the accuracy versus dimension
plot(NPredToSample,cvloss);
xlabel('Number of predictors selected at random');
ylabel('10 fold classification error');
title('k-NN classification with Random Subspace');
```

```
Random Subspace 1 done.
Random Subspace 2 done.
Random Subspace 3 done.
Random Subspace 4 done.
Random Subspace 5 done.
Random Subspace 6 done.
Random Subspace 7 done.
Random Subspace 8 done.
Random Subspace 9 done.
Random Subspace 10 done.
```



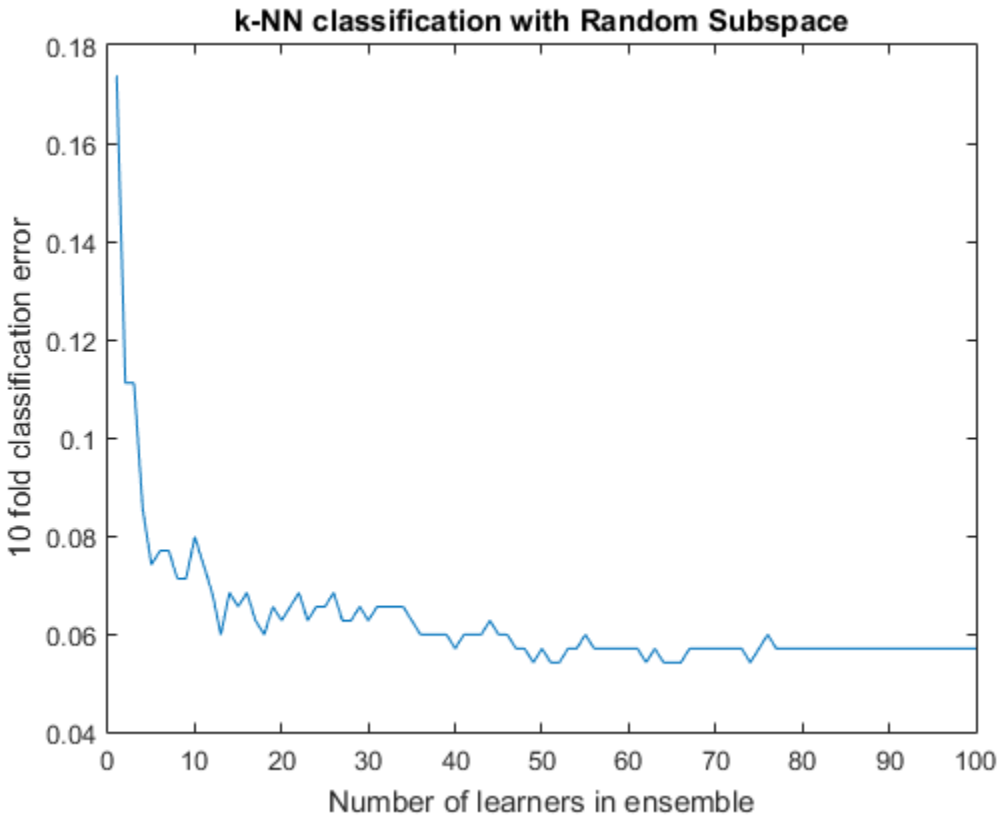
The ensembles that use five and eight predictors per learner have the lowest cross-validated error. The error rate for these ensembles is about 0.06, while the other ensembles have cross-validated error rates that are approximately 0.1 or more.

Find a good ensemble size

Find the smallest number of learners in the ensemble that still give good classification.

```
ens = fitensemble(X,Y,'Subspace',100,learner,...
       'NPredToSample',5,'CrossVal','on');
figure; % Plot the accuracy versus number in ensemble
plot(kfoldLoss(ens,'Mode','Cumulative'))
xlabel('Number of learners in ensemble');
ylabel('10 fold classification error');
```

```
title('k-NN classification with Random Subspace');
```



There seems to be no advantage in an ensemble with more than 50 or so learners. It is possible that 25 learners gives good predictions.

Create a final ensemble

Construct a final ensemble with 50 learners. Compact the ensemble and see if the compacted version saves an appreciable amount of memory.

```
ens = fitensemble(X,Y,'Subspace',50,learner,...
       'NPredToSample',5);
cens = compact(ens);
s1 = whos('ens');
```

```
s2 = whos('cens');
[s1.bytes s2.bytes] % si.bytes = size in bytes


ans =

     1756230     1525678
```

The compact ensemble is about 10% smaller than the full ensemble. Both give the same predictions.

TreeBagger Examples

- "Regression of Insurance Risk Rating for Car Imports Using TreeBagger" on page 16-129
- "Classifying Radar Returns for Ionosphere Data Using TreeBagger" on page 16-141

`TreeBagger` ensembles have more functionality than those constructed with `fitensemble`; see TreeBagger Features Not in fitensemble. Also, some property and method names differ from their `fitensemble` counterparts. This section contains examples of workflow for regression and classification that use this extra `TreeBagger` functionality.

Regression of Insurance Risk Rating for Car Imports Using TreeBagger

In this example, use a database of 1985 car imports with 205 observations, 25 predictors, and 1 response, which is insurance risk rating, or "symboling." The first 15 variables are numeric and the last 10 are categorical. The symboling index takes integer values from -3 to 3.

Load the data set and split it into predictor and response arrays.

```
load imports-85;
Y = X(:,1);
X = X(:,2:end);
isCategorical = [zeros(15,1);ones(size(X,2)-15,1)]; % Categorical variable flag
```

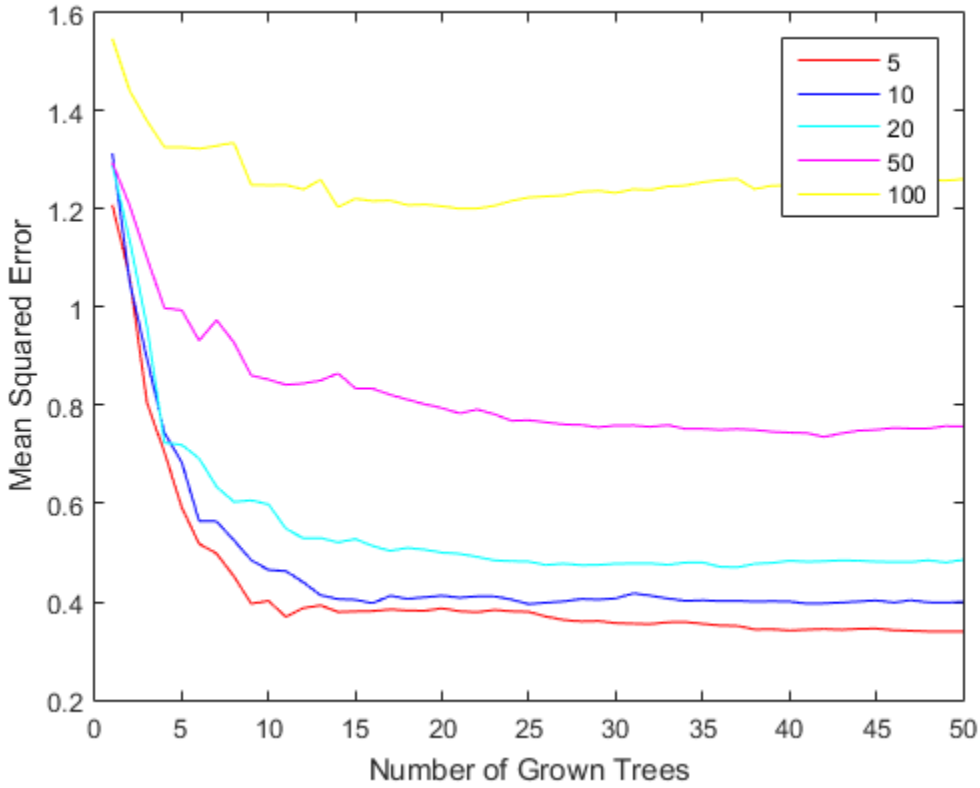
Because bagging uses randomized data drawings, its exact outcome depends on the initial random seed. To reproduce the results in this example, use the random stream settings.

```
rng(1945,'twister')
```

Finding the Optimal Leaf Size

For regression, the general rule is to the set leaf size to 5 and select one third of the input features for decision splits at random. In the following step, verify the optimal leaf size by comparing mean squared errors obtained by regression for various leaf sizes. `oobError` computes MSE versus the number of grown trees. You must set `OOBPred` to `'On'` to obtain out-of-bag predictions later.

```
leaf = [5 10 20 50 100];
col = 'rbcmy';
figure
for i=1:length(leaf)
    b = TreeBagger(50,X,Y,'Method','R','OOBPred','On',...
   'CategoricalPredictors',find(isCategorical == 1),'MinLeaf',leaf(i));
    plot(oobError(b),col(i));
    hold on;
end
xlabel 'Number of Grown Trees';
ylabel 'Mean Squared Error' ;
legend({'5' '10' '20' '50' '100'},'Location','NorthEast');
hold off;
```



The red curve (leaf size 5) yields the lowest MSE values.

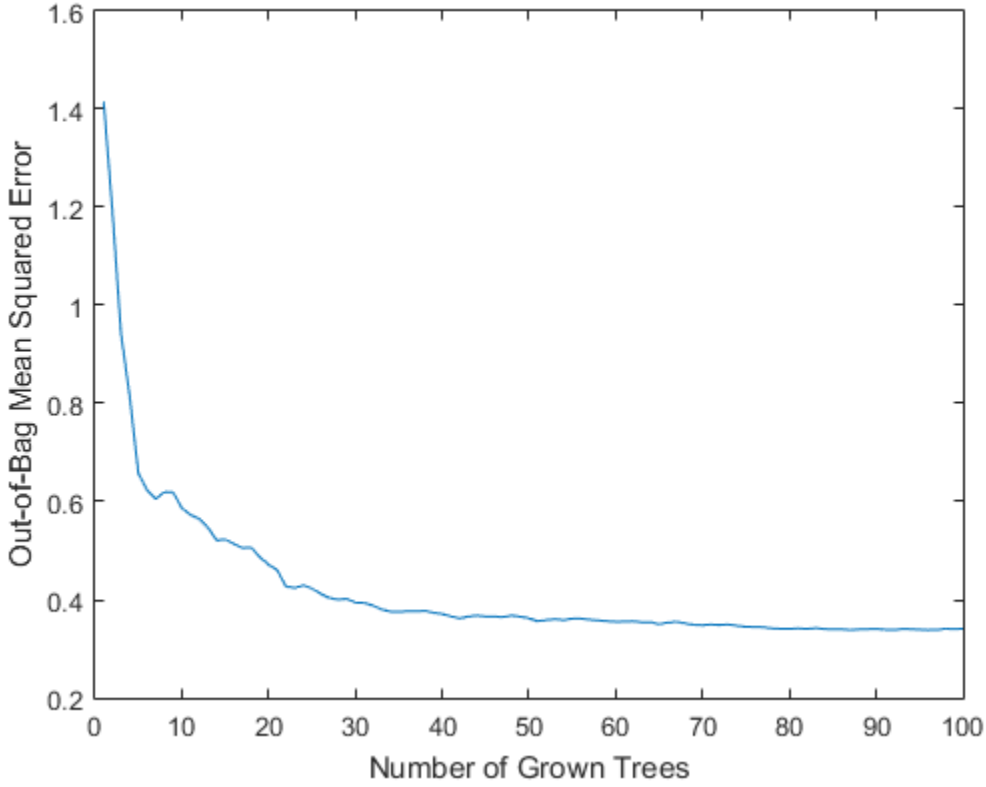
Estimating Feature Importance

In practical applications, you typically grow ensembles with hundreds of trees. For example, the previous code block uses 50 trees for faster processing. Now that you have estimated the optimal leaf size, grow a larger ensemble with 100 trees and use it to estimate feature importance.

```
b = TreeBagger(100,X,Y,'Method','R','OOBVarImp','On',...
    'CategoricalPredictors',find(isCategorical == 1),...
    'MinLeaf',5);
```

Inspect the error curve again to make sure nothing went wrong during training.

```
figure
plot(oobError(b));
xlabel 'Number of Grown Trees';
ylabel 'Out-of-Bag Mean Squared Error';
```



Prediction ability should depend more on important features than unimportant features. You can use this idea to measure feature importance.

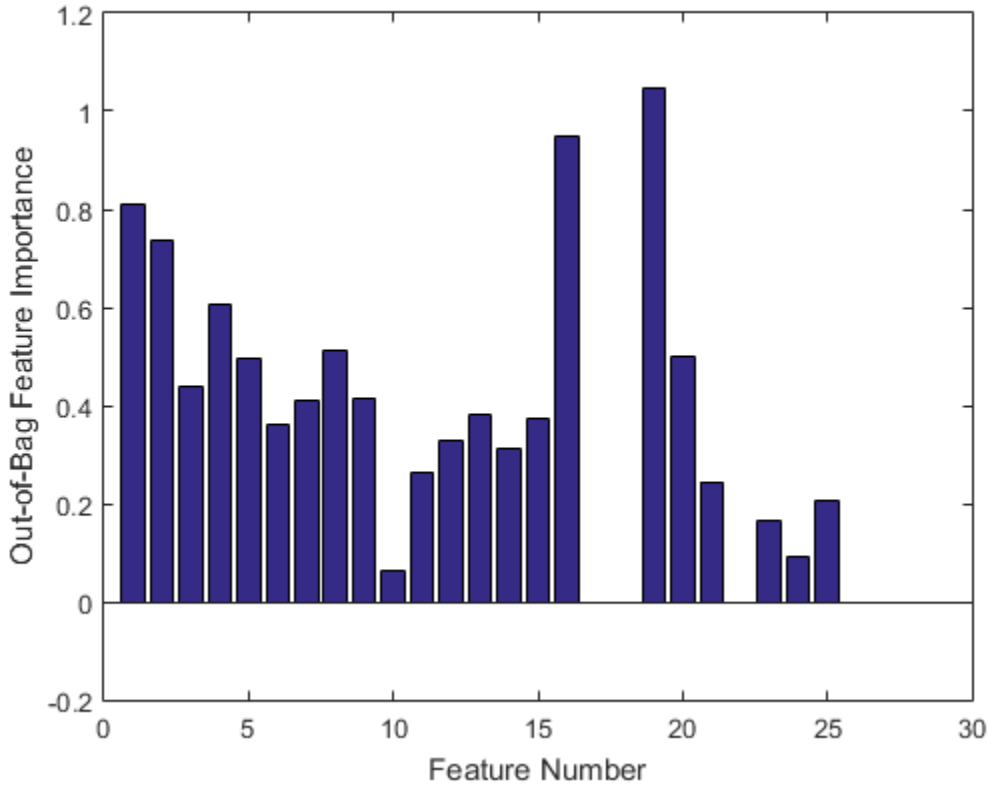
For each feature, permute the values of this feature across every observation in the data set and measure how much worse the MSE becomes after the permutation. You can repeat this for each feature.

Using the following code, plot the increase in MSE due to permuting out-of-bag observations across each input variable. The `OOBPermutedVarDeltaError` array

stores the increase in MSE averaged over all trees in the ensemble and divided by the standard deviation taken over the trees, for each variable. The larger this value, the more important the variable. Imposing an arbitrary cutoff at 0.7, you can select the five most important features.

```
figure
bar(b.OOBPermutedVarDeltaError);
xlabel 'Feature Number' ;
ylabel 'Out-of-Bag Feature Importance';
idxvar = find(b.OOBPermutedVarDeltaError>0.7)
idxCategorical = find(isCategorical(idxvar)==1);
```

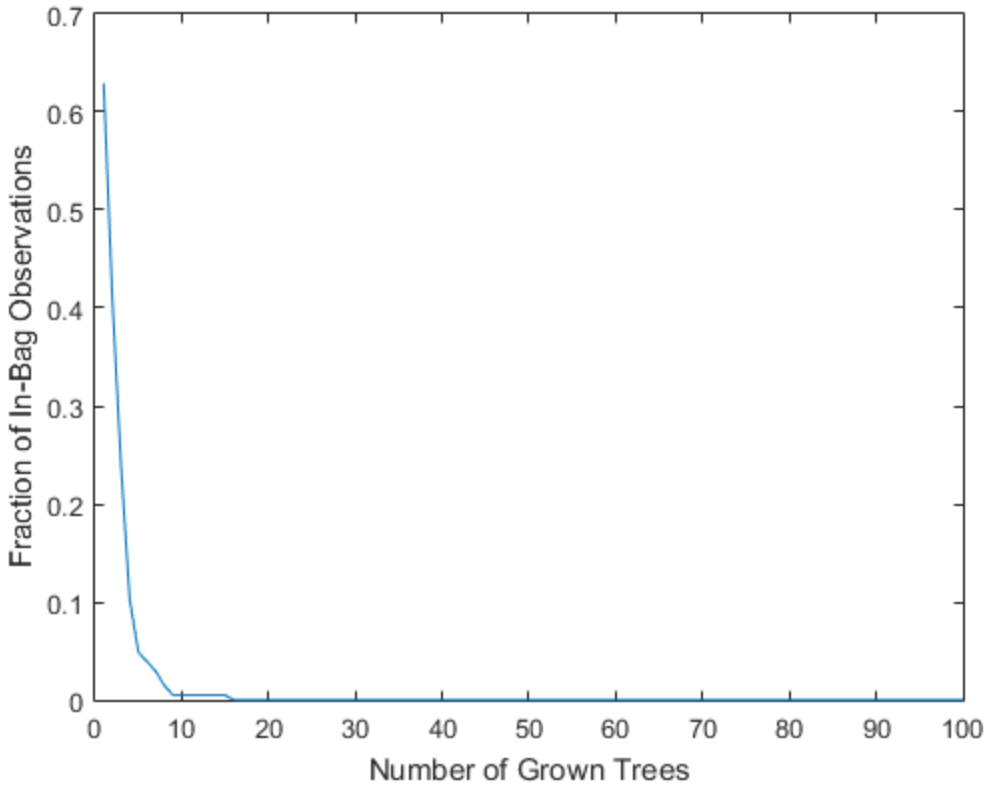
```
idxvar =

     1     2    16    19
```



The `OOBIndices` property of `TreeBagger` tracks which observations are out of bag for what trees. Using this property, you can monitor the fraction of observations in the training data that are in bag for all trees. The curve starts at approximately 2/3, which is the fraction of unique observations selected by one bootstrap replica, and goes down to 0 at approximately 10 trees.

```
finbag = zeros(1,b.NTrees);
for t=1:b.NTrees
    finbag(t) = sum(all(~b.OOBIndices(:,1:t),2));
end
finbag = finbag / size(X,1);
figure
plot(finbag);
xlabel 'Number of Grown Trees';
```

```
ylabel 'Fraction of In-Bag Observations';
```

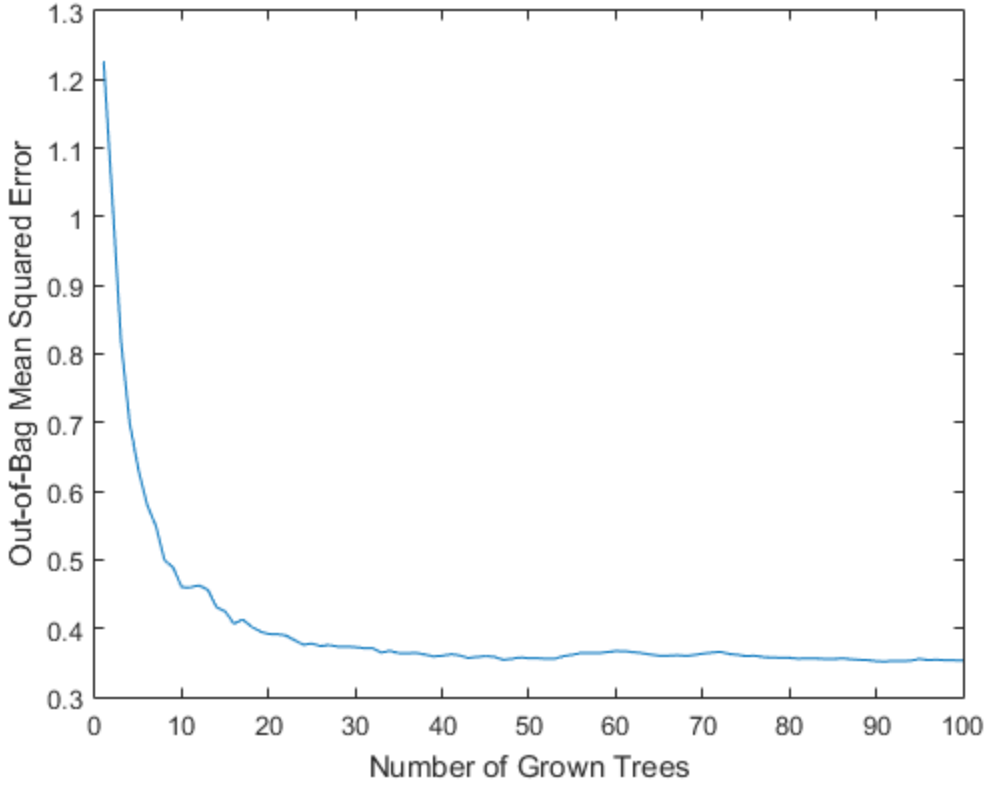


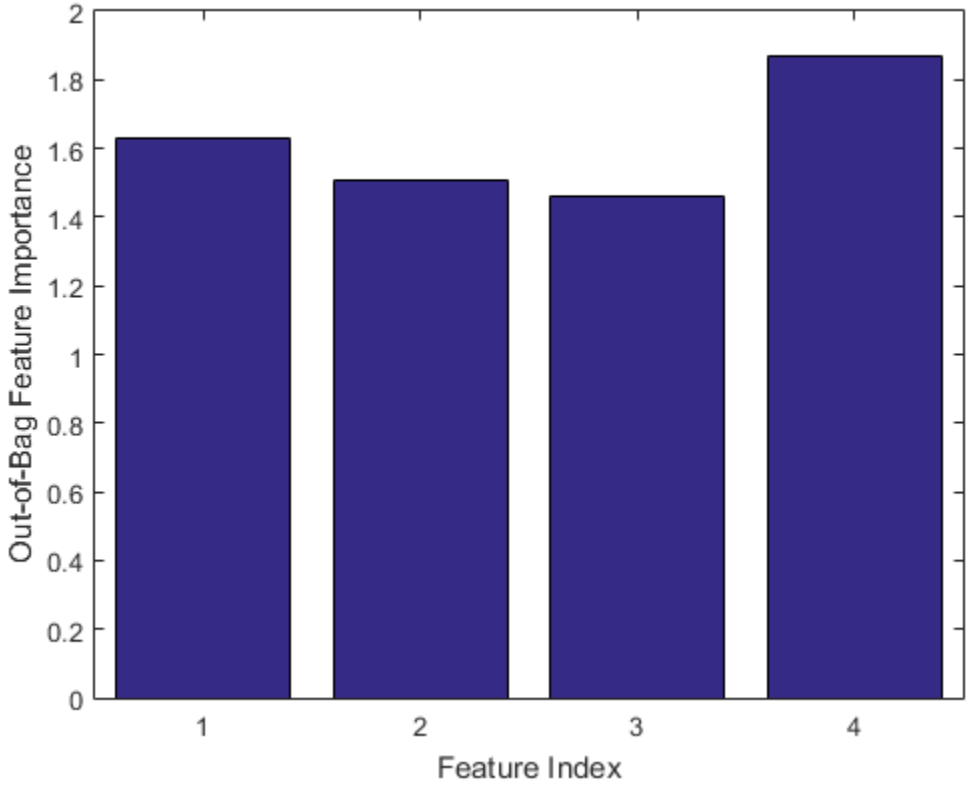
Growing Trees on a Reduced Set of Features

Using just the five most powerful features, determine if it is possible to obtain a similar predictive power. To begin, grow 100 trees on these features only. The first three of the five selected features are numeric and the last two are categorical.

```
b5v = TreeBagger(100,X(:,idxvar),Y,'Method','R',...
    'OOBVarImp','On','CategoricalPredictors',idxCategorical,...
    'MinLeaf',5);
figure
```

```
plot(oobError(b5v));
xlabel 'Number of Grown Trees';
ylabel 'Out-of-Bag Mean Squared Error';
figure
bar(b5v.OOBPermutedVarDeltaError);
xlabel 'Feature Index';
ylabel 'Out-of-Bag Feature Importance';
```





These five most powerful features give the same MSE as the full set, and the ensemble trained on the reduced set ranks these features similarly to each other. If you remove features 1 and 2 from the reduced set, then the predictive power of the algorithm might not decrease significantly.

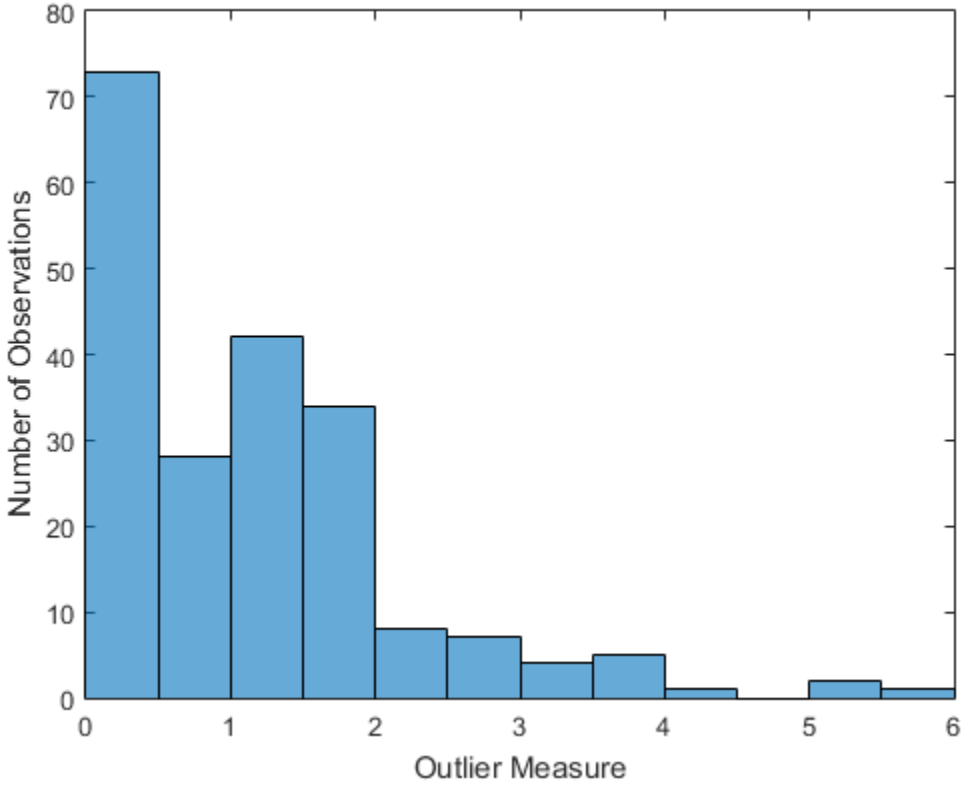
Finding Outliers

To find outliers in the training data, compute the proximity matrix using `fillProximities`.

```
b5v = fillProximities(b5v);
```

The method normalizes this measure by subtracting the mean outlier measure for the entire sample. Then it takes the magnitude of this difference and divides the result by the median absolute deviation for the entire sample.

```
figure
histogram(b5v.OutlierMeasure);
xlabel 'Outlier Measure';
ylabel 'Number of Observations';
```

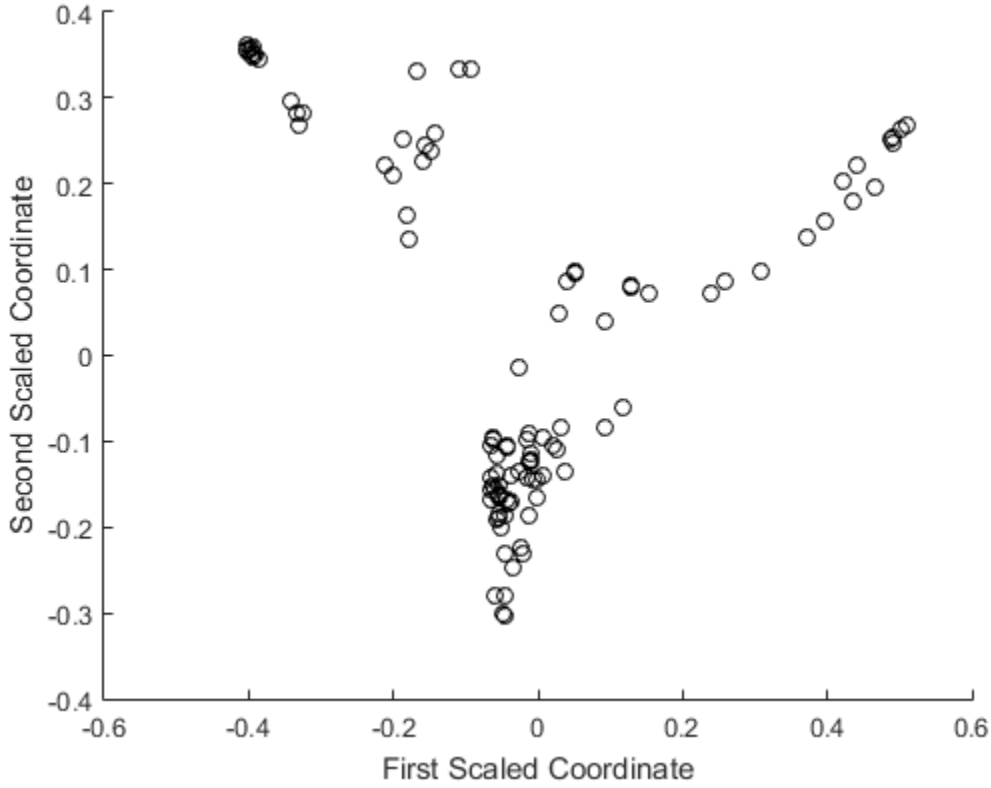


Discovering Clusters in the Data

By applying multidimensional scaling to the computed matrix of proximities, you can inspect the structure of the input data and look for possible clusters of observations. The

`mdsProx` method returns scaled coordinates and eigenvalues for the computed proximity matrix. If you run it with the `Colors` name-value-pair argument, then this method creates a scatter plot of two scaled coordinates.

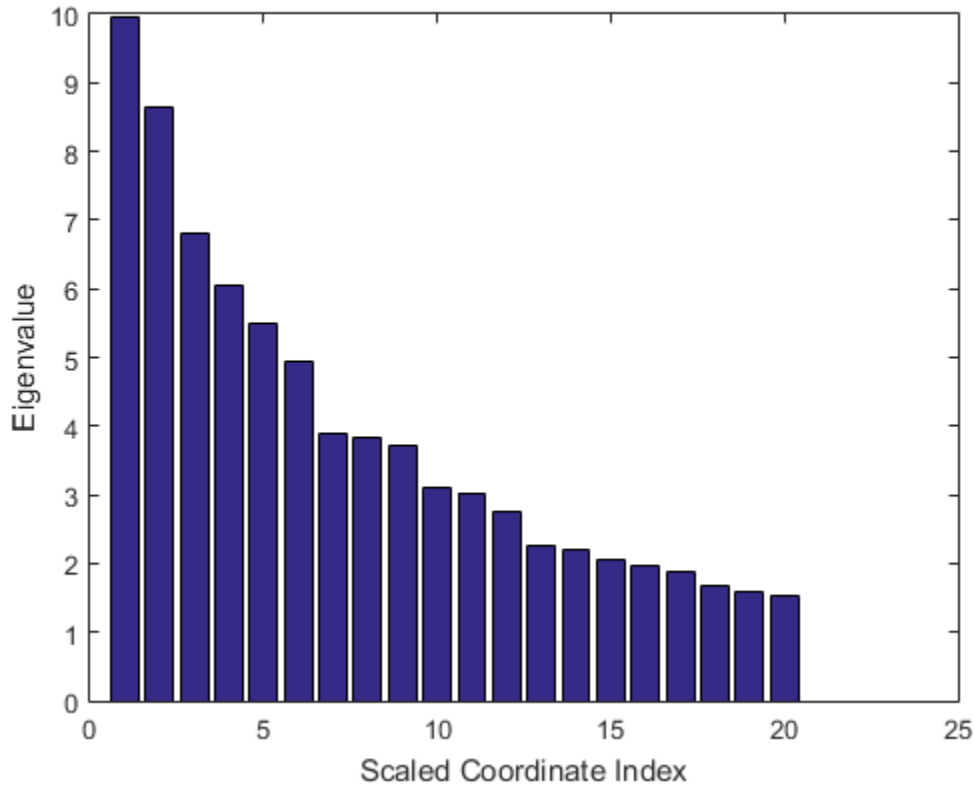
```
figure(8);
[~,e] = mdsProx(b5v,'Colors','K');
xlabel 'First Scaled Coordinate';
ylabel 'Second Scaled Coordinate';
```



Assess the relative importance of the scaled axes by plotting the first 20 eigenvalues.

```
figure
bar(e(1:20));
```

```
xlabel 'Scaled Coordinate Index';
ylabel 'Eigenvalue';
```



Saving the Ensemble Configuration for Future Use

To use the trained ensemble for predicting the response on unseen data, store the ensemble to disk and retrieve it later. If you do not want to compute predictions for out-of-bag data or reuse training data in any other way, there is no need to store the ensemble object itself. Saving the compact version of the ensemble is enough in this case. Extract the compact object from the ensemble.

```
c = compact(b5v)
```

```
c =

  CompactTreeBagger
Ensemble with 100 bagged decision trees:
              Method:           regression
               Nvars:                    4
```

You can save the resulting `CompactTreeBagger` model in a `*.mat` file.

Classifying Radar Returns for Ionosphere Data Using TreeBagger

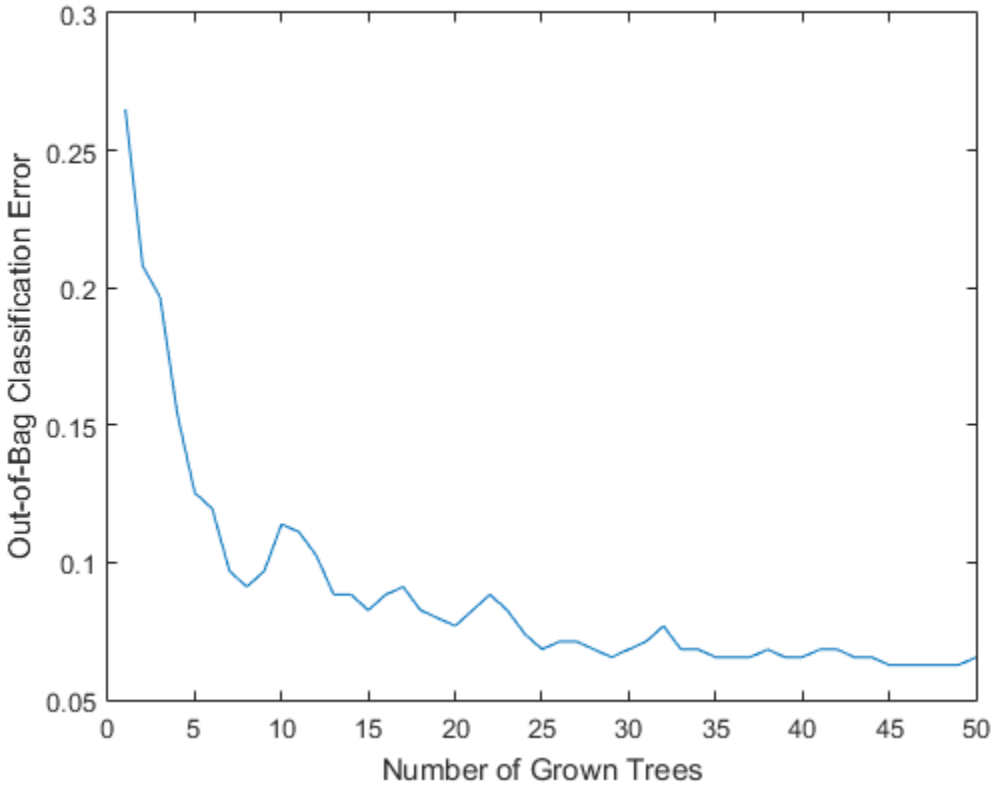
You can also use ensembles of decision trees for classification. For this example, use ionosphere data with 351 observations and 34 real-valued predictors. The response variable is categorical with two levels:

- 'g' represents good radar returns.
- 'b' represents bad radar returns.

The goal is to predict good or bad returns using a set of 34 measurements.

Fix the initial random seed, grow 50 trees, inspect how the ensemble error changes with accumulation of trees, and estimate feature importance. For classification, it is best to set the minimal leaf size to 1 and select the square root of the total number of features for each decision split at random. These settings are defaults for `TreeBagger` used for classification.

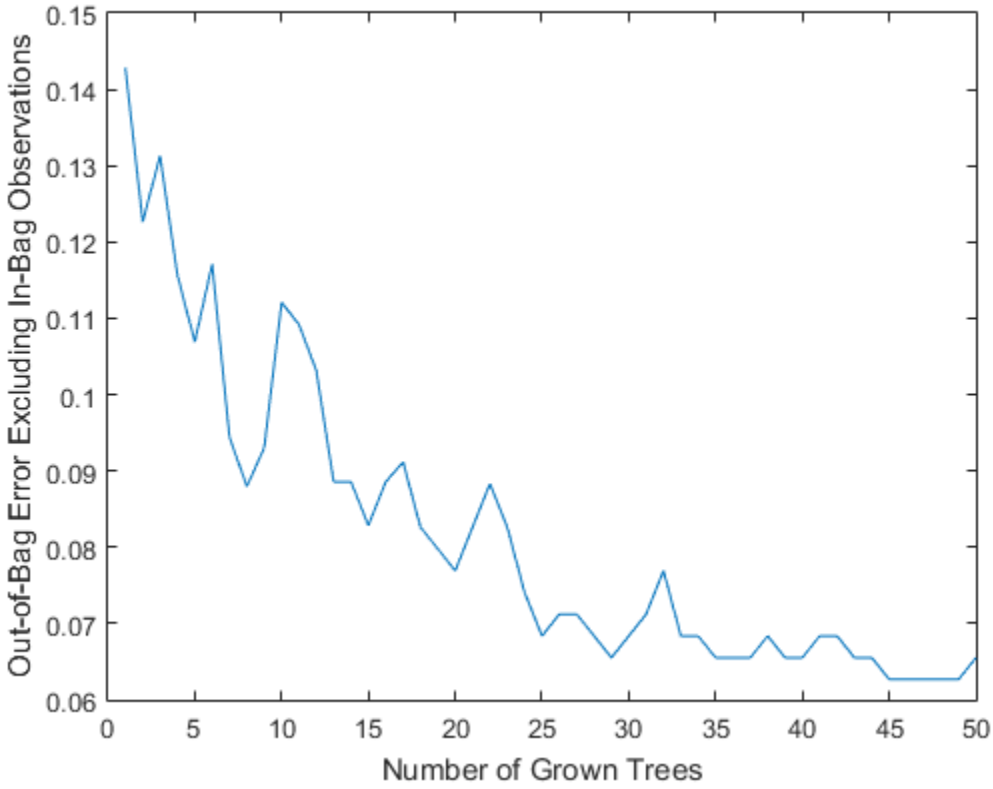
```
load ionosphere;
rng(1945,'twister')
b = TreeBagger(50,X,Y,'OOBVarImp','On');
figure
plot(oobError(b));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Classification Error');
```



The method trains ensembles with few trees on observations that are in bag for all trees. For such observations, it is impossible to compute the true out-of-bag prediction, and `TreeBagger` returns the most probable class for classification and the sample mean for regression. You can change the default value returned for in-bag observations using the `DefaultYfit` property. If you set the default value to an empty string for classification, the method excludes in-bag observations from computation of the out-of-bag error. In this case, the curve is more variable when the number of trees is small, either because some observations are never out of bag (and are therefore excluded) or because their predictions are based on few trees.

```
b.DefaultYfit = '';
figure
plot(oobError(b));
```

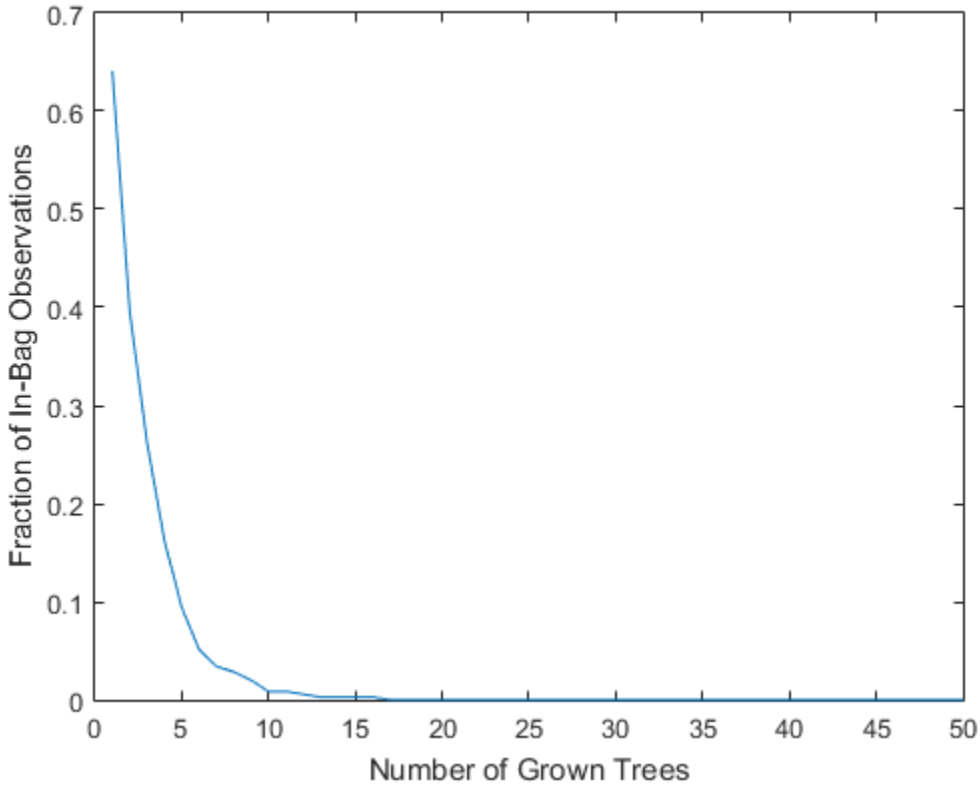
```
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Error Excluding In-Bag Observations');
```



The `OOBIndices` property of `TreeBagger` tracks which observations are out of bag for what trees. Using this property, you can monitor the fraction of observations in the training data that are in bag for all trees. The curve starts at approximately 2/3, which is the fraction of unique observations selected by one bootstrap replica, and goes down to 0 at approximately 10 trees.

```
finbag = zeros(1,b.NTrees);
for t=1:b.NTrees
    finbag(t) = sum(all(~b.OOBIndices(:,1:t),2));
end
finbag = finbag / size(X,1);
```

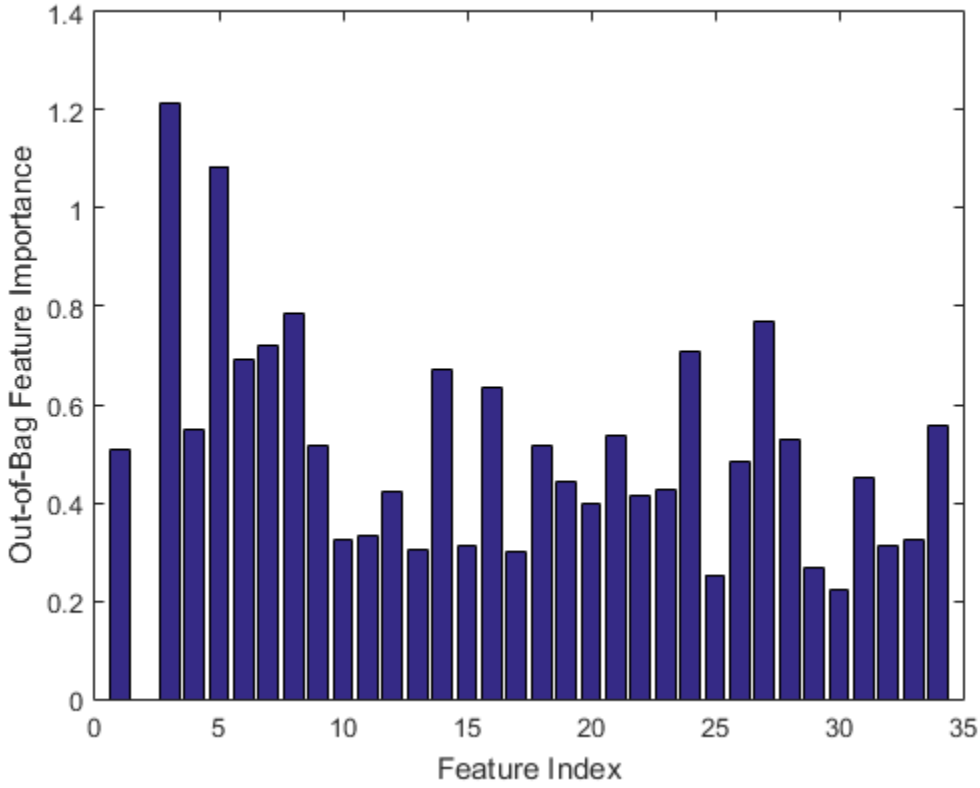
```
figure
plot(finbag);
xlabel('Number of Grown Trees');
ylabel('Fraction of In-Bag Observations');
```



Estimate feature importance.

```
figure
bar(b.OOBPermutedVarDeltaError);
xlabel('Feature Index');
ylabel('Out-of-Bag Feature Importance');
idxvar = find(b.OOBPermutedVarDeltaError>0.75)
```

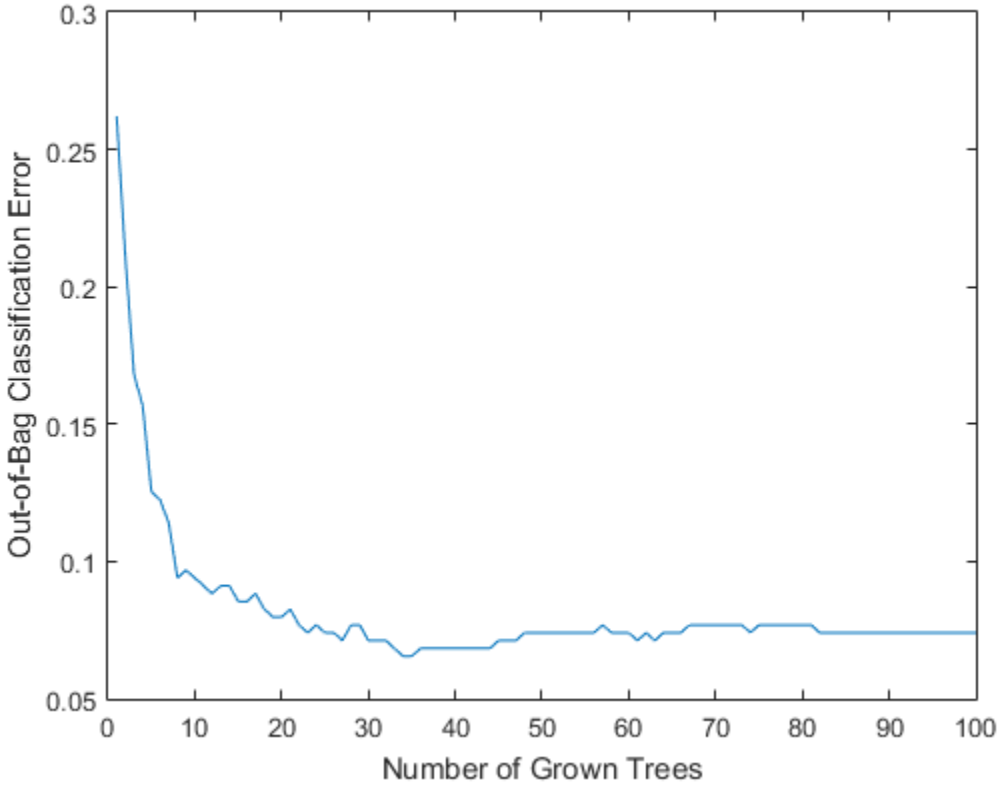
```
idxvar =

     3     5     8    27
```



Having selected the five most important features, grow a larger ensemble on the reduced feature set. Save time by not permuting out-of-bag observations to obtain new estimates of feature importance for the reduced feature set (set `OOBVarImp` to `'off'`). You would still be interested in obtaining out-of-bag estimates of classification error (set `OOBPred` to `'on'`).

```
b5v = TreeBagger(100,X(:,idxvar),Y,'OOBVarImp','off','OOBPred','on');
figure
```

```
plot(oobError(b5v));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Classification Error');
```



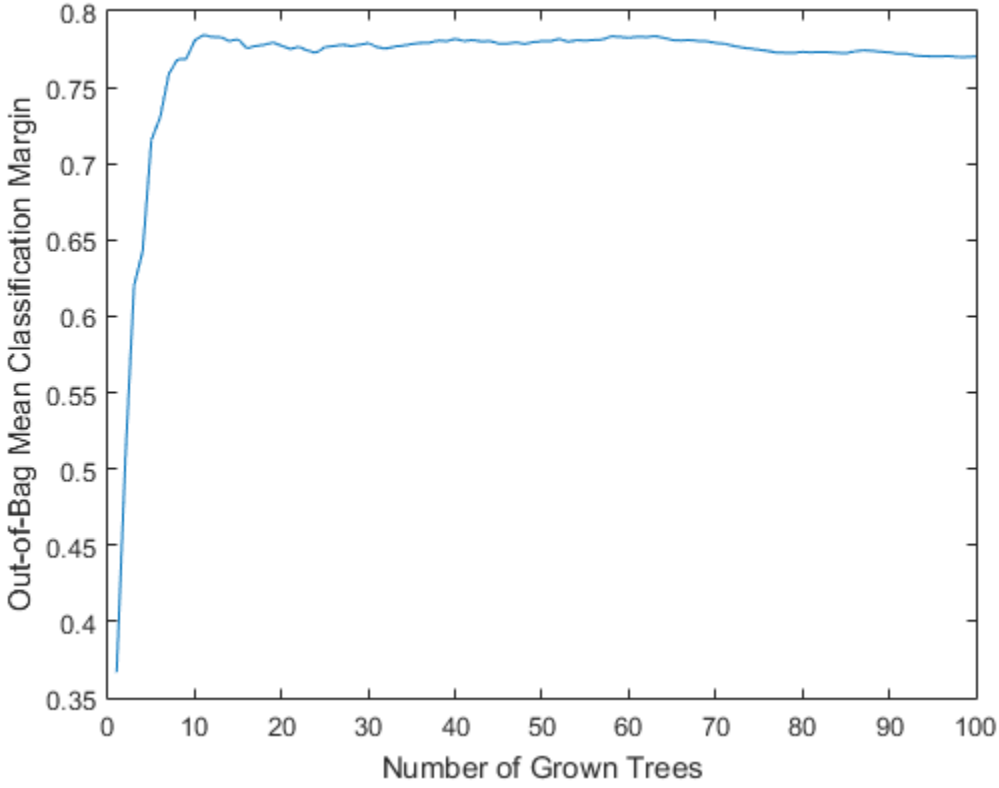
For classification ensembles, in addition to classification error (fraction of misclassified observations), you can also monitor the average classification margin. For each observation, the *margin* is defined as the difference between the score for the true class and the maximal score for other classes predicted by this tree. The cumulative classification margin uses the scores averaged over all trees and the mean cumulative classification margin is the cumulative margin averaged over all observations. The `oobMeanMargin` method with the `'mode'` argument set to `'cumulative'` (default) shows how the mean cumulative margin changes as the ensemble grows: every new element in the returned array represents the cumulative margin obtained by including

a new tree in the ensemble. If training is successful, you would expect to see a gradual increase in the mean classification margin.

The method trains ensembles with few trees on observations that are in bag for all trees. For such observations, it is impossible to compute the true out-of-bag prediction, and `TreeBagger` returns the most probable class for classification and the sample mean for regression.

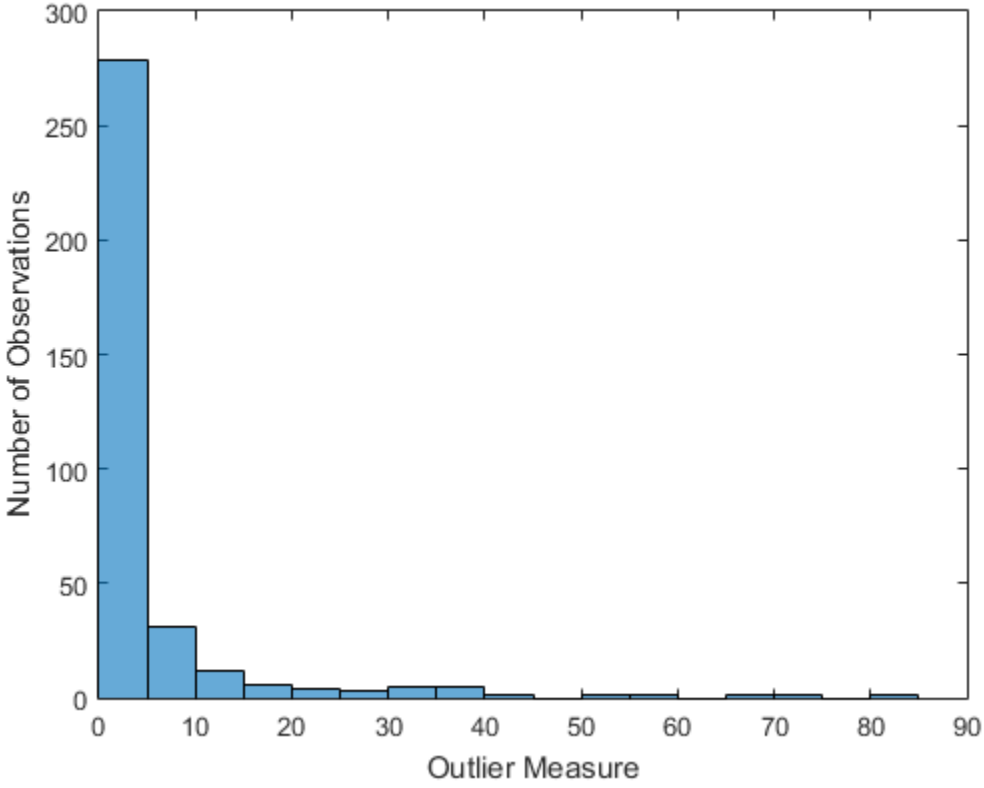
For decision trees, a classification score is the probability of observing an instance of this class in this tree leaf. For example, if the leaf of a grown decision tree has five `'good'` and three `'bad'` training observations in it, the scores returned by this decision tree for any observation fallen on this leaf are 5/8 for the `'good'` class and 3/8 for the `'bad'` class. These probabilities are called `'scores'` for consistency with other classifiers that might not have an obvious interpretation for numeric values of returned predictions.

```
figure
plot(oobMeanMargin(b5v));
xlabel('Number of Grown Trees');
ylabel('Out-of-Bag Mean Classification Margin');
```



Compute the matrix of proximities and examine the distribution of outlier measures. Unlike regression, outlier measures for classification ensembles are computed within each class separately.

```
b5v = fillProximities(b5v);
figure
histogram(b5v.OutlierMeasure);
xlabel('Outlier Measure');
ylabel('Number of Observations');
```



Slightly more than half of the extreme outliers are labeled `'bad'`.

```
extremeOutliers = b5v.Y(b5v.OutlierMeasure>40)
percentBad = 100*sum(strcmp(extremeOutliers,'b'))/numel(extremeOutliers)
```

```
extremeOutliers =

    'g'
    'g'
    'g'
    'g'
    'g'
    'g'
```

```
percentBad =

     0
```

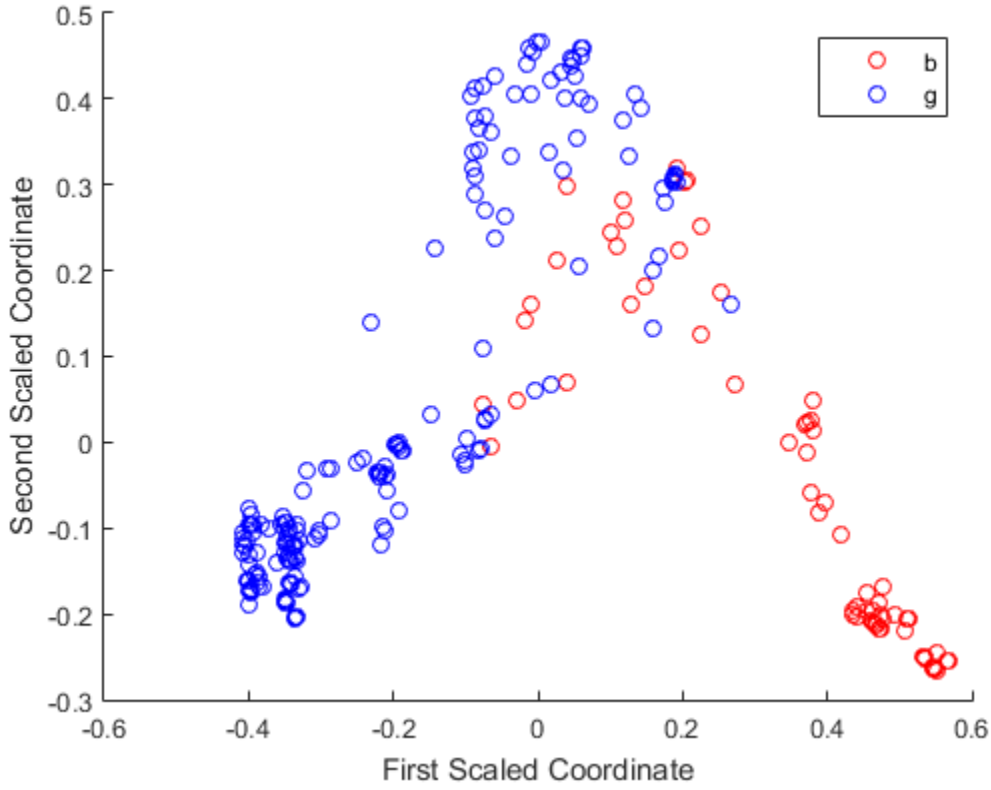
As for regression, you can plot scaled coordinates, displaying the two classes in different colors using the 'Colors' name-value pair argument of `mdsProx`. This argument takes a string in which every character represents a color. The software does not rank class names. Therefore, it is best practice to determine the position of the classes in the `ClassNames` property of the ensemble.

```
gPosition = find(strcmp('g',b5v.ClassNames))
```

```
gPosition =

     2
```

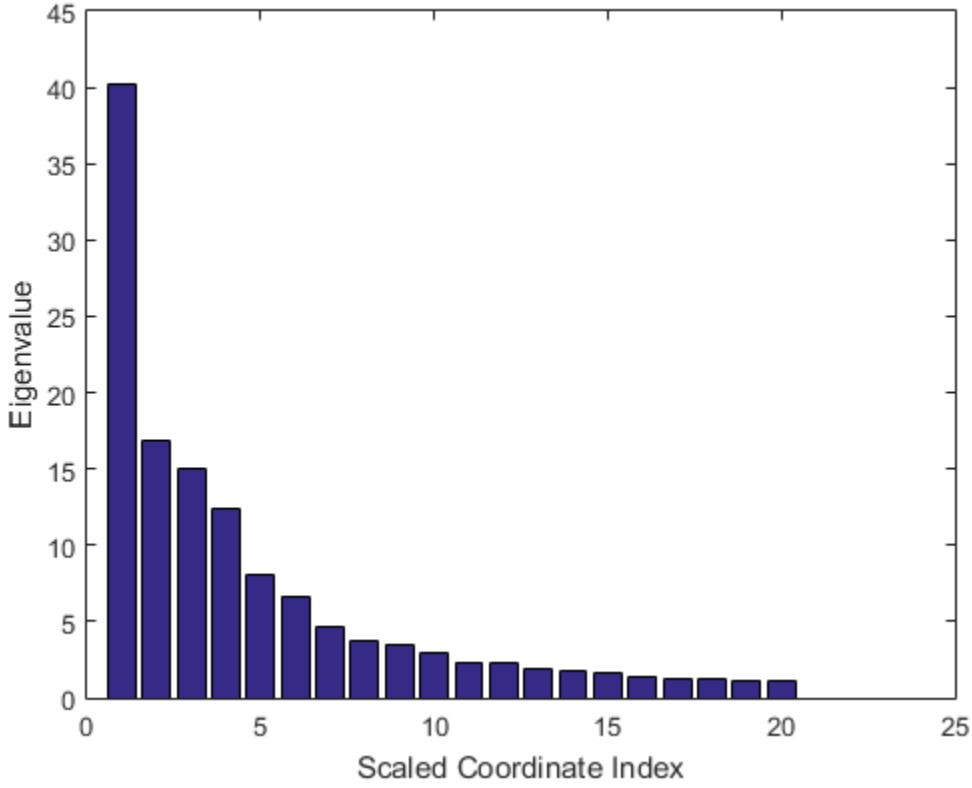
The `'bad'` class is first and the `'good'` class is second. Display scaled coordinates using red for the `'bad'` class and blue for the `'good'` class observations.

```
figure
[s,e] = mdsProx(b5v,'Colors','rb');
xlabel('First Scaled Coordinate');
ylabel('Second Scaled Coordinate');
```



Plot the first 20 eigenvalues obtained by scaling. The first eigenvalue clearly dominates and the first scaled coordinate is most important.

```
figure
bar(e(1:20));
xlabel('Scaled Coordinate Index');
ylabel('Eigenvalue');
```

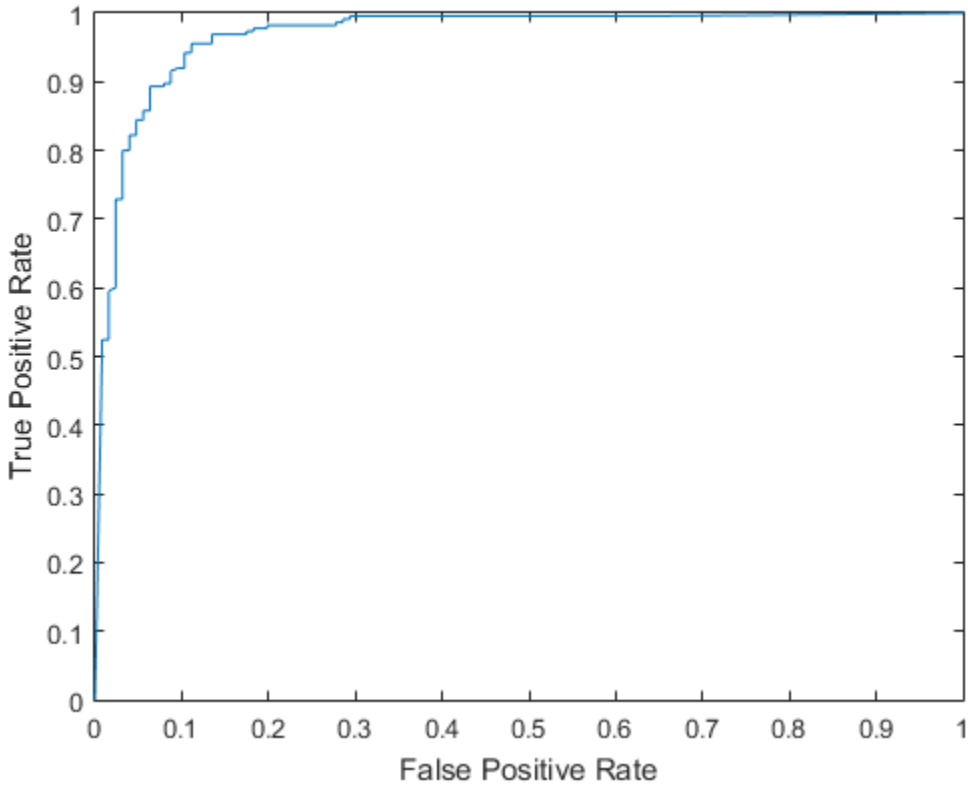


Another way of exploring the performance of a classification ensemble is to plot its Receiver Operating Characteristic (ROC) curve or another performance curve suitable for the current problem. Obtain predictions for out-of-bag observations. For a classification ensemble, the `oobPredict` method returns a cell array of classification labels as the first output argument and a numeric array of scores as the second output argument. The returned array of scores has two columns, one for each class. In this case, the first column is for the `'bad'` class and the second column is for the `'good'` class. One column in the score matrix is redundant because the scores represent class probabilities in tree leaves and by definition add up to 1.

```
[Yfit,Sfit] = oobPredict(b5v);
```

Use `perfcurve` to compute a performance curve. By default, `perfcurve` returns the standard ROC curve, which is the true positive rate versus the false positive rate. `perfcurve` requires true class labels, scores, and the positive class label for input. In this case, choose the `'good'` class as positive.

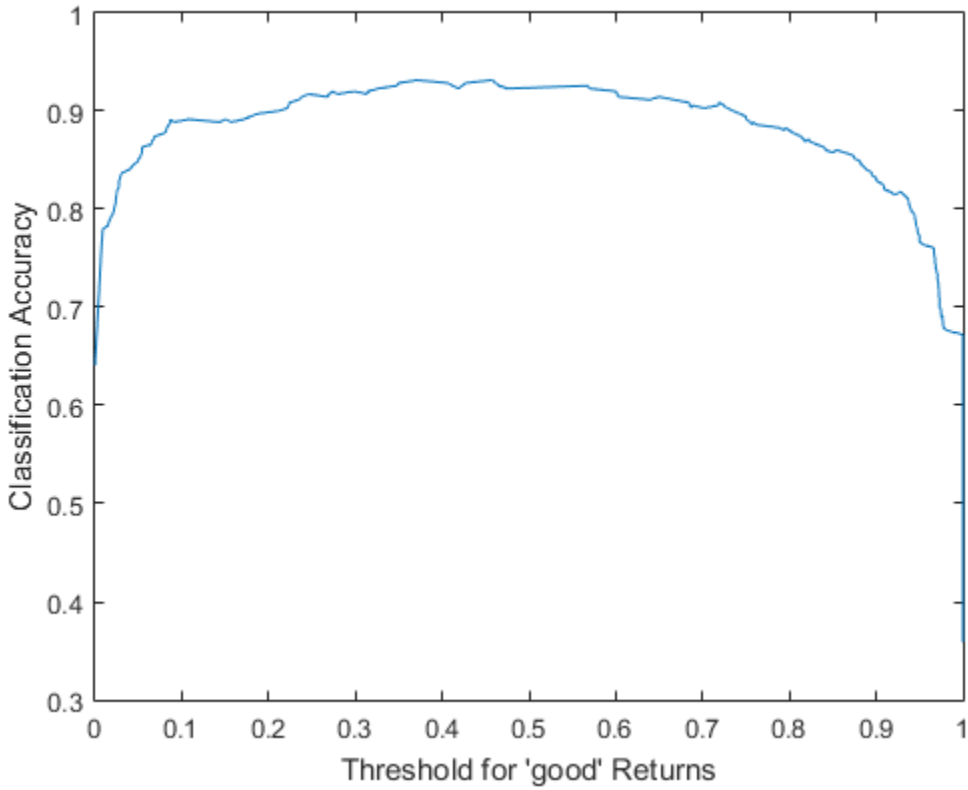
```
[fpr,tpr] = perfcurve(b5v.Y,Sfit(:,gPosition),'g');
figure
plot(fpr,tpr);
xlabel('False Positive Rate');
ylabel('True Positive Rate');
```



Instead of the standard ROC curve, you might want to plot, for example, ensemble accuracy versus threshold on the score for the `'good'` class. The `ycrit` input argument

of `perfcurve` lets you specify the criterion for the `y`-axis, and the third output argument of `perfcurve` returns an array of thresholds for the positive class score. Accuracy is the fraction of correctly classified observations, or equivalently, 1 minus the classification error.

```
[fpr,accu,thre] = perfcurve(b5v.Y,Sfit(:,gPosition),'g','YCrit','Accu');
figure(20);
plot(thre,accu);
xlabel('Threshold for ''good'' Returns');
ylabel('Classification Accuracy');
```



The curve shows a flat region indicating that any threshold from 0.2 to 0.6 is a reasonable choice. By default, the `perfcurve` assigns classification labels using 0.5

as the boundary between the two classes. You can find exactly what accuracy this corresponds to.

```
accu(abs(thre-0.5)<eps)
```

```
ans =

   Empty matrix: 0-by-1
```

The maximal accuracy is a little higher than the default one.

```
[maxaccu,iaccu] = max(accu)
```

```
maxaccu =

    0.9316


iaccu =

   104
```

The optimal threshold is therefore.

```
thre(iaccu)
```

```
ans =

    0.4570
```

Ensemble Algorithms

- “AdaBoostM1” on page 16-156
- “AdaBoostM2” on page 16-158
- “Bag” on page 16-158
- “GentleBoost” on page 16-161

AdaBoostM1

`AdaBoostM1` is a very popular boosting algorithm for binary classification. The algorithm trains learners sequentially. For every learner with index t, `AdaBoostM1` computes the weighted classification error

$$\varepsilon_t = \sum_{n=1}^{N} d_n^{(t)} \mathrm{I}\left(y_n \neq h_t\left(x_n\right)\right),$$

where

- x_n is a vector of predictor values for observation n.
- y_n is the true class label.
- h_t is the prediction of learner (hypothesis) with index t.
- `I` is the indicator function.
- $d_n^{(t)}$ is the weight of observation n at step t.

`AdaBoostM1` then increases weights for observations misclassified by learner t and reduces weights for observations correctly classified by learner t. The next learner $t + 1$ is then trained on the data with updated weights $d_n^{(t+1)}$.

After training finishes, `AdaBoostM1` computes prediction for new data using

$$f\left(x\right) = \sum_{t=1}^{T} \alpha_t h_t\left(x\right),$$

where

$$\alpha_t = \frac{1}{2}\log\frac{1-\varepsilon_t}{\varepsilon_t}$$

are weights of the weak hypotheses in the ensemble.

Training by `AdaBoostM1` can be viewed as stagewise minimization of the exponential loss

$$\sum_{n=1}^{N} w_n \exp\left(-y_n f\left(x_n\right)\right),$$

where

- $y_n \in \{-1,+1\}$ is the true class label.
- w_n are observation weights normalized to add up to 1.
- $f(x_n) \in (-\infty,+\infty)$ is the predicted classification score.

The observation weights w_n are the original observation weights you passed to `fitensemble`.

The second output from the `predict` method of an `AdaBoostM1` classification ensemble is an N-by-2 matrix of classification scores for the two classes and N observations. The second column in this matrix is always equal to minus the first column. `predict` returns two scores to be consistent with multiclass models, though this is redundant because the second column is always the negative of the first.

Most often `AdaBoostM1` is used with decision stumps (default) or shallow trees. If boosted stumps give poor performance, try setting the minimal parent node size to one quarter of the training data.

By default, the learning rate for boosting algorithms is `1`. If you set the learning rate to a lower number, the ensemble learns at a slower rate, but can converge to a better solution. `0.1` is a popular choice for the learning rate. Learning at a rate less than `1` is often called "shrinkage".

For examples using `AdaBoostM1`, see "Tune RobustBoost" on page 16-121.

For references related to AdaBoostM1, see Freund and Schapire [16], Schapire et al. [26], Friedman, Hastie, and Tibshirani [18], and Friedman [17].

AdaBoostM2

AdaBoostM2 is an extension of AdaBoostM1 for multiple classes. Instead of weighted classification error, AdaBoostM2 uses weighted pseudo-loss for N observations and K classes

$$\varepsilon_t = \frac{1}{2}\sum_{n=1}^{N}\sum_{k\neq y_n} d_{n,k}^{(t)}\left(1 - h_t\left(x_n, y_n\right) + h_t\left(x_n, k\right)\right),$$

where

- $h_t(x_n,k)$ is the confidence of prediction by learner at step t into class k ranging from 0 (not at all confident) to 1 (highly confident).
- $d_{n,k}^{(t)}$ are observation weights at step t for class k.
- y_n is the true class label taking one of the K values.
- The second sum is over all classes other than the true class y_n.

Interpreting the pseudo-loss is harder than classification error, but the idea is the same. Pseudo-loss can be used as a measure of the classification accuracy from any learner in an ensemble. Pseudo-loss typically exhibits the same behavior as a weighted classification error for AdaBoostM1: the first few learners in a boosted ensemble give low pseudo-loss values. After the first few training steps, the ensemble begins to learn at a slower pace, and the pseudo-loss value approaches 0.5 from below.

For examples using AdaBoostM2, see “Train a Classification Ensemble” on page 16-76.

For references related to AdaBoostM2, see Freund and Schapire [16].

Bag

Bagging, which stands for “bootstrap aggregation,” is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, generate many bootstrap replicas of this dataset and grow decision trees on these replicas. Obtain each bootstrap replica by

randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, take an average over predictions from individual trees.

Bagged decision trees were introduced in MATLAB R2009a as `TreeBagger`. The `fitensemble` function lets you bag in a manner consistent with boosting. An ensemble of bagged trees, either `ClassificationBaggedEnsemble` or `RegressionBaggedEnsemble`, returned by `fitensemble` offers almost the same functionally as `TreeBagger`. Discrepancies between `TreeBagger` and the new framework are described in detail in TreeBagger Features Not in fitensemble.

Bagging works by training learners on resampled versions of the data. This resampling is usually done by bootstrapping observations, that is, selecting N out of N observations with replacement for every new learner. In addition, every tree in the ensemble can randomly select predictors for decision splits—a technique known to improve the accuracy of bagged trees.

By default, the minimal leaf sizes for bagged trees are set to `1` for classification and `5` for regression. Trees grown with the default leaf size are usually very deep. These settings are close to optimal for the predictive power of an ensemble. Often you can grow trees with larger leaves without losing predictive power. Doing so reduces training and prediction time, as well as memory usage for the trained ensemble.

Another important parameter is the number of predictors selected at random for every decision split. This random selection is made for every split, and every deep tree involves many splits. By default, this parameter is set to a square root of the number of predictors for classification, and one third of predictors for regression.

Several features of bagged decision trees make them a unique algorithm. Drawing `N` out of `N` observations with replacement omits on average 37% of observations for each decision tree. These are “out-of-bag” observations. You can use them to estimate the predictive power and feature importance. For each observation, you can estimate the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. You can then compare the computed prediction against the observed response for this observation. By comparing the out-of-bag predicted responses against the observed responses for all observations used for training, you can estimate the average out-of-bag error. This out-of-bag average is an unbiased estimator of the true ensemble error. You can also obtain out-of-bag estimates of feature importance by randomly permuting out-of-bag data across one variable or column at a time and estimating the increase in the out-of-bag error due to this permutation. The larger the increase, the more important the feature. Thus, you need not supply test data for bagged

ensembles because you obtain reliable estimates of the predictive power and feature importance in the process of training, which is an attractive feature of bagging.

Another attractive feature of bagged decision trees is the proximity matrix. Every time two observations land on the same leaf of a tree, their proximity increases by 1. For normalization, sum these proximities over all trees in the ensemble and divide by the number of trees. The resulting matrix is symmetric with diagonal elements equal to 1 and off-diagonal elements ranging from 0 to 1. You can use this matrix for finding outlier observations and discovering clusters in the data through multidimensional scaling.

For examples using bagging, see:

- "Test Ensemble Quality" on page 16-79
- "Surrogate Splits" on page 16-100
- "Regression of Insurance Risk Rating for Car Imports Using TreeBagger" on page 16-129
- "Classifying Radar Returns for Ionosphere Data Using TreeBagger" on page 16-141

For references related to bagging, see Breiman [7], [8], and [9].

Comparison of TreeBagger and Bagged Ensembles

`fitensemble` produces bagged ensembles that have most, but not all, of the functionality of `TreeBagger` objects. Additionally, some functionality has different names in the new bagged ensembles.

TreeBagger Features Not in fitensemble

Feature	TreeBagger Property	TreeBagger Method
Computation of proximity matrix	`Proximity`	`fillProximities`, `mdsProx`
Computation of outliers	`OutlierMeasure`	N/A
Out-of-bag estimates of predictor importance	`OOBPermutedVarDeltaError`, `OOBPermutedVarDeltaMeanMargin`, `OOBPermutedVarCountRaiseMargir`	N/A
Merging two ensembles trained separately	N/A	`append`
Parallel computation for creating ensemble	Set the `UseParallel` name-value pair to `true`	N/A

Differing Names Between TreeBagger and Bagged Ensembles

Feature	TreeBagger	Bagged Ensembles
Split criterion contributions for each predictor	`DeltaCritDecisionSplit` property	First output of `predictorImportance` (classification) or `predictorImportance` (regression)
Predictor associations	`VarAssoc` property	Second output of `predictorImportance` (classification) or `predictorImportance` (regression)
Error (misclassification probability or mean-squared error)	`error` and `oobError` methods	`loss` and `oobLoss` methods (classification); `loss` and `oobLoss` methods (regression)
Train additional trees and add to ensemble	`growTrees` method	`resume` method (classification); `resume` method (regression)
Mean classification margin per tree	`meanMargin` and `oobMeanMargin` methods	`edge` and `oobEdge` methods (classification)

In addition, two important changes were made to training and prediction for bagged classification ensembles:

- If you pass a misclassification cost matrix to `TreeBagger`, it passes this matrix along to the trees. If you pass a misclassification cost matrix to `fitensemble`, it uses this matrix to adjust the class prior probabilities. `fitensemble` then passes the adjusted prior probabilities and the default cost matrix to the trees. The default cost matrix is `ones(K)-eye(K)` for `K` classes.
- Unlike the `loss` and `edge` methods in the new framework, the `TreeBagger` `error` and `meanMargin` methods do not normalize input observation weights of the prior probabilities in the respective class.

GentleBoost

`GentleBoost` (also known as Gentle AdaBoost) combines features of `AdaBoostM1` and `LogitBoost`. Like `AdaBoostM1`, `GentleBoost` minimizes the exponential loss. But its numeric optimization is set up differently. Like `LogitBoost`, every weak learner fits a

regression model to response values $y_n \in \{-1,+1\}$. This makes `GentleBoost` another good candidate for binary classification of data with multilevel categorical predictors.

`fitensemble` computes and stores the mean-squared error in the `FitInfo` property of the ensemble object. The mean-squared error is

$$\sum_{n=1}^{N} d_n^{(t)} \left(\tilde{y}_n - h_t\left(x_n\right)\right)^2,$$

where

- $d_n^{(t)}$ are observation weights at step t (the weights add up to 1).
- $h_t(x_n)$ are predictions of the regression model h_t fitted to response values y_n.

As the strength of individual learners weakens, the weighted mean-squared error approaches 1.

For examples using `GentleBoost`, see “Example: Unequal Classification Costs” on page 16-91 and “Classification with Many Categorical Levels” on page 16-96.

For references related to `GentleBoost`, see Friedman, Hastie, and Tibshirani [18].

LogitBoost

`LogitBoost` is another popular algorithm for binary classification. `LogitBoost` works similarly to `AdaBoostM1`, except it minimizes binomial deviance

$$\sum_{n=1}^{N} w_n \log\left(1+\exp\left(-2y_n f\left(x_n\right)\right)\right),$$

where

- $y_n \in \{-1,+1\}$ is the true class label.
- w_n are observation weights normalized to add up to 1.
- $f(x_n) \in (-\infty,+\infty)$ is the predicted classification score.

Binomial deviance assigns less weight to badly misclassified observations (observations with large negative values of $y_n f(x_n)$). `LogitBoost` can give better average accuracy than `AdaBoostM1` for data with poorly separable classes.

Learner t in a `LogitBoost` ensemble fits a regression model to response values

$$\tilde{y}_n = \frac{y_n^* - p_t(x_n)}{p_t(x_n)\left(1 - p_t(x_n)\right)},$$

where

- $y^*_n \in \{0,+1\}$ are relabeled classes (0 instead of –1).
- $p_t(x_n)$ is the current ensemble estimate of the probability for observation x_n to be of class 1.

Fitting a regression model at each boosting step turns into a great computational advantage for data with multilevel categorical predictors. Take a categorical predictor with L levels. To find the optimal decision split on such a predictor, classification tree needs to consider $2^{L-1} - 1$ splits. A regression tree needs to consider only $L - 1$ splits, so the processing time can be much shorter. `LogitBoost` is recommended for categorical predictors with many levels.

`fitensemble` computes and stores the mean-squared error in the `FitInfo` property of the ensemble object. The mean-squared error is

$$\sum_{n=1}^{N} d_n^{(t)} \left(\tilde{y}_n - h_t(x_n)\right)^2,$$

where

- $d_n^{(t)}$ are observation weights at step t (the weights add up to 1).
- $h_t(x_n)$ are predictions of the regression model h_t fitted to response values $\tilde{y}_n$.

Values y_n can range from $-\infty$ to $+\infty$, so the mean-squared error does not have well-defined bounds.

For examples using `LogitBoost`, see "Classification with Many Categorical Levels" on page 16-96.

For references related to `LogitBoost`, see Friedman, Hastie, and Tibshirani [18].

LPBoost

`LPBoost` (linear programming boost), like `TotalBoost`, performs multiclass classification by attempting to maximize the minimal *margin* in the training set. This attempt uses optimization algorithms, namely linear programming for `LPBoost`. So you need an Optimization Toolbox license to use `LPBoost` or `TotalBoost`.

The margin of a classification is the difference between the predicted soft classification *score* for the true class, and the largest score for the false classes. For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node. For more information, see "Definitions" on page 22-2839 in `margin`.

Why maximize the minimal margin? For one thing, the generalization error (the error on new data) is the probability of obtaining a negative margin. Schapire and Singer [27] establish this inequality on the probability of obtaining a negative margin:

$$P_{\text{test}}(m \le 0) \le P_{\text{train}}(m \le \theta) + O\left(\frac{1}{\sqrt{N}}\sqrt{\frac{V\log^2(N/V)}{\theta^2} + \log(1/\delta)}\right).$$

Here m is the margin, θ is any positive number, V is the Vapnik-Chervonenkis dimension of the classifier space, N is the size of the training set, and δ is a small positive number. The inequality holds with probability $1–\delta$ over many i.i.d. training and test sets. This inequality says: To obtain a low generalization error, minimize the number of observations below margin θ in the training set.

`LPBoost` iteratively maximizes the minimal margin through a sequence of linear programming problems. Equivalently, by duality, `LPBoost` minimizes the maximal *edge*, where edge is the weighted mean margin (see "Definitions" on page 22-1230). At each iteration, there are more constraints in the problem. So, for large problems, the optimization problem becomes increasingly constrained, and slow to solve.

`LPBoost` typically creates ensembles with many learners having weights that are orders of magnitude smaller than those of other learners. Therefore, to better enable

you to remove the unimportant ensemble members, the `compact` method reorders the members of an `LPBoost` ensemble from largest weight to smallest. Therefore, you can easily remove the least important members of the ensemble using the `removeLearners` method.

For examples using `LPBoost`, see "LPBoost and TotalBoost for Small Ensembles" on page 16-103.

For references related to `LPBoost`, see Warmuth, Liao, and Ratsch [29].

LSBoost

`LSBoost` (least squares boosting) fits regression ensembles. At every step, the ensemble fits a new learner to the difference between the observed response and the aggregated prediction of all learners grown previously. The ensemble fits to minimize mean-squared error.

You can use `LSBoost` with shrinkage by passing in the `LearnRate` parameter. By default this parameter is set to `1`, and the ensemble learns at the maximal speed. If you set `LearnRate` to a value from `0` to `1`, the ensemble fits every new learner to $y_n - \eta f(x_n)$, where

- y_n is the observed response.
- $f(x_n)$ is the aggregated prediction from all weak learners grown so far for observation x_n.
- η is the learning rate.

For examples using `LSBoost`, see "Train a Regression Ensemble" on page 16-78 and "Regularize a Regression Ensemble" on page 16-110.

For references related to `LSBoost`, see Hastie, Tibshirani, and Friedman [19], Chapters 7 (Model Assessment and Selection) and 15 (Random Forests).

RobustBoost

Boosting algorithms such as `AdaBoostM1` and `LogitBoost` increase weights for misclassified observations at every boosting step. These weights can become very large. If this happens, the boosting algorithm sometimes concentrates on a few misclassified observations and neglects the majority of training data. Consequently the average classification accuracy suffers.

In this situation, you can try using `RobustBoost`. This algorithm does not assign almost the entire data weight to badly misclassified observations. It can produce better average classification accuracy.

Unlike `AdaBoostM1` and `LogitBoost`, `RobustBoost` does not minimize a specific loss function. Instead, it maximizes the number of observations with the classification margin above a certain threshold.

`RobustBoost` trains based on time evolution. The algorithm starts at $t = 0$. At every step, `RobustBoost` solves an optimization problem to find a positive step in time Δt and a corresponding positive change in the average margin for training data Δm. `RobustBoost` stops training and exits if at least one of these three conditions is true:

- Time t reaches 1.
- `RobustBoost` cannot find a solution to the optimization problem with positive updates Δt and Δm.
- `RobustBoost` grows as many learners as you requested.

Results from `RobustBoost` can be usable for any termination condition. Estimate the classification accuracy by cross validation or by using an independent test set.

To get better classification accuracy from `RobustBoost`, you can adjust three parameters in `fitensemble`: `RobustErrorGoal`, `RobustMaxMargin`, and `RobustMarginSigma`. Start by varying values for `RobustErrorGoal` from 0 to 1. The maximal allowed value for `RobustErrorGoal` depends on the two other parameters. If you pass a value that is too high, `fitensemble` produces an error message showing the allowed range for `RobustErrorGoal`.

For examples using `RobustBoost`, see "Tune RobustBoost" on page 16-121.

For references related to `RobustBoost`, see Freund [15].

RUSBoost

`RUSBoost` is especially effective at classifying imbalanced data, meaning some class in the training data has many fewer members than another. RUS stands for Random Under Sampling. The algorithm takes N, the number of members in the class with the fewest members in the training data, as the basic unit for sampling. Classes with more members are under sampled by taking only N observations of every class. In other words, if there are K classes, then, for each weak learner in the ensemble, `RUSBoost` takes a subset of the data with N observations from each of the K classes. The boosting procedure follows

the procedure in "AdaBoostM2" on page 16-158 for reweighting and constructing the ensemble.

When you construct a `RUSBoost` ensemble, there is an optional name-value pair called `RatioToSmallest`. Give a vector of K values, each value representing the multiple of N to sample for the associated class. For example, if the smallest class has $N = 100$ members, then `RatioToSmallest = [2,3,4]` means each weak learner has 200 members in class 1, 300 in class 2, and 400 in class 3. If `RatioToSmallest` leads to a value that is larger than the number of members in a particular class, then `RUSBoost` samples the members with replacement. Otherwise, `RUSBoost` samples the members without replacement.

For examples using `RUSBoost`, see "Classification with Imbalanced Data" on page 16-84.

For references related to `RUSBoost`, see Seiffert et al. [28].

Subspace

Use random subspace ensembles (`Subspace`) to improve the accuracy of discriminant analysis (`ClassificationDiscriminant`) or k-nearest neighbor (`ClassificationKNN`) classifiers. `Subspace` ensembles also have the advantage of using less memory than ensembles with all predictors, and can handle missing values (`NaN`s).

The basic random subspace algorithm uses these parameters.

- m is the number of dimensions (variables) to sample in each learner. Set m using the `NPredToSample` name-value pair.
- d is the number of dimensions in the data, which is the number of columns (predictors) in the data matrix `X`.
- n is the number of learners in the ensemble. Set n using the `NLearn` input.

The basic random subspace algorithm performs the following steps:

1. Choose without replacement a random set of m predictors from the d possible values.
2. Train a weak learner using just the m chosen predictors.
3. Repeat steps 1 and 2 until there are n weak learners.
4. Predict by taking an average of the `score` prediction of the weak learners, and classify the category with the highest average `score`.

You can choose to create a weak learner for every possible set of m predictors from the d dimensions. To do so, set n, the number of learners, to `'AllPredictorCombinations'`. In this case, there are `nchoosek(size(X,2),NPredToSample)` weak learners in the ensemble.

`fitensemble` downweights predictors after choosing them for a learner, so subsequent learners have a lower chance of using a predictor that was previously used. This weighting tends to make predictors more evenly distributed among learners than in uniform weighting.

For examples using `Subspace`, see "Random Subspace Classification" on page 16-124.

For references related to random subspace ensembles, see Ho [20].

TotalBoost

`TotalBoost`, like linear programming boost (`LPBoost`), performs multiclass classification by attempting to maximize the minimal *margin* in the training set. This attempt uses optimization algorithms, namely quadratic programming for `TotalBoost`. So you need an Optimization Toolbox license to use `LPBoost` or `TotalBoost`.

The margin of a classification is the difference between the predicted soft classification *score* for the true class, and the largest score for the false classes. For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node. For more information, see "Definitions" on page 22-2839 in `margin`.

Why maximize the minimal margin? For one thing, the generalization error (the error on new data) is the probability of obtaining a negative margin. Schapire and Singer [27] establish this inequality on the probability of obtaining a negative margin:

$$P_{\text{test}}(m \le 0) \le P_{\text{train}}(m \le \theta) + O\left(\frac{1}{\sqrt{N}}\sqrt{\frac{V\log^2(N/V)}{\theta^2} + \log(1/\delta)}\right).$$

Here m is the margin, θ is any positive number, V is the Vapnik-Chervonenkis dimension of the classifier space, N is the size of the training set, and δ is a small positive number. The inequality holds with probability $1–\delta$ over many i.i.d. training and test sets.
This inequality says: To obtain a low generalization error, minimize the number of observations below margin θ in the training set.

`TotalBoost` minimizes a proxy of the Kullback-Leibler divergence between the current weight distribution and the initial weight distribution, subject to the constraint that the *edge* (the weighted margin) is below a certain value. The proxy is a quadratic expansion of the divergence:

$$D(W,W_0) = \sum_{n=1}^{N} \log\frac{W(n)}{W_0(n)} \approx \sum_{n=1}^{N}\left(1+\frac{W(n)}{W_0(n)}\right)\Delta + \frac{1}{2W(n)}\Delta^2,$$

where Δ is the difference between $W(n)$, the weights at the current and next iteration, and W_0, the initial weight distribution, which is uniform. This optimization formulation keeps weights from becoming zero. At each iteration, there are more constraints in the problem. So, for large problems, the optimization problem becomes increasingly constrained, and slow to solve.

`TotalBoost` typically creates ensembles with many learners having weights that are orders of magnitude smaller than those of other learners. Therefore, to better enable you to remove the unimportant ensemble members, the `compact` method reorders the members of a `TotalBoost` ensemble from largest weight to smallest. Therefore you can easily remove the least important members of the ensemble using the `removeLearners` method.

For examples using `TotalBoost`, see “LPBoost and TotalBoost for Small Ensembles” on page 16-103.

For references related to `TotalBoost`, see Warmuth, Liao, and Ratsch [29].

Support Vector Machines (SVM)

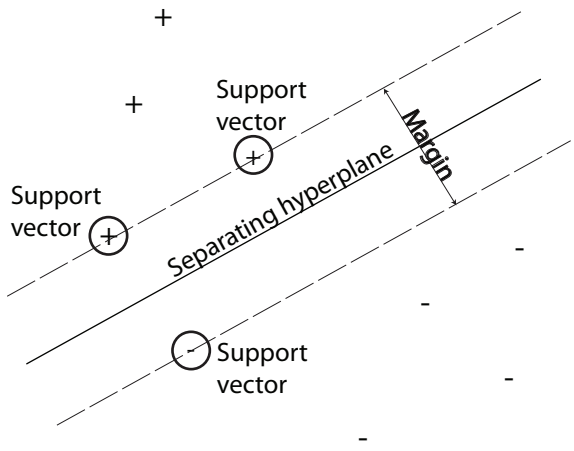
In this section...

Understanding Support Vector Machines

Separable Data

You can use a support vector machine (SVM) when your data has exactly two classes. An SVM classifies data by finding the best hyperplane that separates all data points of one class from those of the other class. The *best* hyperplane for an SVM means the one with the largest *margin* between the two classes. Margin means the maximal width of the slab parallel to the hyperplane that has no interior data points.

The *support vectors* are the data points that are closest to the separating hyperplane; these points are on the boundary of the slab. The following figure illustrates these definitions, with + indicating data points of type 1, and – indicating data points of type –1.



Mathematical Formulation: Primal

This discussion follows Hastie, Tibshirani, and Friedman [19] and Christianini and Shawe-Taylor [11].

The data for training is a set of points (vectors) x_i along with their categories y_i. For some dimension d, the $x_i \in R^d$, and the $y_i = \pm 1$. The equation of a hyperplane is
$\langle w,x\rangle + b = 0$,

where $w \in R^d$, $\langle w,x\rangle$ is the inner (dot) product of w and x, and b is real.

The following problem defines the *best* separating hyperplane. Find w and b that minimize $||w||$ such that for all data points (x_i,y_i),
$y_i(\langle w,x_i\rangle + b) \geq 1$.

The support vectors are the x_i on the boundary, those for which $y_i(\langle w,x_i\rangle + b) = 1$.

For mathematical convenience, the problem is usually given as the equivalent problem of minimizing $\langle w,w\rangle/2$. This is a quadratic programming problem. The optimal solution $\left(\hat{w},\hat{b}\right)$ enables classification of a vector z as follows:

$$\text{class}(z) = \text{sign}\left(\langle w,z\rangle + b\right).$$

Mathematical Formulation: Dual

It is computationally simpler to solve the dual quadratic programming problem. To obtain the dual, take positive Lagrange multipliers α_i multiplied by each constraint, and subtract from the objective function:

$$L_P = \frac{1}{2}\langle w,w\rangle - \sum_i \alpha_i \left(y_i \left(\langle w,x_i \rangle + b \right) - 1 \right),$$

where you look for a stationary point of L_P over w and b. Setting the gradient of L_P to 0, you get

$$w = \sum_i \alpha_i y_i x_i$$
$$0 = \sum_i \alpha_i y_i.$$

Substituting into L_P, you get the dual L_D:

$$L_D = \sum_i \alpha_i - \frac{1}{2} \sum_i \sum_j \alpha_i \alpha_j y_i y_j \left\langle x_i, x_j \right\rangle,$$

which you maximize over $\alpha_i \geq 0$. In general, many α_i are 0 at the maximum. The nonzero α_i in the solution to the dual problem define the hyperplane, as seen in Equation 16-1, which gives w as the sum of $\alpha_i y_i x_i$. The data points x_i corresponding to nonzero α_i are the *support vectors*.

The derivative of L_D with respect to a nonzero α_i is 0 at an optimum. This gives $y_i(<w,x_i> + b) - 1 = 0$.

In particular, this gives the value of b at the solution, by taking any i with nonzero α_i.

The dual is a standard quadratic programming problem. For example, the Optimization Toolbox `quadprog` solver solves this type of problem.

Nonseparable Data

Your data might not allow for a separating hyperplane. In that case, SVM can use a *soft margin*, meaning a hyperplane that separates many, but not all data points.

There are two standard formulations of soft margins. Both involve adding slack variables s_i and a penalty parameter C.

- The L^1-norm problem is:

  $$\min_{w,b,s}\left(\frac{1}{2}\langle w,w\rangle + C\sum_i s_i\right)$$

  such that

  $$\begin{aligned} y_i\left(\langle w,x_i\rangle + b\right) &\geq 1 - s_i \\ s_i &\geq 0. \end{aligned}$$

  The L^1-norm refers to using s_i as slack variables instead of their squares. The three solver options `SMO`, `ISDA`, and `L1Qp` of `fitcsvm` minimize the L^1-norm problem.

- The L^2-norm problem is:

  $$\min_{w,b,s}\left(\frac{1}{2}\langle w,w\rangle + C\sum_i s_i^2\right)$$

  subject to the same constraints.

In these formulations, you can see that increasing C places more weight on the slack variables s_i, meaning the optimization attempts to make a stricter separation between classes. Equivalently, reducing C towards 0 makes misclassification less important.

Mathematical Formulation: Dual

For easier calculations, consider the L^1 dual problem to this soft-margin formulation. Using Lagrange multipliers μ_i, the function to minimize for the L^1-norm problem is:

$$L_P = \frac{1}{2}\langle w,w\rangle + C\sum_i s_i - \sum_i \alpha_i\left(y_i\left(\langle w,x_i\rangle + b\right) - \left(1 - s_i\right)\right) - \sum_i \mu_i s_i,$$

where you look for a stationary point of L_P over w, b, and positive s_i. Setting the gradient of L_P to 0, you get

$$
\begin{aligned}
b &= \sum_i \alpha_i y_i x_i \\
\sum_i \alpha_i y_i &= 0 \\
\alpha_i &= C - \mu_i \\
\alpha_i, \mu_i, s_i &\geq 0.
\end{aligned}
$$

These equations lead directly to the dual formulation:

$$\max_{\alpha} \sum_i \alpha_i - \frac{1}{2} \sum_i \sum_j \alpha_i \alpha_j y_i y_j \left\langle x_i, x_j \right\rangle$$

subject to the constraints

$$
\begin{aligned}
&\sum_i y_i \alpha_i = 0 \\
&0 \leq \alpha_i \leq C.
\end{aligned}
$$

The final set of inequalities, $0 \leq \alpha_i \leq C$, shows why C is sometimes called a *box constraint*. C keeps the allowable values of the Lagrange multipliers α_i in a "box", a bounded region.

The gradient equation for b gives the solution b in terms of the set of nonzero α_i, which correspond to the support vectors.

You can write and solve the dual of the L^2-norm problem in an analogous manner. For details, see Christianini and Shawe-Taylor [11], Chapter 6.

fitcsvm Implementation

Both dual soft-margin problems are quadratic programming problems. Internally, `fitcsvm` has several different algorithms for solving the problems.

- For one-class or binary classification, if you do not set a fraction of expected outliers in the data (see `OutlierFraction`), then the default solver is Sequential Minimal Optimization (SMO). SMO minimizes the one-norm problem by a series of two-point minimizations. During optimization, SMO respects the linear constraint $\sum_i \alpha_i y_i = 0$,

and explicitly includes the bias term in the model. SMO is relatively fast. For more details on SMO, see [13].

- For binary classification, if you set a fraction of expected outliers in the data, then the default solver is the Iterative Single Data Algorithm. Like SMO, ISDA solves the one-norm problem. Unlike SMO, ISDA minimizes by a series on one-point minimizations, does not respect the linear constraint, and does not explicitly include the bias term in the model. For more details on ISDA, see [22].
- For one-class or binary classification, and if you have an Optimization Toolbox license, you can choose to use `quadprog` to solve the one-norm problem. `quadprog` uses a good deal of memory, but solves quadratic programs to a high degree of precision. For more details, see "Quadratic Programming Definition".

Nonlinear Transformation with Kernels

Some binary classification problems do not have a simple hyperplane as a useful separating criterion. For those problems, there is a variant of the mathematical approach that retains nearly all the simplicity of an SVM separating hyperplane.

This approach uses these results from the theory of reproducing kernels:

- There is a class of functions $K(x,y)$ with the following property. There is a linear space S and a function φ mapping x to S such that $K(x,y) = <\varphi(x),\varphi(y)>$.

  The dot product takes place in the space S.
- This class of functions includes:
  - Polynomials: For some positive integer d, $K(x,y) = (1 + <x,y>)^d$.
  - Radial basis function (Gaussian): For some positive number σ, $K(x,y) = \exp(-<(x-y),(x-y)>/(2\sigma^2))$.
  - Multilayer perceptron (neural network): For a positive number p_1 and a negative number p_2, $K(x,y) = \tanh(p_1<x,y> + p_2)$.

    Note:

    - Not every set of p_1 and p_2 gives a valid reproducing kernel.

- `fitcsvm` does not support the sigmoid kernel.

The mathematical approach using kernels relies on the computational method of hyperplanes. All the calculations for hyperplane classification use nothing more than dot products. Therefore, nonlinear kernels can use identical calculations and solution algorithms, and obtain classifiers that are nonlinear. The resulting classifiers are hypersurfaces in some space S, but the space S does not have to be identified or examined.

Using Support Vector Machines

As with any supervised learning model, you first train a support vector machine, and then cross validate the classifier. Use the trained machine to classify (predict) new data. In addition, to obtain satisfactory predictive accuracy, you can use various SVM kernel functions, and you must tune the parameters of the kernel functions.

- "Training an SVM Classifier" on page 16-176
- "Classifying New Data with an SVM Classifier" on page 16-177
- "Tuning an SVM Classifier" on page 16-178

Training an SVM Classifier

Train, and optionally cross validate, an SVM classifier using `fitcsvm`. The most common syntax is:

```
SVMModel = fitcsvm(X,Y,'KernelFunction','rbf','Standardize',true,'ClassNames',{'negClas
```

The inputs are:

- `X` — Matrix of predictor data, where each row is one observation, and each column is one predictor.
- `Y` — Array of class labels with each row corresponding to the value of the corresponding row in `X`. `Y` can be a character array, categorical, logical or numeric vector, or vector cell array of strings. Column vector with each row corresponding to the value of the corresponding row in `X`. `Y` can be a categorical or character array, logical or numeric vector, or cell array of strings.
- `KernelFunction` — The default value is `'linear'` for two-class learning, which separates the data by a hyperplane. The value `'rbf'` is the default for one-class

learning, and uses a Gaussian radial basis function. An important step to successfully train an SVM classifier is to choose an appropriate kernel function.

- `Standardize` — Flag indicating whether the software should standardize the predictors before training the classifier.
- `ClassNames` — Distinguishes between the negative and positive classes, or specifies which classes to include in the data. The negative class is the first element (or row of a character array), e.g., `'negClass'`, and the positive class is the second element (or row of a character array), e.g., `'posClass'`. `ClassNames` must be the same data type as `Y`. It is good practice to specify the class names, especially if you are comparing the performance of different classifiers.

The resulting, trained model (`SVMModel`) contains the optimized parameters from the SVM algorithm, enabling you to classify new data.

For more name-value pairs you can use to control the training, see the `fitcsvm` reference page.

Classifying New Data with an SVM Classifier

Classify new data using `predict`. The syntax for classifying new data using a trained SVM classifier (`SVMModel`) is:

```
[label,score] = predict(SVMModel,newX);
```

The resulting vector, `label`, represents the classification of each row in `X`. `score` is an n-by-2 matrix of soft scores. Each row corresponds to a row in `X`, which is a new observation. The first column contains the scores for the observations being classified in the negative class, and the second column contains the scores observations being classified in the positive class.

To estimate posterior probabilities rather than scores, first pass the trained SVM classifier (`SVMModel`) to `fitPosterior`, which fits a score-to-posterior-probability transformation function to the scores. The syntax is:

```
ScoreSVMModel = fitPosterior(SVMModel,X,Y);
```

The property `ScoreTransform` of the classifier `ScoreSVMModel` contains the optimal transformation function. Pass `ScoreSVMModel` to `predict`. Rather than returning the scores, the output argument `score` contains the posterior probabilities of an observation being classified in the negative (column 1 of `score`) or positive (column 2 of `score`) class.

Tuning an SVM Classifier

Try tuning parameters of your classifier according to this scheme:

1. Pass the data to `fitcsvm`, and set the name-value pair arguments `'KernelScale','auto'`. Suppose that the trained SVM model is called `SVMModel`. The software uses a heuristic procedure to select the kernel scale. The heuristic procedure uses subsampling. Therefore, to reproduce results, set a random number seed using `rng` before training the classifier.
2. Cross validate the classifier by passing it to `crossval`. By default, the software conducts 10-fold cross validation.
3. Pass the cross-validated SVM model to `kFoldLoss` to estimate and retain the classification error.
4. Retrain the SVM classifier, but adjust the `'KernelScale'` and `'BoxConstraint'` name-value pair arguments.

    - `BoxConstraint` — One strategy is to try a geometric sequence of the box constraint parameter. For example, take 11 values, from `1e-5` to `1e5` by a factor of 10. Increasing `BoxConstraint` might decrease the number of support vectors, but also might increase training time.
    - `KernelScale` — One strategy is to try a geometric sequence of the RBF sigma parameter scaled at the original kernel scale. Do this by:

        a. Retrieving the original kernel scale, e.g., `ks`, using dot notation: `ks = SVMModel.KernelParameters.Scale`.

        b. Use as new kernel scales factors of the original. For example, multiply `ks` by the 11 values `1e-5` to `1e5`, increasing by a factor of 10.

Choose the model that yields the lowest classification error.

You might want to further refine your parameters to obtain better accuracy. Start with your initial parameters and perform another cross-validation step, this time using a factor of 1.2. Alternatively, optimize your parameters with `fminsearch`, as shown in “Train and Cross Validate SVM Classifiers” on page 16-189.

Train SVM Classifiers Using a Gaussian Kernel

This example shows how to generate a nonlinear classifier with Gaussian kernel function. First, generate one class of points inside the unit disk in two dimensions,

and another class of points in the annulus from radius 1 to radius 2. Then, generates a classifier based on the data with the Gaussian radial basis function kernel. The default linear classifier is obviously unsuitable for this problem, since the model is circularly symmetric. Set the box constraint parameter to `Inf` to make a strict classification, meaning no misclassified training points. Other kernel functions might not work with this strict box constraint, since they might be unable to provide a strict classification. Even though the rbf classifier can separate the classes, the result can be overtrained.

Generate 100 points uniformly distributed in the unit disk. To do so, generate a radius r as the square root of a uniform random variable, generate an angle t uniformly in $(0, 2\pi)$, and put the point at ($r \cos(t)$, $r \sin(t)$).

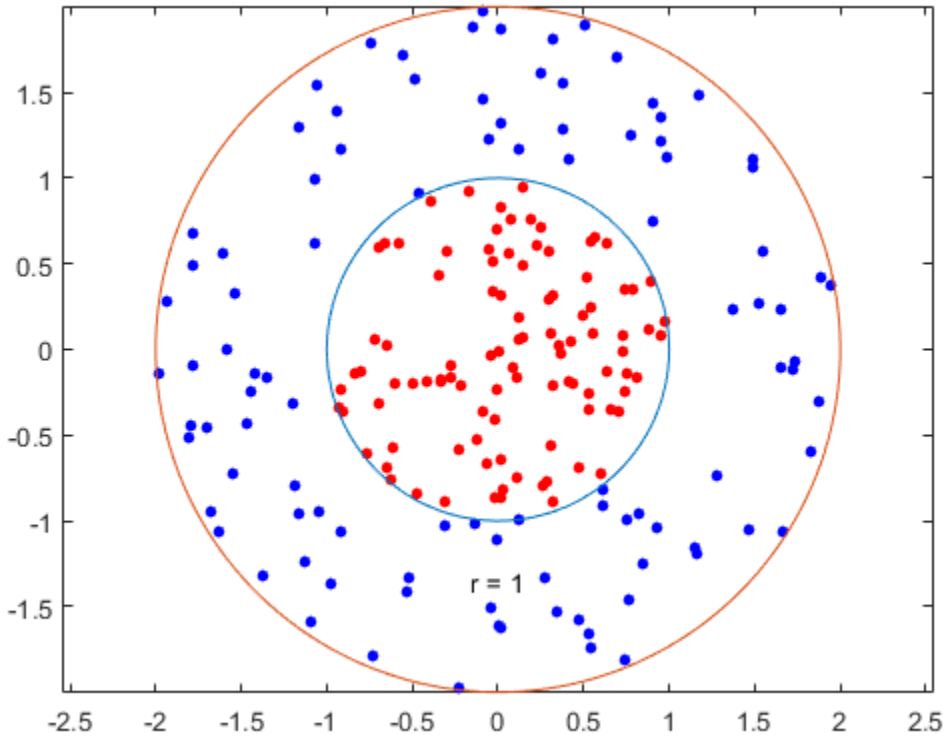
```
rng(1); % For reproducibility
r = sqrt(rand(100,1)); % Radius
t = 2*pi*rand(100,1);  % Angle
data1 = [r.*cos(t), r.*sin(t)]; % Points
```

Generate 100 points uniformly distributed in the annulus. The radius is again proportional to a square root, this time a square root of the uniform distribution from 1 through 4.

```
r2 = sqrt(3*rand(100,1)+1); % Radius
t2 = 2*pi*rand(100,1);      % Angle
data2 = [r2.*cos(t2), r2.*sin(t2)]; % points
```

Plot the points, and plot circles of radii 1 and 2 for comparison.

```
figure;
plot(data1(:,1),data1(:,2),'r.','MarkerSize',15)
hold on
plot(data2(:,1),data2(:,2),'b.','MarkerSize',15)
ezpolar(@(x)1);ezpolar(@(x)2);
axis equal
hold off
```



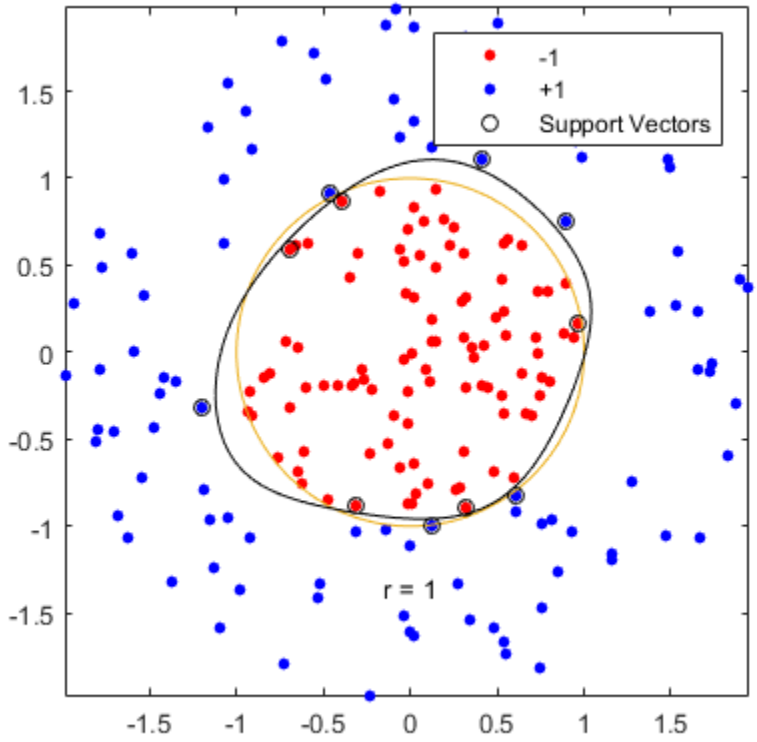
Put the data in one matrix, and make a vector of classifications.

```
data3 = [data1;data2];
theclass = ones(200,1);
theclass(1:100) = -1;
```

Train an SVM classifier with `KernelFunction` set to `'rbf'` and `BoxConstraint` set to `Inf`. Plot the decision boundary and flag the support vectors.

```
%Train the SVM Classifier
cl = fitcsvm(data3,theclass,'KernelFunction','rbf',...
    'BoxConstraint',Inf,'ClassNames',[-1,1]);

% Predict scores over the grid
```

```
d = 0.02;
[x1Grid,x2Grid] = meshgrid(min(data3(:,1)):d:max(data3(:,1)),...
    min(data3(:,2)):d:max(data3(:,2)));
xGrid = [x1Grid(:),x2Grid(:)];
[~,scores] = predict(cl,xGrid);

% Plot the data and the decision boundary
figure;
h(1:2) = gscatter(data3(:,1),data3(:,2),theclass,'rb','.');
hold on
ezpolar(@(x)1);
h(3) = plot(data3(cl.IsSupportVector,1),data3(cl.IsSupportVector,2),'ko');
contour(x1Grid,x2Grid,reshape(scores(:,2),size(x1Grid)),[0 0],'k');
legend(h,{'-1','+1','Support Vectors'});
axis equal
hold off
```

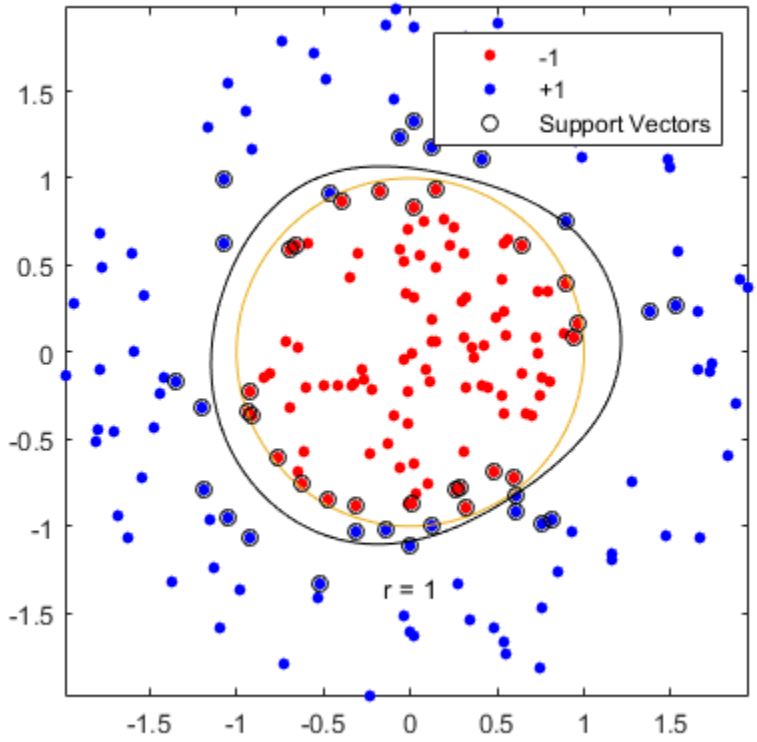


`fitcsvm` generates a classifier that is close to a circle of radius 1. The difference is due to the random training data.

Training with the default parameters makes a more nearly circular classification boundary, but one that misclassifies some training data. Also, the default value of `BoxConstraint` is `1`, and, therefore, there are more support vectors.

```
cl2 = fitcsvm(data3,theclass,'KernelFunction','rbf');
[~,scores2] = predict(cl2,xGrid);

figure;
h(1:2) = gscatter(data3(:,1),data3(:,2),theclass,'rb','.');
hold on
ezpolar(@(x)1);
```

```
h(3) = plot(data3(cl2.IsSupportVector,1),data3(cl2.IsSupportVector,2),'ko');
contour(x1Grid,x2Grid,reshape(scores2(:,2),size(x1Grid)),[0 0],'k');
legend(h,{'-1','+1','Support Vectors'});
axis equal
hold off
```



Train SVM Classifiers Using a Custom Kernel

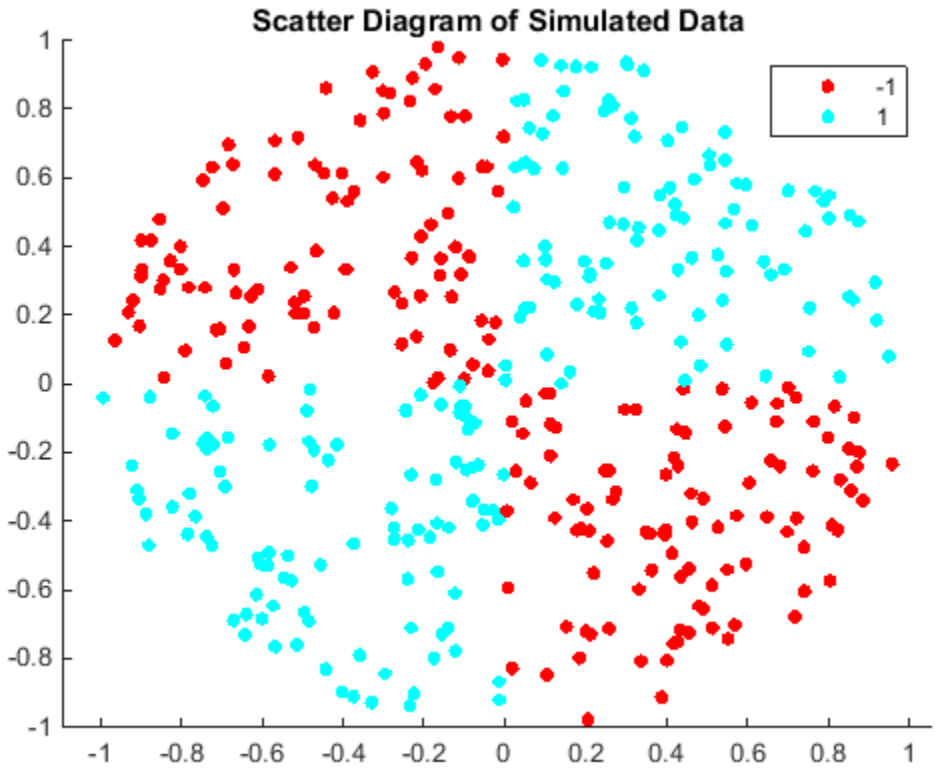
This example shows how to use a custom kernel function, such as the sigmoid kernel, to train SVM classifiers, and adjust custom kernel function parameters.

Generate a random set of points within the unit circle. Label points in the first and third quadrants as belonging to the positive class, and those in the second and fourth quadrants in the negative class.

```
rng(1);  % For reproducibility
n = 100; % Number of points per quadrant

r1 = sqrt(rand(2*n,1));                     % Random radii
t1 = [pi/2*rand(n,1); (pi/2*rand(n,1)+pi)]; % Random angles for Q1 and Q3
X1 = [r1.*cos(t1) r1.*sin(t1)];             % Polar-to-Cartesian conversion

r2 = sqrt(rand(2*n,1));
t2 = [pi/2*rand(n,1)+pi/2; (pi/2*rand(n,1)-pi/2)]; % Random angles for Q2 and Q4
X2 = [r2.*cos(t2) r2.*sin(t2)];

X = [X1; X2];        % Predictors
Y = ones(4*n,1);
Y(2*n + 1:end) = -1; % Labels
```

Plot the data.

```
figure;
gscatter(X(:,1),X(:,2),Y);
title('Scatter Diagram of Simulated Data')
```



Create the function `mysigmoid.m`, which accepts two matrices in the feature space as inputs, and transforms them into a Gram matrix using the sigmoid kernel.

```
function G = mysigmoid(U,V)
% Sigmoid kernel function with slope gamma and intercept c
gamma = 1;
c = -1;
G = tanh(gamma*U*V' + c);
end
```

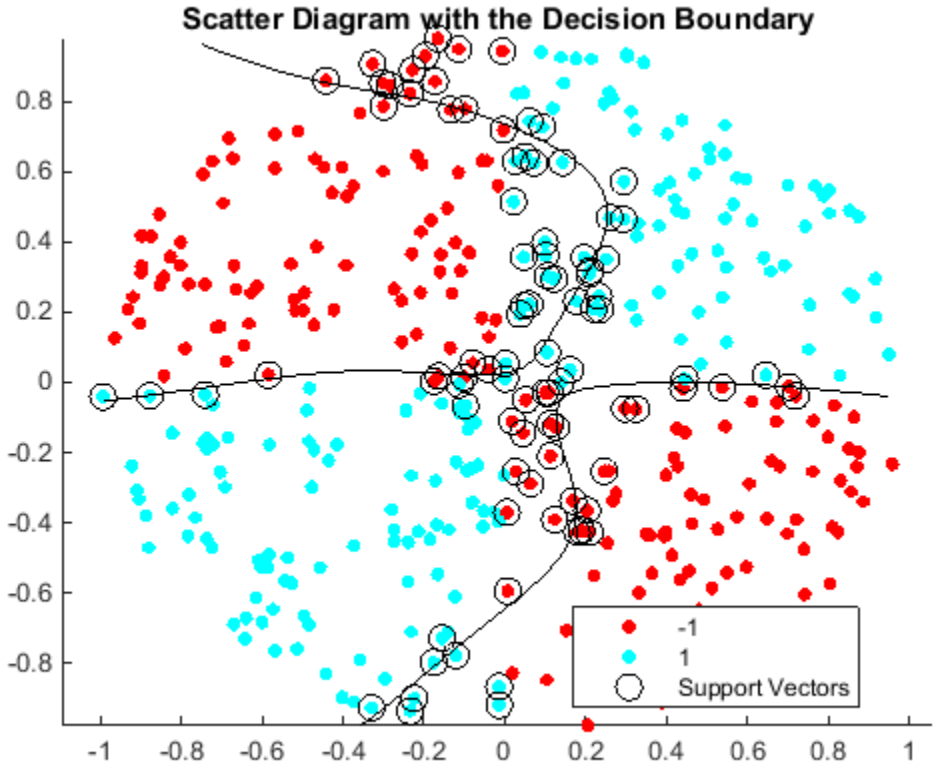
Train an SVM classifier using the sigmoid kernel function. It is good practice to standardize the data.

```
SVMModel1 = fitcsvm(X,Y,'KernelFunction','mysigmoid','Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier containing the estimated parameters.

Plot the data, and identify the support vectors and the decision boundary.

```
% Compute the scores over a grid
d = 0.02; % Step size of the grid
[x1Grid,x2Grid] = meshgrid(min(X(:,1)):d:max(X(:,1)),...
    min(X(:,2)):d:max(X(:,2)));
xGrid = [x1Grid(:),x2Grid(:)];        % The grid
[~,scores1] = predict(SVMModel1,xGrid); % The scores

figure;
h(1:2) = gscatter(X(:,1),X(:,2),Y);
hold on
h(3) = plot(X(SVMModel1.IsSupportVector,1),...
    X(SVMModel1.IsSupportVector,2),'ko','MarkerSize',10);
    % Support vectors
contour(x1Grid,x2Grid,reshape(scores1(:,2),size(x1Grid)),[0 0],'k');
    % Decision boundary
title('Scatter Diagram with the Decision Boundary')
legend({'-1','1','Support Vectors'},'Location','Best');
hold off
```



You can adjust the kernel parameters in an attempt to improve the shape of the decision boundary. This might also decrease the within-sample misclassification rate, but, you should first determine the out-of-sample misclassification rate.

Determine the out-of-sample misclassification rate by using 10-fold cross validation.

```
CVSVMModel1 = crossval(SVMModel1);
misclass1 = kfoldLoss(CVSVMModel1);
misclass1
```

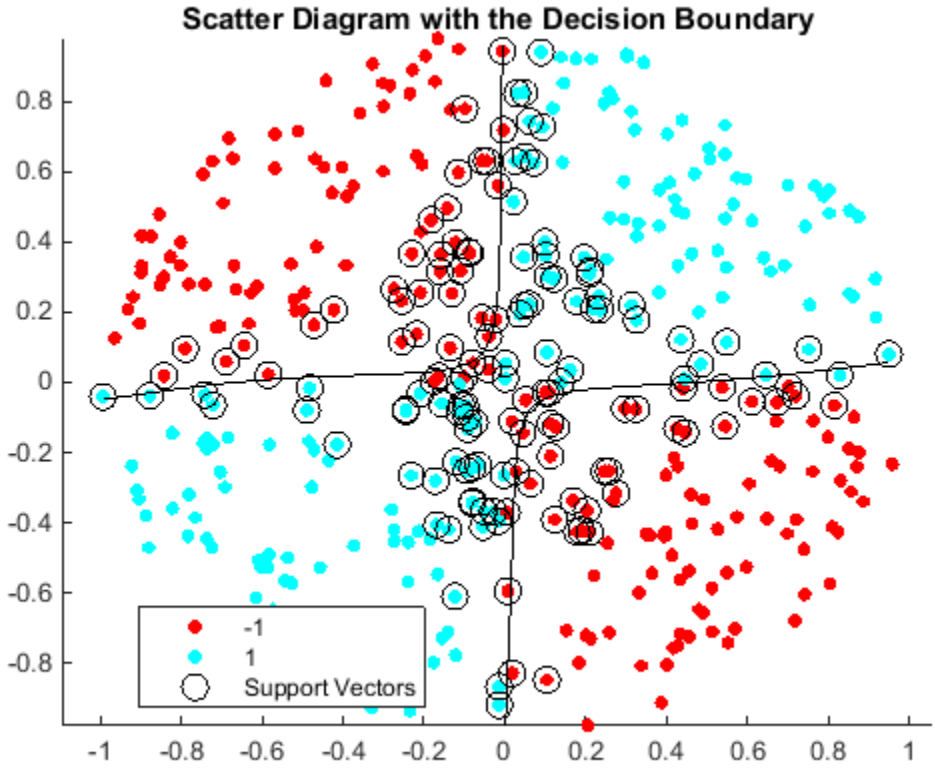
```
misclass1 =

    0.1350
```

The out-of-sample misclassification rate is 13.5%.

Set `gamma = 0.5;` within `mysigmoid.m`. Then, train an SVM classifier using the adjusted sigmoid kernel. Plot the data and the decision region, and determine the out-of-sample misclassification rate.

```
SVMModel2 = fitcsvm(X,Y,'KernelFunction','mysigmoid','Standardize',true);
[~,scores2] = predict(SVMModel2,xGrid);

figure;
h(1:2) = gscatter(X(:,1),X(:,2),Y);
hold on
h(3) = plot(X(SVMModel2.IsSupportVector,1),...
    X(SVMModel2.IsSupportVector,2),'ko','MarkerSize',10);
title('Scatter Diagram with the Decision Boundary')
contour(x1Grid,x2Grid,reshape(scores2(:,2),size(x1Grid)),[0 0],'k');
legend({'-1','1','Support Vectors'},'Location','Best');
hold off

CVSVMModel2 = crossval(SVMModel2);
misclass2 = kfoldLoss(CVSVMModel2);
misclass2
```

```
misclass2 =

    0.0450
```



After the sigmoid slope adjustment, the new decision boundary seems to provide a better within-sample fit, and the cross-validation rate contracts by more than 66%.

Train and Cross Validate SVM Classifiers

This example classifies points from a Gaussian mixture model. In *The Elements of Statistical Learning*, Hastie, Tibshirani, and Friedman (2009), page 17 describe the model. It begins with generating 10 base points for a "green" class, distributed as 2-D independent normals with mean (1,0) and unit variance. It also generates 10 base points for a "red" class, distributed as 2-D independent normals with mean (0,1) and unit variance. For each class (green and red), generate 100 random points as follows:

1 Choose a base point *m* of the appropriate color uniformly at random.

2 Generate an independent random point with 2-D normal distribution with mean m and variance I/5, where I is the 2-by-2 identity matrix.

After generating 100 green and 100 red points, classify them using `fitcsvm`, and tune the classification using cross validation.

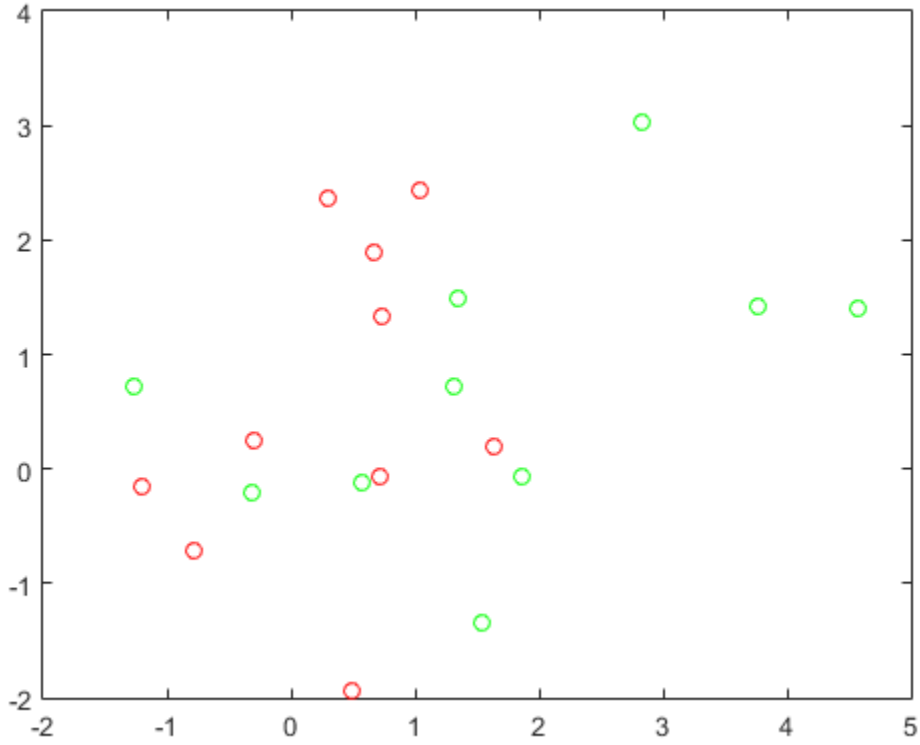
To generate the points and classifier:

Generate the 10 base points for each class.

```
rng('default')
grnpop = mvnrnd([1,0],eye(2),10);
redpop = mvnrnd([0,1],eye(2),10);
```

View the base points:

```
plot(grnpop(:,1),grnpop(:,2),'go')
hold on
plot(redpop(:,1),redpop(:,2),'ro')
hold off
```



Since many red base points are close to green base points, it is difficult to classify the data points.

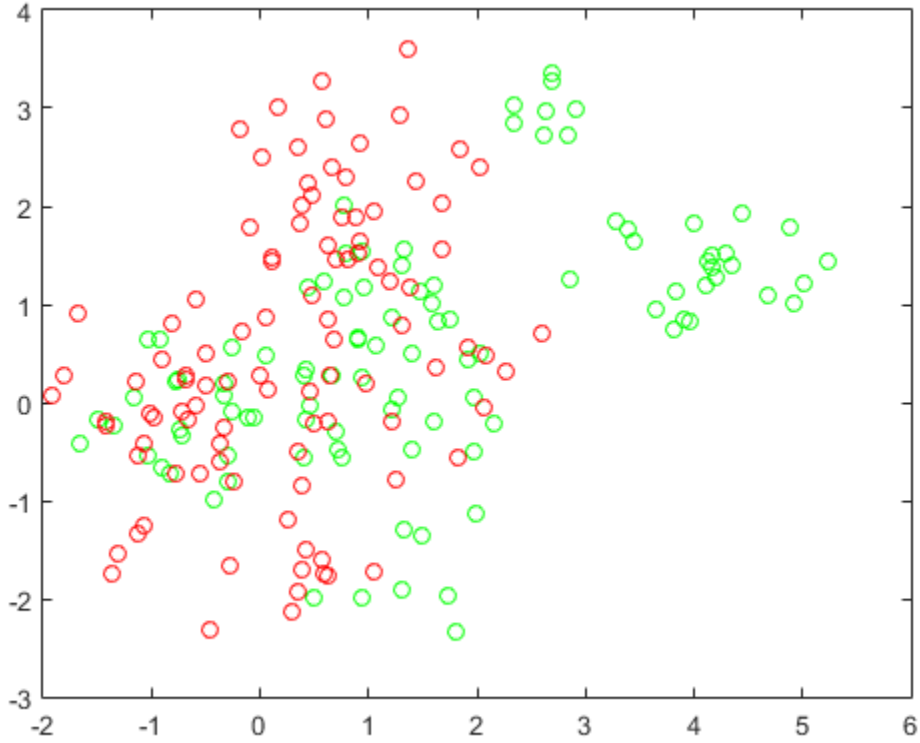
Generate the 100 data points of each class:

```
redpts = zeros(100,2);grnpts = redpts;
for i = 1:100
    grnpts(i,:) = mvnrnd(grnpop(randi(10),:),eye(2)*0.2);
    redpts(i,:) = mvnrnd(redpop(randi(10),:),eye(2)*0.2);
end
```

View the data points:

```
figure
plot(grnpts(:,1),grnpts(:,2),'go')
```

```
hold on
plot(redpts(:,1),redpts(:,2),'ro')
hold off
```



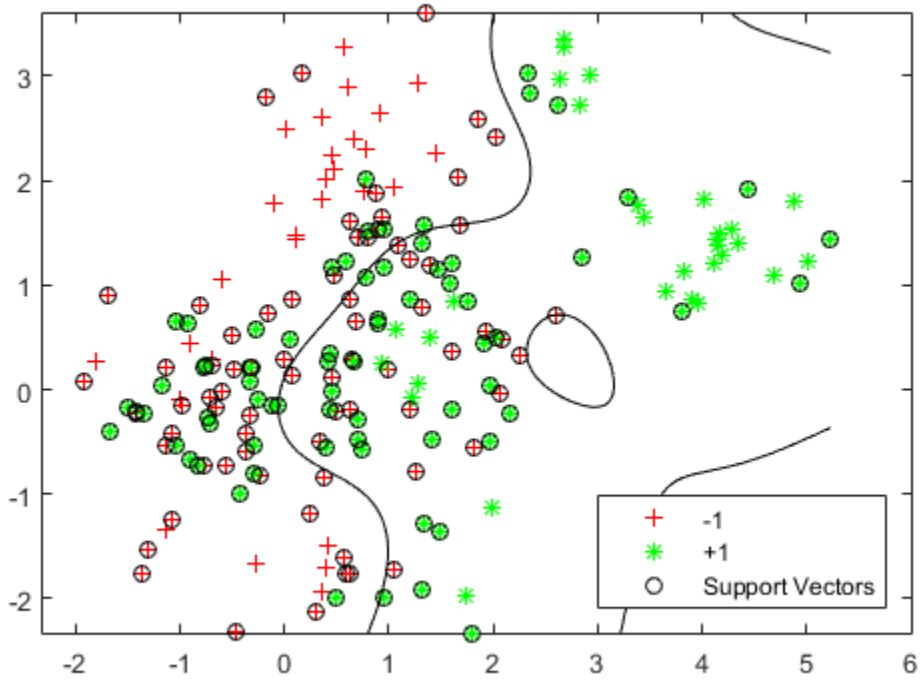
Put the data into one matrix, and make a vector `grp` that labels the class of each point:

```
cdata = [grnpts;redpts];
grp = ones(200,1);
% Green label 1, red label -1
grp(101:200) = -1;
```

Check the basic classification of all the data using the default parameters:

```
% Train the classifier
SVMModel = fitcsvm(cdata,grp,'KernelFunction','rbf','ClassNames',[-1 1]);
```

```
% Predict scores over the grid
d = 0.02;
[x1Grid,x2Grid] = meshgrid(min(cdata(:,1)):d:max(cdata(:,1)),...
    min(cdata(:,2)):d:max(cdata(:,2)));
xGrid = [x1Grid(:),x2Grid(:)];
[~,scores] = predict(SVMModel,xGrid);

% Plot the data and the decision boundary
figure;
h(1:2) = gscatter(cdata(:,1),cdata(:,2),grp,'rg','+*');
hold on
h(3) = plot(cdata(SVMModel.IsSupportVector,1),...
    cdata(SVMModel.IsSupportVector,2),'ko');
contour(x1Grid,x2Grid,reshape(scores(:,2),size(x1Grid)),[0 0],'k');
legend(h,{'-1','+1','Support Vectors'},'Location','Southeast');
axis equal
hold off
```



Set up a partition for cross validation. This step causes the cross validation to be fixed. Without this step, the cross validation is random, so a minimization procedure can find a spurious local minimum.

```
c = cvpartition(200,'KFold',10);
```

Set up a function that takes an input `z=[rbf_sigma,boxconstraint]`, and returns the cross-validation value of `exp(z)`. The reason to take `exp(z)` is twofold:

- `rbf_sigma` and `boxconstraint` must be positive.
- You should look at points spaced approximately exponentially apart.

This function handle computes the cross validation at parameters `exp([rbf_sigma,boxconstraint])`:

```
minfn = @(z)kfoldLoss(fitcsvm(cdata,grp,'CVPartition',c,...
    'KernelFunction','rbf','BoxConstraint',exp(z(2)),...
    'KernelScale',exp(z(1))));
```

Search for the best parameters [rbf_sigma,boxconstraint] with fminsearch, setting looser tolerances than the defaults.

Note that if you have a Global Optimization Toolbox™ license, use `patternsearch` for faster, more reliable minimization. Give bounds on the components of `z` to keep the optimization in a sensible region, such as `[-5,5]`, and give a relatively loose `TolMesh` tolerance.

```
opts = optimset('TolX',5e-4,'TolFun',5e-4);
[searchmin fval] = fminsearch(minfn,randn(2,1),opts)
```

```
searchmin =

    1.0246
   -0.1569


fval =

    0.3100
```

The best parameters `[rbf_sigma;boxconstraint]` in this run are:

```
z = exp(searchmin)
```

```
z =

    2.7861
    0.8548
```

Since the result of `fminsearch` can be a local minimum, not a global minimum, try again with a different starting point to check that your result is meaningful:

```
[searchmin fval] = fminsearch(minfn,randn(2,1),opts)
```

```
searchmin =

    0.2778
    0.6395


fval =

    0.3000
```

The best parameters `[rbf_sigma;boxconstraint]` in this run are:

```
z = exp(searchmin)


z =

    1.3202
    1.8956
```

Try another search:

```
[searchmin fval] = fminsearch(minfn,randn(2,1),opts)


searchmin =

   -0.0810
    0.5409


fval =

    0.3200
```

The best parameters `[rbf_sigma;boxconstraint]` in this run are:

```
z = exp(searchmin)


z =
```

```
    0.9222
    1.7175
```

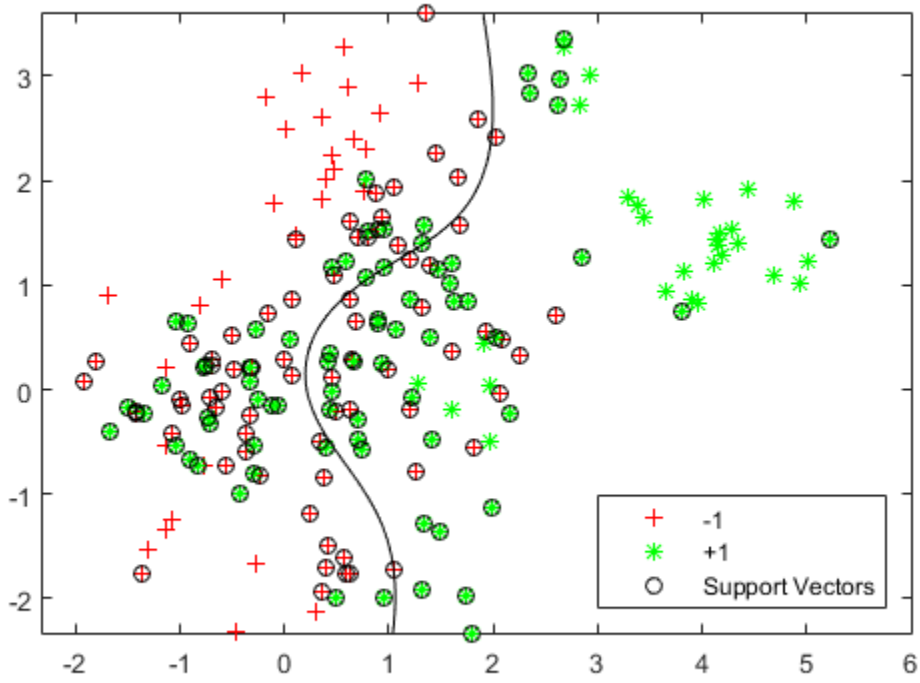
The surface seems to have many local minima. Try a set of 20 random, initial values, and choose the set corresponding to the lowest `fval`.

```
m = 20;
fval = zeros(m,1);
z = zeros(m,2);
for j = 1:m;
    [searchmin fval(j)] = fminsearch(minfn,randn(2,1),opts);
    z(j,:) = exp(searchmin);
end

z = z(fval == min(fval),:)
```

```
z =

    1.9301    0.7507
```

Use the `z` parameters to train a new SVM classifier:

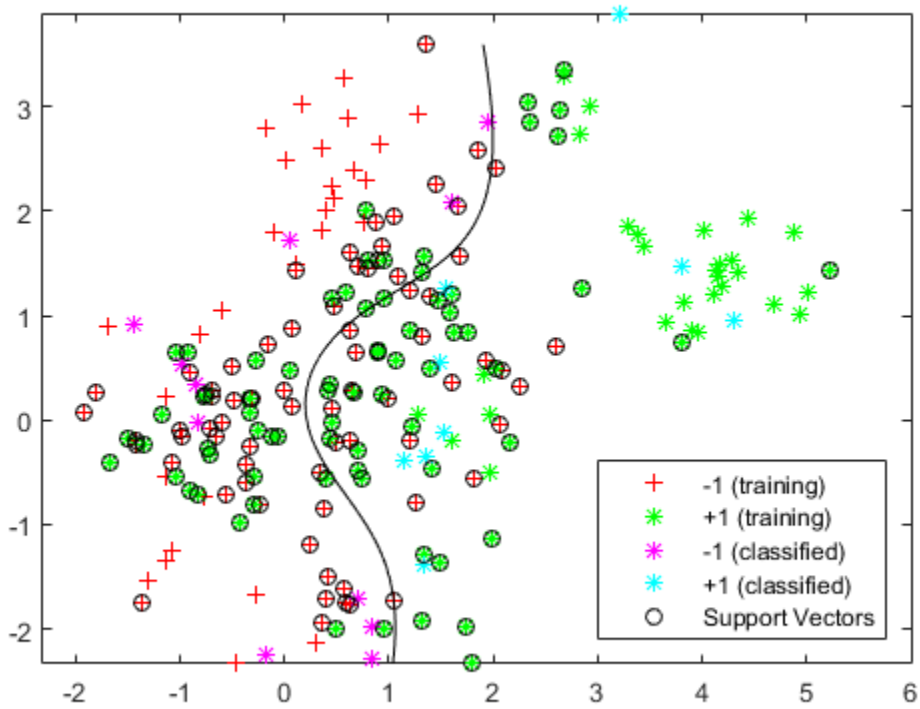
```
SVMModel = fitcsvm(cdata,grp,'KernelFunction','rbf',...
    'KernelScale',z(1),'BoxConstraint',z(2));
[~,scores] = predict(SVMModel,xGrid);

h = nan(3,1); % Preallocation
figure;
h(1:2) = gscatter(cdata(:,1),cdata(:,2),grp,'rg','+*');
hold on
h(3) = plot(cdata(SVMModel.IsSupportVector,1),...
    cdata(SVMModel.IsSupportVector,2),'ko');
contour(x1Grid,x2Grid,reshape(scores(:,2),size(x1Grid)),[0 0],'k');
legend(h,{'-1','+1','Support Vectors'},'Location','Southeast');
axis equal
hold off
```



Generate and classify some new data points:

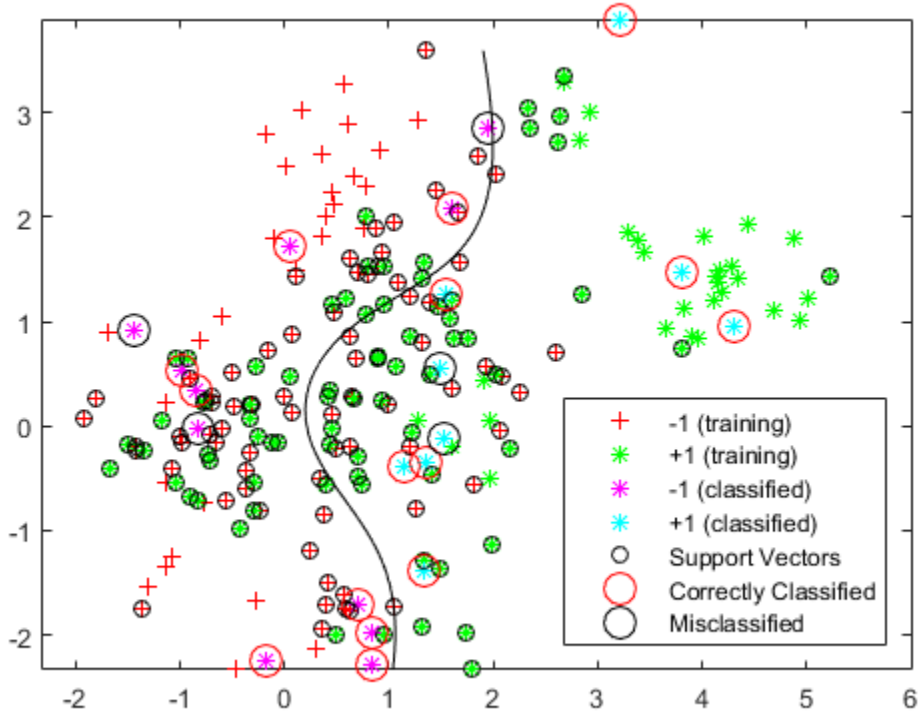
```
grnobj = gmdistribution(grnpop,.2*eye(2));
redobj = gmdistribution(redpop,.2*eye(2));

newData = random(grnobj,10);
newData = [newData;random(redobj,10)];
grpData = ones(20,1);
grpData(11:20) = -1; % red = -1

v = predict(SVMModel,newData);

g = nan(7,1);
figure;
```

```
h(1:2) = gscatter(cdata(:,1),cdata(:,2),grp,'rg','+*');
hold on
h(3:4) = gscatter(newData(:,1),newData(:,2),v,'mc','**');
h(5) = plot(cdata(SVMModel.IsSupportVector,1),...
    cdata(SVMModel.IsSupportVector,2),'ko');
contour(x1Grid,x2Grid,reshape(scores(:,2),size(x1Grid)),[0 0],'k');
legend(h(1:5),{'-1 (training)','+1 (training)','-1 (classified)',...
    '+1 (classified)','Support Vectors'},'Location','Southeast');
axis equal
hold off
```



See which new data points are correctly classified. Circle the correctly classified points in red, and the incorrectly classified points in black.

```
mydiff = (v == grpData); % Classified correctly
hold on
for ii = mydiff % Plot red circles around correct pts
    h(6) = plot(newData(ii,1),newData(ii,2),'ro','MarkerSize',12);
end

for ii = not(mydiff) % Plot black circles around incorrect pts
    h(7) = plot(newData(ii,1),newData(ii,2),'ko','MarkerSize',12);
end
legend(h,{'-1 (training)','+1 (training)','-1 (classified)',...
    '+1 (classified)','Support Vectors','Correctly Classified',...
    'Misclassified'},'Location','Southeast');
hold off
```



Plot Posterior Probability Regions for SVM Classification Models

This example shows how to predict posterior probabilities of SVM models over a grid of observations, and then plot the posterior probabilities over the grid. Plotting posterior probabilities exposes decision boundaries.

Load Fisher's iris data set. Train the classifier using the petal lengths and widths, and remove the virginica species from the data.

```
load fisheriris
classKeep = ~strcmp(species,'virginica');
X = meas(classKeep,3:4);
y = species(classKeep);
```

Train an SVM classifier using the data. It is good practice to specify the order of the classes.

```
SVMModel = fitcsvm(X,y,'ClassNames',{'setosa','versicolor'});
```

Estimate the optimal score transformation function.

```
rng(1); % For reproducibility
[SVMModel,ScoreParameters] = fitPosterior(SVMModel);
ScoreParameters
```

```
Warning: Classes are perfectly separated. The optimal score-to-posterior
transformation is a step function.

ScoreParameters =

                       Type: 'step'
                 LowerBound: -0.8431
                 UpperBound: 0.6897
    PositiveClassProbability: 0.5000
```

The optimal score transformation function is the step function because the classes are separable. The fields `LowerBound` and `UpperBound` of `ScoreParameters` indicate the lower and upper end points of the interval of scores corresponding to observations within the class-separating hyperplanes (the margin). No training observation falls within the margin. If a new score is in the interval, then the software assigns the corresonding observation a positive class posterior probability, i.e., the value in the `PositiveClassProbability` field of `ScoreParameters`.

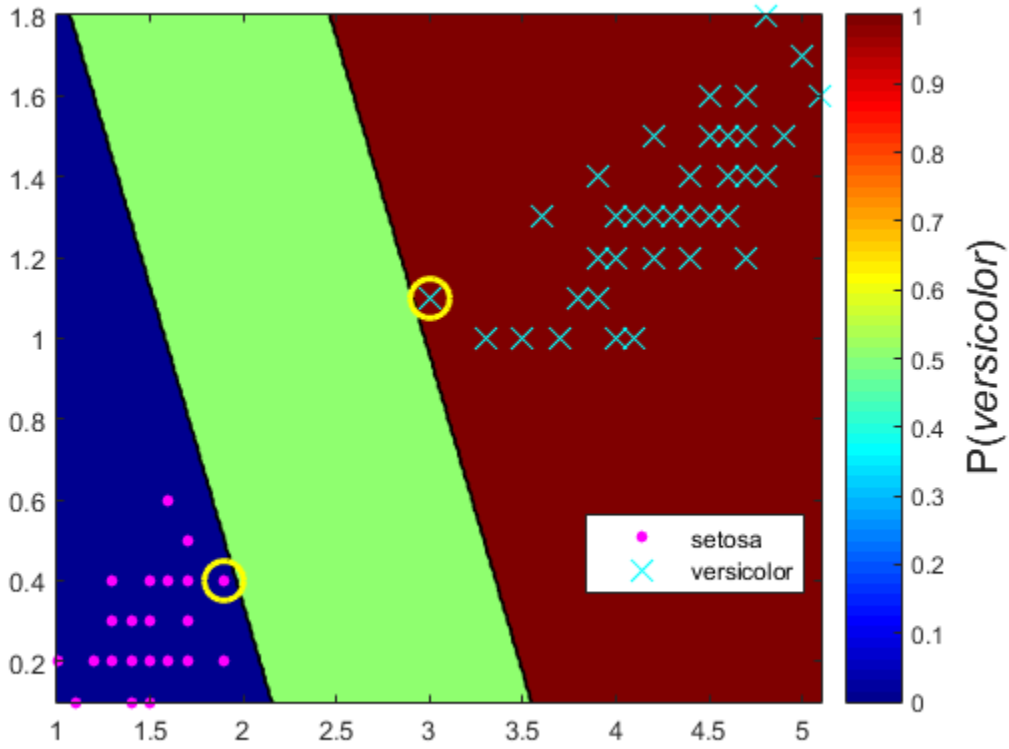
Define a grid of values in the observed predictor space. Predict the posterior probabilities for each instance in the grid.

```
xMax = max(X);
xMin = min(X);
d = 0.01;
[x1Grid,x2Grid] = meshgrid(xMin(1):d:xMax(1),xMin(2):d:xMax(2));

[~,PosteriorRegion] = predict(SVMModel,[x1Grid(:),x2Grid(:)]);
```

Plot the positive class posterior probability region and the training data.

```
figure;
```

```
contourf(x1Grid,x2Grid,...
        reshape(PosteriorRegion(:,2),size(x1Grid,1),size(x1Grid,2)));
h = colorbar;
h.Label.String = 'P({\it{versicolor}})';
h.YLabel.FontSize = 16;
caxis([0 1]);
colormap jet;

hold on
gscatter(X(:,1),X(:,2),y,'mc','.x',[15,10]);
sv = X(SVMModel.IsSupportVector,:);
plot(sv(:,1),sv(:,2),'yo','MarkerSize',15,'LineWidth',2);
axis tight
hold off
```



In two-class learning, if the classes are separable, then there are three regions: one where observations have positive class posterior probability 0, one where it is 1, and the other where it is the postiive class prior probability.

Analyze Images Using Linear Support Vector Machines

This example shows how to determine which quadrant of an image a shape occupies by training an error-correcting output codes (ECOC) model comprised of linear SVM binary learners. This example also illustrates the disk-space consumption of ECOC models that store support vectors, their labels, and the estimated α coefficients.

Create the Data Set

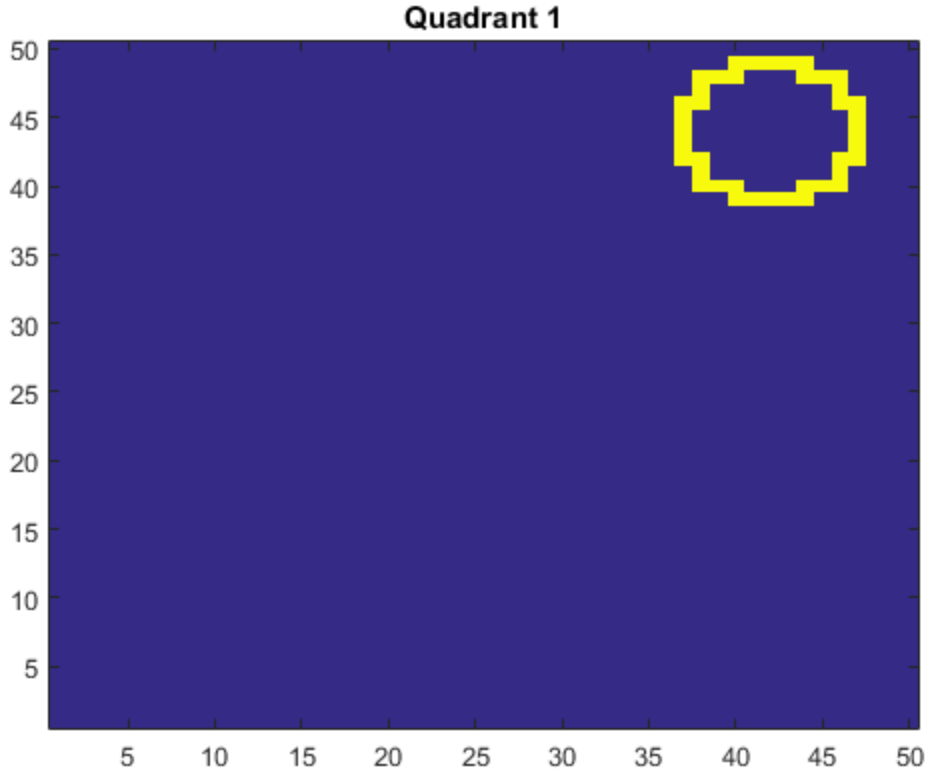
Randomly place a circle with radius five in a 50-by-50 image. Make 10000 images. Create a label for each image indicating the quadrant that the circle occupies. Quadrant 1 is in the upper right, quadrant 2 is in the upper left, quadrant 3 is in the lower left, and quadrant 4 is in the lower right. The predictors are the intensities of each pixel.

```
d = 50;  % Height and width of the images in pixels
n = 1e5; % Sample size

X = zeros(n,d^2); % Predictor matrix preallocation
Y = zeros(n,1);   % Label preallocation
theta = 0:(1/d):(2*pi);
r = 5;            % Circle radius
rng(1);           % For reproducibility

for j = 1:n;
    figmat = zeros(d);                          % Empty image
    c = datasample((r + 1):(d - r - 1),2);   % Random circle center
    x = r*cos(theta) + c(1);                    % Make the circle
    y = r*sin(theta) + c(2);
    idx = sub2ind([d d],round(y),round(x));  % Convert to linear indexing
    figmat(idx) = 1;                            % Draw the circle
    X(j,:) = figmat(:);                 % Store the data
    Y(j) = (c(2) >= floor(d/2)) + 2*(c(2) < floor(d/2)) + ...
        (c(1) < floor(d/2)) + ...
        2*((c(1) >= floor(d/2)) & (c(2) < floor(d/2))); % Determine the quadrant
end
```

Plot an observation.

```
figure;
```

```
imagesc(figmat);
h = gca;
h.YDir = 'normal';
title(sprintf('Quadrant %d',Y(end)));
```



Train the ECOC Model

Use a 25% holdout sample and specify the training and holdout sample indices.

```
p = 0.25;
CVP = cvpartition(Y,'Holdout',p); % Cross-validation data partition
isIdx = training(CVP);            % Training sample indices
oosIdx = test(CVP);               % Test sample indices
```

Create an SVM template that specifies storing the support vectors of the binary learners. Pass it and the training data to `fitcecoc` to train the model. Determine the training sample classification error.

```
t = templateSVM('SaveSupportVectors',true);
MdlSV = fitcecoc(X(isIdx,:),Y(isIdx),'Learners',t);
isLoss = resubLoss(MdlSV)
```

```
isLoss =

     0
```

`MdlSV` is a trained `ClassificationECOC` multiclass model. It stores the training data and the support vectors of each binary learner. For large data sets, such as those in image analysis, the model can consume a lot of memory.

Determine the amount of disk space that the ECOC model consumes.

```
infoMdlSV = whos('MdlSV');
mbMdlSV = infoMdlSV.bytes/1.049e6
```

```
mbMdlSV =

   1.4791e+03
```

The model consumes 1477.5 MB.

Improve Model Efficiency

You can assess out-of-sample performance. You can also assess whether the model has been overfit with a compacted model that does not contain the support vectors, their related parameters, and the training data.

Discard the support vectors and related parameters from the trained ECOC model. Then, discard the training data from the resulting model by using `compact`.

```
Mdl = discardSupportVectors(MdlSV);
CMdl = compact(Mdl);
info = whos('Mdl','CMdl');
[bytesCMdl,bytesMdl] = info.bytes;
```

```
memReduction = 1 - [bytesMdl bytesCMdl]/infoMdlSV.bytes
```

```
memReduction =

    0.0324    0.9999
```

In this case, discarding the support vectors reduces the memory consumption by about 3%. Compacting and discarding support vectors reduces the size by about 99.99%.

An alternative way to manage support vectors is to reduce their numbers during training by specifying a larger box constraint, such as 100. Though SVM models that use fewer support vectors are more desirable and consume less memory, increasing the value of the box constraint tends to increase the training time.

Remove `MdlSV` and `Mdl` from the workspace.

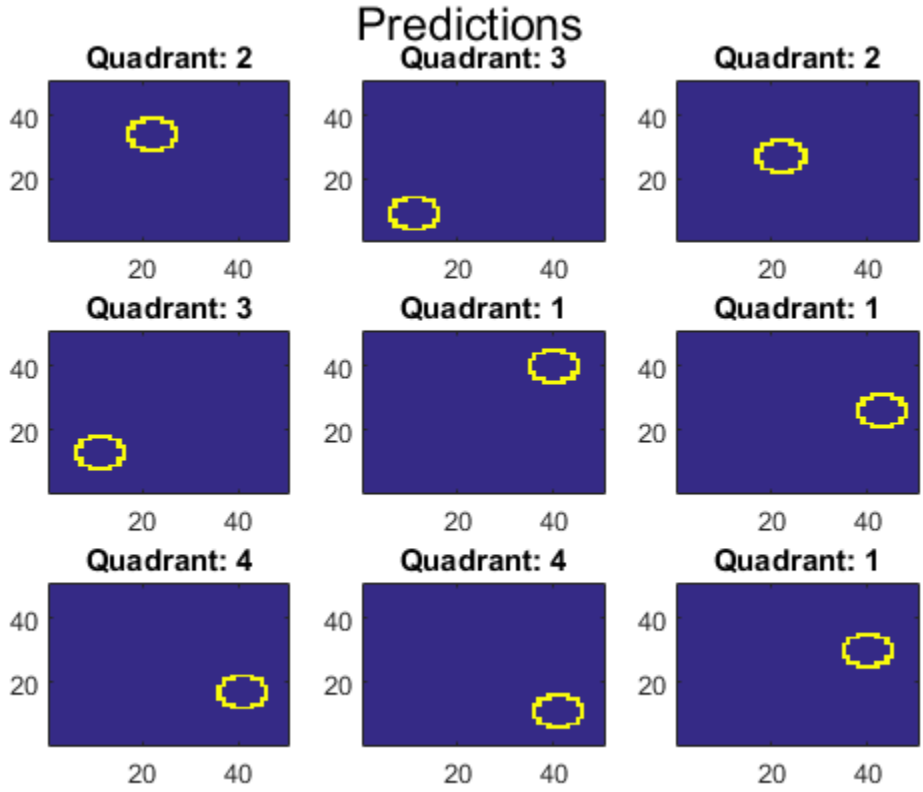
```
clear Mdl MdlSV;
```

Assess Holdout Sample Performance

Calculate the classification error of the holdout sample. Plot a sample of the holdout sample predictions.

```
oosLoss = loss(CMdl,X(oosIdx,:),Y(oosIdx))
yHat = predict(CMdl,X(oosIdx,:));
nVec = 1:size(X,1);
oosIdx = nVec(oosIdx);

figure;
for j = 1:9;
    subplot(3,3,j)
    imagesc(reshape(X(oosIdx(j),:),[d d]));
    h = gca;
    h.YDir = 'normal';
    title(sprintf('Quadrant: %d',yHat(j)))
end
text(-1.33*d,4.5*d + 1,'Predictions','FontSize',17)
```

```
oosLoss =

     0
```



The model does not misclassify any holdout sample observations.

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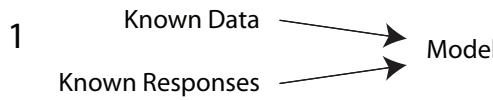
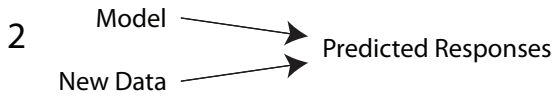
Classification Learner

Explore Classification Models Interactively

You can use the Classification Learner app to train models to classify data. Using this app, you can explore supervised machine learning using various classifiers. You can explore your data, select features, specify cross-validation schemes, train models, and assess results. You can choose from several classification types including decision trees, support vector machines, nearest neighbors, and ensemble classification.

Perform supervised machine learning by supplying a known set of input data (observations or examples) and known responses to the data (i.e., labels or classes). Use the data to train a model that generates predictions for the response to new data. To use the model with new data, or to learn about programmatic classification, you can export the model to the workspace or generate MATLAB code to recreate the trained model.





Use this workflow:

1. Open the app by entering `classificationLearner` at the MATLAB command prompt.
2. Import data and select variables to use as predictors (or features) and a response variable. See "Select Data and Validation for Classification Problem" on page 17-5.
3. Choose a classifier. On the **Classification Learner** tab, in the **Classifier** section, click a classifier type. To see all available classifier options, click the arrow on the far right of the **Classifier** section to expand the list of classifiers. The options in the **Classifier** gallery are starting points with different settings, suitable for a range of different classification problems.

   The table shows typical characteristics of different supervised learning algorithms. To choose a classifier type, decide on tradeoffs between predictive accuracy, speed

of training and prediction, memory usage, and interpretability. For example, for the fastest fitting, try a decision tree first.

4. After selecting a classifier, click **Train**.

   Repeat to try different classifiers. Every time you click **Train**, you create a new model in the history list.

5. Compare model performance by inspecting results in the scatter plot, confusion matrix, and ROC curve. Examine the percentage accuracy reported in the history list for each model. See "Assess Classifier Performance" on page 17-25.

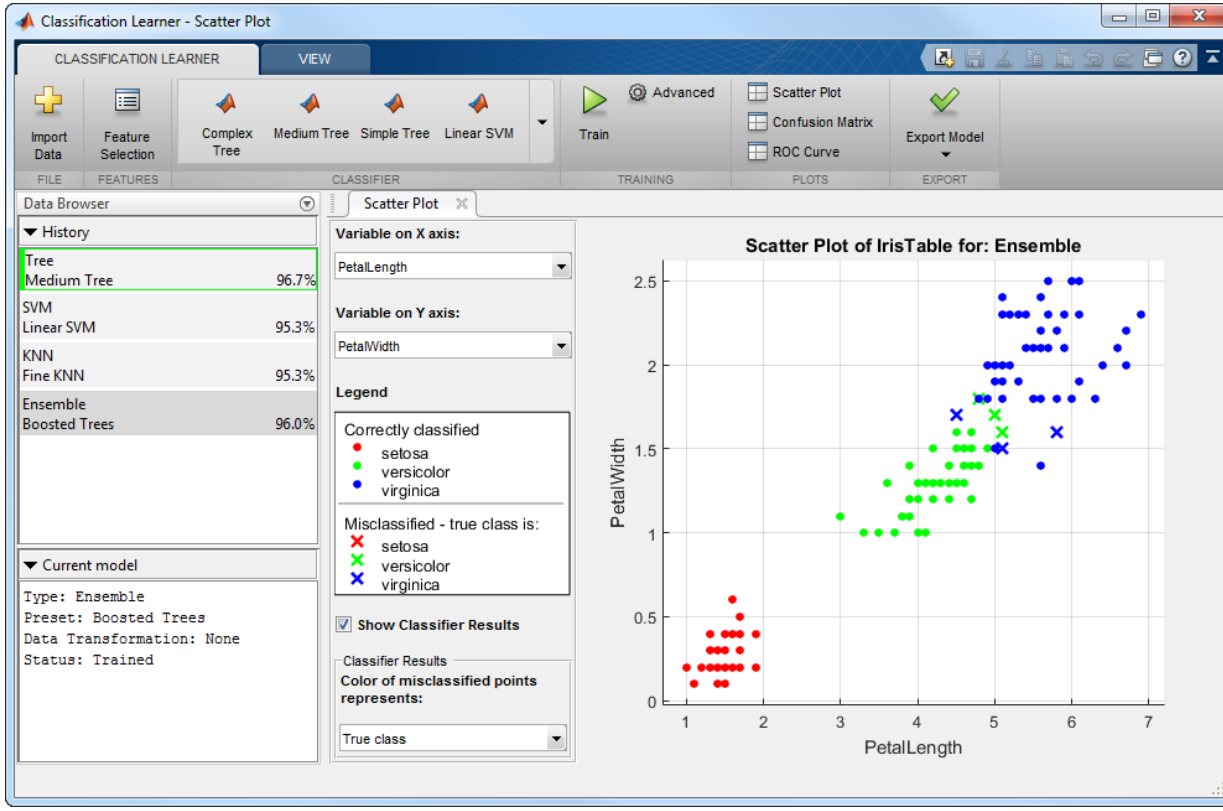
6. Select the best model in the history list and then try including and excluding different features in the model. See if you can improve the model by removing features with low predictive power. Specify predictors to include in the model, and train new models using the new options. Compare results among the models in the history list. See "Select Features" on page 17-23.

7. To improve the model further, you can try changing classifier parameter settings in the Advanced dialog box, and then train using the new options.

8. Generate code to train the model with different data, or export trained models to the workspace to make predictions using new data. See "Export Classification Model to Predict New Data" on page 17-29.

Tip For a step-by-step example, see "Explore Decision Trees Interactively" on page 17-32.

The figure shows the app with a history list containing various classifier types.



Related Examples

- “Select Data and Validation for Classification Problem” on page 17-5
- “Choose a Classifier” on page 17-8
- “Select Features” on page 17-23
- “Assess Classifier Performance” on page 17-25
- “Export Classification Model to Predict New Data” on page 17-29
- “Explore Decision Trees Interactively” on page 17-32

Select Data and Validation for Classification Problem

In this section...

Select Data from the Workspace

1 Load your data into the MATLAB workspace.

Tip Tables are the easiest way to use your data in the Classification Learner app, because they can contain numeric and label data. Use the Import Tool to bring your data into the MATLAB workspace as a table, or use the table functions to create a `table` from workspace variables. See “Tables”.

- Predictor variables must be numeric.
- Response variables can be a categorical array, cell array of strings, character array, logical vector, or a numeric vector the same height (first dimension) as the input predictor data.

2 Open the Classification Learner app by entering:

```
classificationLearner
```

3 In the Classification Learner app, on the **Classification Learner** tab, in the **File** section, click **Import Data**.

4 In the Setup dialog box, select a table or matrix from the workspace variables.

If you select a matrix, choose whether to use rows or columns for observations by clicking the option buttons.

5 Observe the roles the app selects for the variables based on their data type. The app tries to select a suitable response variable, and all other variables are predictors. Change the selections if needed in the column **Import as**. For each variable, you can choose either **Predictor**, **Response**, or **Do not import**.

6 To accept the default validation scheme and continue, click **Import Data**. The default validation option is 5-fold cross-validation, which protects against overfitting.

Tip If you have a large data set you might want to switch to holdout validation. To learn more, see "Choose Validation Scheme" on page 17-6.

Choose Validation Scheme

Choose a validation method to examine the predictive accuracy of the fitted models. Validation estimates model performance on new data compared to the training data, and helps you choose the best model. Validation protects against overfitting. Choose a validation scheme before training any models, so that you can compare all the models in your session using the same validation scheme.

- **Cross Validation**: Select a number of folds (or divisions) to partition the data set using the slider control.

  If you choose k folds, then the app:

  1. Partitions the data into k disjoint sets or folds
  2. For each fold:
     a. Trains a model using the out-of-fold observations
     b. Assesses model performance using in-fold data
  3. Calculates the average test error over all folds

  This method gives a good estimate of the predictive accuracy of the final model trained with all the data. It requires multiple fits but makes efficient use of all the data, so it is recommended for small data sets.

  Tip Try the default number of folds. Click **Import Data** to continue.

- **Holdout**: Select a percentage of the data to use as a test set using the slider control. The app trains the model on the training set and assesses the performance with the test set. The resulting model is based on only a portion of the data, so it is recommended only for large data sets.
- **None**: No validation. The app uses all of the data for training and computes the error rate on the same data. Without any test data, you get an unrealistic estimate of the model's performance on new data. That is, the training sample accuracy is likely to be unrealistically low, and the predictive accuracy is likely to be higher.

To help you avoid overfitting to the training data, choose a validation scheme instead.

All the classification models you train after selecting data use the same validation scheme that you select in this dialog box. You can compare all the models in your session using the same validation scheme.

To change the validation selection and train new models, you can select data again, but you lose any trained models. The app warns you that importing data starts a new session. Save any trained models you want to keep to the workspace, and then import the data.

Tip After you train models, you can view the validation accuracy of your models in the History list. See “Assess Classifier Performance” on page 17-25.

For next steps training models, see “Explore Classification Models Interactively” on page 17-2.

Choose a Classifier

In this section...

Choose a Classifier Type

In the Classification Learner app, you can explore several types of classifiers. To see all available classifier options, on the **Classification Learner** tab, click the arrow on the far right of the **Classifier** section to expand the list of classifiers. The options in the **Classifier** gallery are starting points with different settings, suitable for a range of different classification problems.

For help choosing a classifier type, see the table showing typical characteristics of different supervised learning algorithms. Use the table as a guide for your initial choice of algorithms, but be aware that the table can be inaccurate for some problems.

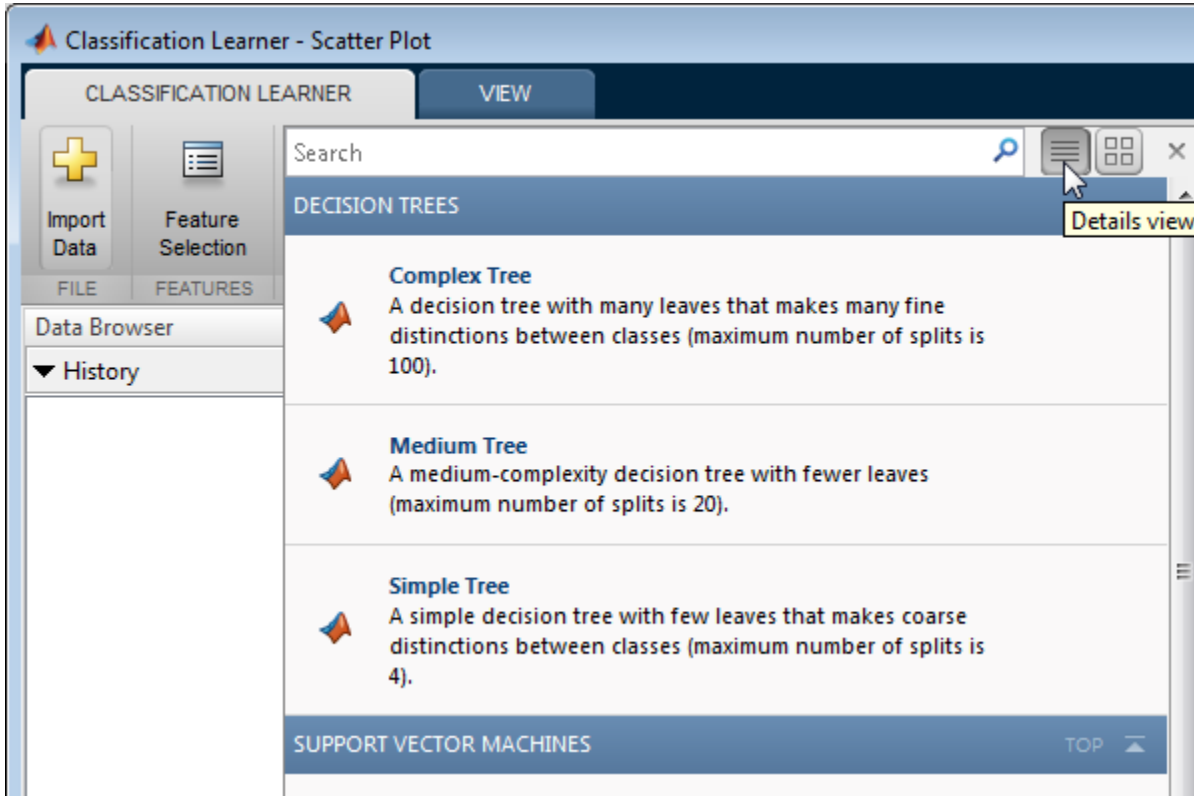
Tip Decide on the tradeoff you want in speed of training, memory usage, accuracy, and interpretability. For example, for the fastest fitting, try a decision tree first.

Choose a Classifier Type

Algorithm	Predictive Accuracy	Fitting Speed	Prediction Speed	Memory Usage	Easy to Interpret
“Decision Trees” on page 17-10	Medium	Fast	Fast	Low	Yes
“Support Vector Machines” on page 17-14	High	Medium	Fast for few support vectors. Slow for many support vectors.	Fast for few support vectors. Slow for many	Yes only for Linear SVM. No for all other kernel types.

Algorithm	Predictive Accuracy	Fitting Speed	Prediction Speed	Memory Usage	Easy to Interpret
				support vectors.	
"Nearest Neighbor Classifiers" on page 17-16	High only in low dimensions. Low for high dimensions.	Fast	Fast for low dimensions (<10), slow for high dimensions (>20)	High	No
"Ensemble Classifiers" on page 17-20	High	Slow	Qualities depend on choice of algorithm.		No

To read a description of each classifier, switch to the details view.



Tip After you choose a classifier type (e.g., decision trees), try training using each of the classifiers. The options in the **Classifier** gallery are starting points with different settings. Try them all to see which option produces the best model with your data.

For workflow instructions, see "Explore Classification Models Interactively" on page 17-2.

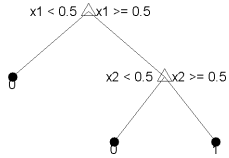
Decision Trees

Decision trees are easy to interpret, fast for fitting and prediction, and low on memory usage, but they can have low predictive accuracy. Try to grow simpler trees to prevent overfitting. Control the depth with the **Maximum number of splits** setting.

Classifier Name	Description
Complex Tree	A decision tree with many leaves that makes many fine distinctions between classes (maximum number of splits is 100).
Medium Tree	A medium-complexity decision tree with fewer leaves (maximum number of splits is 20.
Simple Tree	A simple decision tree with few leaves that makes coarse distinctions between classes (maximum number of splits is 4).

Tip Try training each of the decision tree options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to improve your model, try feature selection, and then try changing some advanced options.

You train classification trees to predict responses to data. To predict a response, follow the decisions in the tree from the root (beginning) node down to a leaf node. The leaf node contains the response. Statistics and Machine Learning Toolbox trees are binary. Each step in a prediction involves checking the value of one predictor (variable). For example, here is a simple classification tree:

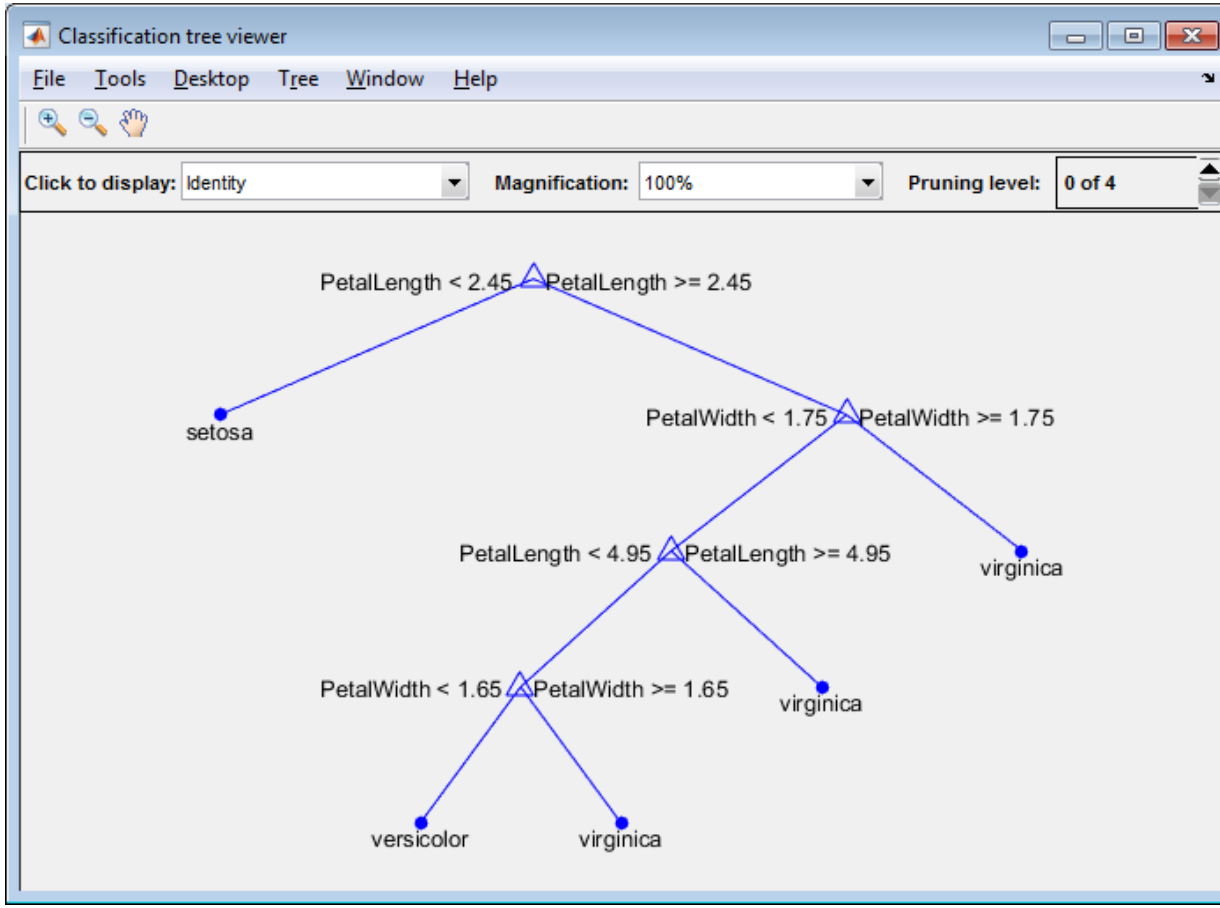


This tree predicts classifications based on two predictors, `x1` and `x2`. To predict, start at the top node. At each decision, check the values of the predictors to decide which branch to follow. When the branches reach a leaf node, the data is classified either as type `0` or `1`.

You can visualize your decision tree model by exporting the model from the app, and then entering:

```
view(trainedClassifier, 'Mode', 'graph')
```

The figure shows an example complex tree trained with the `fisheriris` data.



For an example, see “Explore Decision Trees Interactively” on page 17-32.

Advanced Tree Options

- **Maximum number of splits**

  Specify the maximum number of splits or branch points to control the depth of your tree. When you grow a decision tree, consider its simplicity and predictive power. To change the number of splits, click the buttons or enter a positive integer value in the **Maximum number of splits** box.

  - A complex tree with many leaves is usually highly accurate on the training data. However, the tree might not show comparable accuracy on an independent test set. A leafy tree tends to overtrain, and its validation accuracy is often far lower than its training (or resubstitution) accuracy.
  - In contrast, a simple tree does not attain high training accuracy. But a simple tree can be more robust in that its training accuracy can approach that of a representative test set. Also, a simple tree is easy to interpret.

- **Split Criterion**

  Specify the split criterion measure for deciding when to split nodes. Try each of the three settings to see if they improve the model with your data.

  Split criterion options are `Gini's diversity index`, `Twoing rule`, or `Maximum deviance reduction` (also known as cross entropy).

  The classification tree tries to optimize to pure nodes containing only one class. Gini's diversity index (the default) and the deviance criterion measure node impurity. The twoing rule is a different measure for deciding how to split a node, where maximizing the twoing rule expression increases node purity.

  For details of these split criteria, see `ClassificationTree` "Definitions" on page 22-443.

- **Surrogate Decision Splits** — Only for missing data.

  Specify surrogate use for decision splits. If you have data with missing values, use surrogate splits to improve the accuracy of predictions.

  When you set **Surrogate Decision Splits** to `On`, the classification tree finds at most 10 surrogate splits at each branch node. To change the number, click the buttons or enter a positive integer value in the **Maximum Surrogates Per Node** box.

  When you set **Surrogate Decision Splits** to `Find All`, the classification tree finds all surrogate splits at each branch node. The `Find All` setting can use considerable time and memory.

Support Vector Machines

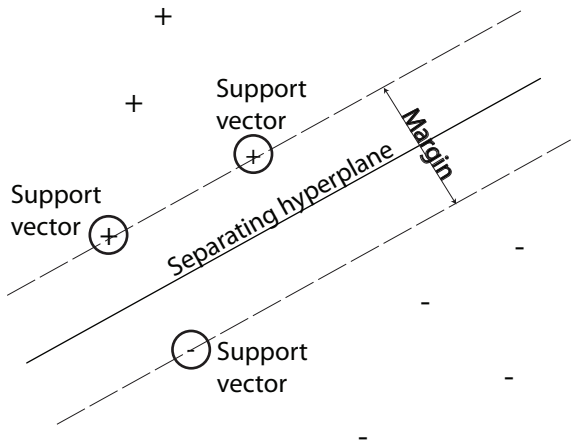
Support vector machines have high predictive accuracy, medium fitting speed, and can have good prediction speed and memory usage with few support vectors. Linear SVM is easy to interpret, but other kernel functions are less easy to interpret.

Classifier Name	Description
Linear SVM	Makes a simple linear separation between classes, using the linear kernel—The easiest SVM to interpret
Fine Gaussian SVM	Makes finely detailed distinctions between classes, using the Gaussian kernel with kernel scale set to `sqrt(P)/4`, where `P` is the number of predictors
Medium Gaussian SVM	Makes fewer distinctions than a fine Gaussian SVM, using the Gaussian kernel with kernel scale set to `sqrt(P)/4`, where P is the number of predictors
Coarse Gaussian SVM	Makes coarse distinctions between classes, using the Gaussian kernel with kernel scale set to `sqrt(P)/4`, where P is the number of predictors
Quadratic SVM	Uses the quadratic kernel
Cubic SVM	Uses the cubic kernel

Tip Try training each of the support vector machine options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to improve your model, try feature selection, and then try changing some advanced options.

An SVM classifies data by finding the best hyperplane that separates data points of one class from those of the other class. The best hyperplane for an SVM means the one with the largest margin between the two classes. Margin means the maximal width of the slab parallel to the hyperplane that has no interior data points.

The *support vectors* are the data points that are closest to the separating hyperplane; these points are on the boundary of the slab. The following figure illustrates these definitions, with + indicating data points of type 1, and – indicating data points of type –1.



SVMs can also use a soft margin, meaning a hyperplane that separates many, but not all data points.

In the Classification Learner app, you can train SVMs when your data has two or more classes. If you have exactly two classes, the app uses the `fitcsvm` function to train the classifier. If you have more than two classes, the app uses the `fitcecoc` function to reduce the multiclass classification problem to a set of binary classification subproblems, with one SVM learner for each subproblem. To examine the code for the binary and multiclass classifier types, you can generate code from your trained classifiers in the app.

For an example, see "Explore Support Vector Machines Interactively" on page 17-43.

Advanced SVM Options

- **Kernel Function**

  Specify the Kernel function to compute the Gram matrix.

  - Linear kernel, easiest to interpret
  - Gaussian or Radial Basis Function (RBF) kernel
  - Quadratic

  - Cubic
- **Box Constraint Level**

  Specify the box constraint to keep the allowable values of the Lagrange multipliers in a box, a bounded region.

  To tune your SVM classifier, try increasing the box constraint level. Click the buttons or enter a positive scalar value in the **Box Constraint Level** box. Increasing the box constraint level can decrease the number of support vectors, but also can increase training time.
- **Kernel Scale Mode**

  Specify manual kernel scaling if desired.

  When you set **Kernel Scale Mode** to `Auto`, then the software uses a heuristic procedure to select the scale value. The heuristic procedure uses subsampling. Therefore, to reproduce results, set a random number seed using `rng` before training the classifier.

  When you set **Kernel Scale Mode** to `Manual`, you can specify a value. Click the buttons or enter a positive scalar value in the **Manual Kernel Scale** box. The software divides all elements of the predictor matrix by the value of the kernel scale. Then, the software applies the appropriate kernel norm to compute the Gram matrix.
- **Multiclass Method**

  Only for data with 3 or more classes. This method reduces the multiclass classification problem to a set of binary classification subproblems, with one SVM learner for each subproblem. `One-vs-One` trains one learner for each pair of classes. It learns to distinguish one class from the other. `One-vs-All` trains one learner for each class. It learns to distinguish one class from all others.
- **Standardize Data**

  Specify whether to scale each coordinate distance. If predictors have widely different scales, standardizing can improve the fit.

Nearest Neighbor Classifiers

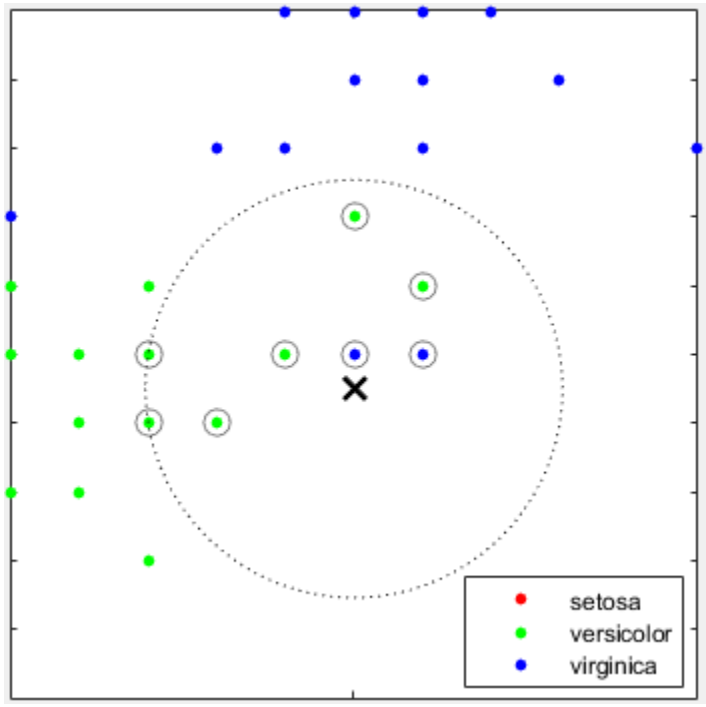
Nearest neighbor classifiers typically have good predictive accuracy in low dimensions, but might not in high dimensions. They have fast fitting speed, and prediction speed

is fast for low dimensions (<10), but slow for high dimensions (>20). They have high memory usage, and are not easy to interpret.

Classifier Name	Description
Fine KNN	Makes finely detailed distinctions between classes. The number of neighbors is set to 1.
Medium KNN	Makes fewer distinctions than a Fine KNN. The number of neighbors is set to 10.
Coarse KNN	Makes coarse distinctions between classes. The number of neighbors is set to 100.
Cosine KNN	Uses the cosine distance metric.
Cubic KNN	Uses the cubic distance metric.
Weighted KNN	Uses distance weighting.

Tip Try training each of the nearest neighbor options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to improve your model, try feature selection, and then (optionally) try changing some advanced options.

What is *k*-Nearest Neighbor classification? Categorizing query points based on their distance to points (or neighbours) in a training dataset can be a simple yet effective way of classifying new points. You can use various metrics to determine the distance. Given a set X of n points and a distance function, *k*-nearest neighbor (*k*NN) search lets you find the k closest points in X to a query point or set of points. *k*NN-based algorithms are widely used as benchmark machine learning rules.



For an example, see “Explore Nearest Neighbor Classification Interactively” on page 17-45.

Advanced KNN Options

- **Number of Neighbors**

  Specify the number of nearest neighbors to find for classifying each point when predicting. Specify a fine (low number) or coarse classifier (high number) by changing the number of neighbors. For example, a fine KNN uses one neighbor, and a coarse KNN uses 100. Many neighbors can be time consuming to fit.

- **Distance Metric**

  You can use various metrics to determine the distance to points. For definitions, see the class `ClassificationKNN`.

- **Distance Weight**

Specify the distance weighting function. You can choose `Equal` (no weights), `Inverse` (weight is 1/distance), or `Squared Inverse` (weight is 1/distance^2).

- **Standardize Data**

  Specify whether to scale each coordinate distance. If predictors have widely different scales, standardizing can improve the fit.

Ensemble Classifiers

Ensemble classifiers meld results from many weak learners into one high-quality ensemble predictor. Qualities depend on the choice of algorithm.

Note: All ensemble classifiers tend to be slow to fit because they often need many learners. Also, ensemble classifiers are difficult to interpret.

This table shows typical characteristics of the various ensemble classifiers. Use the table as a guide for your initial choice of algorithms.

Characteristics of Ensemble Classifiers

Classifier Name	Predictive Accuracy	Ensemble Method	Fitting Speed	Prediction Speed	Memory Usage
Boosted Trees	High, but might require parameter tuning	`AdaBoost`, with `Decision Tree` learners	Fast with few learners, but might need more learners than bagged trees	Fast with few learners	Low
Bagged Trees	Medium to high **Tip** Try this classifier first.	`Bag`, with `Decision Tree` learners	Slow for large data sets	Slow for large data sets	High for large data sets
Subspace KNN	Good for many predictors	`Subspace`, with `Nearest Neighbor` learners	Medium	Medium	High
Subspace Discriminant	Good for many predictors, accuracy dependent on data set	`Subspace`, with `Discriminant` learners	Fast	Fast	Low
RUSBoost Trees	Good for skewed data (with many more observations of 1 class)	`RUSBoost`, with `Decision Tree` learners	Fast with few learners	Fast with few learners	Low
GentleBoost — not available in Classifier gallery. Select manually if you have 2 class data.	For binary classification only	`GentleBoost`, with `Decision Tree` learners Choose `Boosted Trees` and change	Fast with few learners	Fast with few learners	Low

Classifier Name	Predictive Accuracy	Ensemble Method	Fitting Speed	Prediction Speed	Memory Usage
		to `GentleBoost` method.			

Tips

- Try bagged trees first. Boosted trees can usually do better but might require searching many parameter values, which is time-consuming.
- Try training each of the ensemble classifier options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to improve your model, try feature selection, and then (optionally) try changing some advanced options.

For an example, see "Explore Ensemble Classification Interactively" on page 17-47.

Advanced Ensemble Options

- For help choosing **Ensemble Method** and **Learner Type**, see the Ensemble table.
- **Number of Learners**

  Try changing the number of learners to see if you can improve the model. Many learners can produce high accuracy, but can be time consuming to fit. Start with a few dozen learners, and then inspect the performance. An ensemble with good predictive power can need a few hundred leaners.
- **Learning Rate**

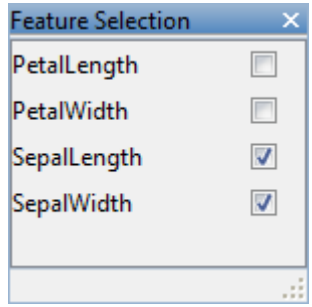
  Specify the learning rate for shrinkage. If you set the learning rate to less than 1, the ensemble requires more learning iterations but often achieves better accuracy. 0.1 is a popular choice.
- **Subspace Dimension**

  For subspace ensembles, specify number of predictors to sample in each learner. The app chooses a random subset of the predictors for each learner. The subsets chosen by different learners are independent.

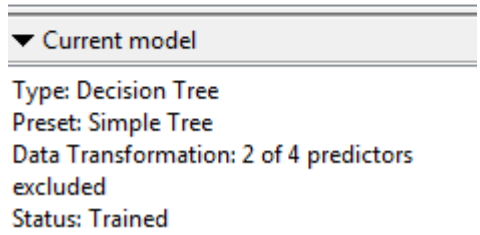
Select Features

In Classification Learner app, you can specify different features (or predictors) to include in the model. See if you can improve models by removing features with low predictive power. If data collection is expensive or difficult, you might prefer a model that performs satisfactorily without some predictors.

1. On the **Classification Learner** tab, in the **Features** section, click **Feature Selection**.
2. In the Feature Selection dialog box, clear the check boxes for the predictors you want to exclude.



3. Click **Train** to train a new model using the new predictor options.
4. Observe the new model in the History list. The Current model pane displays how many predictors are excluded, for example `2 of 4`.



5 To check which predictors are included in a trained model, click the model in the History list and observe the check boxes in the Feature Selection dialog box.

6 You can try to improve the model by including different features in the model.

For an example using feature selection, see “Explore Decision Trees Interactively” on page 17-32.

Assess Classifier Performance

In this section...

Check Performance in the History List

After training a model in the Classification Learner app, check the History list to see which model has the best overall accuracy in percent. The best score is highlighted in a green box. This score is the validation accuracy (unless you opted for no validation scheme). The validation accuracy score estimates a model's performance on new data compared to the training data. Use the score to help you choose the best model.

- For cross-validation, the score is the accuracy on all observations, counting each observation when it was in a held-out fold.

  Note: When you imported data into the app, if you accepted the defaults, you are using cross-validation. To learn more, see “Choose Validation Scheme” on page 17-6.

- For holdout validation, the score is the accuracy on the held-out observations.
- For no validation, the score is the resubstitution accuracy against all the training data observations.

The best overall score might not be the best model for your goal. A model with a slightly lower overall accuracy might be the best classifier for your goal. For example, false positives in a particular class might be important to you. You might want to exclude some predictors where data collection is expensive or difficult.

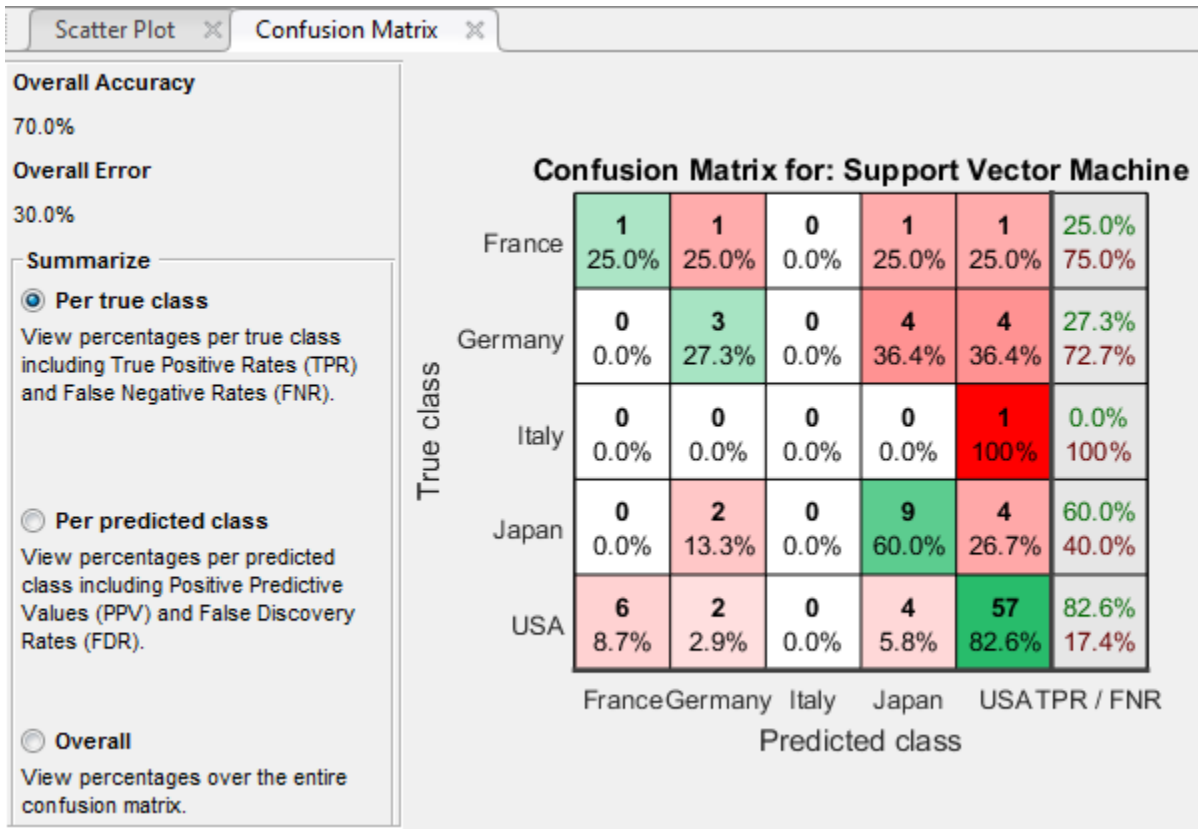
To find out how the classifier performed in each class, examine the confusion matrix.

Understand the Confusion Matrix

To view the confusion matrix after training a model, on the **Classification Learner** tab, in the **Plots** section, click **Confusion Matrix**. Use this plot to understand how the currently selected classifier performed in each class.

On the plot, the rows show the true class, and the columns show the predicted class. The diagonal cells show where the true class and predicted class match. If these cells are green and display high percentages, the classifier has performed well and classified observations of this true class correctly.

Tip Look for areas where the classifier performed poorly by examining cells off the diagonal that display high percentages and are red. In these red cells, the true class and the predicted class do not match. The data points are misclassified.



The default view shows a summary per true class in the last column on the right.

In this example, using the `carsmall` data set, the top row shows all cars with true class France. The columns show the predicted classes. In the top row, one out of four cars from France is correctly classified, so the summary cell on the right shows **25%** in green. 25% is the true positive rate for correctly classified points in this class.

The other three cars in this row are misclassified: one car is incorrectly classified as from Germany, one from Japan, and one from the USA. The summary cell on the right shows **75%** in red, under the green **25%**. 75% is the false negative rate for incorrectly classified points in this class.

If you want to see a summary per predicted class instead, under **Summarize**, select **Per predicted class**. The plot shows a summary row underneath the table. Positive predictive values are shown in green for the correctly predicted points in each class, and false discovery rates are shown below it in red for the incorrectly predicted points in each class. If false positives are important in your classification problem, use this view to investigate false discovery rates.

If you want to see percentages across the whole data set instead of by class, under **Summarize**, select **Overall**. The views per class are more useful for identifying the areas where the classifier has performed poorly. The higher the percentage, the brighter the hue of the cell color.

The **Overall Accuracy** is the validation accuracy you can also view in the History list.

The confusion matrix shows no numbers in the cells if you have more than five classes or the pane is too small.

If you decide there are too many misclassified points in the classes of interest, try changing classifier settings or feature selection to search for a better model.

Understand the ROC Curve

To view the ROC curve after training a model, on the **Classification Learner** tab, in the **Plots** section, click **ROC Curve**. View the receiver operating characteristic (ROC) curve showing true and false positive rates. The ROC curve shows true positive rate versus false positive rate for the currently selected trained classifier. You can select different classes to plot.

A perfect result with no misclassified points is a right angle to the top left of the plot. A poor result that is no better than random is a line at 45 degrees. The **Area Under**

Curve number is a measure of the overall quality of the classifier. Compare classes and trained models to see if they perform differently in the ROC curve.

For more information, see `perfcurve`.

Related Examples

- "Explore Classification Models Interactively" on page 17-2
- "Export Classification Model to Predict New Data" on page 17-29

Export Classification Model to Predict New Data

In this section...

Export the Model to the Workspace to Make Predictions for New Data

After you create classification models interactively in the Classification Learner app, you can export your best model to the workspace. You can then use the trained model to make predictions using new data.

1. In the Classification Learner app, select the model you want to export in the History list.
2. On the **Classification Learner** tab, in the **Export** section, click one of the export options:

   - If you want to include the data used for training the model, then select **Export Model**.

     You export the trained model to the workspace as a classification object, such as a `ClassificationTree`, `ClassificationSVM`, `CompactClassificationTree`, `ClassificationKNN`, `ClassificationBaggedEnsemble`, etc.
   - If you do not want to include the training data, select **Export compacted**. This option exports the model as a compact classification object that does not include the training data (e.g., `CompactClassificationTree`). You can use a compact classification object for making predictions of new data, but you can use fewer other methods with it.

   The app displays information about the exported model in the command window.
3. To use the exported classifier to make predictions for new data, `T`, use the form:

   ```
   yfit = predict(trainedClassifier,T{:,trainedClassifier.PredictorNames})
   ```
   Replace the table `T` with your training data or new data. The output `yfit` contains a class prediction for each data point.

Generate MATLAB Code to Train the Model with New Data

After you create classification models interactively in the Classification Learner app, you can generate MATLAB code for your best model. You can then use the code to train the model with new data.

1. In the Classification Learner app, in the History list, select the model you want to generate code for.
2. On the **Classification Learner** tab, in the **Export** section, click **Export Model** > **Generate Code**.

   The app generates code from your session and displays the file in the MATLAB Editor. The file includes the predictors and response, the classifier training methods, and validation methods. Save the file.
3. To retrain your classifier model, call the function from the command line with your original data or new data as the input argument. New data must be the same shape.

   Copy the first line of the generated code excluding the word `function`, and edit the datasetTable input argument to the variable name of your training data or new data. For example, to retrain a classifier trained with the `fisheriris` data set, enter:

   ```
   [trainedClassifier, validationAccuracy] = trainClassifier(fisheriris)
   ```
4. If you want to automate training the same classifier with new data, or learn how to programmatically train classifiers, examine the generated code. The code shows you how to:

   - Process the data into the right shape
   - Train a classifier and specify all the classifier options
   - Perform cross-validation
   - Compute validation accuracy
   - Compute validation predictions and scores

See Also

Functions

`fitcecoc` | `fitcknn` | `fitcsvm` | `fitctree` | `fitensemble`

Classes

`ClassificationBaggedEnsemble` | `ClassificationKNN` | `ClassificationSVM` | `ClassificationTree` | `CompactClassificationEnsemble` | `CompactClassificationSVM` | `CompactClassificationTree`

Related Examples

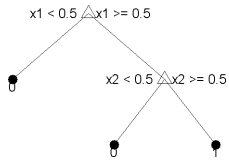
- “Explore Classification Models Interactively” on page 17-2

Explore Decision Trees Interactively

This example shows how to create and compare various classification trees using Classification Learner app, and export trained models to the workspace to make predictions for new data.

You can train classification trees to predict responses to data. To predict a response, follow the decisions in the tree from the root (beginning) node down to a leaf node. The leaf node contains the response.

Statistics and Machine Learning Toolbox trees are binary. Each step in a prediction involves checking the value of one predictor (variable). For example, here is a simple classification tree:



This tree predicts classifications based on two predictors, `x1` and `x2`. To predict, start at the top node. At each decision, check the values of the predictors to decide which branch to follow. When the branches reach a leaf node, the data is classified either as type `0` or `1`.

This example use Fisher's 1936 iris data. The iris data contains measurements of flowers: the petal length, petal width, sepal length, and sepal width for specimens from three species. Train a classifier to predict the species based on the predictor measurements.

1. In MATLAB, load the `fisheriris` data set.

   ```
   load fisheriris;
   ```

2. Create a table of measurement predictors (or features) using variables from the data set to use for a classification.

   ```
   IrisTable = array2table(meas,'VariableNames',{'SepalLength','SepalWidth',...
   'PetalLength','PetalWidth'});
   ```

3. Add the species response variable to the table. `Species` is the response you want to train a model to predict.

   ```
   IrisTable.Species = categorical(species);
   ```

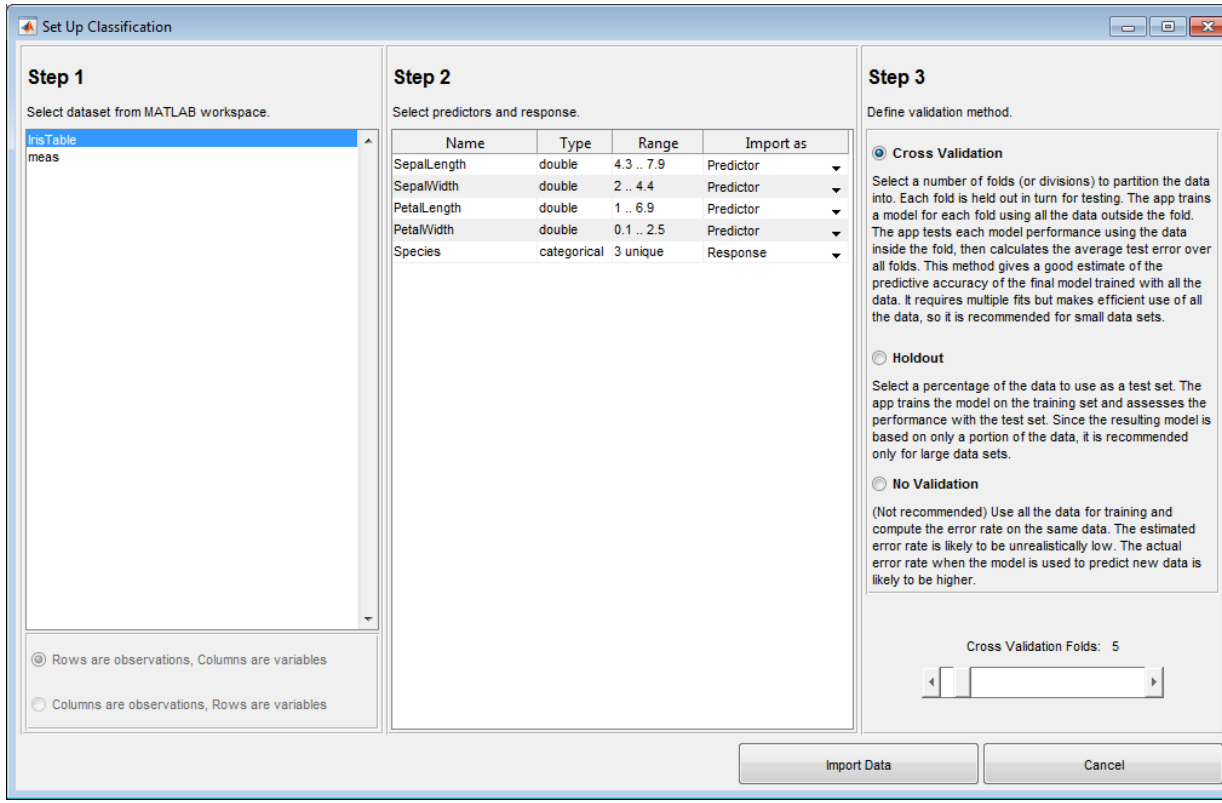
4. Open the Classification Learner app by entering:

```
classificationLearner
```

5 On the **Classification Learner** tab, in the **File** section, click **Import Data**.

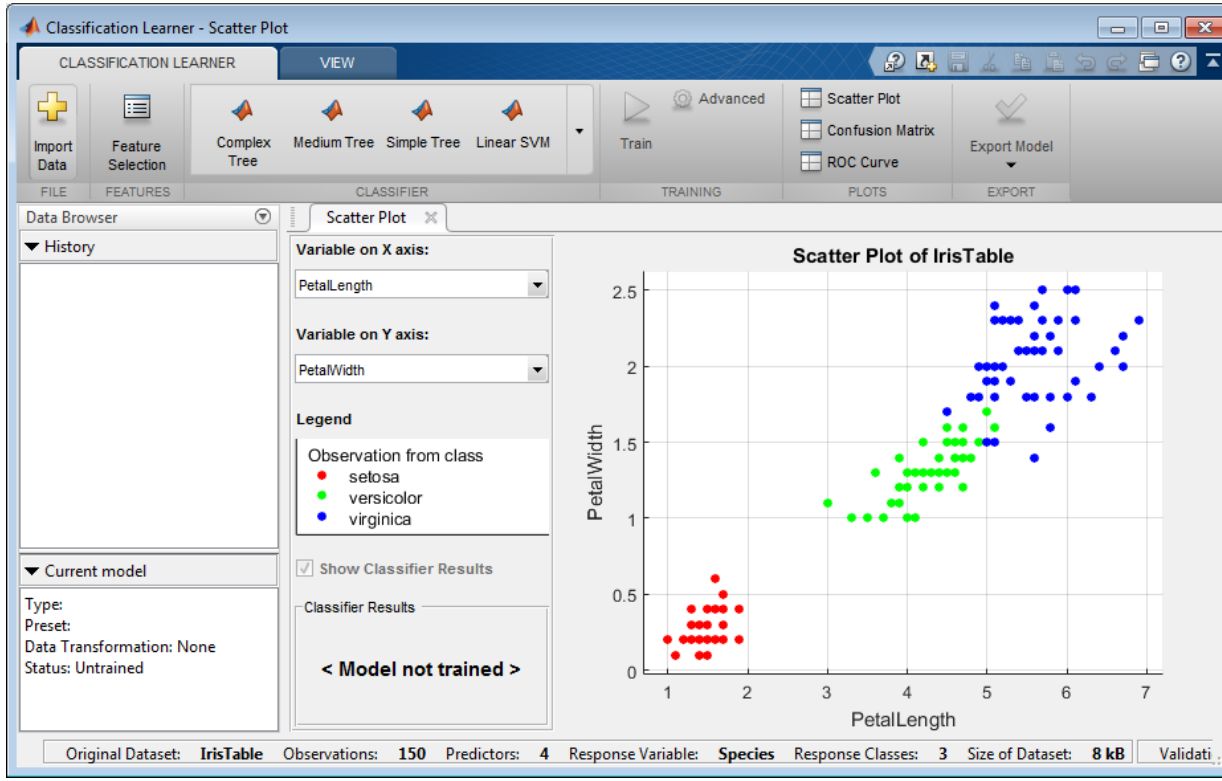
6 In the Set Up Classification dialog box, select the table `IrisTable` from the workspace list.

Observe the roles the app has selected for the variables based on their data type. Petal and sepal length and width are predictors, and species is the response that you want to classify. For this example, do not change the role selections.

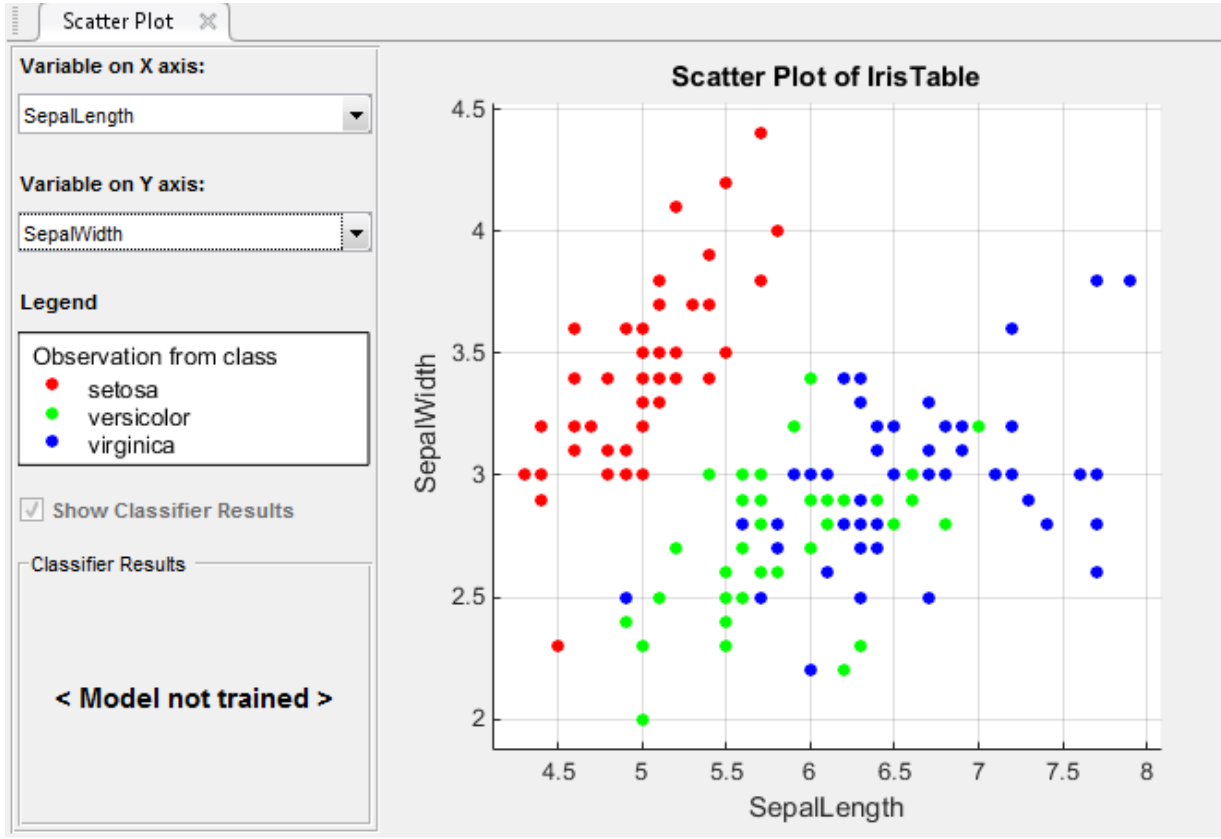


7 To accept the default validation scheme and continue, click **Import Data**. The default validation option is cross validation, to protect against overfitting.

Classification Learner app creates a scatter plot of the data.



8 Use the scatter plot to investigate which variables are useful for predicting the response. Select different options on the **Variable on X axis** and **Variable on Y axis** menus to visualize the distribution of species and measurements. Observe which variables separate the species colors most clearly.



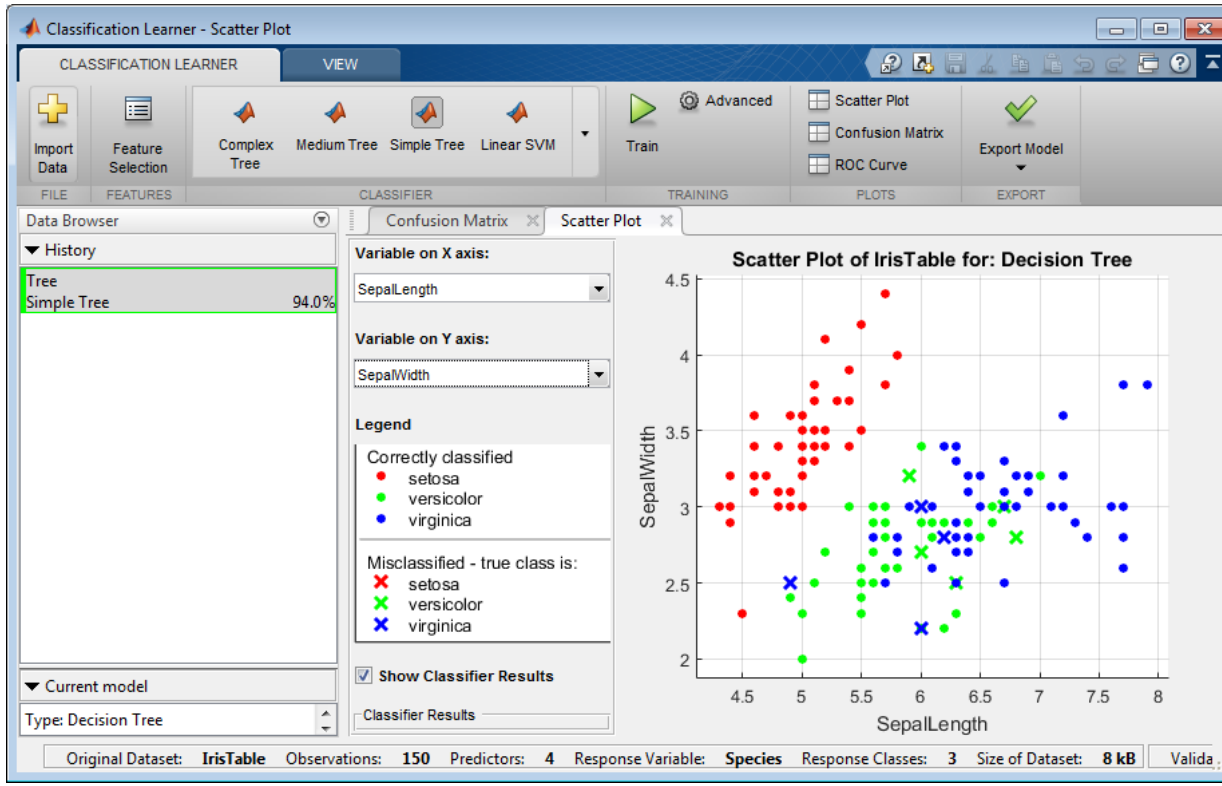
Observe that the `setosa` species (red points) is easy to separate from the other two species with all four predictors. The `versicolor` and `virginica` species are much closer together in all predictor measurements, and overlap especially when you plot sepal length and width. `setosa` is easier to predict than the other two species.

9 To create a classification tree model, on the **Classification Learner** tab, in the **Classifier** section, click **Simple Tree**, and then click **Train**.

The app creates a simple classification tree, and plots the results.

Observe the **Simple Tree** model in the History list. Check the model validation score. The model has performed well.

Note: With cross validation, there is some randomness in the results, so your model validation score results can vary from those shown.



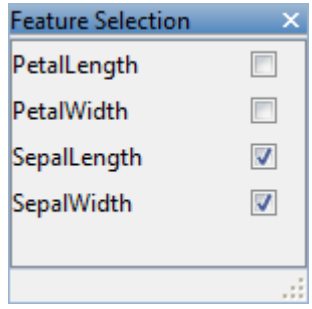
10 Examine the scatter plot. An X indicates misclassified points. The red points (`setosa` species) are all correctly classified, but some of the other two species are misclassified. Under **Classifier Results**, change the color of misclassified points from `True class` to `Predicted class`. Observe the color of the X points.

11 Train a different model to compare. Click **Medium Tree**, and then click **Train**.

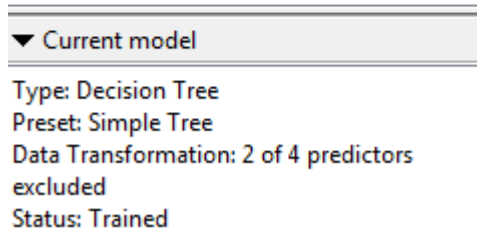
When you click **Train**,the app displays a new model in the History list.

12. Observe the **Medium Tree** model in the History list. The model validation score is no better than the simple tree score. The app outlines the best model in a green box. Click each model in the History list to view and compare the results.
13. Examine the scatter plot for the **Medium Tree** model. The medium tree classifies as many points correctly as the previous simple tree. You want to avoid overfitting, and the simple tree performs well, so base all further models on the simple tree.
14. Select **Simple Tree** in the History list. To try to improve the model, try including different features in the model. See if you can improve the model by removing features with low predictive power.

    On the **Classification Learner** tab, in the **Features** section, click **Feature Selection**. In the Feature Selection dialog box, clear the check boxes for **PetalLength** and **PetalWidth** to exclude them from the predictors. Click **Train** to train a new medium tree model using the new predictor options.



15. Observe the third model in the History list. It is also a **Simple Tree** model, trained using only 2 of 4 predictors. The Current model pane displays how many predictors are excluded. To check which predictors are included, click a model in the History list and observe the check boxes in the Feature Selection dialog box.



The model with only sepal measurements has a much lower score than the petals-only model.

16 Train another model including only the petal measurements. Change the selections in the Feature Selection dialog box and click **Train**.

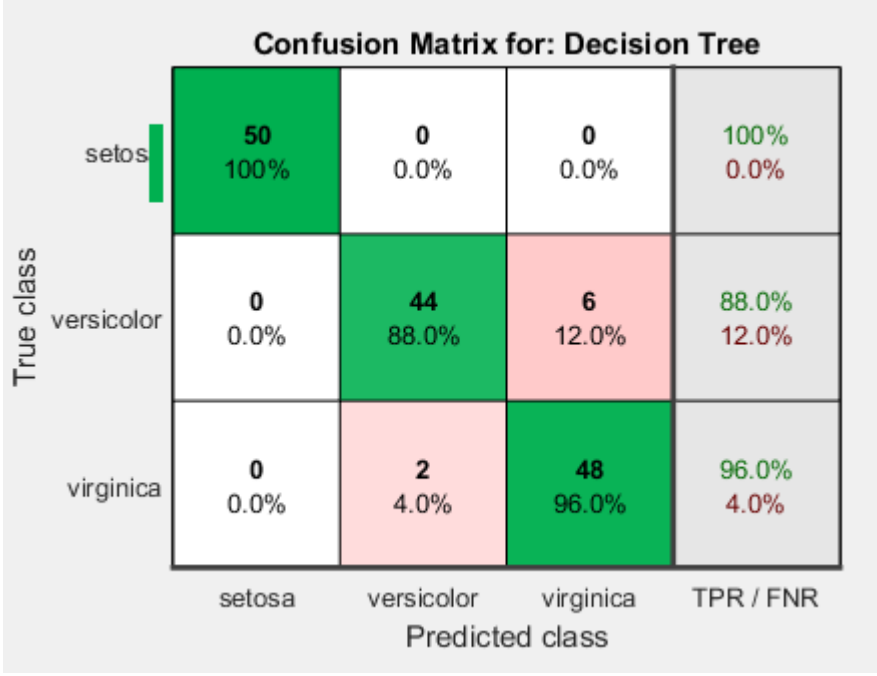
The model trained using only petal measurements performs comparably to the models containing all predictors. The models predict no better using all the measurements compared to only the petal measurements. If data collection is expensive or difficult, you might prefer a model that performs satisfactorily without some predictors.

17 Repeat to train two more models including only the width measurements and then the length measurements. There is not much difference in scores between all the models with 2 of 4 predictors.

18 Choose a best model among those of similar scores by examining the performance in each class. Select the simple tree that includes all the predictors. To inspect the accuracy of the predictions in each class, on the **Classification Learner** tab, in

the **Plots** section, click **Confusion Matrix**. Use this plot to understand how the currently selected classifier performed in each class. View the matrix of true class and predicted class results.

Look for areas where the classifier performed poorly by examining cells off the diagonal that display high percentages and are red. In these red cells, the true class and the predicted class do not match. The data points are misclassified.



Note: With cross validation, there is some randomness in the results, so your confusion matrix results can vary from those shown.

In this figure, examine the third cell in the middle row. In this cell, true class is `versicolor`, but the model misclassified the points as `virginica`. For this model, the cell shows 12% misclassified.

You can use this information to help you choose the best model for your goal. If false positives in this class are very important to your classification problem, then choose the best model at predicting this class. If false positives in this class are not very important, and models with fewer predictors do better in other classes, then choose a model to tradeoff some overall accuracy to exclude some predictors and make future data collection easier.

19 Compare the confusion matrix for each model in the History list. Check the Feature Selection dialog box to see which predictors are included in each model.

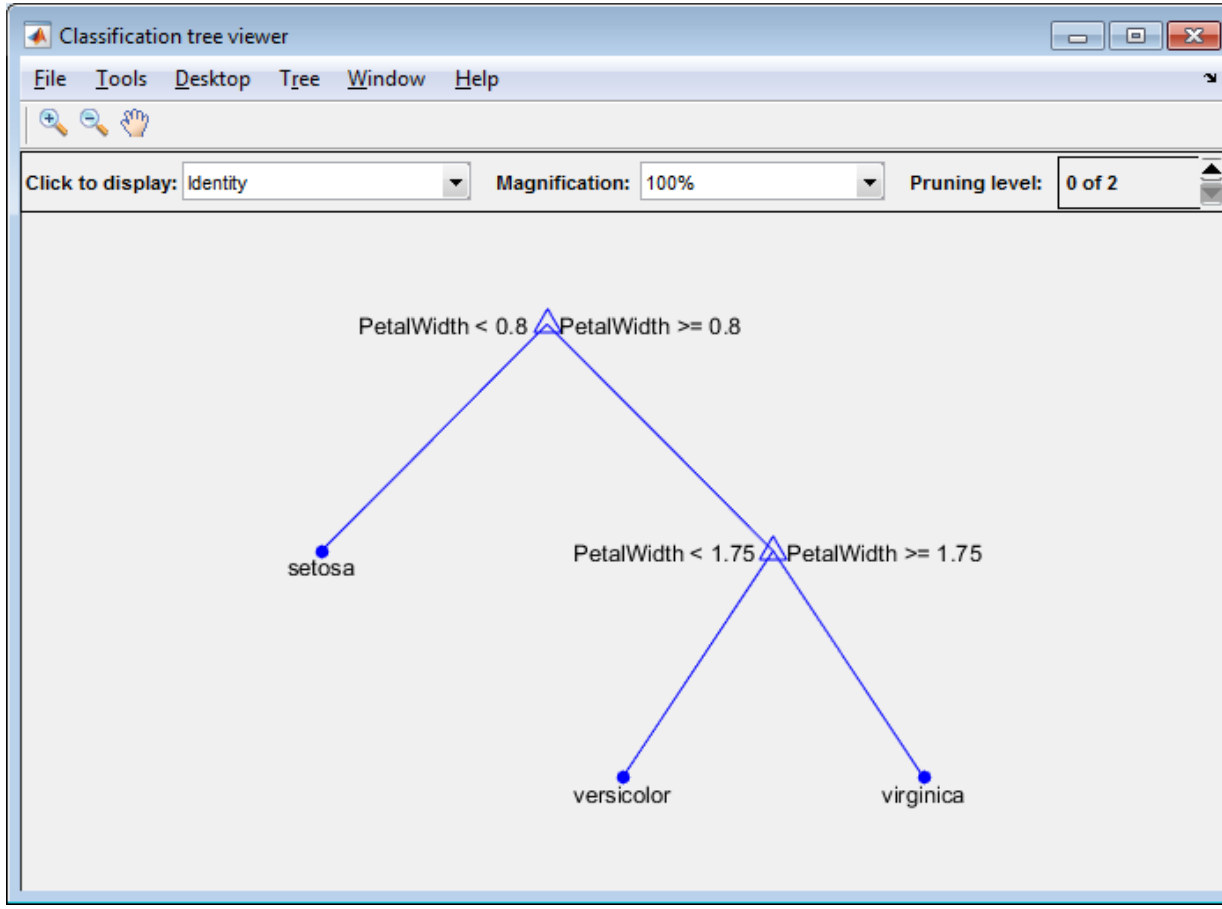
20 To learn about model settings, choose a model in the History list and view the advanced settings. The options in the **Classifier** gallery are preset starting points, and you can change further settings. On the **Classification Learner** tab, in the **Training** section, click **Advanced**. Compare the simple and medium tree models in the history, and observe the differences in the Advanced Tree Options dialog box. The **Maximum Number of Splits** setting controls tree depth.

To try to improve the simple tree model further, try changing the **Maximum Number of Splits** setting, then train a new model by clicking **Train**.

21 To export the best trained model to the workspace, on the **Classification Learner** tab, in the **Export** section, click **Export Model**. In the Export Model dialog box, click **OK** to accept the default variable name `trainedClassifier`. Look in the command window to see information about the results.

22 To visualize your decision tree model, enter:

```
view(trainedClassifier, 'Mode', 'graph')
```



23 You can use the exported classifier to make predictions on new data. For example, to make predictions for the `IrisTable` data in your workspace, enter:

```
yfit = predict(trainedClassifier,IrisTable{:,trainedClassifier.PredictorNames});
```

The output `yfit` contains a class prediction for each data point.

24 If you want to automate training the same classifier with new data, or learn how to programmatically train classifiers, you can generate code from the app. To generate code for the best trained model, on the **Classification Learner** tab, in the **Export** section, click **Export Model** > **Generate Code**.

The app generates code from your model and displays the file in the MATLAB Editor. To learn more, see “Generate MATLAB Code to Train the Model with New Data” on page 17-30.

Use the same workflow to evaluate and compare the other classifier types you can train in Classification Learner app: support vector machines, nearest neighbour classifiers, and ensemble classifiers. To learn about other classifier types, see “Explore Classification Models Interactively” on page 17-2.

Related Examples

- “Explore Classification Models Interactively” on page 17-2
- “Select Data and Validation for Classification Problem” on page 17-5
- “Choose a Classifier” on page 17-8
- “Select Features” on page 17-23
- “Assess Classifier Performance” on page 17-25
- “Export Classification Model to Predict New Data” on page 17-29

Explore Support Vector Machines Interactively

This example shows how to construct a support vector machine (SVM) classifier using the `ionosphere` data set that contains two classes. You can use a support vector machine (SVM) with two or more classes in the Classification Learner app. An SVM classifies data by finding the best hyperplane that separates all data points of one class from those of another class. In the `ionosphere` data, the response variable is categorical with two levels: `g` represents good radar returns, and `b` represents bad radar returns.

1. In MATLAB, load the `ionosphere` data set and define some variables from the data set to use for a classification.

   ```
   load ionosphere
   ionosphere = table(X,categorical(Y));
   ```

2. Open the Classification Learner app.

   ```
   classificationLearner
   ```

3. On the **Classification Learner** tab, in the **File** section, click **Import Data**.

   In the Setup dialog, observe the roles the app has selected for the variables based on their data type. The response variable `Var2` is categorical with two levels.

4. Click **Import Data**.

   Classification Learner app creates a scatter plot of the data.

5. Use the scatter plot to visualize which variables are useful for predicting the response. Select different variables in the X- and Y-axis controls. Observe which variables separate the class colors most clearly.

6. To create an SVM model, on the **Classification Learner** tab, in the **Classifier** section, click the down arrow to expand the list of classifiers, and click one of the SVM options (e.g., **Linear SVM**). Then click **Train**.

   Classification Learner app creates an SVM classification using the default settings.

7. Examine the scatter plot for the trained model. Misclassified points are shown as an X.

8. To inspect the accuracy of the classifier predictions, click the Confusion Matrix tab. View the matrix of true class and predicted class results.

9. To inspect the classifier performance, click the ROC curve tab. View the Receiver Operating Characteristic (ROC) curve showing true and false positive rates.

10 To create more models to compare, try the other SVM options in the **Classifier** gallery. Click one of the other SVM options and then click **Train**. Repeat to try all the SVM options. Every time you click **Train**, you create a new model in the History list.

   For information on the strengths of different model types, see “Support Vector Machines” on page 17-14.

11 Choose the best model in the History list (the best score is highlighted in a green box). To improve the model, try including different features in the model. See if you can improve the model by removing features with low predictive power.

   On the **Classification Learner** tab, in the **Data Transformation** section, click **Features**. In the Feature Selection dialog box, specify predictors to include in the model, and click **Train** to train a new model using the new options. Compare results among the classifiers in the History list.

12 Choose the best model in the History list. To try to improve the model further, try changing SVM settings. On the **Classification Learner** tab, in the **Training** section, click **Advanced**. Try changing a setting, then retrain the model by clicking **Train**. Every time you click **Train**, you create a new model. For information on settings, see “Support Vector Machines” on page 17-14.

13 To export the trained model to the workspace, select the Classification Learner App tab and click **Export model**. See “Export Classification Model to Predict New Data” on page 17-29.

Use the same workflow to evaluate and compare the other classifier types you can train in Classification Learner app. To learn about other classifier types, see “Explore Classification Models Interactively” on page 17-2.

Explore Nearest Neighbor Classification Interactively

This example shows how to construct a nearest neighbors classifier.

1. In MATLAB, load the `fisheriris` data set and define some variables from the data set to use for a classification.

   ```
   load fisheriris
   fisheririsCategorical = table(meas(:,1),meas(:,2),meas(:,3),...
    meas(:,4),categorical(species));
   fisheririsCategorical.Properties.VariableNames = {'SepalLength',...
    'SepalWidth','PetalLength','PetalWidth','Species'};
   ```

2. Open the Classification Learner app.

   ```
   classificationLearner
   ```

3. On the **Classification Learner** tab, in the **File** section, click **Import Data**.

   In the Set Up Classification dialog, observe the roles the app selected for the variables based on their data type. Petal and sepal length and width are predictors, and species is the response that you want to classify. For this example, do not change the role selections.

4. Click **Import Data**.

   The app creates a scatter plot of the data.

5. Use the scatter plot to investigate which variables are useful for predicting the response. To visualize the distribution of species and measurements, select different options on the **Variable on X axis** and **Variable on Y axis** menus. Observe which variables separate the species colors most clearly.

6. To create a nearest neighbors model, on the **Classification Learner** tab, on the far right of the **Classifier** section, click the arrow to expand the list of classifiers, and then click **k-Nearest Neighbor**.

7. In the **Training** section, click **Train**.

   The app creates a classification tree using the default settings.

8. Examine the scatter plot for the trained model. An X indicates a misclassified point.

9. To inspect the accuracy of the classifier predictions, in the **Plot** section, click **Confusion Matrix**. View the matrix of true class and predicted class results.

10. To inspect the classifier performance, in the **Plot** section, click **ROC Curve**. View the receiver operating characteristic (ROC) curve showing true- and false- positive rates.
11. To create more models to compare, try the other nearest neighbor options in the **Classifier** gallery. Click one of the other nearest neighbor options and then click **Train**. Repeat to try all the nearest neighbor options. Every time you click **Train**, you create a new model in the History list.
12. Choose the best model in the History list (the best score is highlighted in a green box). To improve the model, try including different features in the model. See if you can improve the model by removing features with low predictive power.

    On the **Classification Learner** tab, in the **Data Transformation** section, click **Features**. In the Feature Selection dialog box, select predictors to include in the model, and click **Train** to train a new model using the new options. Compare results among the classifiers in the History list.
13. Choose the best model in the History list. To try to improve the model further, try changing settings. On the **Classification Learner** tab, in the **Training** section, click **Advanced**. Try changing a setting, and then retrain the model by clicking **Train**. Every time you click **Train**, you create a new model. For information on settings, see "Nearest Neighbor Classifiers" on page 17-16.
14. To export the trained model to the workspace, in the **Export** section of the toolstrip, click **Export model**. See "Export Classification Model to Predict New Data" on page 17-29.

For information on the strengths of different nearest neighbour model types, see "Nearest Neighbor Classifiers" on page 17-16.

Use the same workflow to evaluate and compare the other classifier types you can train in Classification Learner app. To learn about other classifier types, see "Explore Classification Models Interactively" on page 17-2.

Explore Ensemble Classification Interactively

This example shows how to construct an ensemble of classifiers. Ensemble classifiers meld results from many weak learners into one high-quality ensemble predictor. Qualities depend on the choice of algorithm, but ensemble classifiers tend to be slow to fit because they often need many learners.

1. In MATLAB, load the `fisheriris` data set and define some variables from the data set to use for a classification.

   ```
   load fisheriris
   fisheririsCategorical = table(meas(:,1), meas(:,2), meas(:,3),...
    meas(:,4), categorical(species));
   fisheririsCategorical.Properties.VariableNames = {'SepalLength',...
    'SepalWidth', 'PetalLength', 'PetalWidth', 'Species'};
   ```

2. Open Classification Learner app.

   ```
   classificationLearner
   ```

3. On the **Classification Learner** tab, in the **File** section, click **Import Data**.

   In the Setup dialog, observe the roles the app has selected for the variables based on their data type. Petal and sepal length and width are predictors, and species is the response that you want to classify. For this example, do not change the role selections.

4. Click **Import Data**.

   Classification Learner app creates a scatter plot of the data.

5. Use the scatter plot to investigate which variables are useful for predicting the response. Select different variables in the X- and Y-axis controls to visualize the distribution of species and measurements. Observe which variables separate the species colors most clearly.

6. To create an ensemble model, on the **Classification Learner** tab, in the **Classifier** section, click the down arrow to expand the list of classifiers, then under **Ensemble Classifiers**, click **Boosted Trees**. Then click **Train**.

   Classification Learner app creates a classification tree using the default settings.

7. Examine the scatter plot for the trained model. Misclassified points are shown as an X.

8. To inspect the accuracy of the classifier predictions, click the Confusion Matrix tab. View the matrix of true class and predicted class results.

9. To inspect the classifier performance, click the ROC curve tab. View the Receiver Operating Characteristic (ROC) curve showing true and false positive rates.
10. To create more models to compare, try training models using the other classifier types under **Ensemble Classifiers**.
11. Choose the best model in the History list (the best score is highlighted in a green box). To improve the model, try including different features in the model. See if you can improve the model by removing features with low predictive power.

    On the **Classification Learner** tab, in the **Data Transformation** section, click **Features**. In the Feature Selection dialog box, specify predictors to include in the model, and click **Train** to train a new model using the new options. Compare results among the classifiers in the History list.
12. Choose the best model in the History list. To try to improve the model further, try changing settings. On the **Classification Learner** tab, in the Training section, click **Advanced**. Try changing a setting, then retrain the model by clicking **Train**. Every time you click **Train**, you create a new model.
13. To export the trained model to the workspace, select the Classification Learner App tab and click **Export model**. See "Export Classification Model to Predict New Data" on page 17-29.

For information on the strengths of different ensemble model types, see "Ensemble Classifiers" on page 17-20.

Use the same workflow to evaluate and compare the other classifier types you can train in Classification Learner app. To learn about other classifier types, see "Explore Classification Models Interactively" on page 17-2.

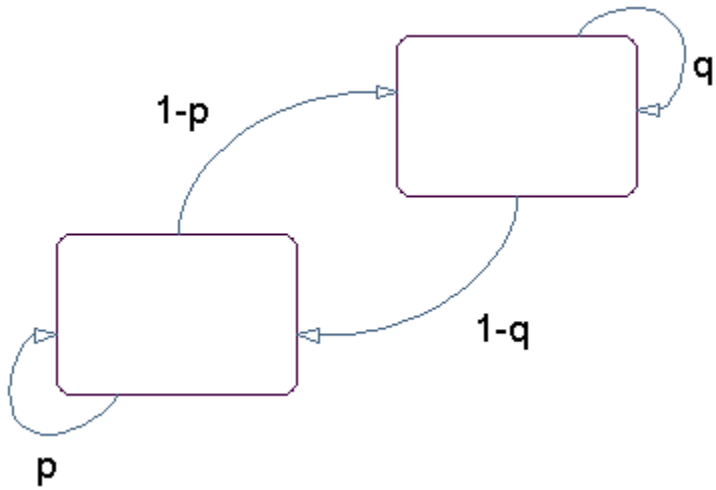
Markov Models

Introduction to Markov Models

Markov processes are examples of stochastic processes—processes that generate random sequences of outcomes or *states* according to certain probabilities. Markov processes are distinguished by being memoryless—their next state depends only on their current state, not on the history that led them there. Models of Markov processes are used in a wide variety of applications, from daily stock prices to the positions of genes in a chromosome.

Markov Chains

A Markov model is given visual representation with a *state diagram*, such as the one below.



State Diagram for a Markov Model

The rectangles in the diagram represent the possible states of the process you are trying to model, and the arrows represent transitions between states. The label on each arrow represents the probability of that transition. At each step of the process, the model may generate an output, or *emission*, depending on which state it is in, and then make a transition to another state. An important characteristic of Markov models is that the next state depends only on the current state, and not on the history of transitions that lead to the current state.

For example, for a sequence of coin tosses the two states are heads and tails. The most recent coin toss determines the current state of the model and each subsequent toss determines the transition to the next state. If the coin is fair, the transition probabilities are all 1/2. The emission might simply be the current state. In more complicated models, random processes at each state will generate emissions. You could, for example, roll a die to determine the emission at any step.

Markov chains are mathematical descriptions of Markov models with a discrete set of states. Markov chains are characterized by:

- A set of states {1, 2, ..., *M*}
- An *M*-by-*M transition matrix T* whose *i*,*j* entry is the probability of a transition from state *i* to state *j*. The sum of the entries in each row of *T* must be 1, because this is the sum of the probabilities of making a transition from a given state to each of the other states.
- A set of possible outputs, or *emissions*, $\{s_1, s_2, \ldots, s_N\}$. By default, the set of emissions is {1, 2, ... , *N*}, where *N* is the number of possible emissions, but you can choose a different set of numbers or symbols.
- An *M*-by-*N emission matrix E* whose *i*,*k* entry gives the probability of emitting symbol s_k given that the model is in state *i*.

Markov chains begin in an *initial state* i_0 at step 0. The chain then transitions to state i_1 with probability T_{1i_1}, and emits an output s_{k_1} with probability $E_{i_1 k_1}$. Consequently, the probability of observing the sequence of states $i_1 i_2 \ldots i_r$ and the sequence of emissions $s_{k_1} s_{k_2} \ldots s_{k_r}$ in the first *r* steps, is

$$T_{1i_1} E_{i_1 k_1} T_{i_1 i_2} E_{i_2 k_2} \ldots T_{i_{r-1} i_r} E_{i_r k}$$

Hidden Markov Models (HMM)

In this section...

Introduction to Hidden Markov Models (HMM)

A *hidden Markov model* (HMM) is one in which you observe a sequence of emissions, but do not know the sequence of states the model went through to generate the emissions. Analyses of hidden Markov models seek to recover the sequence of states from the observed data.

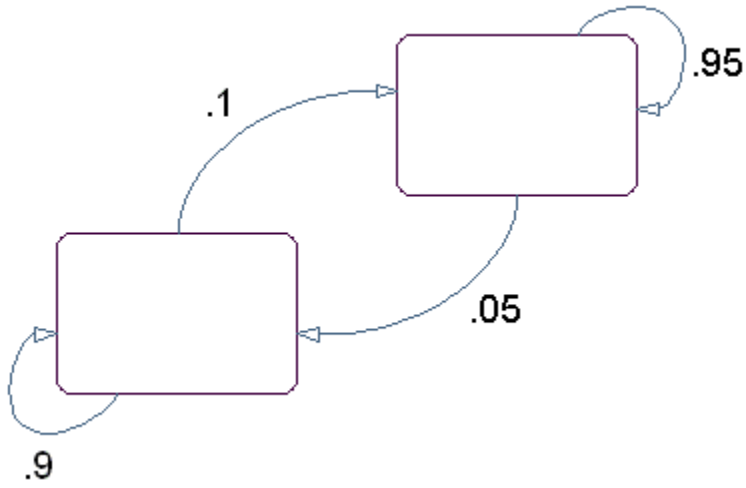
As an example, consider a Markov model with two states and six possible emissions. The model uses:

- A red die, having six sides, labeled 1 through 6.
- A green die, having twelve sides, five of which are labeled 2 through 6, while the remaining seven sides are labeled 1.
- A weighted red coin, for which the probability of heads is .9 and the probability of tails is .1.
- A weighted green coin, for which the probability of heads is .95 and the probability of tails is .05.

The model creates a sequence of numbers from the set {1, 2, 3, 4, 5, 6} with the following rules:

- Begin by rolling the red die and writing down the number that comes up, which is the emission.
- Toss the red coin and do one of the following:
  - If the result is heads, roll the red die and write down the result.
  - If the result is tails, roll the green die and write down the result.
- At each subsequent step, you flip the coin that has the same color as the die you rolled in the previous step. If the coin comes up heads, roll the same die as in the previous step. If the coin comes up tails, switch to the other die.

The state diagram for this model has two states, red and green, as shown in the following figure.



You determine the emission from a state by rolling the die with the same color as the state. You determine the transition to the next state by flipping the coin with the same color as the state.

The transition matrix is:

$$T = \begin{bmatrix} 0.9 & 0.1 \\ 0.05 & 0.95 \end{bmatrix}$$

The emissions matrix is:

$$E = \begin{bmatrix} \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} & \frac{1}{6} \\ \frac{7}{12} & \frac{1}{12} & \frac{1}{12} & \frac{1}{12} & \frac{1}{12} & \frac{1}{12} \end{bmatrix}$$

The model is not hidden because you know the sequence of states from the colors of the coins and dice. Suppose, however, that someone else is generating the emissions without showing you the dice or the coins. All you see is the sequence of emissions. If you start

seeing more 1s than other numbers, you might suspect that the model is in the green state, but you cannot be sure because you cannot see the color of the die being rolled.

Hidden Markov models raise the following questions:

- Given a sequence of emissions, what is the most likely state path?
- Given a sequence of emissions, how can you estimate transition and emission probabilities of the model?
- What is the *forward probability* that the model generates a given sequence?
- What is the *posterior probability* that the model is in a particular state at any point in the sequence?

Analyzing Hidden Markov Models

Statistics and Machine Learning Toolbox functions related to hidden Markov models are:

- `hmmgenerate` — Generates a sequence of states and emissions from a Markov model
- `hmmestimate` — Calculates maximum likelihood estimates of transition and emission probabilities from a sequence of emissions and a known sequence of states
- `hmmtrain` — Calculates maximum likelihood estimates of transition and emission probabilities from a sequence of emissions
- `hmmviterbi` — Calculates the most probable state path for a hidden Markov model
- `hmmdecode` — Calculates the posterior state probabilities of a sequence of emissions

This section shows how to use these functions to analyze hidden Markov models.

Generating a Test Sequence

The following commands create the transition and emission matrices for the model described in the "Introduction to Hidden Markov Models (HMM)" on page 18-5:

```
TRANS = [.9 .1; .05 .95;];
```

```
EMIS = [1/6, 1/6, 1/6, 1/6, 1/6, 1/6;...
7/12, 1/12, 1/12, 1/12, 1/12, 1/12];
```

To generate a random sequence of states and emissions from the model, use `hmmgenerate`:

```
[seq,states] = hmmgenerate(1000,TRANS,EMIS);
```

The output `seq` is the sequence of emissions and the output `states` is the sequence of states.

`hmmgenerate` begins in state 1 at step 0, makes the transition to state i_1 at step 1, and returns i_1 as the first entry in `states`. To change the initial state, see "Changing the Initial State Distribution" on page 18-11.

Estimating the State Sequence

Given the transition and emission matrices `TRANS` and `EMIS`, the function `hmmviterbi` uses the Viterbi algorithm to compute the most likely sequence of states the model would go through to generate a given sequence `seq` of emissions:

```
likelystates = hmmviterbi(seq, TRANS, EMIS);
```

`likelystates` is a sequence the same length as `seq`.

To test the accuracy of `hmmviterbi`, compute the percentage of the actual sequence `states` that agrees with the sequence `likelystates`.

```
sum(states==likelystates)/1000
ans =
   0.8200
```

In this case, the most likely sequence of states agrees with the random sequence 82% of the time.

Estimating Transition and Emission Matrices

- "Using hmmestimate" on page 18-9
- "Using hmmtrain" on page 18-9

The functions `hmmestimate` and `hmmtrain` estimate the transition and emission matrices `TRANS` and `EMIS` given a sequence `seq` of emissions.

Using hmmestimate

The function `hmmestimate` requires that you know the sequence of states `states` that the model went through to generate `seq`.

The following takes the emission and state sequences and returns estimates of the transition and emission matrices:

```
[TRANS_EST, EMIS_EST] = hmmestimate(seq, states)

TRANS_EST =
0.8989    0.1011
0.0585    0.9415

EMIS_EST =
0.1721    0.1721    0.1749    0.1612    0.1803    0.1393
0.5836    0.0741    0.0804    0.0789    0.0726    0.1104
```

You can compare the outputs with the original transition and emission matrices, `TRANS` and `EMIS`:

```
TRANS
TRANS =
0.9000    0.1000
0.0500    0.9500

EMIS
EMIS =
0.1667    0.1667    0.1667    0.1667    0.1667    0.1667
0.5833    0.0833    0.0833    0.0833    0.0833    0.0833
```

Using hmmtrain

If you do not know the sequence of states `states`, but you have initial guesses for `TRANS` and `EMIS`, you can still estimate `TRANS` and `EMIS` using `hmmtrain`.

Suppose you have the following initial guesses for `TRANS` and `EMIS`.

```
TRANS_GUESS = [.85 .15; .1 .9];
EMIS_GUESS = [.17 .16 .17 .16 .17 .17;.6 .08 .08 .08 .08 08];
```

You estimate `TRANS` and `EMIS` as follows:

```
[TRANS_EST2, EMIS_EST2] = hmmtrain(seq, TRANS_GUESS, EMIS_GUESS)

TRANS_EST2 =
```

```
0.2286    0.7714
0.0032    0.9968

EMIS_EST2 =
0.1436    0.2348    0.1837    0.1963    0.2350    0.0066
0.4355    0.1089    0.1144    0.1082    0.1109    0.1220
```

`hmmtrain` uses an iterative algorithm that alters the matrices `TRANS_GUESS` and `EMIS_GUESS` so that at each step the adjusted matrices are more likely to generate the observed sequence, `seq`. The algorithm halts when the matrices in two successive iterations are within a small tolerance of each other.

If the algorithm fails to reach this tolerance within a maximum number of iterations, whose default value is `100`, the algorithm halts. In this case, `hmmtrain` returns the last values of `TRANS_EST` and `EMIS_EST` and issues a warning that the tolerance was not reached.

If the algorithm fails to reach the desired tolerance, increase the default value of the maximum number of iterations with the command:

```
hmmtrain(seq,TRANS_GUESS,EMIS_GUESS,'maxiterations',maxiter)
```

where `maxiter` is the maximum number of steps the algorithm executes.

Change the default value of the tolerance with the command:

```
hmmtrain(seq, TRANS_GUESS, EMIS_GUESS, 'tolerance', tol)
```

where `tol` is the desired value of the tolerance. Increasing the value of `tol` makes the algorithm halt sooner, but the results are less accurate.

Two factors reduce the reliability of the output matrices of `hmmtrain`:

- The algorithm converges to a local maximum that does not represent the true transition and emission matrices. If you suspect this, use different initial guesses for the matrices `TRANS_EST` and `EMIS_EST`.
- The sequence `seq` may be too short to properly train the matrices. If you suspect this, use a longer sequence for `seq`.

Estimating Posterior State Probabilities

The posterior state probabilities of an emission sequence `seq` are the conditional probabilities that the model is in a particular state when it generates a symbol in `seq`, given that `seq` is emitted. You compute the posterior state probabilities with `hmmdecode`:

```
PSTATES = hmmdecode(seq,TRANS,EMIS)
```

The output PSTATES is an M-by-L matrix, where M is the number of states and L is the length of seq. PSTATES(i,j) is the conditional probability that the model is in state i when it generates the jth symbol of seq, given that seq is emitted.

hmmdecode begins with the model in state 1 at step 0, prior to the first emission. PSTATES(i,1) is the probability that the model is in state i at the following step 1. To change the initial state, see "Changing the Initial State Distribution" on page 18-11.

To return the logarithm of the probability of the sequence seq, use the second output argument of hmmdecode:

```
[PSTATES,logpseq] = hmmdecode(seq,TRANS,EMIS)
```

The probability of a sequence tends to 0 as the length of the sequence increases, and the probability of a sufficiently long sequence becomes less than the smallest positive number your computer can represent. hmmdecode returns the logarithm of the probability to avoid this problem.

Changing the Initial State Distribution

By default, Statistics and Machine Learning Toolbox hidden Markov model functions begin in state 1. In other words, the distribution of initial states has all of its probability mass concentrated at state 1. To assign a different distribution of probabilities, $p = [p_1, p_2, ..., p_M]$, to the M initial states, do the following:

1. Create an M+1-by-M+1 augmented transition matrix, $\hat{T}$ of the following form:

$$\hat{T} = \begin{bmatrix} 0 & p \\ 0 & T \end{bmatrix}$$

   where T is the true transition matrix. The first column of $\hat{T}$ contains M+1 zeros. p must sum to 1.

2. Create an M+1-by-N augmented emission matrix, $\hat{E}$, that has the following form:

$$\hat{E} = \begin{bmatrix} 0 \\ E \end{bmatrix}$$

If the transition and emission matrices are TRANS and EMIS, respectively, you create the augmented matrices with the following commands:

```
TRANS_HAT = [0 p; zeros(size(TRANS,1),1) TRANS];

EMIS_HAT = [zeros(1,size(EMIS,2)); EMIS];
```

Design of Experiments

Design of Experiments

Passive data collection leads to a number of problems in statistical modeling. Observed changes in a response variable may be correlated with, but not caused by, observed changes in individual *factors* (process variables). Simultaneous changes in multiple factors may produce interactions that are difficult to separate into individual effects. Observations may be dependent, while a model of the data considers them to be independent.

Designed experiments address these problems. In a designed experiment, the data-producing process is actively manipulated to improve the quality of information and to eliminate redundant data. A common goal of all experimental designs is to collect data as parsimoniously as possible while providing sufficient information to accurately estimate model parameters.

For example, a simple model of a response y in an experiment with two controlled factors x_1 and x_2 might look like this:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_1 x_2 + \varepsilon$$

Here ε includes both experimental error and the effects of any uncontrolled factors in the experiment. The terms $\beta_1 x_1$ and $\beta_2 x_2$ are *main effects* and the term $\beta_3 x_1 x_2$ is a two-way *interaction effect*. A designed experiment would systematically manipulate x_1 and x_2 while measuring y, with the objective of accurately estimating β_0, β_1, β_2, and β_3.

Full Factorial Designs

In this section...

Multilevel Designs

To systematically vary experimental factors, assign each factor a discrete set of *levels*. Full factorial designs measure response variables using every *treatment* (combination of the factor levels). A full factorial design for n factors with N_1, ..., N_n levels requires $N_1 \times ... \times N_n$ experimental runs—one for each treatment. While advantageous for separating individual effects, full factorial designs can make large demands on data collection.

As an example, suppose a machine shop has three machines and four operators. If the same operator always uses the same machine, it is impossible to determine if a machine or an operator is the cause of variation in production. By allowing every operator to use every machine, effects are separated. A full factorial list of treatments is generated by the Statistics and Machine Learning Toolbox function `fullfact`:

```
dFF = fullfact([3,4])
dFF =
     1     1
     2     1
     3     1
     1     2
     2     2
     3     2
     1     3
     2     3
     3     3
     1     4
     2     4
     3     4
```

Each of the 3×4 = 12 rows of `dFF` represent one machine/operator combination.

Two-Level Designs

Many experiments can be conducted with two-level factors, using *two-level designs*. For example, suppose the machine shop in the previous example always keeps the same

operator on the same machine, but wants to measure production effects that depend on the composition of the day and night shifts. The Statistics and Machine Learning Toolbox function `ff2n` generates a full factorial list of treatments:

```
dFF2 = ff2n(4)
dFF2 =
     0     0     0     0
     0     0     0     1
     0     0     1     0
     0     0     1     1
     0     1     0     0
     0     1     0     1
     0     1     1     0
     0     1     1     1
     1     0     0     0
     1     0     0     1
     1     0     1     0
     1     0     1     1
     1     1     0     0
     1     1     0     1
     1     1     1     0
     1     1     1     1
```

Each of the $2^4 = 16$ rows of `dFF2` represent one schedule of operators for the day (`0`) and night (`1`) shifts.

Fractional Factorial Designs

In this section...

Introduction to Fractional Factorial Designs

Two-level designs are sufficient for evaluating many production processes. Factor levels of ±1 can indicate categorical factors, normalized factor extremes, or simply "up" and "down" from current factor settings. Experimenters evaluating process *changes* are interested primarily in the factor directions that lead to process improvement.

For experiments with many factors, two-level full factorial designs can lead to large amounts of data. For example, a two-level full factorial design with 10 factors requires $2^{10} = 1024$ runs. Often, however, individual factors or their interactions have no distinguishable effects on a response. This is especially true of higher order interactions. As a result, a well-designed experiment can use fewer runs for estimating model parameters.

Fractional factorial designs use a fraction of the runs required by full factorial designs. A subset of experimental treatments is selected based on an evaluation (or assumption) of which factors and interactions have the most significant effects. Once this selection is made, the experimental design must separate these effects. In particular, significant effects should not be *confounded*, that is, the measurement of one should not depend on the measurement of another.

Plackett-Burman Designs

Plackett-Burman designs are used when only main effects are considered significant. Two-level Plackett-Burman designs require a number of experimental runs that are a multiple of 4 rather than a power of 2. The MATLAB function `hadamard` generates these designs:

```
dPB = hadamard(8)
dPB =
     1     1     1     1     1     1     1     1
```

```
     1    -1     1    -1     1    -1     1    -1
     1     1    -1    -1     1     1    -1    -1
     1    -1    -1     1     1    -1    -1     1
     1     1     1     1    -1    -1    -1    -1
     1    -1     1    -1    -1     1    -1     1
     1     1    -1    -1    -1    -1     1     1
     1    -1    -1     1    -1     1     1    -1
```

Binary factor levels are indicated by ±1. The design is for eight runs (the rows of `dPB`) manipulating seven two-level factors (the last seven columns of `dPB`). The number of runs is a fraction $8/2^7 = 0.0625$ of the runs required by a full factorial design. Economy is achieved at the expense of confounding main effects with any two-way interactions.

General Fractional Designs

At the cost of a larger fractional design, you can specify which interactions you wish to consider significant. A design of *resolution* R is one in which no n-factor interaction is confounded with any other effect containing less than $R - n$ factors. Thus, a resolution III design does not confound main effects with one another but may confound them with two-way interactions (as in "Plackett-Burman Designs" on page 19-5), while a resolution IV design does not confound either main effects or two-way interactions but may confound two-way interactions with each other.

Specify general fractional factorial designs using a full factorial design for a selected subset of *basic factors* and *generators* for the remaining factors. Generators are products of the basic factors, giving the levels for the remaining factors. Use the Statistics and Machine Learning Toolbox function `fracfact` to generate these designs:

```
dfF = fracfact('a b c d bcd acd')
dfF =
    -1    -1    -1    -1    -1    -1
    -1    -1    -1     1     1     1
    -1    -1     1    -1     1     1
    -1    -1     1     1    -1    -1
    -1     1    -1    -1     1    -1
    -1     1    -1     1    -1     1
    -1     1     1    -1    -1     1
    -1     1     1     1     1    -1
     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1
     1    -1     1    -1     1    -1
     1    -1     1     1    -1     1
```

```
     1     1    -1    -1     1     1
     1     1    -1     1    -1    -1
     1     1     1    -1    -1    -1
     1     1     1     1     1     1
```

This is a six-factor design in which four two-level basic factors (`a`, `b`, `c`, and `d` in the first four columns of `dfF`) are measured in every combination of levels, while the two remaining factors (in the last three columns of `dfF`) are measured only at levels defined by the generators `bcd` and `acd`, respectively. Levels in the generated columns are products of corresponding levels in the columns that make up the generator.

The challenge of creating a fractional factorial design is to choose basic factors and generators so that the design achieves a specified resolution in a specified number of runs. Use the Statistics and Machine Learning Toolbox function `fracfactgen` to find appropriate generators:

```
generators = fracfactgen('a b c d e f',4,4)
generators =
    'a'
    'b'
    'c'
    'd'
    'bcd'
    'acd'
```

These are generators for a six-factor design with factors `a` through `f`, using $2^4 = 16$ runs to achieve resolution IV. The `fracfactgen` function uses an efficient search algorithm to find generators that meet the requirements.

An optional output from `fracfact` displays the *confounding pattern* of the design:

```
[dfF,confounding] = fracfact(generators);
confounding
confounding =
    'Term'     'Generator'    'Confounding'
    'X1'       'a'            'X1'
    'X2'       'b'            'X2'
    'X3'       'c'            'X3'
    'X4'       'd'            'X4'
    'X5'       'bcd'          'X5'
    'X6'       'acd'          'X6'
    'X1*X2'    'ab'           'X1*X2 + X5*X6'
    'X1*X3'    'ac'           'X1*X3 + X4*X6'
    'X1*X4'    'ad'           'X1*X4 + X3*X6'
```

```
'X1*X5'    'abcd'          'X1*X5 + X2*X6'
'X1*X6'    'cd'            'X1*X6 + X2*X5 + X3*X4'
'X2*X3'    'bc'            'X2*X3 + X4*X5'
'X2*X4'    'bd'            'X2*X4 + X3*X5'
'X2*X5'    'cd'            'X1*X6 + X2*X5 + X3*X4'
'X2*X6'    'abcd'          'X1*X5 + X2*X6'
'X3*X4'    'cd'            'X1*X6 + X2*X5 + X3*X4'
'X3*X5'    'bd'            'X2*X4 + X3*X5'
'X3*X6'    'ad'            'X1*X4 + X3*X6'
'X4*X5'    'bc'            'X2*X3 + X4*X5'
'X4*X6'    'ac'            'X1*X3 + X4*X6'
'X5*X6'    'ab'            'X1*X2 + X5*X6'
```

The confounding pattern shows that main effects are effectively separated by the design, but two-way interactions are confounded with various other two-way interactions.

Response Surface Designs

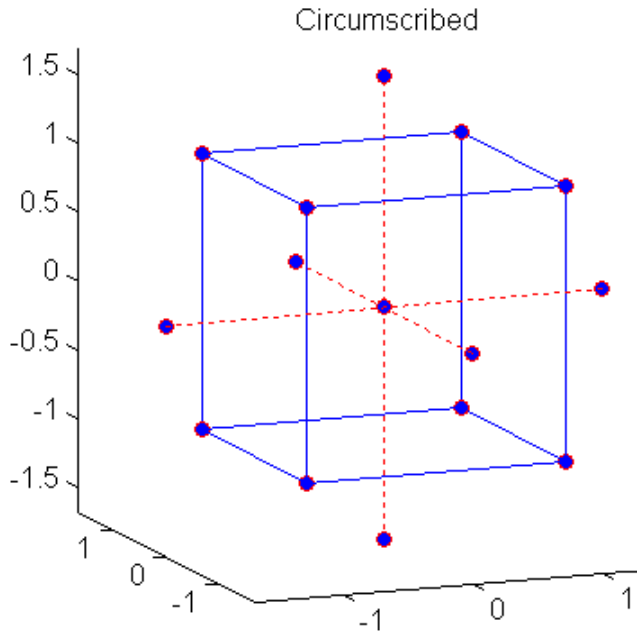
In this section...

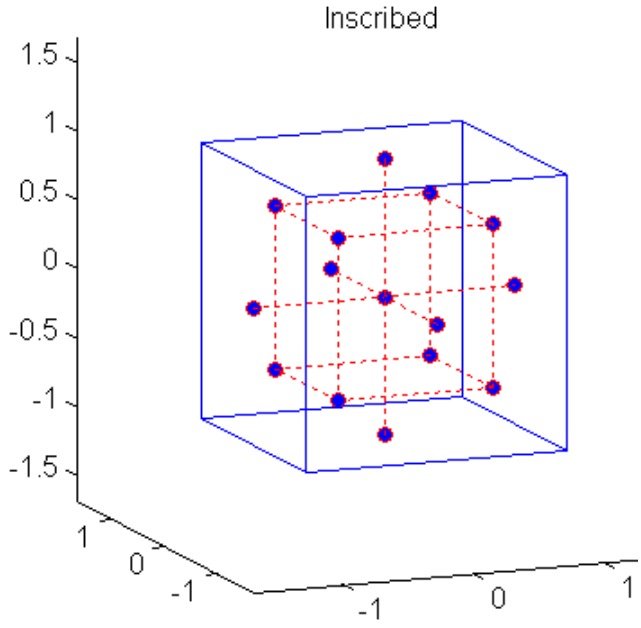
Introduction to Response Surface Designs

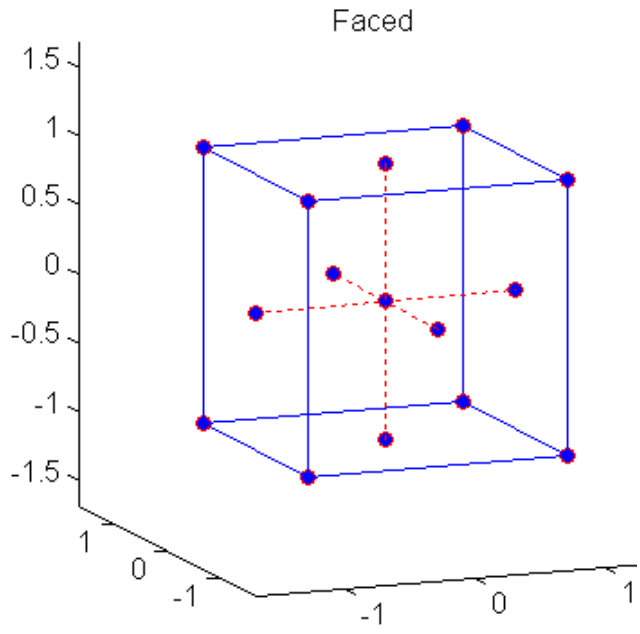
Quadratic response surfaces are simple models that provide a maximum or minimum without making additional assumptions about the form of the response. Quadratic models can be calibrated using full factorial designs with three or more levels for each factor, but these designs generally require more runs than necessary to accurately estimate model parameters. This section discusses designs for calibrating quadratic models that are much more efficient, using three or five levels for each factor, but not using all combinations of levels.

Central Composite Designs

Central composite designs (CCDs), also known as Box-Wilson designs, are appropriate for calibrating full quadratic models. There are three types of CCDs—circumscribed, inscribed, and faced—pictured below:


Circumscribed
1.5
1
0.5
0
-0.5
-1
-1.5
1
0
-1
-1
0
1


Inscribed
1.5
1
0.5
0
-0.5
-1
-1.5
1
0
-1
-1
0
1


Faced
1.5
1
0.5
0
-0.5
-1
-1.5
1
0
-1
-1
0
1

Each design consists of a factorial design (the corners of a cube) together with *center* and *star* points that allow for estimation of second-order effects. For a full quadratic model with n factors, CCDs have enough design points to estimate the $(n+2)(n+1)/2$ coefficients in a full quadratic model with n factors.

The type of CCD used (the position of the factorial and star points) is determined by the number of factors and by the desired properties of the design. The following table summarizes some important properties. A design is *rotatable* if the prediction variance depends only on the distance of the design point from the center of the design.

Design	Rotatable	Factor Levels	Uses Points Outside ±1	Accuracy of Estimates
Circumscribed (CCC)	Yes	5	Yes	Good over entire design space
Inscribed (CCI)	Yes	5	No	Good over central subset of design space
Faced (CCF)	No	3	No	Fair over entire design space; poor for pure quadratic coefficients

Generate CCDs with the Statistics and Machine Learning Toolbox function `ccdesign`:

```
dCC = ccdesign(3,'type','circumscribed')
dCC =
   -1.0000   -1.0000   -1.0000
   -1.0000   -1.0000    1.0000
   -1.0000    1.0000   -1.0000
   -1.0000    1.0000    1.0000
    1.0000   -1.0000   -1.0000
    1.0000   -1.0000    1.0000
    1.0000    1.0000   -1.0000
    1.0000    1.0000    1.0000
   -1.6818         0         0
    1.6818         0         0
         0   -1.6818         0
         0    1.6818         0
         0         0   -1.6818
         0         0    1.6818
         0         0         0
         0         0         0
         0         0         0
         0         0         0
```

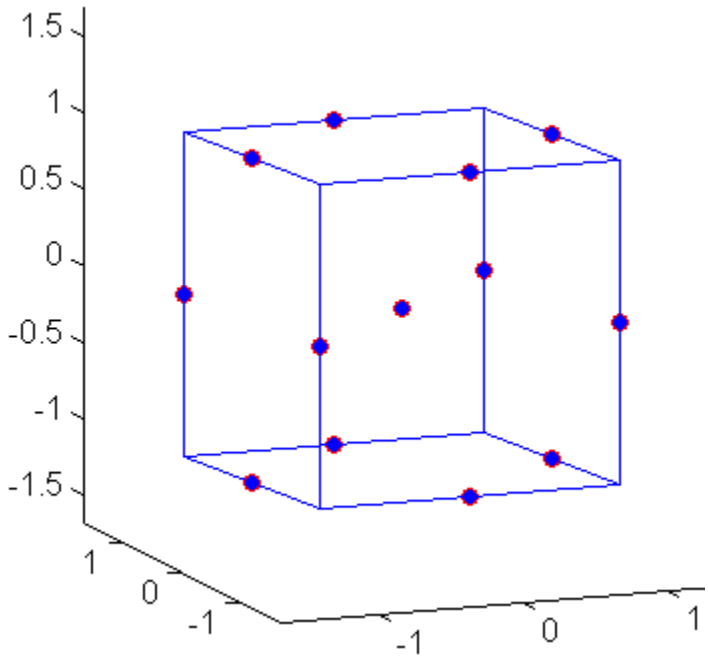
```
0     0     0
0     0     0
0     0     0
0     0     0
0     0     0
0     0     0
```

The repeated center point runs allow for a more uniform estimate of the prediction variance over the entire design space.

Box-Behnken Designs

Like the designs described in "Central Composite Designs" on page 19-9, Box-Behnken designs are used to calibrate full quadratic models. Box-Behnken designs are rotatable and, for a small number of factors (four or less), require fewer runs than CCDs. By avoiding the corners of the design space, they allow experimenters to work around extreme factor combinations. Like an inscribed CCD, however, extremes are then poorly estimated.

The geometry of a Box-Behnken design is pictured in the following figure.



Design points are at the midpoints of edges of the design space and at the center, and do not contain an embedded factorial design.

Generate Box-Behnken designs with the Statistics and Machine Learning Toolbox function `bbdesign`:

```
dBB = bbdesign(3)
dBB =
     -1     -1      0
     -1      1      0
      1     -1      0
      1      1      0
     -1      0     -1
     -1      0      1
      1      0     -1
      1      0      1
      0     -1     -1
      0     -1      1
      0      1     -1
      0      1      1
      0      0      0
      0      0      0
      0      0      0
```

Again, the repeated center point runs allow for a more uniform estimate of the prediction variance over the entire design space.

D-Optimal Designs

In this section...

Introduction to D-Optimal Designs

Traditional experimental designs ("Full Factorial Designs" on page 19-3, "Fractional Factorial Designs" on page 19-5, and "Response Surface Designs" on page 19-9) are appropriate for calibrating linear models in experimental settings where factors are relatively unconstrained in the region of interest. In some cases, however, models are necessarily nonlinear. In other cases, certain treatments (combinations of factor levels) may be expensive or infeasible to measure. *D-optimal designs* are model-specific designs that address these limitations of traditional designs.

A D-optimal design is generated by an iterative search algorithm and seeks to minimize the covariance of the parameter estimates for a specified model. This is equivalent to maximizing the determinant $D = |X^TX|$, where X is the design matrix of model terms (the columns) evaluated at specific treatments in the design space (the rows). Unlike traditional designs, D-optimal designs do not require orthogonal design matrices, and as a result, parameter estimates may be correlated. Parameter estimates may also be locally, but not globally, D-optimal.

There are several Statistics and Machine Learning Toolbox functions for generating D-optimal designs:

Function	Description
`candexch`	Uses a row-exchange algorithm to generate a D-optimal design with a specified number of runs for a specified model and a specified candidate set. This is the second component of the algorithm used by `rowexch`.
`candgen`	Generates a candidate set for a specified model. This is the first component of the algorithm used by `rowexch`.

Function	Description
`cordexch`	Uses a coordinate-exchange algorithm to generate a D-optimal design with a specified number of runs for a specified model.
`daugment`	Uses a coordinate-exchange algorithm to augment an existing D-optimal design with additional runs to estimate additional model terms.
`dcovary`	Uses a coordinate-exchange algorithm to generate a D-optimal design with fixed covariate factors.
`rowexch`	Uses a row-exchange algorithm to generate a D-optimal design with a specified number of runs for a specified model. The algorithm calls `candgen` and then `candexch`. (Call `candexch` separately to specify a candidate set.)

The following sections explain how to use these functions to generate D-optimal designs.

Note: The Statistics and Machine Learning Toolbox function `rsmdemo` generates simulated data for experimental settings specified by either the user or by a D-optimal design generated by `cordexch`. It uses the `rstool` interface to visualize response surface models fit to the data, and it uses the `nlintool` interface to visualize a nonlinear model fit to the data.

Generate D-Optimal Designs

Two Statistics and Machine Learning Toolbox algorithms generate D-optimal designs:

- The `cordexch` function uses a coordinate-exchange algorithm
- The `rowexch` function uses a row-exchange algorithm

Both `cordexch` and `rowexch` use iterative search algorithms. They operate by incrementally changing an initial design matrix X to increase $D = |X^TX|$ at each step. In both algorithms, there is randomness built into the selection of the initial design and into the choice of the incremental changes. As a result, both algorithms may return locally, but not globally, D-optimal designs. Run each algorithm multiple times and select the best result for your final design. Both functions have a `'tries'` parameter that automates this repetition and comparison.

At each step, the row-exchange algorithm exchanges an entire row of X with a row from a design matrix C evaluated at a *candidate set* of feasible treatments. The `rowexch`

function automatically generates a C appropriate for a specified model, operating in two steps by calling the `candgen` and `candexch` functions in sequence. Provide your own C by calling `candexch` directly. In either case, if C is large, its static presence in memory can affect computation.

The coordinate-exchange algorithm, by contrast, does not use a candidate set. (Or rather, the candidate set is the entire design space.) At each step, the coordinate-exchange algorithm exchanges a single element of X with a new element evaluated at a neighboring point in design space. The absence of a candidate set reduces demands on memory, but the smaller scale of the search means that the coordinate-exchange algorithm is more likely to become trapped in a local minimum than the row-exchange algorithm.

For example, suppose you want a design to estimate the parameters in the following three-factor, seven-term interaction model:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{12} x_1 x_2 + \beta_{13} x_1 x_3 + \beta_{23} x_2 x_3 + \varepsilon$$

Use `cordexch` to generate a D-optimal design with seven runs:

```
nfactors = 3;
nruns = 7;
[dCE,X] = cordexch(nfactors,nruns,'interaction','tries',10)
dCE =
    -1     1     1
    -1    -1    -1
     1     1     1
    -1     1    -1
     1    -1     1
     1    -1    -1
    -1    -1     1
X =
     1    -1     1     1    -1    -1     1
     1    -1    -1    -1     1     1     1
     1     1     1     1     1     1     1
     1    -1     1    -1    -1     1    -1
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1    -1
```

Columns of the design matrix `X` are the model terms evaluated at each row of the design `dCE`. The terms appear in order from left to right:

1. Constant term
2. Linear terms (1, 2, 3)
3. Interaction terms (12, 13, 23)

Use `X` in a linear regression model fit to response data measured at the design points in `dCE`.

Use `rowexch` in a similar fashion to generate an equivalent design:

```
[dRE,X] = rowexch(nfactors,nruns,'interaction','tries',10)
dRE =
    -1    -1     1
     1    -1     1
     1    -1    -1
     1     1     1
    -1    -1    -1
    -1     1    -1
    -1     1     1
X =
     1    -1    -1     1     1    -1    -1
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1     1     1     1     1     1     1
     1    -1    -1    -1     1     1     1
     1    -1     1    -1    -1     1    -1
     1    -1     1     1    -1    -1     1
```

Augment D-Optimal Designs

In practice, you may want to add runs to a completed experiment to learn more about a process and estimate additional model coefficients. The `daugment` function uses a coordinate-exchange algorithm to augment an existing D-optimal design.

For example, the following eight-run design is adequate for estimating main effects in a four-factor model:

```
dCEmain = cordexch(4,8)
dCEmain =
     1    -1    -1     1
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
     1     1     1     1
```

```
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
```

To estimate the six interaction terms in the model, augment the design with eight additional runs:

```
dCEinteraction = daugment(dCEmain,8,'interaction')
dCEinteraction =
     1    -1    -1     1
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
     1     1     1     1
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
    -1     1     1     1
    -1    -1    -1    -1
     1    -1     1    -1
     1     1    -1     1
    -1     1     1    -1
     1     1    -1    -1
     1    -1     1     1
     1     1     1    -1
```

The augmented design is full factorial, with the original eight runs in the first eight rows.

The `'start'` parameter of the `candexch` function provides the same functionality as `daugment`, but uses a row exchange algorithm rather than a coordinate-exchange algorithm.

Specify Fixed Covariate Factors

In many experimental settings, certain factors and their covariates are constrained to a fixed set of levels or combinations of levels. These cannot be varied when searching for an optimal design. The `dcovary` function allows you to specify fixed covariate factors in the coordinate exchange algorithm.

For example, suppose you want a design to estimate the parameters in a three-factor linear additive model, with eight runs that necessarily occur at different times. If the process experiences temporal linear drift, you may want to include the run time as a variable in the model. Produce the design as follows:

```
time = linspace(-1,1,8)';
[dCV,X] = dcovary(3,time,'linear')
dCV =
   -1.0000    1.0000    1.0000   -1.0000
    1.0000   -1.0000   -1.0000   -0.7143
   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000   -1.0000    1.0000   -0.1429
    1.0000    1.0000   -1.0000    0.1429
   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    0.7143
   -1.0000   -1.0000    1.0000    1.0000
X =
    1.0000   -1.0000    1.0000    1.0000   -1.0000
    1.0000    1.0000   -1.0000   -1.0000   -0.7143
    1.0000   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000    1.0000   -1.0000    1.0000   -0.1429
    1.0000    1.0000    1.0000   -1.0000    0.1429
    1.0000   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    1.0000    0.7143
    1.0000   -1.0000   -1.0000    1.0000    1.0000
```

The column vector `time` is a fixed factor, normalized to values between ±1. The number of rows in the fixed factor specifies the number of runs in the design. The resulting design `dCV` gives factor settings for the three controlled model factors at each time.

Specify Categorical Factors

Categorical factors take values in a discrete set of levels. Both `cordexch` and `rowexch` have a `'categorical'` parameter that allows you to specify the indices of categorical factors and a `'levels'` parameter that allows you to specify a number of levels for each factor.

For example, the following eight-run design is for a linear additive model with five factors in which the final factor is categorical with three levels:

```
dCEcat = cordexch(5,8,'linear','categorical',5,'levels',3)
dCEcat =
    -1    -1     1     1     2
    -1    -1    -1    -1     3
     1     1     1     1     3
     1     1    -1    -1     2
     1    -1    -1     1     3
    -1     1    -1     1     1
```

```
    -1     1     1    -1     3
     1    -1     1    -1     1
```

Specify Candidate Sets

The row-exchange algorithm exchanges rows of an initial design matrix X with rows from a design matrix C evaluated at a candidate set of feasible treatments. The `rowexch` function automatically generates a C appropriate for a specified model, operating in two steps by calling the `candgen` and `candexch` functions in sequence. Provide your own C by calling `candexch` directly.

For example, the following uses `rowexch` to generate a five-run design for a two-factor pure quadratic model using a candidate set that is produced internally:

```
dRE1 = rowexch(2,5,'purequadratic','tries',10)
dRE1 =
    -1     1
     0     0
     1    -1
     1     0
     1     1
```

The same thing can be done using `candgen` and `candexch` in sequence:

```
[dC,C] = candgen(2,'purequadratic') % Candidate set, C
dC =
    -1    -1
     0    -1
     1    -1
    -1     0
     0     0
     1     0
    -1     1
     0     1
     1     1
C =
     1    -1    -1     1     1
     1     0    -1     0     1
     1     1    -1     1     1
     1    -1     0     1     0
     1     0     0     0     0
     1     1     0     1     0
     1    -1     1     1     1
```

```
     1     0     1     0     1
     1     1     1     1     1
treatments = candexch(C,5,'tries',10) % D-opt subset
treatments =
     2
     1
     7
     3
     4
dRE2 = dC(treatments,:) % Display design
dRE2 =
     0    -1
    -1    -1
    -1     1
     1    -1
    -1     0
```

You can replace `C` in this example with a design matrix evaluated at your own candidate set. For example, suppose your experiment is constrained so that the two factors cannot have extreme settings simultaneously. The following produces a restricted candidate set:

```
constraint = sum(abs(dC),2) < 2; % Feasible treatments
my_dC = dC(constraint,:)
my_dC =
     0    -1
    -1     0
     0     0
     1     0
     0     1
```

Use the `x2fx` function to convert the candidate set to a design matrix:

```
my_C = x2fx(my_dC,'purequadratic')
my_C =
     1     0    -1     0     1
     1    -1     0     1     0
     1     0     0     0     0
     1     1     0     1     0
     1     0     1     0     1
```

Find the required design in the same manner:

```
my_treatments = candexch(my_C,5,'tries',10) % D-opt subset
my_treatments =
     2
```

```
     4
     5
     1
     3
my_dRE = my_dC(my_treatments,:) % Display design
my_dRE =
    -1     0
     1     0
     0     1
     0    -1
     0     0
```

Improve an Engine Cooling Fan Using Design for Six Sigma Techniques

This example shows how to improve the performance of an engine cooling fan through a Design for Six Sigma approach using Define, Measure, Analyze, Improve, and Control (DMAIC). The initial fan does not circulate enough air through the radiator to keep the engine cool during difficult conditions. First the example shows how to design an experiment to investigate the effect of three performance factors: fan distance from the radiator, blade-tip clearance, and blade pitch angle. It then shows how to estimate optimum values for each factor, resulting in a design that produces airflows beyond the goal of 875 ft^3 per minute using test data. Finally it shows how to use simulations to verify that the new design produces airflow according to the specifications in more than 99.999% of the fans manufactured. This example uses MATLAB, Statistics and Machine Learning Toolbox, and Optimization Toolbox.

Define the Problem

This example addresses an engine cooling fan design that is unable to pull enough air through the radiator to keep the engine cool during difficult conditions, such as stop-and-go traffic or hot weather). Suppose you estimate that you need airflow of at least 875 ft^3/min to keep the engine cool during difficult conditions. You need to evaluate the current design and develop an alternative design that can achieve the target airflow.

Assess Cooling Fan Performance

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

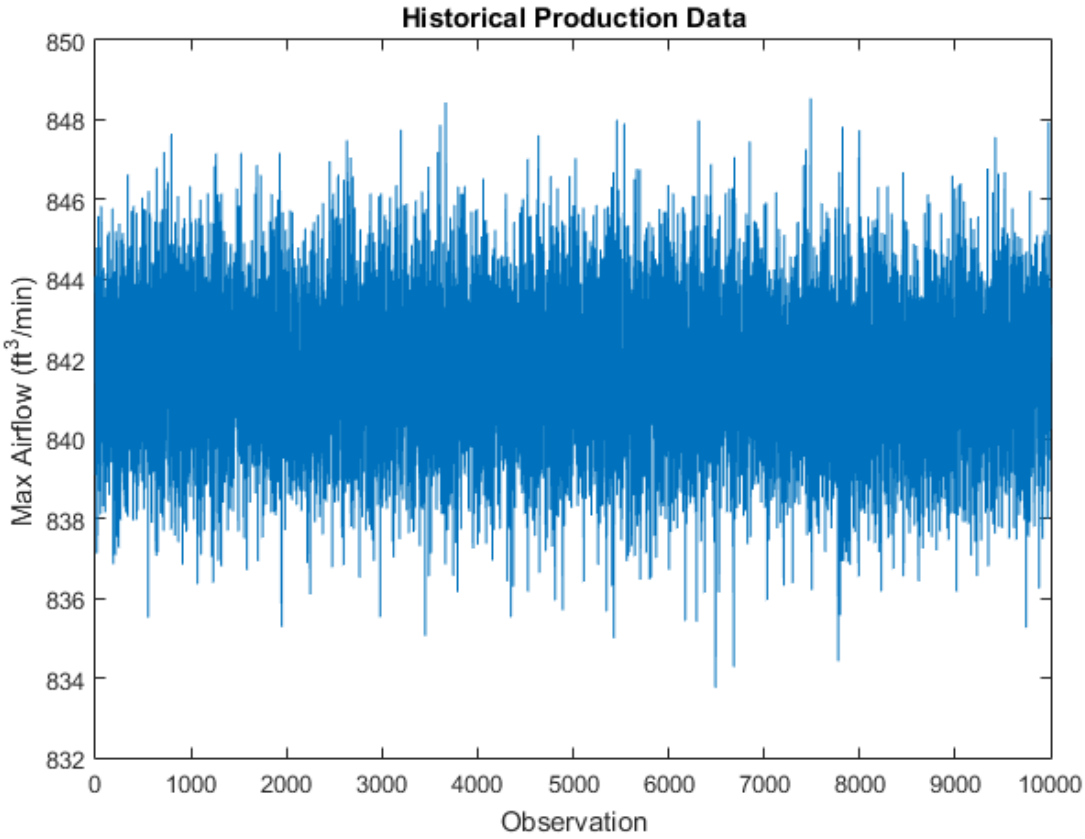
```
load OriginalFan
```

The data consists of 10,000 measurements (historical production data) of the existing cooling fan performance.

Plot the data to analyze the current fan's performance.

```
plot(originalfan)
xlabel('Observation')
```

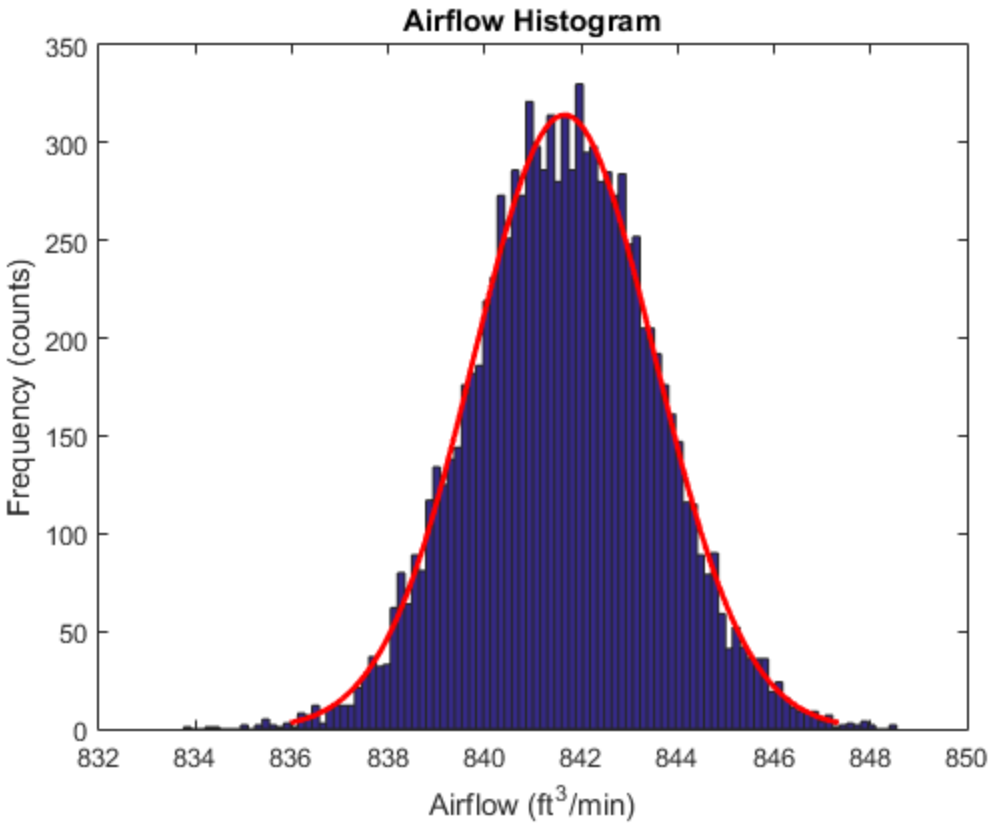
```
ylabel('Max Airflow (ft^3/min)')
title('Historical Production Data')
```



The data is centered around 842 ft^3/min and most values fall within the range of about 8 ft^3/min. The plot does not tell much about the underlying distribution of data, however. Plot the histogram and fit a normal distribution to the data.

```
figure()
histfit(originalfan) % Plot histogram with normal distribution fit
format shortg
xlabel('Airflow (ft^3/min)')
ylabel('Frequency (counts)')
```

```
title('Airflow Histogram')
```




```
pd = fitdist(originalfan,'normal') % Fit normal distribution to data
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 841.652   [841.616, 841.689]
    sigma =  1.8768   [1.85114, 1.90318]
```

`fitdist` fits a normal distribution to data and estimates the parameters from data. The estimate for the mean airflow speed is 841.652 ft^3/min, and the 95% confidence interval

for the mean airflow speed is (841.616, 841.689). This estimate makes it clear that the current fan is not close to the required 875 ft^3/min. There is need to improve the fan design to achieve the target airflow.

Determine Factors That Affect Fan Performance

Evaluate the factors that affect cooling fan performance using design of experiments (DOE). The response is the cooling fan airflow rate (ft^3/min). Suppose that the factors that you can modify and control are:

- Distance from radiator
- Pitch angle
- Blade tip clearance

In general, fluid systems have nonlinear behavior. Therefore, use a response surface design to estimate any nonlinear interactions among the factors. Generate the experimental runs for a Box-Behnken design in coded (normalized) variables [-1, 0, +1].

```
CodedValue = bbdesign(3)
```

```
CodedValue =

    -1    -1     0
    -1     1     0
     1    -1     0
     1     1     0
    -1     0    -1
    -1     0     1
     1     0    -1
     1     0     1
     0    -1    -1
     0    -1     1
     0     1    -1
     0     1     1
     0     0     0
     0     0     0
     0     0     0
```

The first column is for the distance from radiator, the second column is for the pitch angle, and the third column is for the blade tip clearance. Suppose you want to test the effects of the variables at the following minimum and maximum values.

Distance from radiator: 1 to 1.5 inches

Pitch angle: 15 to 35 degrees
Blade tip clearance: 1 to 2 inches

Randomize the order of the runs, convert the coded design values to real-world units, and perform the experiment in the order specified.

```
runorder = randperm(15);     % Random permutation of the runs
bounds = [1 1.5;15 35;1 2];  % Min and max values for each factor

RealValue = zeros(size(CodedValue));
for i = 1:size(CodedValue,2) % Convert coded values to real-world units
    zmax = max(CodedValue(:,i));
    zmin = min(CodedValue(:,i));
    RealValue(:,i) = interp1([zmin zmax],bounds(i,:),CodedValue(:,i));
end
```

Suppose the at the end of the experiments, you collect the following response values in the variable `TestResult`.

```
TestResult = [837 864 829 856 880 879 872 874 834 833 860 859 874 876 875]';
```

Display the design values and the response.

```
disp({'Run Number','Distance','Pitch','Clearance','Airflow'})
disp(sortrows([runorder' RealValue TestResult]))
```

```
'Run Number'    'Distance'    'Pitch'    'Clearance'    'Airflow'

           1          1.5         35          1.5          856
           2         1.25         25          1.5          876
           3          1.5         25            1          872
           4         1.25         25          1.5          875
           5            1         35          1.5          864
           6         1.25         25          1.5          874
           7         1.25         15            2          833
           8          1.5         15          1.5          829
           9         1.25         15            1          834
          10            1         15          1.5          837
          11          1.5         25            2          874
          12            1         25            1          880
          13         1.25         35            1          860
          14            1         25            2          879
          15         1.25         35            2          859
```

Save the design values and the response in a `table`.

```
Exp = table(runorder', CodedValue(:,1), CodedValue(:,2), CodedValue(:,3), ...
    TestResult,'VariableNames',{'RunNumber','D','P','C','Airflow'});
```

`D` stands for `Distance`, `P` stands for `Pitch`, and C stands for `Clearance`. Based on the experimental test results, the airflow rate is sensitive to the changing factors values. Also, four experimental runs meet or exceed the target airflow rate of 875 ft^3/min (runs 2, 4,12, and 14). However, it is not clear which, if any, of these runs is the optimal one. In addition, it is not obvious how robust the design is to variation in the factors. Create a model based on the current experimental data and use the model to estimate the optimal factor settings.

Improve the Cooling Fan Performance

The Box-Behnken design enables you to test for nonlinear (quadratic) effects. The form of the quadratic model is:

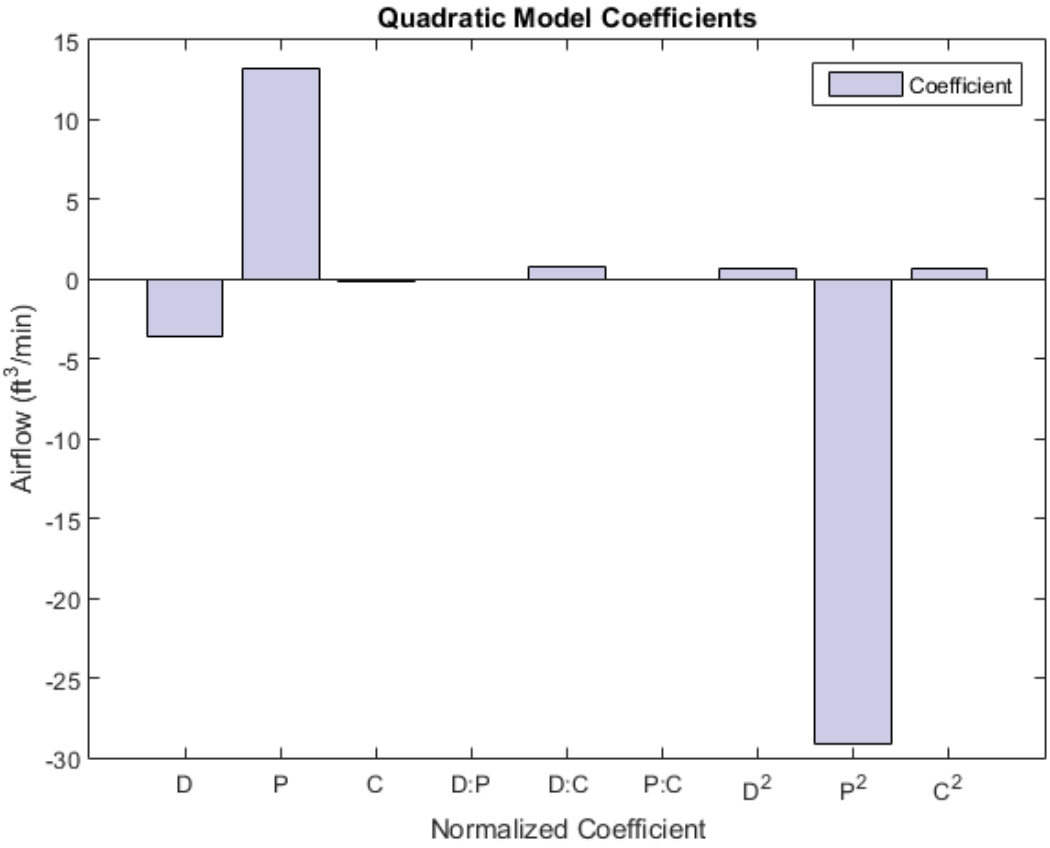
$$\begin{aligned} AF &= \beta_0 + \beta_1 * Distance + \beta_2 * Pitch + \beta_3 * Clearance + \beta_4 * Distance * Pitch \\ &+ \beta_5 * Distance * Clearance + \beta_6 * Pitch * Clearance + \beta_7 * Distance^2 \\ &+ \beta_8 * Pitch^2 + \beta_9 * Clearance^2, \end{aligned}$$

where AF is the airflow rate and B_i is the coefficient for the term i. Estimate the coefficients of this model using the `fitlm` function from Statistics and Machine Learning Toolbox.

```
mdl = fitlm(Exp,'Airflow~D*P*C-D:P:C+D^2+P^2+C^2');
```

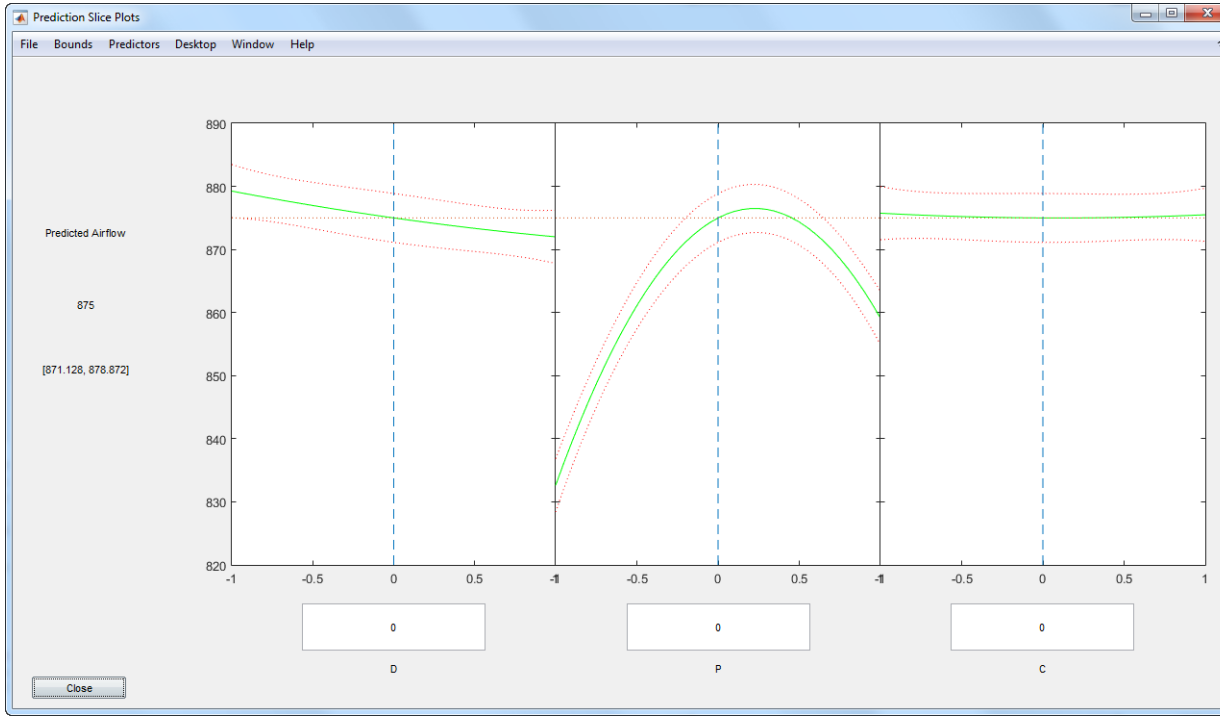
Display the magnitudes of the coefficients (for normalized values) in a bar chart.

```
figure()
h = bar(mdl.Coefficients.Estimate(2:10));
set(h,'facecolor',[.8 .8 .9]);
legend('Coefficient');
set(gcf,'units','normalized','position',[.05 .4 .35 .4]);
set(gca,'xticklabel',mdl.CoefficientNames(2:10));
ylabel('Airflow (ft^3/min)')
xlabel('Normalized Coefficient')
title('Quadratic Model Coefficients')
```



The bar chart shows that *Pitch* and $Pitch^2$ are dominant factors. You can look at the relationship between multiple input variables and one output variable by generating a response surface plot. Use`plotSlice` to generate response surface plots for the model `mdl` interactively.

```
plotSlice(mdl)
```



The plot shows the nonlinear relationship of airflow with pitch. Move the blue dashed lines around and see the effect the different factors have on airflow. Although you can use `plotSlice` to determine the optimum factor settings, you can also use Optimization Toolbox to automate the task.

Find the optimal factor settings using the constrained optimization function `fmincon`.

Write the objective function.

```
f = @(x) -x2fx(x,'quadratic')*mdl.Coefficients.Estimate;
```

The objective function is a quadratic response surface fit to the data. Minimizing the negative airflow using `fmincon` is the same as maximizing the original objective function. The constraints are the upper and lower limits tested (in coded values). Set the initial starting point to be the center of the design of the experimental test matrix.

```
lb = [-1 -1 -1]; ub = [1 1 1];                % Lower/upper bounds
x0 = [0 0 0];                                 % Starting point
```

```
options = optimset('LargeScale','off');                    % Medium scale problem
[optfactors,fval] = fmincon(f,x0,[],[],[],[],lb,ub,[],options); % Invoke the solver

Local minimum found that satisfies the constraints.

Optimization completed because the objective function is non-decreasing in
feasible directions, to within the default value of the function tolerance,
and constraints are satisfied to within the default value of the constraint tolerance.
```

Convert the results to a maximization problem and real-world units.

```
maxval = -fval;
maxloc = (optfactors + 1)';
bounds = [1 1.5;15 35;1 2];
maxloc=bounds(:,1)+maxloc .* ((bounds(:,2) - bounds(:,1))/2);
disp('Optimal Values:')
disp({'Distance','Pitch','Clearance','Airflow'})
disp([maxloc' maxval])

Optimal Values:
    'Distance'    'Pitch'    'Clearance'    'Airflow'

            1       27.275             1       882.26
```

The optimization result suggests placing the new fan one inch from the radiator, with a one-inch clearance between the tips of the fan blades and the shroud.

Because pitch angle has such a significant effect on airflow, perform additional analysis to verify that a 27.3 degree pitch angle is optimal.

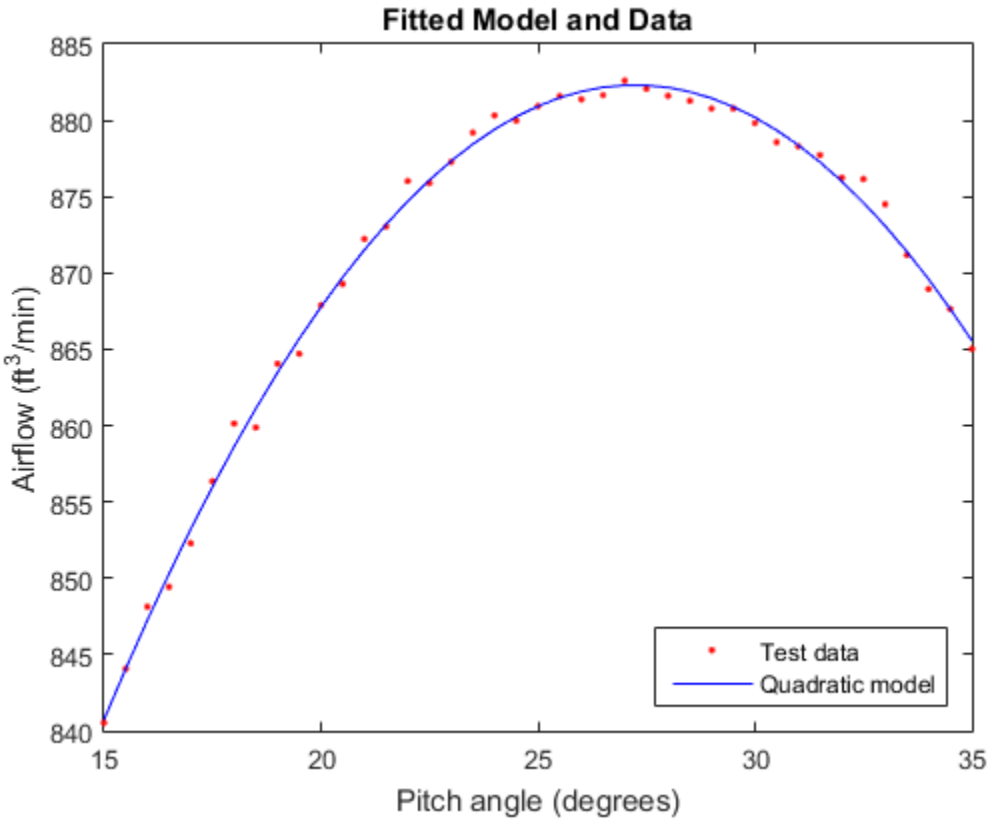
```
load AirflowData
tbl = table(pitch,airflow,'VariableNames',{'pitch','airflow'});
mdl2 = fitlm(tbl,'airflow~pitch^2');
mdl2.Rsquared.Ordinary

ans =

      0.99632
```

The results show that a quadratic model explains the effect of pitch on the airflow well.

Plot the pitch angle against airflow and impose the fitted model.

```
figure()
plot(pitch,airflow,'.r'); hold on
ylim([840 885]);
```

```
line(pitch,mdl2.Fitted,'color','b');
title('Fitted Model and Data')
xlabel('Pitch angle (degrees)');
ylabel('Airflow (ft^3/min)')
legend('Test data','Quadratic model','Location','se')
hold off
```



Find the pitch value that corresponds to the maximum airflow.

```
pitch(find(airflow==max(airflow)))
```

```
ans =

    27
```

The additional analysis confirms that a 27.3 degree pitch angle is optimal.

The improved cooling fan design meets the airflow requirements. You also have a model that approximates the fan performance well based on the factors you can modify in the design. Ensure that the fan performance is robust to variability in manufacturing and installation by performing a sensitivity analysis.

Sensitivity Analysis

Suppose that, based on historical experience, the manufacturing uncertainty is as follows.

Factor	Real Values	Coded Values
Distance from radiator	1.00 +/- 0.05 inch	1.00 +/- 0.20 inch
Blade pitch angle	27.3 +/- 0.25 degrees	0.227 +/- 0.028 degrees
Blade tip clearance	1.00 +/- 0.125 inch	-1.00 +/- 0.25 inch

Verify that these variations in factors will enable to maintain a robust design around the target airflow. The philosophy of Six Sigma targets a defect rate of no more than 3.4 per 1,000,000 fans. That is, the fans must hit the 875 ft^3/min target 99.999% of the time.

You can verify the design using Monte Carlo simulation. Generate 10,000 random numbers for three factors with the specified tolerance. First, set the state of the random number generators so results are consistent across different runs.

```
rng('default')
```

Perform he Monte Carlo simulation. Include a noise variable that is proportional to the noise in the fitted model, `mdl` (that is, the RMS error of the model). Because the model coefficients are in coded variables, you must generate `dist`, `pitch`, and `clearance` using the coded definition.

```
dist = random('normal',optfactors(1),0.20,[10000 1]);
pitch = random('normal',optfactors(2),0.028,[10000 1]);
clearance = random('normal',optfactors(3),0.25,[10000 1]);
noise = random('normal',0,mdl2.RMSE,[10000 1]);
```

Calculate airflow for 10,000 random factor combinations using the model.

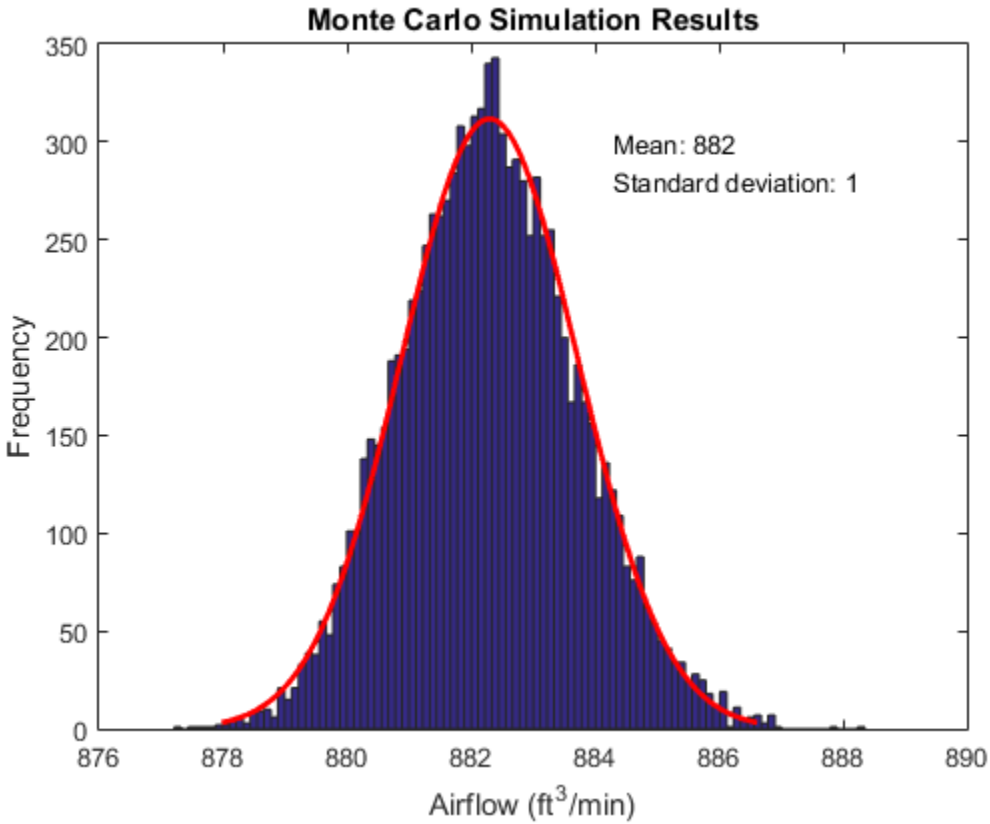
```
simfactor = [dist pitch clearance];
X = x2fx(simfactor,'quadratic');
```

Add noise to the model (the variation in the data that the model did not account for).

```
simflow = X*mdl.Coefficients.Estimate+noise;
```

Evaluate the variation in the model's predicted airflow using a histogram. To estimate the mean and standard deviation, fit a normal distribution to data.

```
pd = fitdist(simflow,'normal');
histfit(simflow); hold on
text(pd.mu+2,300,['Mean: ' num2str(round(pd.mu))])
text(pd.mu+2,280,['Standard deviation: ' num2str(round(pd.sigma))])
hold off
xlabel('Airflow (ft^3/min)')
ylabel('Frequency')
title('Monte Carlo Simulation Results')
```



The results look promising. The average airflow is 882 ft^3/min and appears to be better than 875 ft^3/min for most of the data.

Determine the probability that the airflow is at 875 ft^3/min or below.

```
format long
pfail = cdf(pd,875)
pass = (1-pfail)*100
```

```
pfail =

     1.509289008603141e-07


pass =

  99.999984907109919
```

The design appears to achieve at least 875 ft^3/min of airflow 99.999% of the time.

Use the simulation results to estimate the process capability.

```
S = capability(simflow,[875.0 890])
pass = (1-S.Pl)*100
```

```
S =

       mu: 8.822982645666709e+02
    sigma: 1.424806876923940
        P: 0.999999816749816
       Pl: 1.509289008603141e-07
       Pu: 3.232128339675335e-08
       Cp: 1.754623760237126
      Cpl: 1.707427788957002
      Cpu: 1.801819731517250
      Cpk: 1.707427788957002


pass =

  99.9999849071099
```

The `Cp` value is 1.75. A process is considered high quality when `Cp` is greater than or equal to 1.6. The `Cpk` is similar to the `Cp` value, which indicates that the process is

centered. Now implement this design. Monitor it to verify the design process and to ensure that the cooling fan delivers high-quality performance.

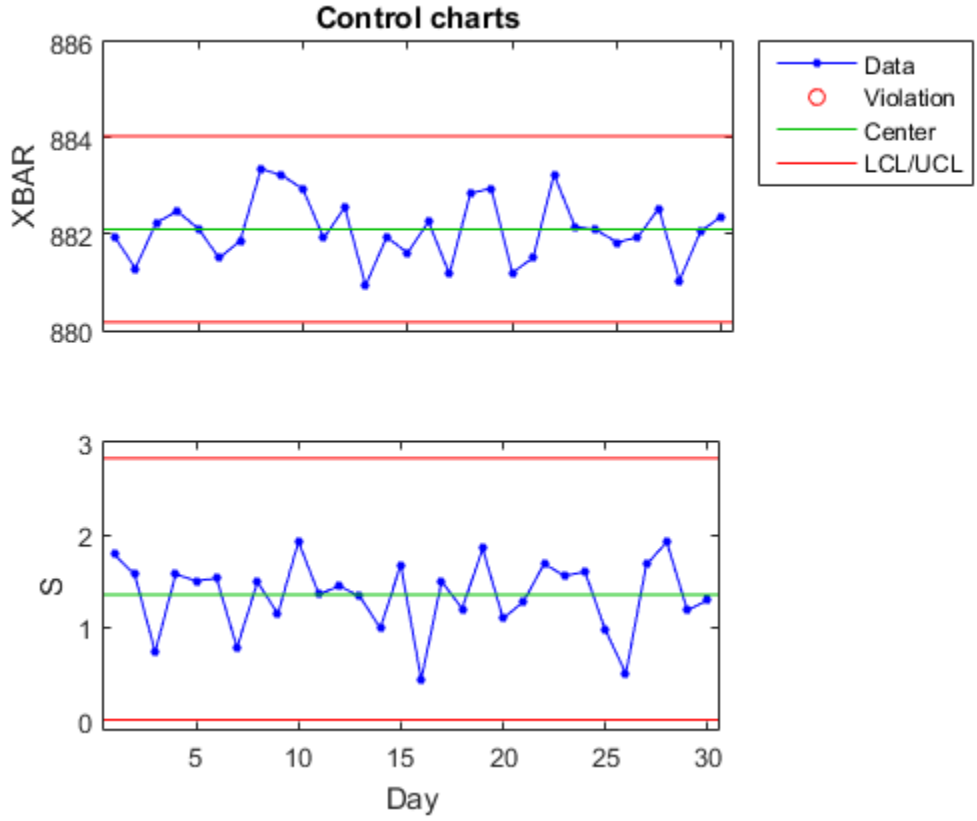
Control Manufacturing of the Improved Cooling Fan

You can monitor and evaluate the manufacturing and installation process of the new fan using control charts. Evaluate the first 30 days of production of the new cooling fan. Initially, five cooling fans per day were produced. First, load the sample data from the new process.

```
load spcdata
```

Plot the X-bar and S charts.

```
figure()
controlchart(spcflow,'chart',{'xbar','s'}) % Reshape the data into daily sets
xlabel('Day')
```



According to the results, the manufacturing process is in statistical control, as indicated by the absence of violations of control limits or nonrandom patterns in the data over time. You can also run a capability analysis on the data to evaluate the process.

```
[row,col] = size(spcflow);
S2 = capability(reshape(spcflow,row*col,1),[875.0 890])
pass = (1-S.Pl)*100
```

```
S2 =

       mu: 8.821061141685465e+02
    sigma: 1.423887508874697
        P: 0.999999684316149
       Pl: 3.008932155898586e-07
```

```
       Pu: 1.479063578225176e-08
       Cp: 1.755756676295137
      Cpl: 1.663547652525458
      Cpu: 1.847965700064817
      Cpk: 1.663547652525458


pass =

  99.9999699106784
```

The `Cp` value of 1.755 is very similar to the estimated value of 1.73. The `Cpk` value of 1.66 is smaller than the `Cp` value. However, only a `Cpk` value less than 1.33, which indicates that the process shifted significantly toward one of the process limits, is a concern. The process is well within the limits and it achieves the target airflow (875 ft^3/min) more than 99.999% of the time.

20

Statistical Process Control

Introduction to Statistical Process Control

Statistical process control (SPC) refers to a number of different methods for monitoring and assessing the quality of manufactured goods. Combined with methods from the design of experiments, SPC is used in programs that define, measure, analyze, improve, and control development and production processes. These programs are often implemented using “Design for Six Sigma” methodologies.

Control Charts

A control chart displays measurements of process samples over time. The measurements are plotted together with user-defined *specification limits* and process-defined *control limits*. The process can then be compared with its specifications—to see if it is *in control* or *out of control*.

The chart is just a monitoring tool. Control activity might occur if the chart indicates an undesirable, systematic change in the process. The control chart is used to discover the variation, so that the process can be adjusted to reduce it.

Control charts are created with the `controlchart` function. Any of the following chart types may be specified:

- Xbar or mean
- Standard deviation
- Range
- Exponentially weighted moving average
- Individual observation
- Moving range of individual observations
- Moving average of individual observations
- Proportion defective
- Number of defectives
- Defects per unit
- Count of defects

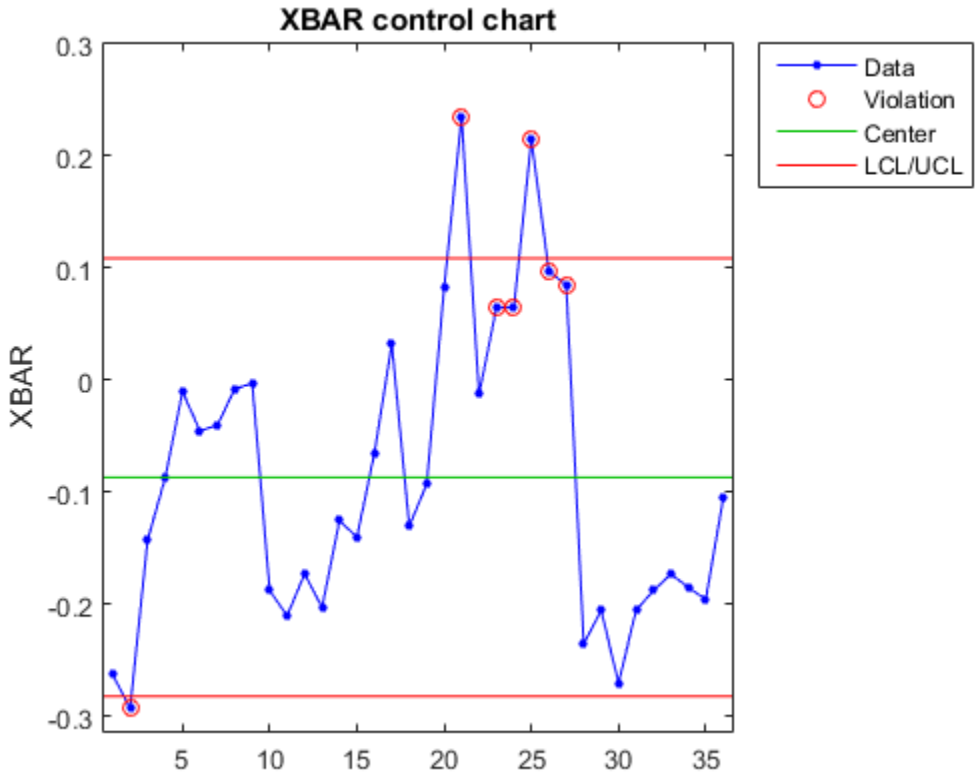
Control rules are specified with the `controlrules` function. The following example illustrates how to use Western Electric rules to mark out of control measurements on an Xbar chart.

First load the sample data.

```
load parts;
```

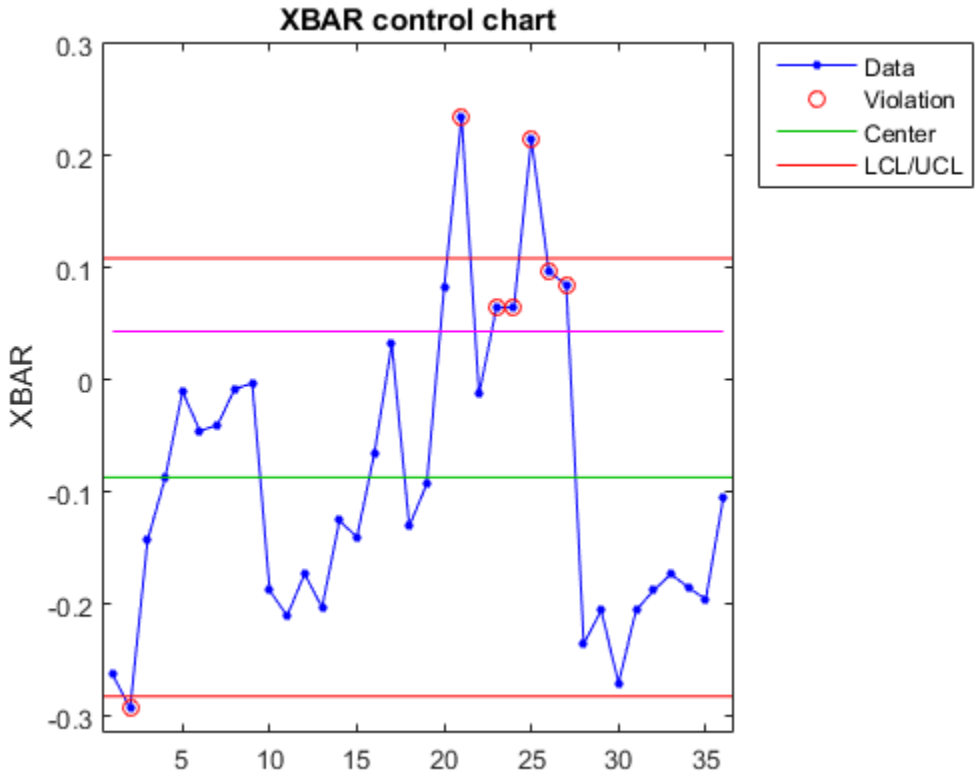
Construct the Xbar control chart using the Western Electric 2 rule (2 of 3 points at least 2 standard errors above the center line) to mark the out of control measurements.

```
st = controlchart(runout,'rules','we2');
```



For a better understanding of the Western Electric 2 rule, calculate and plot the 2 standard errors line on the chart.

```
x = st.mean;
cl = st.mu;
se = st.sigma./sqrt(st.n);
hold on
plot(cl+2*se,'m')
```



Identify the measurements that violate the control rule.

```
R = controlrules('we2',x,cl,se);
I = find(R)
```

```
I =

    21
    23
    24
    25
    26
    27
```

Capability Studies

Before going into production, many manufacturers run a *capability study* to determine if their process will run within specifications enough of the time. *Capability indices* produced by such a study are used to estimate expected percentages of defective parts.

Capability studies are conducted with the `capability` function. The following capability indices are produced:

- `mu` — Sample mean
- `sigma` — Sample standard deviation
- `P` — Estimated probability of being within the lower (`L`) and upper (`U`) specification limits
- `Pl` — Estimated probability of being below `L`
- `Pu` — Estimated probability of being above `U`
- `Cp` — `(U-L)/(6*sigma)`
- `Cpl` — `(mu-L)./(3.*sigma)`
- `Cpu` — `(U-mu)./(3.*sigma)`
- `Cpk` — `min(Cpl,Cpu)`

As an example, simulate a sample from a process with a mean of 3 and a standard deviation of 0.005:

```
rng default; % For reproducibility
data = normrnd(3,0.005,100,1);
```

Compute capability indices if the process has an upper specification limit of 3.01 and a lower specification limit of 2.99:

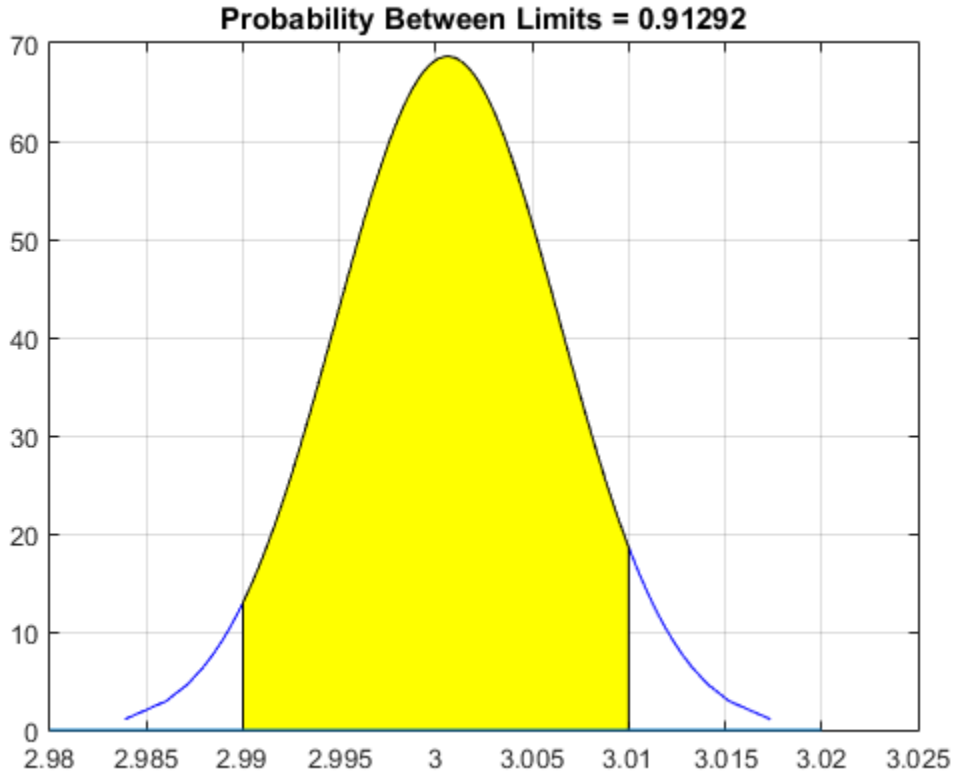
```
S = capability(data,[2.99 3.01])
```

```
S =

       mu: 3.0006
    sigma: 0.0058
        P: 0.9129
       Pl: 0.0339
       Pu: 0.0532
       Cp: 0.5735
```

```
Cpl: 0.6088
Cpu: 0.5382
Cpk: 0.5382
```

Visualize the specification and process widths:

```
capaplot(data,[2.99 3.01]);
grid on
```



Parallel Statistics

Quick Start Parallel Computing for Statistics and Machine Learning Toolbox

Note: To use parallel computing as described in this chapter, you must have a Parallel Computing Toolbox license.

In this section...

What Is Parallel Statistics Functionality?

You can use any of the Statistics and Machine Learning Toolbox functions with Parallel Computing Toolbox constructs such as `parfor` and `spmd`. However, some functions, such as those with interactive displays, can lose functionality in parallel. In particular, displays and interactive usage are not effective on workers (see "Vocabulary for Parallel Computation" on page 21-7).

Additionally, the following functions are enhanced to use parallel computing internally. These functions use `parfor` internally to parallelize calculations.

- `bootci`
- `bootstrp`
- `candexch`
- `cordexch`
- `crossval`
- `daugment`
- `dcovary`
- `jackknife`
- `kmeans`
- `lasso`
- `lassoglm`

- `nnmf`
- `plsregress`
- `rowexch`
- `sequentialfs`
- `TreeBagger`
- `TreeBagger.growTrees`

The following functions for fitting multiclass models for support vector machines and other classifiers are also enhanced to use parallel computing internally.

- `fitcecoc`
- Methods of the class `ClassificationECOC`:
  - `resubEdge`
  - `resubLoss`
  - `resubMargin`
  - `resubPredict`
  - `crossval`
- Methods of the class `CompactClassificationECOC`
  - `edge`
  - `loss`
  - `margin`
  - `predict`
- Methods of the class `ClassificationPartitionedECOC`
  - `kfoldEdge`
  - `kfoldLoss`
  - `kfoldMargin`
  - `kfoldPredict`

This chapter gives the simplest way to use these enhanced functions in parallel. For more advanced topics, including the issues of reproducibility and nested `parfor` loops, see the other sections in this chapter.

For information on parallel statistical computing at the command line, enter

```
help parallelstats
```

How To Compute in Parallel

To have a function compute in parallel:

1. “Set Up a Parallel Environment” on page 21-4
2. “Set the UseParallel Option to true” on page 21-4
3. “Call the Function Using the Options Structure” on page 21-4

Set Up a Parallel Environment

To run a statistical computation in parallel, first set up a parallel environment.

Note: Setting up a parallel environment can take several seconds.

For a multicore machine, enter the following at the MATLAB command line:

`parpool(`*n*`)`

n is the number of workers you want to use.

Set the UseParallel Option to true

Create an options structure with the `statset` function. To run in parallel, set the `UseParallel` option to `true`:

```
paroptions = statset('UseParallel',true);
```

Call the Function Using the Options Structure

Call your function with syntax that uses the options structure. For example:

```
% Run crossval in parallel
cvMse = crossval('mse',x,y,'predfun',regf,'Options',paroptions);

% Run bootstrp in parallel
sts = bootstrp(100,@(x)[mean(x) std(x)],y,'Options',paroptions);

% Run TreeBagger in parallel
b = TreeBagger(50,meas,spec,'OOBPred','on','Options',paroptions);
```

For more complete examples of parallel statistical functions, see “Parallel Treebagger” on page 21-5 and “Examples of Parallel Statistical Functions” on page 21-18.

After you have finished computing in parallel, close the parallel environment:

```
delete mypool
```

Tip To save time, keep the pool open if you expect to compute in parallel again soon.

Parallel Treebagger

To run the example “Regression of Insurance Risk Rating for Car Imports Using TreeBagger” on page 16-129 in parallel:

1. Set up the parallel environment to use two cores:

```
mypool = parpool(2)
Starting parpool using the 'local' profile ... connected to 2 workers.

mypool =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
          Cluster: [1x1 parallel.cluster.Local]
      SpmdEnabled: 1
```

2. Set the options to use parallel processing:

```
paroptions = statset('UseParallel',true);
```

3. Load the problem data and separate it into input and response:

```
load imports-85;
Y = X(:,1);
X = X(:,2:end);
```

4. Estimate feature importance using leaf size 1 and 1000 trees in parallel. Time the function for comparison purposes:

```
tic
b = TreeBagger(1000,X,Y,'Method','r','OOBVarImp','on',...
    'cat',16:25,'MinLeaf',1,'Options',paroptions);
toc
```

```
Elapsed time is 16.696336 seconds.
```

5 Perform the same computation in serial for timing comparison:

```
tic
b = TreeBagger(1000,X,Y,'Method','r','OOBVarImp','on',...
    'cat',16:25,'MinLeaf',1); % No options gives serial
toc

Elapsed time is 21.747950 seconds.
```

Computing in parallel took about 75% of the time of computing serially.

Concepts of Parallel Computing in Statistics and Machine Learning Toolbox

In this section...

Subtleties in Parallel Computing

There are two main subtleties in parallel computations:

- Nested parallel evaluations (see "No Nested parfor Loops" on page 21-11). Only the outermost `parfor` loop runs in parallel, the others run serially.
- Reproducible results when using random numbers (see "Reproducibility in Parallel Statistical Computations" on page 21-13). How can you get exactly the same results when repeatedly running a parallel computation that uses random numbers?

Vocabulary for Parallel Computation

- *worker* — An independent MATLAB session that runs code distributed by the *client*.
- *client* — The MATLAB session with which you interact, and that distributes jobs to workers.
- `parfor` — A Parallel Computing Toolbox function that distributes independent code segments to workers (see "Working with parfor" on page 21-10).
- *random stream* — A pseudorandom number generator, and the sequence of values it generates. MATLAB implements random streams with the `RandStream` class.
- *reproducible computation* — A computation that can be exactly replicated, even in the presence of random numbers (see "Reproducibility in Parallel Statistical Computations" on page 21-13).

When to Run Statistical Functions in Parallel

In this section...

Why Run in Parallel?

The main reason to run statistical computations in parallel is to gain speed, meaning to reduce the execution time of your program or functions. "Factors Affecting Speed" on page 21-8 discusses the main items affecting the speed of programs or functions. "Factors Affecting Results" on page 21-9 discusses details that can cause a parallel run to give different results than a serial run.

Factors Affecting Speed

Some factors that can affect the speed of execution of parallel processing are:

- Parallel environment setup. It takes time to run `parpool` to begin computing in parallel. If your computation is fast, the setup time can exceed any time saved by computing in parallel.
- Parallel overhead. There is overhead in communication and coordination when running in parallel. If function evaluations are fast, this overhead could be an appreciable part of the total computation time. Thus, solving a problem in parallel can be slower than solving the problem serially. For an example, see Improving Optimization Performance with Parallel Computing in MATLAB Digest, March 2009.
- No nested `parfor` loops. This is described in "Working with parfor" on page 21-10. `parfor` does not work in parallel when called from within another `parfor` loop. If you have programmed your custom functions to take advantage of parallel processing, the limitation of no nested `parfor` loops can cause a parallel function to run slower than expected.
- When executing serially, `parfor` loops run slightly slower than `for` loops.
- Passing parameters. Parameters are automatically passed to worker sessions during the execution of parallel computations. If there are many parameters, or they take a large amount of memory, passing parameters can slow the execution of your computation.

- Contention for resources: network and computing. If the pool of workers has low bandwidth or high latency, parallel computation can be slow.

Factors Affecting Results

Some factors can affect results when using parallel processing. There are several caveats related to `parfor` listed in "parfor Limitations" in the Parallel Computing Toolbox documentation. Some important factors are:

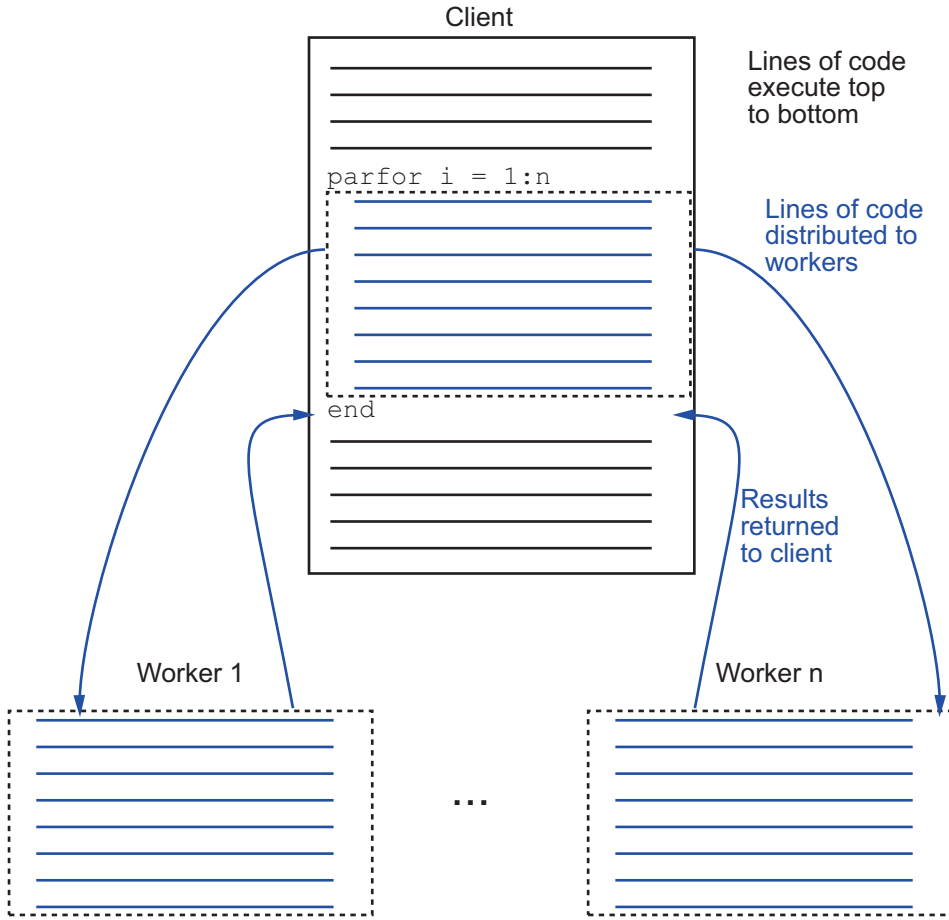
- Persistent or global variables. If any functions use persistent or global variables, these variables can take different values on different worker processors. Furthermore, they might not be cleared properly on the worker processors.
- Accessing external files. External files can be accessed unpredictably during a parallel computation. The order of computations is not guaranteed during parallel processing, so external files can be accessed in unpredictable order, leading to unpredictable results. Furthermore, if multiple processors try to read an external file simultaneously, the file can become locked, leading to a read error, and halting function execution.
- Noncomputational functions, such as `input`, `plot`, and `keyboard`, can behave badly when used in your custom functions. When called in a `parfor` loop, these functions are executed on worker machines. This can cause a worker to become nonresponsive, since it is waiting for input.
- `parfor` does not allow `break` or `return` statements.
- The random numbers you use can affect the results of your computations. See "Reproducibility in Parallel Statistical Computations" on page 21-13.

Working with parfor

In this section...

How Statistical Functions Use parfor

`parfor` is a Parallel Computing Toolbox function similar to a `for` loop. Parallel statistical functions call `parfor` internally. `parfor` distributes computations to worker processors.



Characteristics of parfor

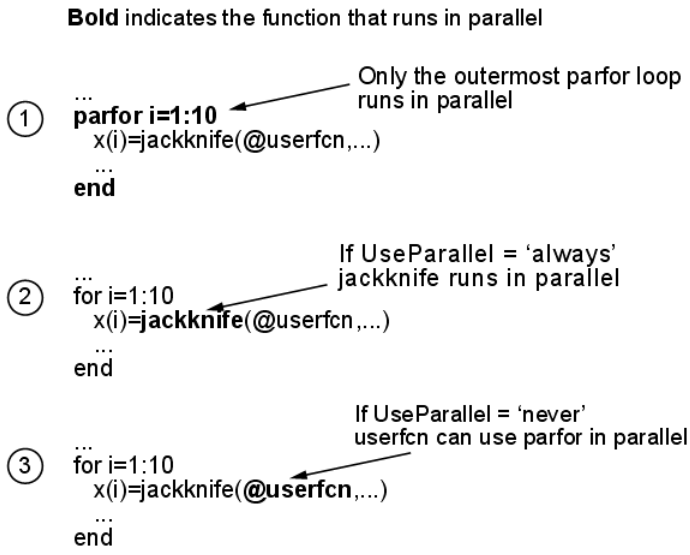
More caveats related to `parfor` appear in "parfor Limitations" in the Parallel Computing Toolbox documentation.

No Nested parfor Loops

`parfor` does not work in parallel when called from within another `parfor` loop, or from an `spmd` block. Parallelization occurs only at the outermost level.

Suppose, for example, you want to apply `jackknife` to your function `userfcn`, which calls `parfor`, and you want to call `jackknife` in a loop. The following figure shows three cases:

1. The outermost loop is `parfor`. Only that loop runs in parallel.
2. The outermost `parfor` loop is in `jackknife`. Only `jackknife` runs in parallel.
3. The outermost `parfor` loop is in `userfcn`. `userfcn` uses `parfor` in parallel.



When parfor Runs in Parallel

Reproducibility in Parallel Statistical Computations

In this section...

Issues and Considerations in Reproducing Parallel Computations

A *reproducible* computation is one that gives the same results every time it runs. Reproducibility is important for:

- Debugging — To correct an anomalous result, you need to reproduce the result.
- Confidence — When you can reproduce results, you can investigate and understand them.
- Modifying existing code — When you change existing code, you want to ensure that you do not break anything.

Generally, you do not need to ensure reproducibility for your computation. Often, when you want reproducibility, the simplest technique is to run in serial instead of in parallel. In serial computation you can simply call the `rng` function as follows:

```
s = rng % Obtain the current state of the random stream
% run the statistical function
rng(s) % Reset the stream to the previous state
% run the statistical function again, obtain identical results
```

This section addresses the case when your function uses random numbers, and you want reproducible results in parallel. This section also addresses the case when you want the same results in parallel as in serial.

Running Reproducible Parallel Computations

To run a Statistics and Machine Learning Toolbox function reproducibly:

1. Set the `UseSubstreams` option to `true`.
2. Set the `Streams` option to a type that supports substreams: `'mlfg6331_64'` or `'mrg32k3a'`. For information on these streams, see " Choosing a Random Number Generator" in the MATLAB Mathematics documentation.

3 To compute in parallel, set the `UseParallel` option to `true`.
4 Call the function with the options structure.
5 To reproduce the computation, reset the stream, then call the function again.

To understand why this technique gives reproducibility, see "How Substreams Enable Reproducible Parallel Computations" on page 21-15.

For example, to use the `'mlfg6331_64'` stream for reproducible computation:

1 Create an appropriate options structure:

```
s = RandStream('mlfg6331_64');
options = statset('UseParallel',true, ...
    'Streams',s,'UseSubstreams',true);
```

2 Run your parallel computation. For instructions, see "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2.
3 Reset the random stream:

```
reset(s);
```

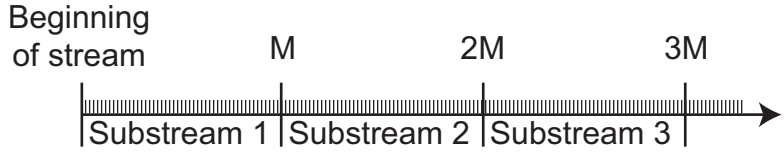
4 Rerun your parallel computation. You obtain identical results.

For an example of a parallel computation run this reproducible way, see "Reproducible Parallel Bootstrap" on page 21-23.

Parallel Statistical Computation Using Random Numbers

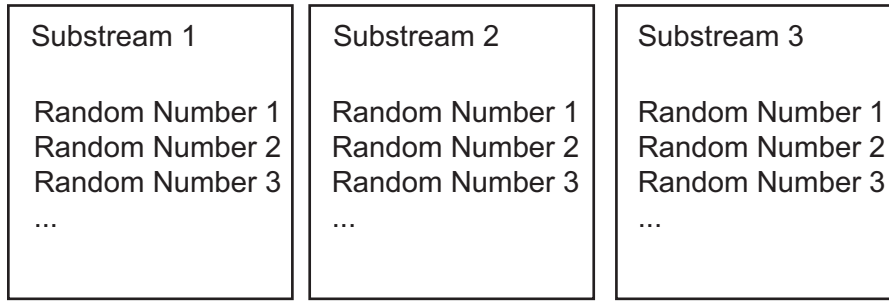
What Are Substreams?

A *substream* is a portion of a random stream that `RandStream` can access quickly. There is a number `M` such that for any positive integer `k`, `RandStream` can go the `k`Mth pseudorandom number in the stream. From that point, `RandStream` can generate the subsequent entries in the stream. Currently, `RandStream` has `M` = 2^{72}, about 5e21, or more.



The entries in different substreams have good statistical properties, similar to the properties of entries in a single stream: independence, and lack of k-way correlation at

various lags. The substreams are so long that you can view the substreams as being independent streams, as in the following picture.



Two `RandStream` stream types support substreams: `'mlfg6331_64'` and `'mrg32k3a'`.

How Substreams Enable Reproducible Parallel Computations

When MATLAB performs computations in parallel with `parfor`, each worker receives loop iterations in an unpredictable order. Therefore, you cannot predict which worker gets which iteration, so cannot determine the random numbers associated with each iteration.

Substreams allow MATLAB to tie each iteration to a particular sequence of random numbers. `parfor` gives each iteration an index. The iteration uses the index as the substream number. Since the random numbers are associated with the iterations, not with the workers, the entire computation is reproducible.

To obtain reproducible results, simply reset the stream, and all the substreams generate identical random numbers when called again. This method succeeds when all the workers use the same stream, and the stream supports substreams. This concludes the discussion of how the procedure in “Running Reproducible Parallel Computations” on page 21-13 gives reproducible parallel results.

Random Numbers on the Client or Workers

A few functions generate random numbers on the client before distributing them to parallel workers. The workers do not use random numbers, so operate purely deterministically. For these functions, you can run a parallel computation reproducibly using any random stream type.

The functions that operate this way include:

- `crossval`
- `plsregress`
- `sequentialfs`

To obtain identical results, reset the random stream on the client, or the random stream you pass to the client. For example:

```
s = rng % Obtain the current state of the random stream
% run the statistical function
rng(s) % Reset the stream to the previous state
% run the statistical function again, obtain identical results
```

While this method enables you to run reproducibly in parallel, the results can differ from a serial computation. The reason for the difference is `parfor` loops run in reverse order from `for` loops. Therefore, a serial computation can generate random numbers in a different order than a parallel computation. For unequivocal reproducibility, use the technique in "Running Reproducible Parallel Computations" on page 21-13.

Distributing Streams Explicitly

For testing or comparison using particular random number algorithms, you must set the random number generators. How do you set these generators in parallel, or initialize streams on each worker in a particular way? Or you might want to run a computation using a different sequence of random numbers than any other you have run. How can you ensure the sequence you use is statistically independent?

Parallel Statistics and Machine Learning Toolbox functions allow you to set random streams on each worker explicitly. For information on *creating* multiple streams, enter `help RandStream/create` at the command line. To create four independent streams using the `'mrg32k3a'` generator:

```
s = RandStream.create('mrg32k3a','NumStreams',4,...
    'CellOutput',true);
```

Pass these streams to a statistical function using the `Streams` option. For example:

```
parpool(4) % if you have at least 4 cores
s = RandStream.create('mrg32k3a','NumStreams',4,...
    'CellOutput',true); % create 4 independent streams
paroptions = statset('UseParallel',true,...
    'Streams',s); % set the 4 different streams
x = [randn(700,1); 4 + 2*randn(300,1)];
```

```
latt = -4:0.01:12;
myfun = @(X) ksdensity(X,latt);
pdfestimate = myfun(x);
B = bootstrp(200,myfun,x,'Options',paroptions);
```

This method of distributing streams gives each worker a different stream for the computation. However, it does not allow for a reproducible computation, because the workers perform the 200 bootstraps in an unpredictable order. If you want to perform a reproducible computation, use substreams as described in "Running Reproducible Parallel Computations" on page 21-13.

If you set the `UseSubstreams` option to `true`, then set the `Streams` option to a single random stream of the type that supports substreams (`'mlfg6331_64'` or `'mrg32k3a'`). This setting gives reproducible computations.

Examples of Parallel Statistical Functions

In this section...

Parallel Jackknife

This example is from the `jackknife` function reference page, but runs in parallel.

```
mypool=parpool()
Starting parpool using the 'local' profile ... connected to 2 workers.

mypool =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
      IdleTimeout: 30
          Cluster: [1x1 parallel.cluster.Local]
     RequestQueue: [1x1 parallel.RequestQueue]
      SpmdEnabled: 1

opts = statset('UseParallel',true);
sigma = 5;
rng('default')
y = normrnd(0,sigma,100,1);
m = jackknife(@var, y,1,'Options',opts);
n = length(y);
bias = -sigma^2 / n % known bias formula
jbias = (n - 1)*(mean(m)-var(y,1)) % jackknife bias estimate

bias =

   -0.2500


jbias =
```

```
   -0.3378
```

This simple example is not a good candidate for parallel computation:

```
% How long to compute in serial?
tic;m = jackknife(@var,y,1);toc
Elapsed time is 0.022771 seconds.

% How long to compute in parallel?
tic;m = jackknife(@var,y,1,'Options',opts);toc
Elapsed time is 0.299066 seconds.
```

`jackknife` does not use random numbers, so gives the same results every time, whether run in parallel or serial.

Parallel Cross Validation

Simple Parallel Cross Validation

This example is the same as the first in the `crossval` function reference page, but runs in parallel.

```
mypool = parpool()
Starting parpool using the 'local' profile ... connected to 2 workers.

mypool =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
      IdleTimeout: 30
          Cluster: [1x1 parallel.cluster.Local]
     RequestQueue: [1x1 parallel.RequestQueue]
      SpmdEnabled: 1opts = statset('UseParallel',true);


load('fisheriris');
```

```
y = meas(:,1);
X = [ones(size(y,1),1),meas(:,2:4)];
regf=@(XTRAIN,ytrain,XTEST)(XTEST*regress(ytrain,XTRAIN));

cvMse = crossval('mse',X,y,'Predfun',regf,'Options',opts)

cvMse =

    0.1028
```

This simple example is not a good candidate for parallel computation:

```
% How long to compute in serial?
tic;cvMse = crossval('mse',X,y,'Predfun',regf);toc
Elapsed time is 0.073438 seconds.

% How long to compute in parallel?
tic;cvMse = crossval('mse',X,y,'Predfun',regf,...
    'Options',opts);toc
Elapsed time is 0.289585 seconds.
```

Reproducible Parallel Cross Validation

To run `crossval` in parallel in a reproducible fashion, set the options and reset the random stream appropriately (see "Running Reproducible Parallel Computations" on page 21-13).

```
mypool = parpool()

Starting parpool using the 'local' profile ... connected to 2 workers.

mypool =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
      IdleTimeout: 30
          Cluster: [1x1 parallel.cluster.Local]
     RequestQueue: [1x1 parallel.RequestQueue]
      SpmdEnabled: 1

s = RandStream('mlfg6331_64');
opts = statset('UseParallel',true,...
```

```
    'Streams',s,'UseSubstreams',true);

load('fisheriris');
y = meas(:,1);
X = [ones(size(y,1),1),meas(:,2:4)];
regf=@(XTRAIN,ytrain,XTEST)(XTEST*regress(ytrain,XTRAIN));

cvMse = crossval('mse',X,y,'Predfun',regf,'Options',opts)

cvMse =

    0.1020
```

Reset the stream:

```
reset(s)
cvMse = crossval('mse',X,y,'Predfun',regf,'Options',opts)

cvMse =

    0.1020
```

Parallel Bootstrap

Bootstrap in Serial and Parallel

Here is an example timing a bootstrap in parallel versus in serial. The example generates data from a mixture of two Gaussians, constructs a nonparametric estimate of the resulting data, and uses a bootstrap to get a sense of the sampling variability.

1. Generate the data:

```
% Generate a random sample of size 1000,
% from a mixture of two Gaussian distributions
x = [randn(700,1); 4 + 2*randn(300,1)];
```

2. Construct a nonparametric estimate of the density from the data:

```
latt = -4:0.01:12;
myfun = @(X) ksdensity(X,latt);
pdfestimate = myfun(x);
```

3 Bootstrap the estimate to get a sense of its sampling variability. Run the bootstrap in serial for timing comparison.

```
tic;B = bootstrp(200,myfun,x);toc

Elapsed time is 10.878654 seconds.
```

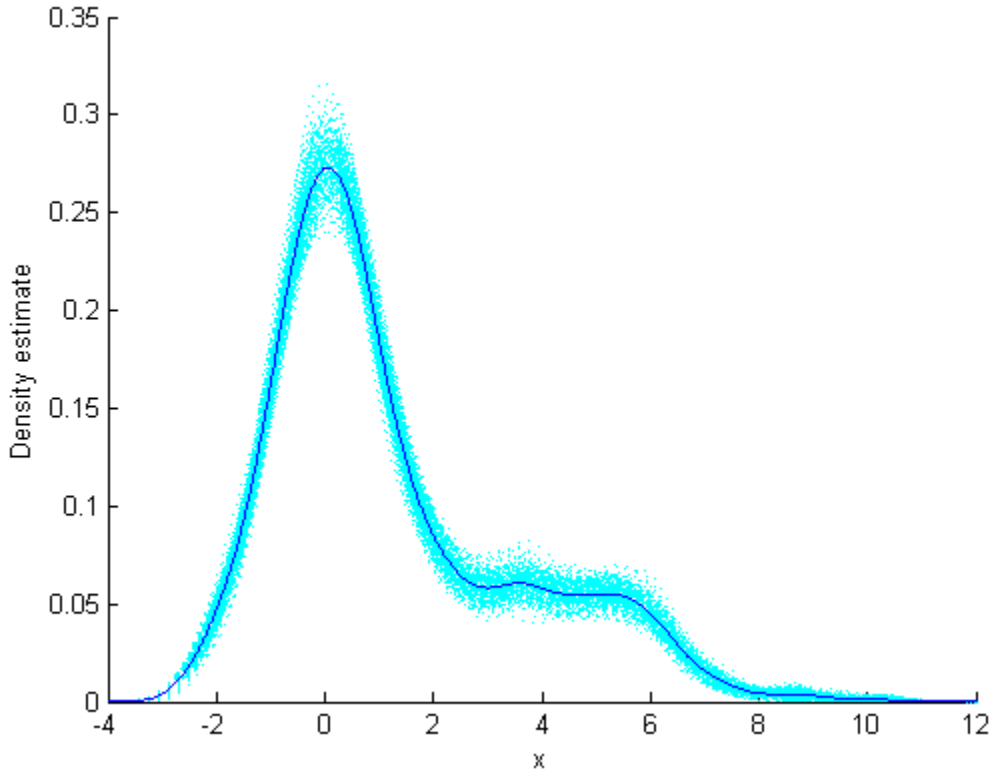
4 Run the bootstrap in parallel for timing comparison:

```
mypool = parpool()
Starting parpool using the 'local' profile ... connected to 2 workers.

mypool =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
      IdleTimeout: 30
          Cluster: [1x1 parallel.cluster.Local]
     RequestQueue: [1x1 parallel.RequestQueue]
      SpmdEnabled: 1

opt = statset('UseParallel',true);
tic;B = bootstrp(200,myfun,x,'Options',opt);toc

Elapsed time is 6.304077 seconds.
```

Computing in parallel is nearly twice as fast as computing in serial for this example.

Overlay the `ksdensity` density estimate with the 200 bootstrapped estimates obtained in the parallel bootstrap. You can get a sense of how to assess the accuracy of the density estimate from this plot.

```
hold on
for i=1:size(B,1),
    plot(latt,B(i,:),'c:')
end
plot(latt,pdfestimate);
xlabel('x');ylabel('Density estimate')
```



Reproducible Parallel Bootstrap

To run the example in parallel in a reproducible fashion, set the options appropriately (see "Running Reproducible Parallel Computations" on page 21-13). First set up the problem and parallel environment as in "Bootstrap in Serial and Parallel" on page 21-21. Then set the options to use substreams along with a stream that supports substreams.

```
s = RandStream('mlfg6331_64'); % has substreams
opts = statset('UseParallel',true,...
    'Streams',s,'UseSubstreams',true);
B2 = bootstrp(200,myfun,x,'Options',opts);
```

To rerun the bootstrap and get the same result:

```
reset(s) % set the stream to initial state
B3 = bootstrp(200,myfun,x,'Options',opts);
isequal(B2,B3) % check if same results

ans =
     1
```

Functions — Alphabetical List

addedvarplot

Added variable plot

Syntax

```
addedvarplot(X,y,num,inmodel)
addedvarplot(X,y,num,inmodel,stats)
```

Description

`addedvarplot(X,y,num,inmodel)` displays an added variable plot using the predictive terms in `X`, the response values in `y`, the added term in column `num` of `X`, and the model with current terms specified by `inmodel`. `X` is an n-by-p matrix of n observations of p predictive terms. `y` is vector of n response values. `num` is a scalar index specifying the column of `X` with the term to be added. `inmodel` is a logical vector of p elements specifying the columns of `X` in the current model. By default, all elements of `inmodel` are `false`.

Note: `addedvarplot` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`addedvarplot(X,y,num,inmodel,stats)` uses the `stats` output from the `stepwisefit` function to improve the efficiency of repeated calls to `addedvarplot`. Otherwise, this syntax is equivalent to the previous syntax.

Added variable plots are used to determine the unique effect of adding a new term to a multilinear model. The plot shows the relationship between the part of the response unexplained by terms already in the model and the part of the new term unexplained by terms already in the model. The "unexplained" parts are measured by the residuals of the respective regressions. A scatter of the residuals from the two regressions forms the added variable plot.

In addition to the scatter of residuals, the plot produced by `addedvarplot` shows 95% confidence intervals on predictions from the fitted line. The fitted line has intercept zero

because, under typical linear model assumptions, both of the plotted variables have mean zero. The slope of the fitted line is the coefficient that the new term would have if it were added to the model with terms `inmodel`.

Added variable plots are sometimes known as partial regression leverage plots.

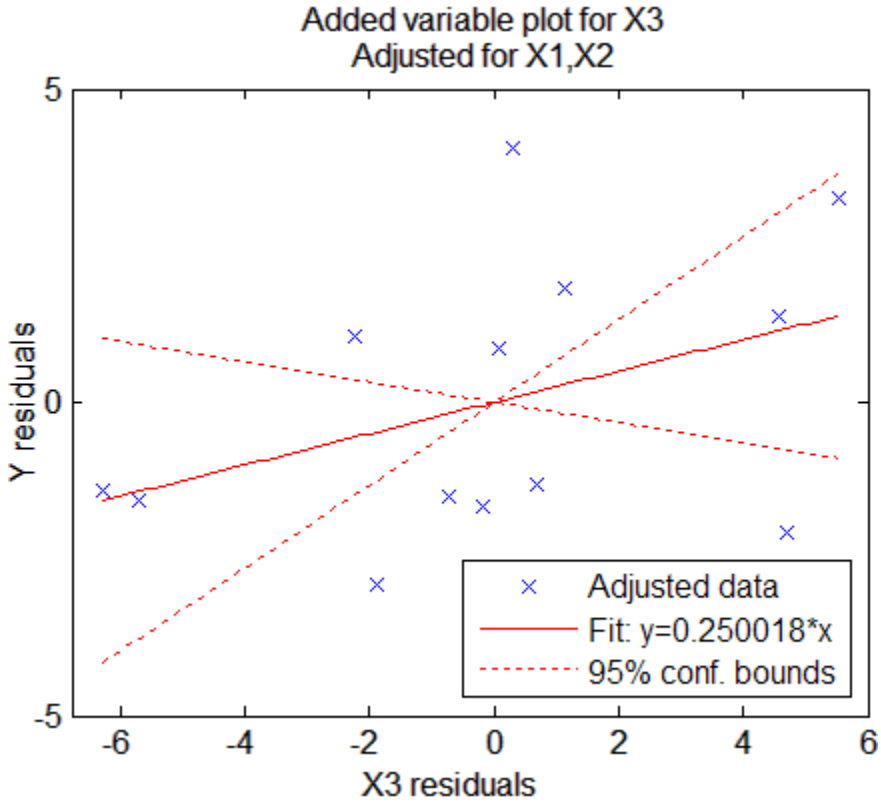
Examples

Load the data in `hald.mat`, which contains observations of the heat of reaction of various cement mixtures:

```
load hald
whos
  Name          Size    Bytes   Class   Attributes

  Description   22x58   2552    char
  hald          13x5     520    double
  heat          13x1     104    double
  ingredients   13x4     416    double
```

Create an added variable plot to investigate the addition of the third column of `ingredients` to a model consisting of the first two columns:

```
inmodel = [true true false false];
addedvarplot(ingredients,heat,3,inmodel)
```



The wide scatter and the low slope of the fitted line are evidence against the statistical significance of adding the third column to the model.

See Also

`stepwisefit` | `stepwise`

addK

Class: clustering.evaluation.ClusterCriterion
Package: clustering.evaluation

Evaluate additional numbers of clusters

Syntax

```
eva_out = addK(eva,klist)
```

Description

`eva_out = addK(eva,klist)` returns a clustering evaluation object eva_out that contains the evaluation data stored in the input object eva, plus additional evaluation data for the proposed number of clusters specified in klist.

Input Arguments

`eva` — Clustering evaluation data

clustering evaluation object

Clustering evaluation data, specified as a clustering evaluation object. Create a clustering evaluation object using `evalclusters`.

`klist` — Additional numbers of clusters to evaluate

vector of positive integer values

Additional numbers of clusters to evaluate, specified as a vector of positive integer values. If any values in klist overlap with clustering solutions already evaluated in the input object eva, then `addK` ignores the overlapping values.

Output Arguments

`eva_out` — Updated clustering evaluation data

clustering evaluation object

Updated clustering evaluation data, returned as a clustering evaluation object. eva_out contains data on the proposed clustering solutions included in the input clustering evaluation object eva, plus data on the additional proposed numbers of clusters specified in klist.

For all clustering evaluation object classes, `addK` updates the `InspectedK` and `CriterionValues` properties to include the proposed clustering solutions specified in klist and their corresponding criterion values. `addK` might also update the `OptimalK` and `OptimalY` properties to reflect the new optimal number of clusters and optimal clustering solution.

For certain cluster evaluation objects classes, `addK` might also update the following additional property values:

- For gap evaluation objects — `LogW`, `ExpectedLogW`, `StdLogW`, and `SE`
- For silhouette evaluation objects — `ClusterSilhouettes`

Examples

Evaluate Additional Numbers of Clusters

Create a clustering evaluation object using `evalclusters`, then use `addK` to evaluate additional numbers of clusters.

Load the sample data.

```
load fisheriris;
```

The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Cluster the flower measurement data using `kmeans`, and use the Calinski-Harabasz criterion to evaluate proposed solutions of one through five clusters.

```
eva = evalclusters(meas,'kmeans','calinski','klist',1:5)
```

```
eva =

  CalinskiHarabaszEvaluation with properties:

    NumObservations: 150
```

```
        InspectedK: [1 2 3 4 5]
    CriterionValues: [NaN 513.9245 561.6278 530.7658 459.5058]
           OptimalK: 3
```

The clustering evaluation object `eva` contains data on each proposed clustering solution. The returned value of `OptimalK` indicates that the optimal solution is three clusters.

Evaluate proposed solutions of 6 through 10 clusters using the same criteria. Add these evaluations to the original clustering evaluation object `eva`.

```
eva = addK(eva,6:10)
```

```
eva =

  CalinskiHarabaszEvaluation with properties:

    NumObservations: 150
        InspectedK: [1 2 3 4 5 6 7 8 9 10]
    CriterionValues: [1x10 double]
           OptimalK: 3
```

The updated values for `InspectedK` and `CriterionValues` show that `eva` now evaluates proposed solutions of 1 through 10 clusters. The `OptimalK` value still equals `3`, indicating that three clusters remain the optimal solution.

See Also

`clustering.evaluation.CalinskiHarabaszEvaluation` | `clustering.evaluation.DaviesBouldinEvaluation` | `clustering.evaluation.GapEvaluation` | `clustering.evaluation.SilhouetteEvaluation` | `evalclusters`

addlevels

Add levels to nominal or ordinal arrays

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
B = addlevels(A,newlevels)
```

Description

`B = addlevels(A,newlevels)` adds new levels specified by newlevels to the `nominal` or `ordinal` array A. `addlevels` adds the new levels at the end of the list of possible levels in A, but does not modify the value of any element. B does not contain elements at the new levels.

Examples

Add Levels To A Nominal Array

Add levels for additional species to Fisher's iris data.

Create a nominal array of the existing species in Fisher's iris data.

```
load fisheriris
species = nominal(species);
getlevels(species)


ans =
```

```
     setosa      versicolor      virginica
```

Add two additional species.

```
species = addlevels(species,{'spuria','ruthenica'});
getlevels(species)
```

```
ans =

     setosa      versicolor      virginica      spuria      ruthenica
```

Even though there are new levels, there are no elements in `species` that are in these new levels.

```
sum(species=='spuria')
sum(species=='ruthenica')
```

```
ans =

     0


ans =

     0
```

- “Add and Drop Category Levels” on page 2-21

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

newlevels — Levels to add

cell array of strings | 2-D character matrix

Levels to add to the input `nominal` or `ordinal` array, specified as a cell array of strings or 2-D character matrix.

Data Types: `char | cell`

Output Arguments

B — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, returned as a `nominal` or `ordinal` array object.

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`droplevels | mergelevels | nominal | ordinal | reorderlevels`

addlistener

Class: qrandstream

Add listener for event

Syntax

```
el = addlistener(hsource,'eventname',callback)
el = addlistener(hsource,property,'eventname',callback)
```

Description

`el = addlistener(hsource,'eventname',callback)` creates a listener for the event named `eventname`, the source of which is handle object `hsource`. If `hsource` is an array of source handles, the listener responds to the named event on any handle in the array. `callback` is a function handle that is invoked when the event is triggered.

`el = addlistener(hsource,property,'eventname',callback)` adds a listener for a property event. `eventname` must be one of the strings `'PreGet'`, `'PostGet'`, `'PreSet'`, and `'PostSet'`. `property` must be either a property name or cell array of property names, or a `meta.property` or array of `meta.property`. The properties must belong to the class of `hsource`. If `hsource` is scalar, `property` can include dynamic properties.

For all forms, `addlistener` returns an `event.listener`. To remove a listener, delete the object returned by `addlistener`. For example, `delete(el)` calls the handle class delete method to remove the listener and delete it from the workspace.

See Also

`notify` | `qrandstream` | `delete` | `dynamicprops` | `event.listener` | `events` | `meta.property` | `reset`

anova

Class: GeneralizedLinearMixedModel

Analysis of variance for generalized linear mixed-effects model

Syntax

```
stats = anova(glme)
stats = anova(glme,Name,Value)
```

Description

`stats = anova(glme)` returns a table, stats, that contains the results of *F*-tests to determine if all coefficients representing each fixed-effects term in the generalized linear mixed-effects model glme are equal to 0.

`stats = anova(glme,Name,Value)` returns a table, stats, using additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the method used to compute the approximate denominator degrees of freedom for the *F*-tests.

Tips

- For each fixed-effects term, `anova` performs an *F*-test (marginal test) to determine if all coefficients representing the fixed-effects term are equal to 0.

  When fitting a generalized linear mixed-effects (GLME) model using `fitglme` and one of the maximum likelihood fit methods (`'Laplace'` or `'ApproximateLaplace'`):

  - If you specify the `'CovarianceMethod'` name-value pair argument as `'conditional'`, then the *F*-tests are conditional on the estimated covariance parameters.
  - If you specify the `'CovarianceMethod'` name-value pair as `'JointHessian'`, then the *F*-tests account for the uncertainty in estimation of covariance parameters.

When fitting a GLME model using `fitglme` and one of the pseudo likelihood fit methods (`'MPL'` or `'REMPL'`), `anova` uses the fitted linear mixed effects model from the final pseudo likelihood iteration for inference on fixed effects.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'DFMethod'` — Method for computing approximate denominator degrees of freedom

`'residual'` (default) | `'none'`

Method for computing approximate denominator degrees of freedom to use in the F-test, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'residual'`	The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'none'`	All degrees of freedom are set to infinity.

The denominator degrees of freedom for the F-statistic correspond to the column `DF2` in the output structure `stats`.

Example: `'DFMethod','none'`

Output Arguments

`stats` — Results of *F*-tests for fixed-effects terms

table

Results of *F*-tests for fixed-effects terms, returned as a table with one row for each fixed-effects term in glme and the following columns.

`Term`	Name of the fixed-effects term
`FStat`	*F*-statistic for the term
`DF1`	Numerator degrees of freedom for the *F*-statistic
`DF2`	Denominator degrees of freedom for the *F*-statistic
`pValue`	*p*-value for the term

Each fixed-effects term is a continuous variable, a grouping variable, or an interaction between two or more continuous or grouping variables. For each fixed-effects term, `anova` performs an *F*-test (marginal test) to determine if all coefficients representing the fixed-effects term are equal to 0.

To perform tests for the type III hypothesis, when fitting the generalized linear mixed-effects model `fitglme`, you must use the `'effects'` contrasts for the `'DummyVarCoding'` name-value pair argument.

Examples

F-Tests for Fixed Effects

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The

company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.

- μ_{ij} is the mean number of defects corresponding to factory i (where $i = 1, 2, ..., 20$) during batch j (where $j = 1, 2, ..., 5$).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
'Distribution','Poisson','Link','log','FitMethod','Laplace','DummyVarCoding','effects')
```

```
glme =


Generalized linear mixed-effects model fit by ML

Model information:
    Number of observations             100
    Fixed effects coefficients           6
    Random effects coefficients         20
    Covariance parameters                1
    Distribution                   Poisson
    Link                           Log
    FitMethod                      Laplace

Formula:
    Linear Mixed Formula with 5 predictors.

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    416.35    434.58    -201.17          402.35

Fixed effects coefficients (95% CIs):
    Name                 Estimate     SE          tStat       DF
    '(Intercept)'           1.4689    0.15988      9.1875     94
    'newprocess'          -0.36766    0.17755     -2.0708     94
    'time_dev'            -0.094521   0.82849     -0.11409    94
    'temp_dev'             -0.28317    0.9617     -0.29444    94
    'supplier_C'          -0.071868   0.078024     -0.9211    94
```

```
    'supplier_B'          0.071072     0.07739     0.91836    94


    pValue        Lower        Upper
    9.8194e-15       1.1515       1.7864
      0.041122     -0.72019    -0.015134
       0.90941      -1.7395       1.5505
       0.76907      -2.1926       1.6263
       0.35936     -0.22679     0.083051
       0.36078    -0.082588      0.22473

Random effects covariance parameters:
Group: factory (20 Levels)
    Name1               Name2               Type         Estimate
    '(Intercept)'       '(Intercept)'       'std'        0.31381

Group: Error
    Name                       Estimate
    'sqrt(Dispersion)'         1
```

Perform an F-test to determine if all fixed-effects coefficients are equal to 0.

```
stats = anova(glme)
```

```
stats =


    ANOVA marginal tests: DFMethod = 'residual'

    Term                FStat       DF1    DF2    pValue
    '(Intercept)'          84.41    1      94     9.8194e-15
    'newprocess'          4.2881    1      94       0.041122
    'time_dev'          0.013016    1      94        0.90941
    'temp_dev'          0.086696    1      94        0.76907
    'supplier'           0.59212    2      94         0.5552
```

The p-values for the intercept, `newprocess`, `time_dev`, and `temp_dev` are the same as in the coefficient table of the `glme` display. The small p-values for the intercept and `newprocess` indicate that these are significant predictors at the 5% significance level. The large p-values for `time_dev` and `temp_dev` indicate that these are not significant predictors at this level.

The p-value of 0.5552 for `supplier` measures the combined significance for both coefficients representing the categorical variable `supplier`. This includes the dummy

variables `supplier_C` and `supplier_B` as shown in the coefficient table of the `glme` display. The large *p*-value indicates that `supplier` is not a significant predictor at the 5% significance level.

See Also

`GeneralizedLinearMixedModel` | `coefCI` | `coefTest` | `disp` | `fitglme` | `fixedEffects`

addTerms

Class: GeneralizedLinearModel

Add terms to generalized linear model

Syntax

```
mdl1 = addTerms(mdl,terms)
```

Description

`mdl1 = addTerms(mdl,terms)` returns a generalized linear model the same as `mdl` but with additional terms.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`terms`

Terms to add to the `mdl` regression model. Specify as either a:

- Text string representing one or more terms to add. For details, see "Wilkinson Notation" on page 22-20.
- Row or rows in the terms matrix (see `modelspec` in `fitglm`). For example, if there are three variables `A`, `B`, and `C`:

```
[0 0 0] represents a constant term or intercept
[0 1 0] represents B; equivalently, A^0 * B^1 * C^0
[1 0 1] represents A*C
[2 0 0] represents A^2
[0 1 2] represents B*(C^2)
```

Output Arguments

`mdl1`

Generalized linear model, the same as `mdl` but with additional terms given in `terms`. You can set `mdl1` equal to `mdl` to overwrite `mdl`.

Definitions

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

For details, see Wilkinson and Rogers [1].

Examples

Add a term to a generalized linear regression model

Create a model using just one predictor, then add a second.

Generate artificial data for the model, Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data. Use just the first predictor in the model.

```
mdl = fitglm(X,y,...
    'y ~ x1','distr','poisson')

mdl =

Generalized Linear regression model:
    log(y) ~ 1 + x1
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE           tStat     pValue
    (Intercept)    2.7784       0.014043    197.85    0
    x1             1.1732      0.0033653     348.6    0

100 observations, 98 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 1.25e+05, p-value = 0
```

Add the second predictor to the model.

```
mdl1 = addTerms(mdl,'x2')

mdl1 =

Generalized Linear regression model:
    log(y) ~ 1 + x1 + x2
```

```
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE           tStat     pValue
    (Intercept)    1.0405       0.022122    47.034    0
    x1             0.9968       0.003362    296.49    0
    x2              1.987      0.0063433    313.24    0

100 observations, 97 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 2.95e+05, p-value = 0
```

References

[1] Wilkinson, G. N., and C. E. Rogers. *Symbolic description of factorial models for analysis of variance.* J. Royal Statistics Society 22, pp. 392–399, 1973.

Alternatives

`step` adds or removes terms from a model using a greedy one-step algorithm.

See Also

`GeneralizedLinearModel` | `removeTerms` | `step` | `stepwiseglm`

More About

- “Generalized Linear Models” on page 10-12

addTerms

Class: LinearModel

Add terms to linear regression model

Syntax

```
mdl1 = addTerms(mdl,terms)
```

Description

`mdl1 = addTerms(mdl,terms)` returns a linear model the same as `mdl` but with additional terms.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`terms`

Terms to add to the `mdl` regression model. Specify as either a:

- Text string representing one or more terms to add. For details, see "Wilkinson Notation" on page 22-24.
- Row or rows in the terms matrix (see `modelspec` in `fitlm`). For example, if there are three variables `A`, `B`, and `C`:

```
[0 0 0] represents a constant term or intercept
[0 1 0] represents B; equivalently, A^0 * B^1 * C^0
[1 0 1] represents A*C
[2 0 0] represents A^2
[0 1 2] represents B*(C^2)
```

Output Arguments

`mdl1`

Linear model, the same as `mdl` but with additional terms given in `terms`. You can set `mdl1` equal to `mdl` to overwrite `mdl`.

Definitions

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

For details, see Wilkinson and Rogers [1].

Examples

Add a Term to a Model

Create a model of the `carsmall` data without any interactions, then add an interaction term.

Load the `carsmall` data and make a model of the MPG as a function of weight and model year.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
mdl = fitlm(ds,'MPG ~ Year + Weight^2');
```

Add an interaction term to `mdl`.

```
terms = 'Year*Weight';
mdl1 = addTerms(mdl,terms)
```

```
mdl1 =

Linear regression model:
    MPG ~ 1 + Weight*Year + Weight^2

Estimated Coefficients:
                       Estimate       SE            tStat       pValue
    (Intercept)            48.045        6.779       7.0874    3.3967e-10
    Weight               -0.012624    0.0041455      -3.0454     0.0030751
    Year_76                2.7768        3.0538      0.90931        0.3657
    Year_82                16.416        4.9802       3.2962     0.0014196
    Weight:Year_76     -0.00020693    0.00092403     -0.22394       0.82333
    Weight:Year_82      -0.0032574     0.0018919      -1.7217       0.088673
    Weight^2           1.0121e-06      6.12e-07       1.6538       0.10177

Number of observations: 94, Error degrees of freedom: 87
Root Mean Squared Error: 2.76
R-squared: 0.89,  Adjusted R-Squared 0.882
F-statistic vs. constant model: 117, p-value = 1.88e-39
```

References

[1] Wilkinson, G. N., and C. E. Rogers. *Symbolic description of factorial models for analysis of variance.* J. Royal Statistics Society 22, pp. 392–399, 1973.

Alternatives

Use `stepwiselm` to select a model from a starting model, continuing until no single step is beneficial.

Use `removeTerms` to remove particular terms.

Use `step` to optimally improve the model by adding or removing terms.

See Also

`removeTerms` | `LinearModel` | `step` | `stepwiselm`

How To

- “Linear Regression” on page 9-11

adtest

Anderson-Darling test

Syntax

```
h = adtest(x)
h = adtest(x,Name,Value)
[h,p] = adtest(___)
[h,p,adstat,cv] = adtest(___)
```

Description

`h = adtest(x)` returns a test decision for the null hypothesis that the data in vector x is from a population with a normal distribution, using the Anderson-Darling test. The alternative hypothesis is that x is not from a population with a normal distribution. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, or `0` otherwise.

`h = adtest(x,Name,Value)` returns a test decision for the Anderson-Darling test with additional options specified by one or more name-value pair arguments. For example, you can specify a null distribution other than normal, or select an alternative method for calculating the *p*-value.

`[h,p] = adtest(___)` also returns the *p*-value, p, of the Anderson-Darling test, using any of the input arguments from the previous syntaxes.

`[h,p,adstat,cv] = adtest(___)` also returns the test statistic, adstat, and the critical value, cv, for the Anderson-Darling test.

Examples

Test for a Normal Distribution

Load the data set. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that the exam grades come from a normal distribution. You do not need to specify values for the population parameters.

```
[h,p,adstat,cv] = adtest(x);
```

```
h =
     0

p =
    0.1854

adstat =
    0.5194

cv =
    0.7470
```

The returned value of `h = 0` indicates that `adtest` fails to reject the null hypothesis at the default 5% significance level.

Test for an Extreme Value Distribution

Load the data set. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that the exam grades come from an extreme value distribution. You do not need to specify values for the population parameters.

```
[h,p] = adtest(x,'Distribution','ev')
```

```
h =
     0

p =
    0.0714
```

The returned value of `h = 0` indicates that `adtest` fails to reject the null hypothesis at the default 5% significance level.

Specify the Hypothesized Distribution Using a Probability Distribution Object

Load the data set. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Create a normal probability distribution object with mean `mu = 75` and standard deviation `sigma = 10`.

```
dist = makedist('normal','mu',75,'sigma',10)
```

```
dist =

  prob.NormalDistribution
  Package: prob

  Normal distribution
       mu = 75
    sigma = 10

  Properties, Methods
```

Test the null hypothesis that `x` comes from the hypothesized normal distribution.

```
[h,p] = adtest(x,'Distribution',dist)
```

```
h =
     0

p =
    0.4687
```

The returned value of `h = 0` indicates that `adtest` fails to reject the null hypothesis at the default 5% significance level.

Input Arguments

x — Sample data

vector

Sample data, specified as a vector. Missing observations in x, indicated by `NaN`, are ignored.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alpha',0.01,'MCTol',0.01` conducts the hypothesis test at the 1% significance level, and determines the p-value, `p`, using a Monte Carlo simulation with a maximum Monte Carlo standard error for `p` of 0.01.

`'Distribution'` — Hypothesized distribution

`'norm'` (default) | `'exp'` | `'ev'` | `'logn'` | `'weibull'` | probability distribution object

Hypothesized distribution of data vector x, specified as the comma-separated pair consisting of `'Distribution'` and one of the following.

`'norm'`	Normal distribution
`'exp'`	Exponential distribution
`'ev'`	Extreme value distribution
`'logn'`	Lognormal distribution
`'weibull'`	Weibull distribution

In this case, you do not need to specify population parameters. Instead, `adtest` estimates the distribution parameters from the sample data and tests x against a composite hypothesis that it comes from the selected distribution family with parameters unspecified.

Alternatively, you can specify any continuous probability distribution object for the null distribution. In this case, you must specify all the distribution parameters, and `adtest` tests x against a simple hypothesis that it comes from the given distribution with its specified parameters.

Example: `'Distribution','exp'`

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'MCTol'` — Maximum Monte Carlo standard error

positive scalar value

Maximum Monte Carlo standard error for the *p*-value, p, specified as the comma-separated pair consisting of `'MCTol'` and a positive scalar value. If you use `MCTol`, `adtest` determines p using a Monte Carlo simulation, and the name-value pair argument `Asymptotic` must have the value `false`.

Example: `'MCTol',0.01`

Data Types: `single` | `double`

`'Asymptotic'` — Method for calculating *p*-value

`false` (default) | `true`

Method for calculating the *p*-value of the Anderson-Darling test, specified as the comma-separated pair consisting of `'Asymptotic'` and either `true` or `false`. If you specify `'true'`, `adtest` estimates the *p*-value using the limiting distribution of the Anderson-Darling test statistic. If you specify `false`, `adtest` calculates the *p*-value based on an analytical formula. For sample sizes greater than 120, the limiting distribution estimate is likely to be more accurate than the small sample size approximation method.

- If you specify a distribution family with unknown parameters for the `Distribution` name-value pair, `Asymptotic` must be `false`.
- If you use `MCTol` to calculate the *p*-value using a Monte Carlo simulation, `Asymptotic` must be `false`.

Example: `'Asymptotic',true`

Data Types: `logical`

Output Arguments

h — Hypothesis test result

1 | 0

Hypothesis test result, returned as a logical value.

- If h = `1`, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = `0`, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the Anderson-Darling test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. p is calculated using one of these methods:

- If the hypothesized distribution is a fully specified probability distribution object, `adtest` calculates p analytically. If `'Asymptotic'` is `true`, `adtest` uses the asymptotic distribution of the test statistic. If you specify a value for `'MCTol'`, `adtest` uses a Monte Carlo simulation.
- If the hypothesized distribution is specified as a distribution family with unknown parameters, `adtest` retrieves the critical value from a table and uses inverse interpolation to determine the *p*-value. If you specify a value for `'MCTol'`, `adtest` uses a Monte Carlo simulation.

`adstat` — Test statistic

scalar value

Test statistic for the Anderson-Darling test, returned as a scalar value.

- If the hypothesized distribution is a fully specified probability distribution object, `adtest` computes adstat using specified parameters.
- If the hypothesized distribution is specified as a distribution family with unknown parameters, `adtest` computes adstat using parameters estimated from the sample data.

`cv` — Critical value

scalar value

Critical value for the Anderson-Darling test at the significance level `Alpha`, returned as a scalar value. `adtest` determines cv by interpolating into a table based on the specified `Alpha` significance level.

More About

Anderson-Darling Test

The Anderson-Darling test is commonly used to test whether a data sample comes from a normal distribution. However, it can be used to test for another hypothesized distribution, even if you do not fully specify the distribution parameters. Instead, the test estimates any unknown parameters from the data sample.

The test statistic belongs to the family of quadratic empirical distribution function statistics, which measure the distance between the hypothesized distribution, $F(x)$ and the empirical cdf, $F_n(x)$ as

$$n\int_{-\infty}^{\infty}\left(F_n(x)-F(x)\right)^2 w(x)\,dF(x),$$

over the ordered sample values $x_1 < x_2 < \ldots < x_n$, where $w(x)$ is a weight function and n is the number of data points in the sample.

The weight function for the Anderson-Darling test is

$$w(x)=\left[F(x)\left(1-F(x)\right)\right]^{-1},$$

which places greater weight on the observations in the tails of the distribution, thus making the test more sensitive to outliers and better at detecting departure from normality in the tails of the distribution.

The Anderson-Darling test statistic is

$$A_n^2 = -n-\sum_{i=1}^{n}\frac{2i-1}{n}\left[\ln\left(F\left(X_i\right)\right)+\ln\left(1-F\left(X_{n+1-i}\right)\right)\right],$$

where $\{X_1 < ... < X_n\}$ are the ordered sample data points and n is the number of data points in the sample.

In `adtest`, the decision to reject or not reject the null hypothesis is based on comparing the p-value for the hypothesis test with the specified significance level, not on comparing the test statistic with the critical value.

Monte Carlo Standard Error

The Monte Carlo standard error is the error due to simulating the p-value.

The Monte Carlo standard error is calculated as

$$SE = \sqrt{\frac{(\hat{p})(1-\hat{p})}{\text{mcreps}}},$$

where $\hat{p}$ is the estimated p-value of the hypothesis test, and `mcreps` is the number of Monte Carlo replications performed.

`adtest` chooses the number of Monte Carlo replications, `mcreps`, large enough to make the Monte Carlo standard error for $\hat{p}$ less than the value specified for `MCTol`.

See Also

`jbtest` | `kstest`

AIC property

Class: gmdistribution

Akaike Information Criterion

Description

The Akaike Information Criterion: `2*NlogL + 2*m`, where `NlogL` is the negative loglikelihood and `m` is the number of estimated parameters.

Note: This property applies only to gmdistribution objects constructed with `fitgmdist`.

andrewsplot

Andrews plot

Syntax

```
andrewsplot(X)
andrewsplot(X,...,'Standardize',standopt)
andrewsplot(X,...,'Quantile',alpha)
andrewsplot(X,...,'Group',group)
andrewsplot(X,...,'PropName',PropVal,...)
h = andrewsplot(X,...)
```

Description

`andrewsplot(X)` creates an Andrews plot of the multivariate data in the matrix `X`. The rows of `X` correspond to observations, the columns to variables. Andrews plots represent each observation by a function $f(t)$ of a continuous dummy variable t over the interval [0,1]. $f(t)$ is defined for the i th observation in `X` as

$$f(t) = X(i,1)/\sqrt{2} + X(i,2)\sin(2\pi t) + X(i,3)\cos(2\pi t) + \ldots$$

`andrewsplot` treats `NaN` values in `X` as missing values and ignores the corresponding rows.

`andrewsplot(X,...,'Standardize',standopt)` creates an Andrews plot where *`standopt`* is one of the following:

- `'on'` — scales each column of `X` to have mean `0` and standard deviation `1` before making the plot.
- `'PCA'` — creates an Andrews plot from the principal component scores of `X`, in order of decreasing eigenvalue. (See `pca`.)
- `'PCAStd'` — creates an Andrews plot using the standardized principal component scores. (See `pca`.)

`andrewsplot(X,...,'Quantile',alpha)` plots only the median and the `alpha` and (1 – `alpha`) quantiles of $f(t)$ at each value of t. This is useful if `X` contains many observations.

`andrewsplot(X,...,'Group',group)` plots the data in different groups with different colors. Groups are defined by `group`, a numeric array containing a group index for each observation. `group` can also be a categorical array, character matrix, or cell array of strings containing a group name for each observation.

`andrewsplot(X,...,'PropName',PropVal,...)` sets optional lineseries object properties to the specified values for all lineseries objects created by `andrewsplot`. (See Chart Line Properties.)

`h = andrewsplot(X,...)` returns a column vector of handles to the lineseries objects created by `andrewsplot`, one handle per row of `X`. If you use the `'Quantile'` input parameter, `h` contains one handle for each of the three lineseries objects created. If you use both the `'Quantile'` and the `'Group'` input parameters, `h` contains three handles for each group.

Examples

Create Andrews Plot to Visualize Grouped Data

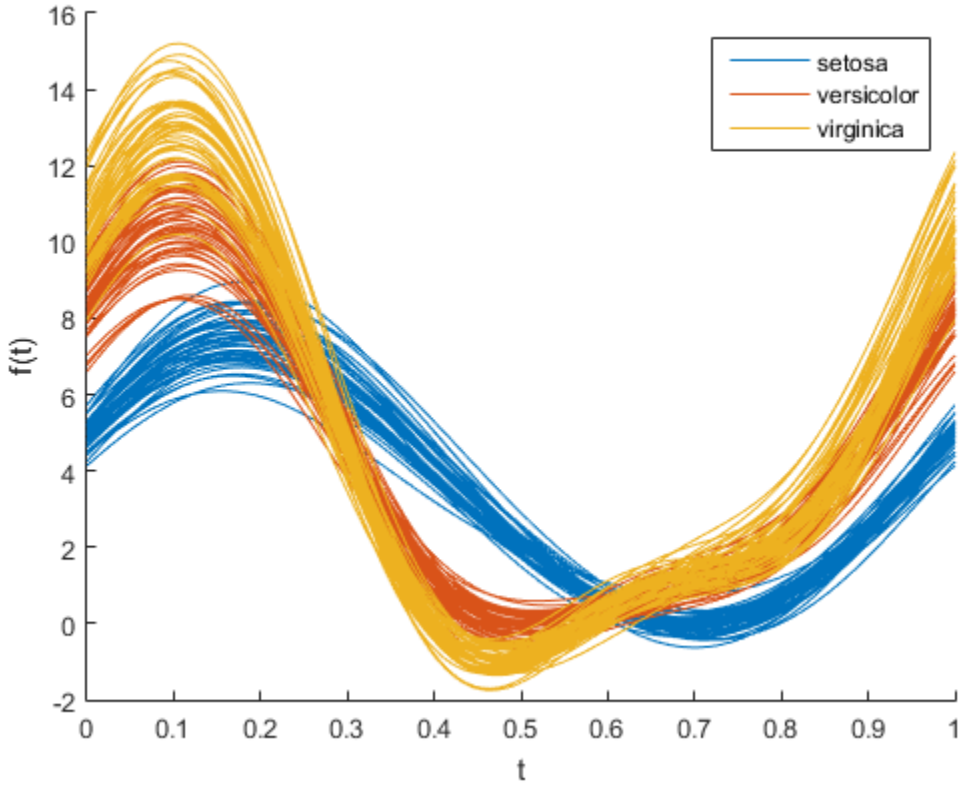
This example shows how to create an Andrews plot to visualize grouped sample data.

Load the sample data.

```
load fisheriris
```

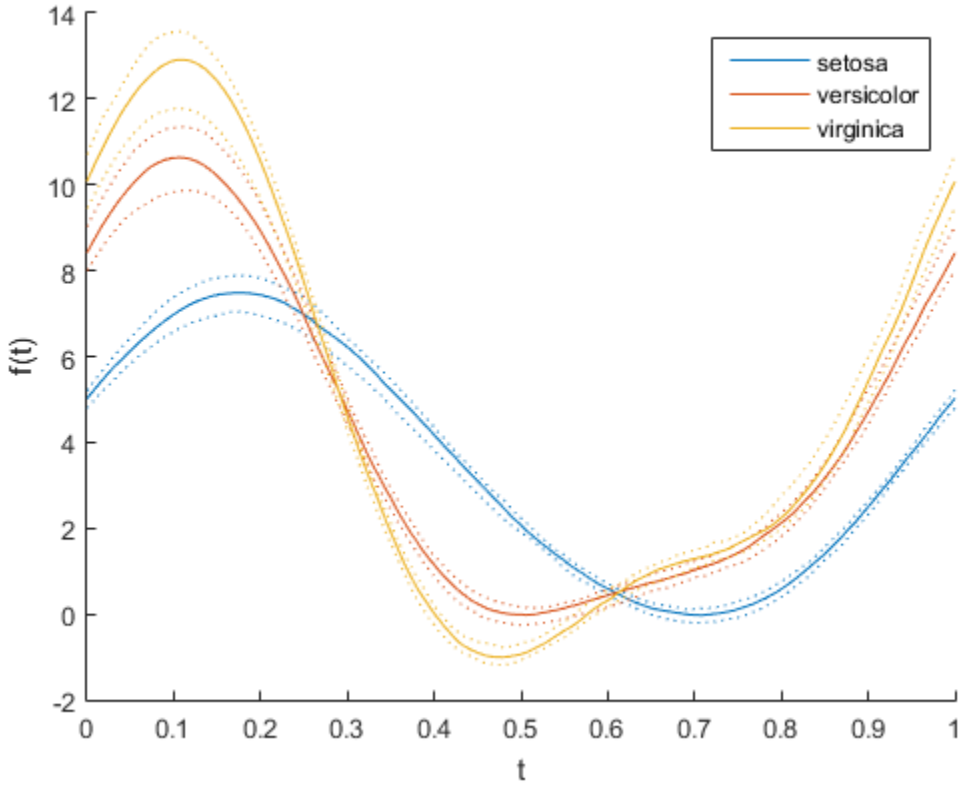
Create an Andrews plot, grouping the sample data by `species`.

```
andrewsplot(meas,'group',species)
```



Create a second, simplified Andrews plot that only displays the median and quartiles of each group.

```
andrewsplot(meas,'group',species,'quantile',.25)
```



More About

- "Grouping Variables" on page 2-52

See Also

`parallelcoords` | `glyphplot`

anova

Class: LinearModel

Analysis of variance for linear model

Syntax

```
tbl = anova(mdl)
tbl = anova(mdl,anovatype)
tbl = anova(mdl,anovatype,sstype)
```

Description

`tbl = anova(mdl)` returns a table with summary ANOVA statistics.

`tbl = anova(mdl,anovatype)` returns ANOVA statistics of the chosen type.

`tbl = anova(mdl,anovatype,sstype)` computes ANOVA statistics using the chosen type of sum of squares.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`anovatype`

ANOVA type:

- `'component'` — `tbl` displays a 'components' ANOVA table, with sums of squares and *F* tests attributable to each term in the model except the constant term.
- `'summary'` — `tbl` displays a summary ANOVA table with an *F* test for the model as a whole.
  - If there are both linear and higher-order terms, there is also an *F* test for the higher-order terms as a group.

- If there are replications (multiple observations sharing the same predictor values), there is also an *F* test for lack-of-fit computed by decomposing the residual sum of squares into a sum of squares for the replicated observations and the remaining sum of squares.

Default: `'component'`

`sstype`

When `anovatype` is `'component'`, choose the sum of squares type:

- `1`
- `2`
- `3`
- `'h'`

For details, see sstype.

Default: `'h'`

Output Arguments

`tbl`

Table containing summary ANOVA statistics. `tbl` depends on `anovatype`:

- `'component'`:
  - Sum of squares
  - Degrees of freedom
  - Mean squares
  - *F* statistic
  - *p*-value
  - Formula used for model
- `'summary'`:
  - Total Sum of Squares

- Model Sum of Squares
  - Linear Sum of Squares (present if model has powers or interactions)
  - Nonlinear Sum of Squares (present if model has powers or interactions)
- Residual Sum of Squares
  - Lack-of-fit Sum of Squares (present if model has replicates)
  - Pure error Sum of Squares (present if model has replicates)

Examples

Component ANOVA Table

Create a component ANOVA table from a model of the `carsmall` data.

Load the `carsmall` data and make a model of the MPG as a function of weight and model year.

```
load carsmall
cars = table(MPG,Weight);
cars.Year = ordinal(Model_Year);
mdl = fitlm(cars,'MPG ~ Year + Weight^2');
```

Create an ANOVA table.

```
tbl = anova(mdl)
```

```
tbl =

               SumSq     DF    MeanSq      F         pValue
               ______    __    ______    ______    __________

    Weight     2050.2     1    2050.2    265.11    1.9885e-28
    Year       849.55     2    424.77    54.927    2.9042e-16
    Weight^2   76.688     1    76.688    9.9164     0.0022303
    Error      688.27    89    7.7334
```

Summary ANOVA Table

Create a summary ANOVA table from a model of the `carsmall` data.

Load the `carsmall` data and make a model of the MPG as a function of weight and model year.

```
load carsmall
cars = table(MPG,Weight);
cars.Year = ordinal(Model_Year);
mdl = fitlm(cars,'MPG ~ Year + Weight^2');
```

Create a summary ANOVA table.

```
tbl = anova(mdl,'summary')
```

```
tbl =

                    SumSq     DF    MeanSq      F
                    ______    __    ______    ______

    Total           6005.3    93    64.573
    Model             5317     4    1329.3    171.88
    . Linear        5240.3     3    1746.8    225.87
    . Nonlinear     76.688     1    76.688    9.9164
    Residual        688.27    89    7.7334
    . Lack of fit   663.77    86    7.7183    0.9451
    . Pure error      24.5     3    8.1667


                      pValue
                    __________

    Total
    Model           5.5208e-41
    . Linear        1.7302e-41
    . Nonlinear      0.0022303
    Residual
    . Lack of fit      0.62874
    . Pure error
```

The summary ANOVA table shows tests for groups of terms. The nonlinear group consists of just the `Weight^2` term, so it has the same *p*-value as that term in "Component ANOVA Table" on page 22-42. The *F* statistic comparing the residual sum of squares to a "pure error" estimate from replicated observations shows no evidence of lack of fit.

- "ANOVA" on page 9-21

Alternatives

More complete ANOVA statistics are available in the `anova1`, `anova2`, and `anovan` functions.

See Also

`LinearModel` | `table`

How To

- “Linear Regression” on page 9-11

anova

Class: LinearMixedModel

Analysis of variance for linear mixed-effects model

Syntax

```
stats = anova(lme)
stats = anova(lme,Name,Value)
```

Description

`stats = anova(lme)` returns the dataset array `stats` that includes the results of the *F*-tests for each fixed-effects term in the linear mixed-effects model `lme`.

`stats = anova(lme,Name,Value)` also returns the dataset array `stats` with additional options specified by one or more Name,Value pair arguments.

Tips

- For each fixed-effects term, `anova` performs an *F*-test (marginal test), that all coefficients representing the fixed-effects term are 0. To perform tests for type III hypotheses, you must set the `'DummyVarCoding'` name-value pair argument to `'effects'` contrasts while fitting your linear mixed-effects model.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'DFMethod'` — Method for computing approximate degrees of freedom
`'Residual'` (default) | `'Satterthwaite'` | `'None'`

Method for computing approximate degrees of freedom to use in the F-test, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'Residual'`	Default. The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'Satterthwaite'`	Satterthwaite approximation.
`'None'`	All degrees of freedom are set to infinity.

For example, you can specify the Satterthwaite approximation as follows.

Example: `'DFMethod','Satterthwaite'`

Output Arguments

`stats` — Results of *F*-tests for fixed-effects terms
dataset array

Results of *F*-tests for fixed-effects terms, returned as a dataset array with the following columns.

`Term`	Name of the fixed effects term
`Fstat`	*F*-statistic for the term
`DF1`	Numerator degrees of freedom for the *F*-statistic
`DF2`	Denominator degrees of freedom for the *F*-statistic

`pValue`	*p*-value of the test for the term

There is one row for each fixed-effects term. Each term is a continuous variable, a grouping variable, or an interaction between two or more continuous or grouping variables. For each fixed-effects term, `anova` performs an *F*-test (marginal test) to determine if all coefficients representing the fixed-effects term are 0. To perform tests for the type III hypothesis, you must use the `'effects'` contrasts while fitting the linear mixed-effects model.

Examples

F-Tests for Fixed Effects

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data shows the deviations from the target quality characteristic measured from the products that five operators manufacture during three shifts: morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the deviation of the quality characteristics from the target value. This is simulated data.

`Shift` and `Operator` are nominal variables.

```
shift.Shift = nominal(shift.Shift);
shift.Operator = nominal(shift.Operator);
```

Fit a linear mixed-effects model with a random intercept grouped by operator to assess if performance significantly differs according to the time of the shift. Use the restricted maximum likelihood method and `'effects'` contrasts.

`'effects'` contrasts indicate that the coefficients sum to 0, and `fitlme` creates two contrast-coded variables in the fixed-effects design matrix, $X1$ and $X2$, where

$$Shift\_Evening = \begin{cases} 0, & if\ Morning \\ 1, & if\ Evening \\ -1, & if\ Night \end{cases} \quad and \quad Shift\_Morning = \begin{cases} 1, & if\ Morning \\ 0, & if\ Evening \\ -1, & if\ Night \end{cases}.$$

The model corresponds to

$$\begin{aligned} &\text{Morning Shift: } QCDev_{im} = \beta_0 + \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \quad m = 1,2,\ldots,5, \\ &\text{Evening Shift: } QCDev_{im} = \beta_0 + \beta_1 Shift\_Evening_i + b_{0m} + \varepsilon_{im}, \\ &\text{Night Shift: } \quad QCDev_{im} = \beta_0 - \beta_1 Shift\_Evening_i - \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \end{aligned}$$

where $b \sim N(0,\sigma^2_b)$ and $\varepsilon \sim N(0,\sigma^2)$.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)',...
'FitMethod','REML','DummyVarCoding','effects')
```

```
lme =


Linear mixed-effects model fit by REML

Model information:
    Number of observations             15
    Fixed effects coefficients          3
    Random effects coefficients         5
    Covariance parameters               2

Formula:
    QCDev ~ 1 + Shift + (1 | Operator)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    58.913    61.337    -24.456          48.913

Fixed effects coefficients (95% CIs):
    Name                  Estimate    SE         tStat      DF    pValue       Lower
    '(Intercept)'           3.6525    0.94109     3.8812    12    0.0021832     1.602
    'Shift_Evening'        -0.53293   0.31206    -1.7078    12      0.11339    -1.212
    'Shift_Morning'        -0.91973   0.31206    -2.9473    12     0.012206    -1.599

Random effects covariance parameters (95% CIs):
Group: Operator (5 Levels)
    Name1               Name2               Type         Estimate    Lower      Upper
```

```
    '(Intercept)'        '(Intercept)'        'std'        2.0457      0.98207    4.26

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.85462     0.52357    1.395
```

Perform an F-test to determine if all fixed-effects coefficients are 0.

```
anova(lme)
```

```
ans =


    ANOVA marginal tests: DFMethod = 'Residual'

    Term                 FStat     DF1    DF2    pValue
    '(Intercept)'        15.063    1      12     0.0021832
    'Shift'              11.091    2      12     0.0018721
```

The p-value for the constant term, 0.0021832, is the same as in the coefficient table in the `lme` display. The p-value of 0.0018721 for `Shift` measures the combined significance for both coefficients representing `Shift`.

Split-Plot Experiment

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
```

```
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type) and the plots within blocks (tomato types within soil types) independently. Use the `'effects'` contrasts when fitting the data for the type III sum of squares.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)',...
'DummyVarCoding','effects')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             60
    Fixed effects coefficients         20
    Random effects coefficients        18
    Covariance parameters               3

Formula:
    Yield ~ 1 + Tomato*Fertilizer + (1 | Soil) + (1 | Soil:Tomato)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    522.57    570.74    -238.29          476.57

Fixed effects coefficients (95% CIs):
    Name                                  Estimate    SE        tStat       DF    pValu
    '(Intercept)'                            104.6    3.3008      31.69     40    5.908
    'Tomato_Cherry'                            1.4    5.9353     0.23588    40       0
    'Tomato_Grape'                          -7.7667    5.9353     -1.3085    40       0
    'Tomato_Heirloom'                       -11.183    5.9353     -1.8842    40     0.0
    'Tomato_Plum'                            30.233    5.9353      5.0938    40    8.77
    'Fertilizer_1'                          -28.267    2.3475     -12.041    40    7.026
    'Fertilizer_2'                          -1.9333    2.3475    -0.82356    40       0
    'Fertilizer_3'                           10.733    2.3475      4.5722    40    4.57
    'Tomato_Cherry:Fertilizer_1'            -0.73333    4.6951    -0.15619    40       0
    'Tomato_Grape:Fertilizer_1'             -7.5667    4.6951     -1.6116    40       0
    'Tomato_Heirloom:Fertilizer_1'           5.1833    4.6951       1.104    40       0
    'Tomato_Plum:Fertilizer_1'               2.7667    4.6951     0.58927    40       0
    'Tomato_Cherry:Fertilizer_2'                7.6    4.6951      1.6187    40       0
    'Tomato_Grape:Fertilizer_2'                -1.9    4.6951    -0.40468    40       0
```

```
    'Tomato_Heirloom:Fertilizer_2'          5.5167    4.6951       1.175    40        0.
    'Tomato_Plum:Fertilizer_2'                -3.9    4.6951    -0.83066    40         0
    'Tomato_Cherry:Fertilizer_3'            -6.0667    4.6951     -1.2921    40        0.
    'Tomato_Grape:Fertilizer_3'              3.7667    4.6951     0.80226    40        0.
    'Tomato_Heirloom:Fertilizer_3'           3.1833    4.6951     0.67802    40        0.
    'Tomato_Plum:Fertilizer_3'                  1.1    4.6951     0.23429    40        0.

Random effects covariance parameters (95% CIs):
Group: Soil (3 Levels)
    Name1               Name2               Type         Estimate    Lower       Uppe
    '(Intercept)'       '(Intercept)'       'std'        2.5028      0.027711    226.

Group: Soil:Tomato (15 Levels)
    Name1               Name2               Type         Estimate    Lower     Upper
    '(Intercept)'       '(Intercept)'       'std'        10.225      6.1497    17.001

Group: Error
    Name            Estimate    Lower     Upper
    'Res Std'       10.499      8.5389    12.908
```

Perform an analysis of variance to test for the fixed-effects.

```
anova(lme)
```

```
ans =


    ANOVA marginal tests: DFMethod = 'Residual'

    Term                      FStat     DF1    DF2    pValue
    '(Intercept)'             1004.2     1     40     5.9086e-30
    'Tomato'                  7.1663     4     40     0.00018935
    'Fertilizer'              58.833     3     40     1.0024e-14
    'Tomato:Fertilizer'       1.4182    12     40        0.19804
```

The *p*-value for the constant term, 5.9086e-30, is the same as in the coefficient table in the `lme` display. The *p*-values of 0.00018935, 1.0024e-14, and 0.19804 for `Tomato`, `Fertilizer`, and `Tomato:Fertilizer` represent the combined significance for all tomato coefficients, fertilizer coefficients, and coefficients representing the interaction between the tomato and fertilizer, respectively. The *p*-value of 0.19804 indicates that the interaction between tomato and fertilizer is not significant.

Satterthwaite Approximation for Degrees of Freedom

Navigate to a folder containing sample data.

```
 cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit the model using the `'effects'` contrasts.

```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)',...
  'DummyVarCoding','effects')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           9
    Random effects coefficients         40
    Covariance parameters                4

Formula:
    Linear Mixed Formula with 4 predictors.

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -22.981    13.257    24.49            -48.981

Fixed effects coefficients (95% CIs):
    Name                    Estimate     SE           tStat
    '(Intercept)'             0.77122      0.24309      3.1725
    'InitialWeight'         0.0031879    0.0013814      2.3078
```

```
    'Program_A'              -0.11017     0.080377     -1.3707
    'Program_B'               0.25061      0.08045      3.1151
    'Program_C'              -0.14344     0.080475     -1.7824
    'Week'                    0.19881     0.033727      5.8946
    'Program_A:Week'         -0.025607     0.058417    -0.43835
    'Program_B:Week'          0.013164     0.058417     0.22535
    'Program_C:Week'         0.0049357     0.058417    0.084492


    DF     pValue         Lower          Upper
    111     0.0019549        0.28951        1.2529
    111      0.022863     0.00045067     0.0059252
    111       0.17323       -0.26945        0.0491
    111     0.0023402       0.091195       0.41003
    111      0.077424        -0.3029      0.016031
    111    4.1099e-08        0.13198       0.26564
    111       0.66198       -0.14136      0.090149
    111       0.82212       -0.10259       0.12892
    111       0.93282       -0.11082       0.12069

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1                Name2                Type
    '(Intercept)'        '(Intercept)'        'std'
    'Week'               '(Intercept)'        'corr'
    'Week'               'Week'               'std'


    Estimate    Lower      Upper
    0.18407     0.12281    0.27587
    0.66841     0.21076    0.88573
    0.15033     0.11004    0.20537

Group: Error
    Name             Estimate    Lower       Upper
    'Res Std'        0.10261     0.087882    0.11981
```

The *p*-values 0.022863 and 4.1099e-08 indicate significant effects of the initial weights of the subjects and the time factor in the amount of weight lost. The weight loss of subjects who are in program B is significantly different relative to the weight loss of subjects that are in program A. The lower and upper limits of the covariance parameters for the random effects do not include zero, thus they are significant.

Perform an F-test that all fixed-effects coefficients are zero.

```
anova(lme)

ans =


    ANOVA marginal tests: DFMethod = 'Residual'

    Term                    FStat       DF1    DF2
    '(Intercept)'             10.065    1      111
    'InitialWeight'            5.326    1      111
    'Program'                 3.6798    3      111
    'Week'                    34.747    1      111
    'Program:Week'          0.066648    3      111


    pValue
     0.0019549
      0.022863
      0.014286
    4.1099e-08
       0.97748
```

The *p*-values for the constant term, initial weight, and week are the same as in the coefficient table in the previous `lme` output display. The *p*-value of 0.014286 for `Program` represents the combined significance for all program coefficients. Similarly, the *p*-value for the interaction between program and week (`Program:Week`) measures the combined significance for all coefficients representing this interaction.

Now, use the Satterthwaite method to compute the degrees of freedom.

```
anova(lme,'DFMethod','Satterthwaite')

ans =


    ANOVA marginal tests: DFMethod = 'Satterthwaite'

    Term                    FStat       DF1    DF2
    '(Intercept)'             10.065    1      20.445
    'InitialWeight'            5.326    1          20
    'Program'                 3.6798    3       19.14
    'Week'                    34.747    1          20
    'Program:Week'          0.066648    3          20
```

```
pValue
  0.004695
  0.031827
  0.030233
9.1346e-06
   0.97697
```

The Satterthwaite method produces smaller denominator degrees of freedom and slightly larger *p*-values.

See Also

`fitlme` | `fitlmematrix` | `LinearMixedModel`

anova1

One-way analysis of variance

Syntax

```
p = anova1(y)
p = anova1(y,group)
p = anova1(y,group,displayopt)
[p,tbl] = anova1(___)
[p,tbl,stats] = anova1(___)
```

Description

`p = anova1(y)` returns the *p*-value for a balanced one-way ANOVA. It also displays the standard ANOVA table (tbl) and a box plot of the columns of y. `anova1` tests the hypothesis that the samples in `y` are drawn from populations with the same mean against the alternative hypothesis that the population means are not all the same.

`p = anova1(y,group)` returns the *p*-value for a balanced one-way ANOVA by group. It also displays the standard ANOVA table and a box-plot of the observations of y by group.

`p = anova1(y,group,displayopt)` enables the ANOVA table and box plot displays when displayopt is `'on'` (default) and suppresses the displays when displayopt is `'off'`.

`[p,tbl] = anova1(___)` returns the ANOVA table (including column and row labels) in the cell array `tbl`. To copy a text version of the ANOVA table to the clipboard, select **Edit > Copy Text**.

`[p,tbl,stats] = anova1(___)` returns a structure, `stats`, which you can use to perform a multiple comparison test. A multiple comparison test enables you to determine which pairs of group means are significantly different. To perform this test, use `multcompare`, providing the `stats` structure as an input argument.

Examples

One-Way ANOVA

Create sample data matrix `y` with columns that are constants, plus random normal disturbances with mean 0 and standard deviation 1.

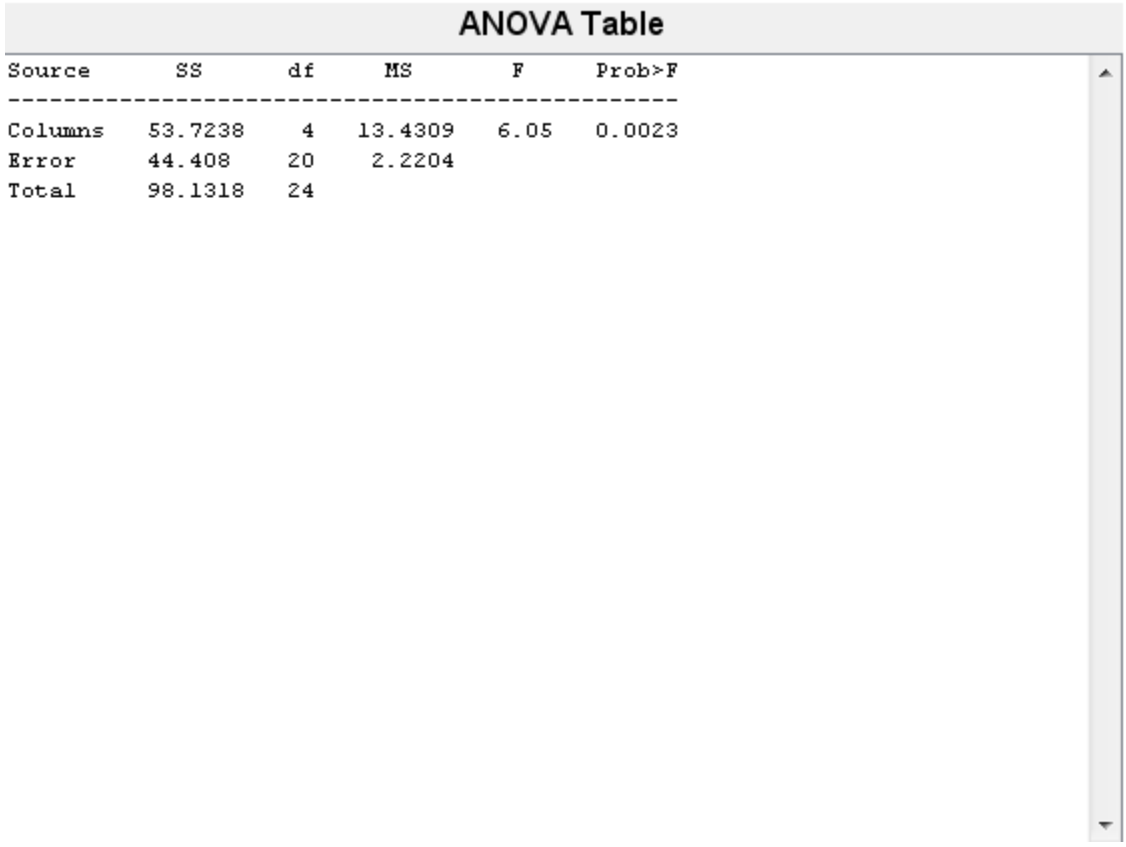
```
y = meshgrid(1:5);
rng default; % For reproducibility
y = y + normrnd(0,1,5,5)
```

```
y =

    1.5377    0.6923    1.6501    3.7950    5.6715
    2.8339    1.5664    6.0349    3.8759    3.7925
   -1.2588    2.3426    3.7254    5.4897    5.7172
    1.8622    5.5784    2.9369    5.4090    6.6302
    1.3188    4.7694    3.7147    5.4172    5.4889
```

Perform one-way ANOVA.

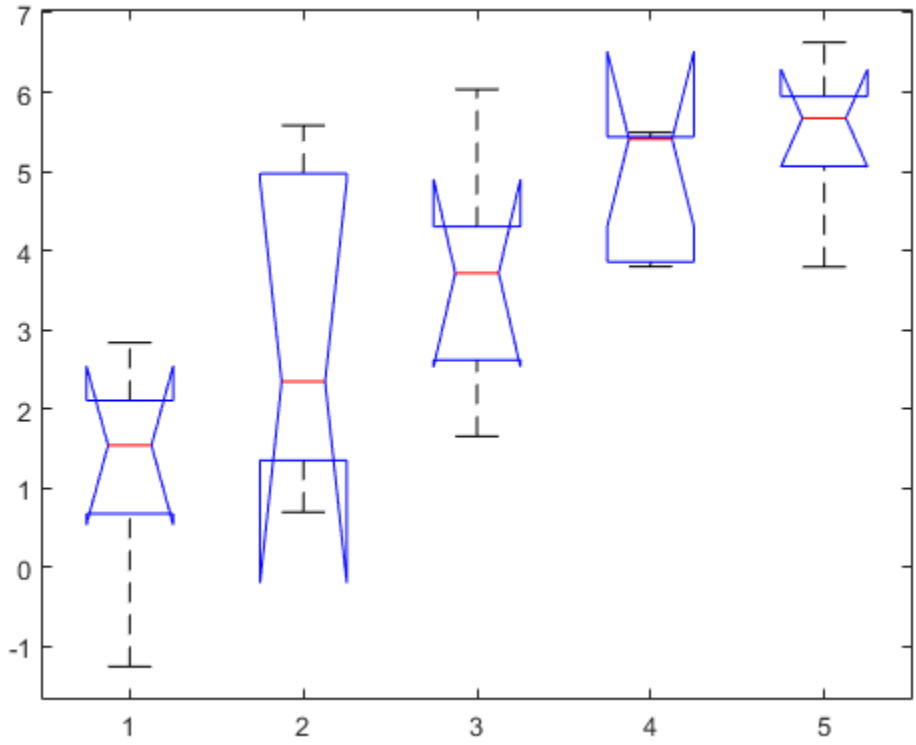
```
p = anova1(y)
```

```
p =

    0.0023
```



ANOVA Table

Source	SS	df	MS	F	Prob>F
Columns	53.7238	4	13.4309	6.05	0.0023
Error	44.408	20	2.2204		
Total	98.1318	24			



The ANOVA table shows the between-groups variation (`Columns`) and within-groups variation (`Error`). `SS` is the sum of squares, and `df` is the degrees of freedom. The total degrees of freedom is total number of observations minus one, which is 25 - 1 = 24. The between-groups degrees of freedom is number of groups minus one, which is 5 - 1 = 4. The within-groups degrees of freedom is total degrees of freedom minus the between groups degrees of freedom, which is 24 - 4 = 20.

`MS` is the mean squared error, which is `SS/df` for each source of variation. The *F*-statistic is the ratio of the mean squared errors (13.4309/2.2204). The *p*-value is the probability that the test statistic can take a value greater than or equal to the value of the test

statistic, i.e., P(F > 6.05). The small *p*-value of 0.0023 indicates that differences between column means are significant.

Compare Beam Strength Using One-Way ANOVA

Input the sample data.

```
strength = [82 86 79 83 84 85 86 87 74 82 ...
            78 75 76 77 79 79 77 78 82 79];
alloy = {'st','st','st','st','st','st','st','st',...
         'al1','al1','al1','al1','al1','al1',...
         'al2','al2','al2','al2','al2','al2'};
```

The data are from a study of the strength of structural beams in Hogg (1987). The vector strength measures deflections of beams in thousandths of an inch under 3000 pounds of force. The vector alloy identifies each beam as steel (`'st'`), alloy 1 (`'al1'`), or alloy 2 (`'al2'`). Although alloy is sorted in this example, grouping variables do not need to be sorted.

Test the null hypothesis that the steel beams are equal in strength to the beams made of the two more expensive alloys. Turn the figure display off and return the ANOVA results in a cell array.

```
[p,tbl] = anova1(strength,alloy,'off')
```

```
p =

   1.5264e-04


tbl =

    'Source'    'SS'          'df'    'MS'         'F'          'Prob>F'
    'Groups'    [184.8000]    [ 2]    [92.4000]    [15.4000]    [1.5264e-04]
    'Error'     [102.0000]    [17]    [ 6.0000]          []             []
    'Total'     [286.8000]    [19]          []           []             []
```

The total degrees of freedom is total number of observations minus one, which is $20 - 1 = 19$. The between-groups degrees of freedom is number of groups minus one, which is $3 - 1 = 2$. The within-groups degrees of freedom is total degrees of freedom minus the between groups degrees of freedom, which is $19 - 2 = 17$.

MS is the mean squared error, which is SS/df for each source of variation. The F-statistic is the ratio of the mean squared errors. The p-value is the probability that the test statistic can take a value greater than or equal to the value of the test statistic. The p-value of 1.5264e-04 suggests rejection of the null hypothesis.

You can retrieve the values in the ANOVA table by indexing into the cell array. Save the F-statistic value and the p-value in the new variables Fstat and pvalue.

```
Fstat = tbl{2,5}
pvalue = tbl{2,6}
```

```
Fstat =

   15.4000


pvalue =

   1.5264e-04
```

Multiple Comparisons for One-Way ANOVA

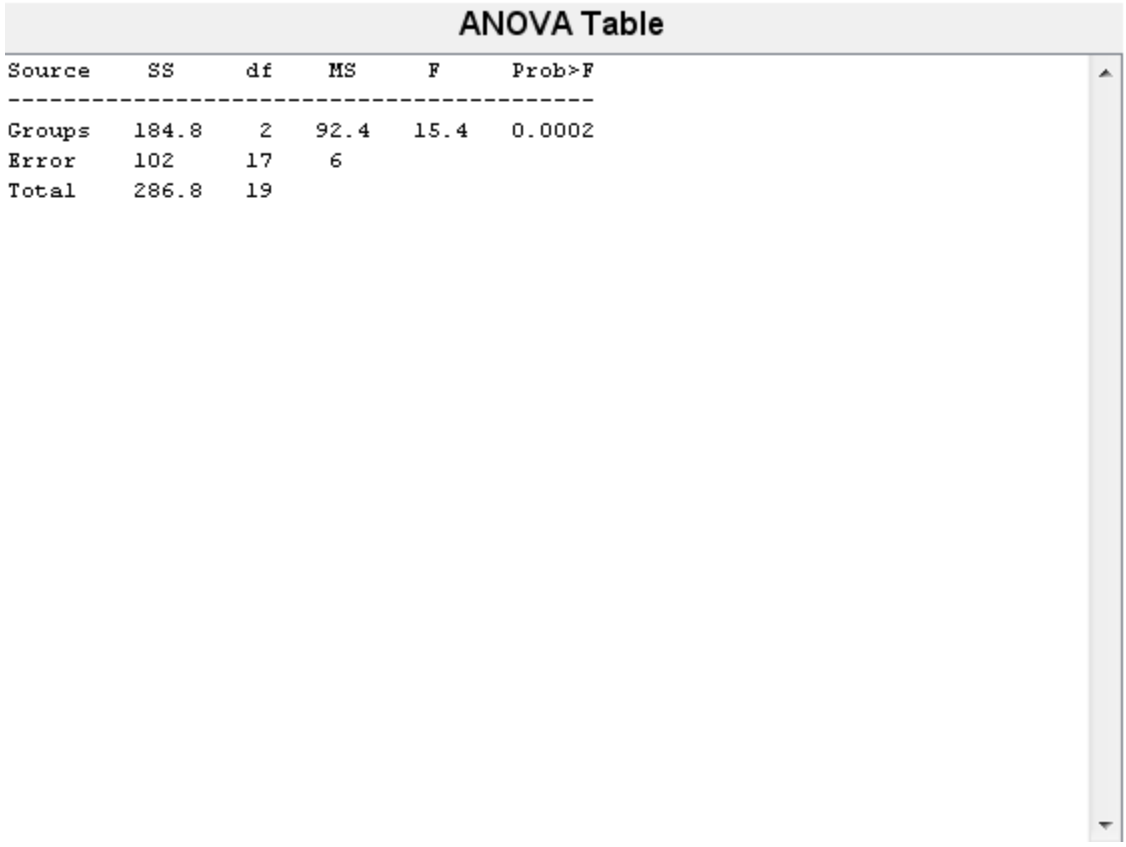
Input the sample data.

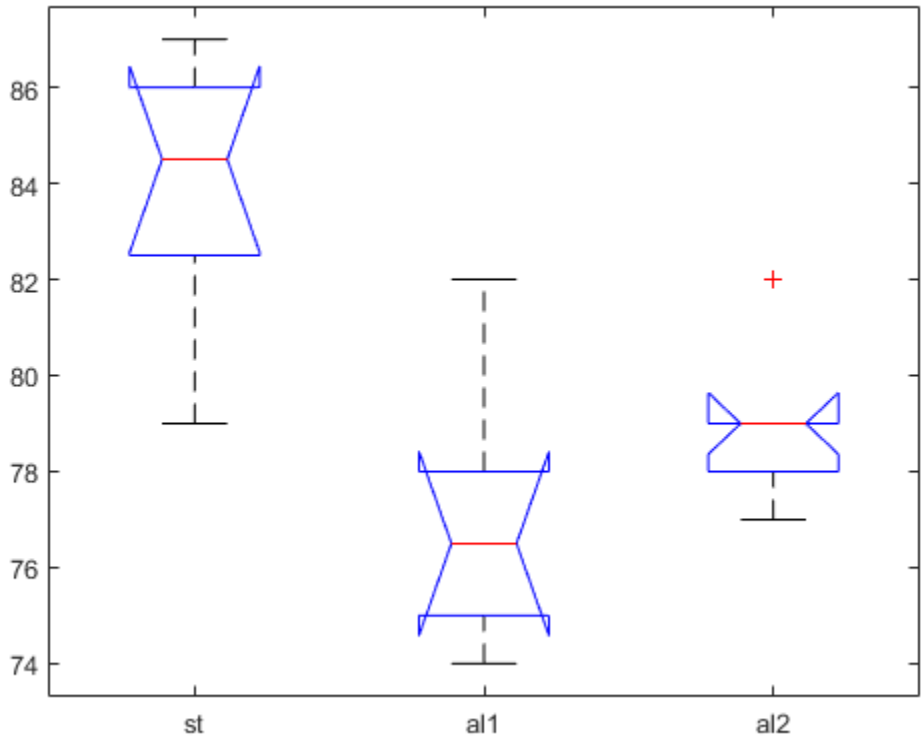
```
strength = [82 86 79 83 84 85 86 87 74 82 ...
            78 75 76 77 79 79 77 78 82 79];
alloy = {'st','st','st','st','st','st','st','st',...
         'al1','al1','al1','al1','al1','al1',...
         'al2','al2','al2','al2','al2','al2'};
```

The data are from a study of the strength of structural beams in Hogg (1987). The vector strength measures deflections of beams in thousandths of an inch under 3000 pounds of force. The vector alloy identifies each beam as steel (st), alloy 1 (al1), or alloy 2 (al2). Although alloy is sorted in this example, grouping variables do not need to be sorted.

Perform one-way ANOVA using anova1. Return the structure stats, which contains the statistics multcompare needs for performing “Multiple Comparisons”.

```
[~,~,stats] = anova1(strength,alloy);
```

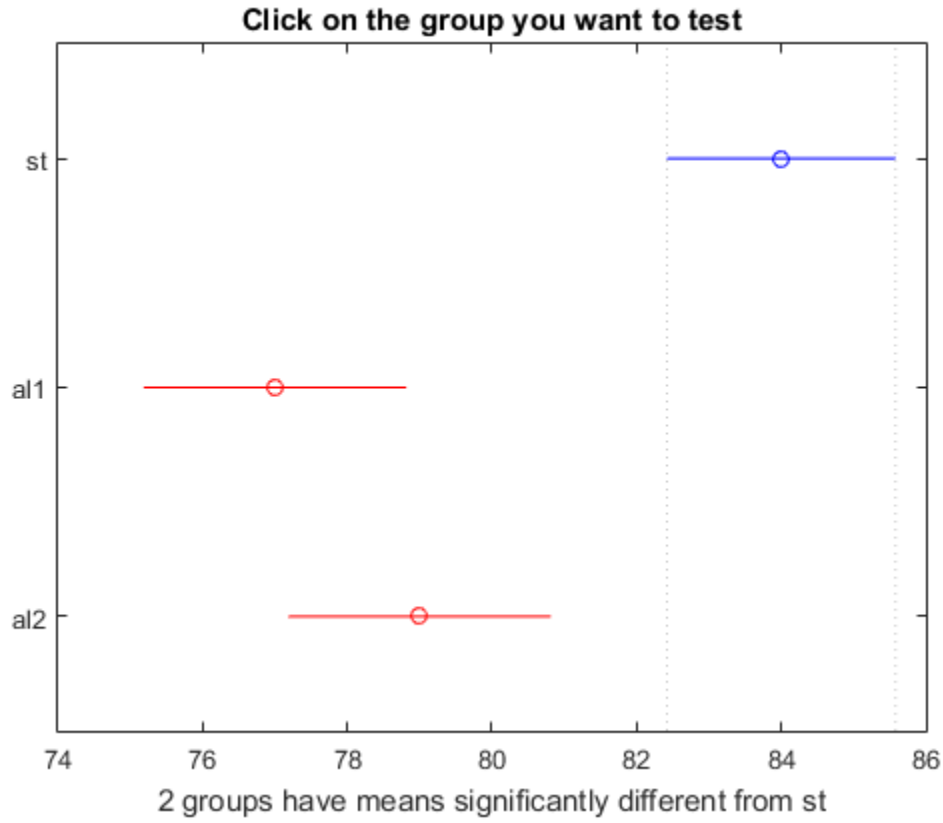

ANOVA Table
Source SS df MS F Prob>F
Groups 184.8 2 92.4 15.4 0.0002
Error 102 17 6
Total 286.8 19



The small *p*-value of 0.0002 suggests that the strength of the beams is not the same.

Perform a multiple comparison of the mean strength of the beams.

```
[c,~,~,gnames] = multcompare(stats);
```



Display the comparison results with the corresponding group names.

```
[gnames(c(:,1)), gnames(c(:,2)), num2cell(c(:,3:6))]
```

```
ans =

    'st'     'al1'    [ 3.6064]    [ 7]    [10.3936]    [1.6831e-04]
    'st'     'al2'    [ 1.6064]    [ 5]    [ 8.3936]    [    0.0040]
    'al1'    'al2'    [-5.6280]    [-2]    [ 1.6280]    [    0.3560]
```

The first two columns show the pair of groups that are compared. The fourth column shows the difference between the estimated group means. The third and fifth columns

show the lower and upper limits for the 95% confidence intervals of the true difference of means. The sixth column shows the *p*-value for a hypothesis that the true difference of means for the corresponding groups is equal to zero.

The first two rows show that both comparisons involving the first group (steel) have confidence intervals that do not include zero. Because the corresponding *p*-values (1.6831e-04 and 0.0040, respectively) are small, those differences are significant.

The third row shows that the differences in strength between the two alloys is not significant. A 95% confidence interval for the difference is [-5.6,1.6], so you cannot reject the hypothesis that the true difference is zero. The corresponding *p*-value of 0.3560 in the sixth column confirms this result.

In the figure, the blue bar represents the comparison interval for mean material strength for steel. The red bars represent the comparison intervals for the mean material strength for alloy 1 and alloy 2. Neither of the red bars overlap with the blue bar, which indicates that the mean material strength for steel is significantly different from that of alloy 1 and alloy 2. To confirm the significant difference by clicking the bars that represent alloy 1 and 2.

- "Perform One-Way ANOVA" on page 8-6

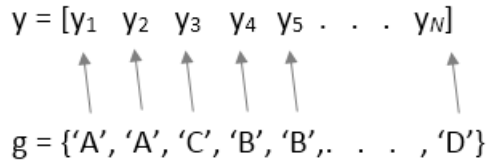
Input Arguments

y — sample data

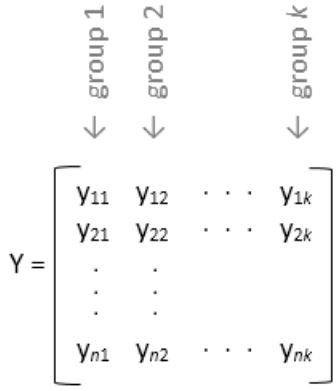
vector | matrix

Sample data, specified as a vector or a matrix.

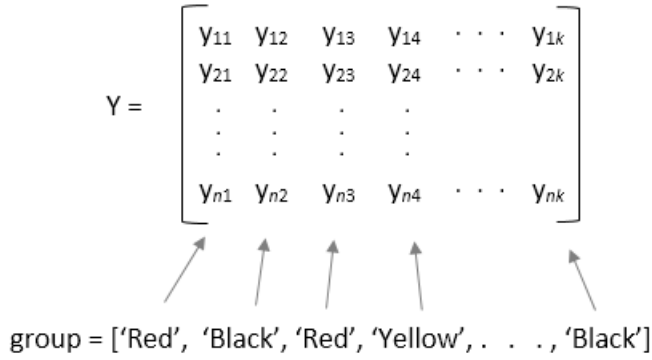
- If y is a vector, you must specify the group input argument. group must be a categorical variable, numeric vector, logical vector, string array, or cell array of strings, with one name for each element of y. The `anova1` function treats the y values corresponding to the same value of group as part of the same group. Use this design when groups have different numbers of elements (unbalanced ANOVA).



- If y is a matrix and you do not specify group, `anova1` treats each column of y as a separate group. In this design, the function evaluates whether the population means of the columns are equal. Use this design when each group has the same number of elements (balanced ANOVA).



- If `y` is a matrix and you specify group, then group must be a character array or cell array of strings, with one name for each column of y. The `anova1` function treats the columns that have the same group name as part of the same group.



If group contains empty or `NaN` valued cells or strings, `anova1` disregards the corresponding observations in y.

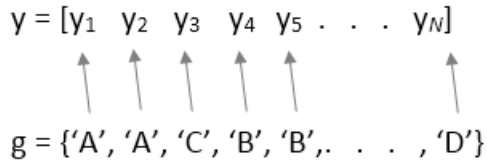
Data Types: `single` | `double`

`group` — Grouping variable

numeric vector | logical vector | character array | cell array of strings

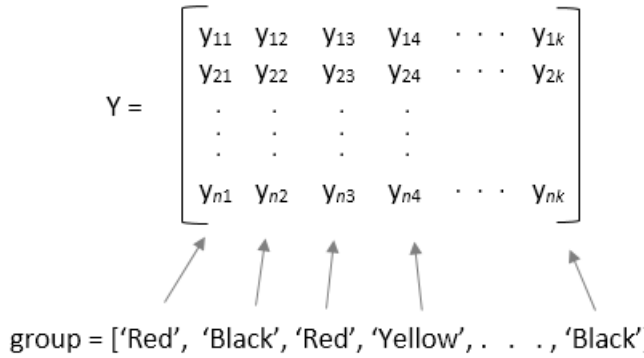
Grouping variable, specified as a numeric or logical vector, character array, or a cell array of strings, containing group names.

- If y is a vector, group must be a categorical variable, numeric vector, logical vector, string array, or cell array of strings, with one name for each element of y. The `anova1` function treats the y values corresponding to the same value of group as part of the same group.



  N is the total number of observations.

- If y is a matrix, then group must be a character array or cell array of strings, with one group name for each column of y. The `anova1` function treats the columns of y that have the same group name as part of the same group.



  If you do not want to specify group names, enter an empty array ([ ]) or omit this argument.

If group contains empty or `NaN` valued cells or strings, the corresponding observations in y are disregarded.

For more information on grouping variables, see “Grouping Variables” on page 2-52.

For example, if y is a vector, with observations categorized into groups 1, 2, and 3, then you can specify the grouping variables as follows.

Example: `'group',[1,2,1,3,1,...,3,1]`

For example, if y is a matrix, with six columns categorized into groups red, white, and black, then you can specify the grouping variables as follows.

Example: `'group',{'white','red','white','black','red'}`

Data Types: `single` | `double` | `logical` | `char` | `cell`

`displayopt` — Indicator to display ANOVA table and box plot

`'on'` (default) | `'off'`

Indicator to display ANOVA table and box plot, specified as `'on'` or `'off'`. When `displayopt` is `'off'`, `anova1` returns the output arguments, only. It does not display the standard ANOVA table and box-plot of the columns of y.

Example: `p = anova(x,group,'off')`

Output Arguments

`p` — *p*-value for the *F*-test

scalar value

p-value for the *F*-test, returned as a scalar value. *p*-value is the probability that the *F*-statistic can take a value larger than the computed test-statistic value. `anova1` tests the null hypothesis that all group means are equal to each other against the alternative hypothesis that at least one group mean is different from the others. The function derives the *p*-value from the cdf of the *F*-distribution.

A*p*-value that is smaller than the significance level indicates that at least one of the sample means is significantly different from the others. Common significance levels are 0.05 or 0.01.

`tbl` — ANOVA table

cell array

ANOVA table, returned as a cell array. `tbl` has six columns.

Column	Definition
`source`	The source of the variability.
`SS`	The sum of squares due to each source.
`df`	The degrees of freedom associated with each source. Suppose N is the total number of observations and k is the number of groups. Then, $N-k$ is the within-groups degrees of freedom (`Error`), $k-1$ is the between-groups degrees of freedom (`Columns`), and $N-1$ is the total degrees of freedom. $N-1=(N-k)+(k-1)$
`MS`	The mean squares for each source, which is the ratio `SS/df`.
`F`	F-statistic, which is the ratio of the mean squares.
`Prob>F`	The p-value, which is the probability that the F-statistic can take a value larger than the computed test-statistic value. `anova1` derives this probability from the cdf of F-distribution.

The rows of the ANOVA table show the variability in the data that is divided by the source.

Row	Definition
`Groups`	Variability due to the differences among the group means (variability *between* groups)
`Error`	Variability due to the differences between the data in each group and the group mean (variability *within* groups)
`Total`	Total variability

`stats` — Statistics for multiple comparison tests

structure

Statistics for multiple comparison tests, returned as a structure. stats has six fields.

Field name	Definition
`gnames`	Names of the groups
`n`	Number of observations in each group
`source`	Source of the stats output
`means`	Estimated values of the means
`df`	Error (within-groups) degrees of freedom ($N - k$, where N is the total number of observations and k is the number of groups)
`s`	Square root of the mean squared error

More About

Box-Plot

`anova1` returns box plots of the observations in y, by group. Box plots provide a visual comparison of the group location parameters.

If y is a vector, then the plot shows one box for each value of group. If `y` is a matrix and you do not specify group, then the plot shows one box for each column of y. On each box, the central mark is the median and the edges of the box are the 25th and 75th percentiles (1st and 3rd quantiles). The whiskers extend to the most extreme data points that are not considered outliers. The outliers are plotted individually. The interval endpoints are the extremes of the notches. The extremes correspond to $q2 - 1.57(q3 - q1)/\text{sqrt}(n)$ and $q2 + 1.57(q3 - q1)/\text{sqrt}(n)$, where $q2$ is the median (50th percentile), $q1$ and $q3$ are the 25th and 75th percentiles, respectively, and n is the number of observations without any `NaN` values.

Two medians are significantly different at the 5% significance level if their intervals do not overlap. This test is different from the F-test that ANOVA performs, but large differences in the center lines of the boxes correspond to large F-statistic values and correspondingly small p-values. For more information about box plots, see `boxplot`.

- “One-Way ANOVA” on page 8-3

- "Multiple Comparisons" on page 8-26

References

[1] Hogg, R. V., and J. Ledolter. *Engineering Statistics*. New York: MacMillan, 1987.

See Also

`anova2` | `anovan` | `boxplot` | `multcompare`

anova2

Two-way analysis of variance

`anova2` performs two-way analysis of variance (ANOVA) with balanced designs. To perform two-way ANOVA with unbalanced designs, see `anovan`.

Syntax

```
p = anova2(y,reps)
p = anova2(y,reps,displayopt)
[p,tbl] = anova2( ___ )
[p,tbl,stats] = anova2( ___ )
```

Description

`p = anova2(y,reps)` returns the *p*-values for a balanced two-way ANOVA for comparing the means of two or more columns and two or more rows of the observations in y.

reps is the number of replicates for each combination of factor groups, which must be constant, indicating a balanced design. For unbalanced designs, use `anovan`. The `anova2` function tests the main effects for column and row factors and their interaction effect. To test the interaction effect, reps must be greater than 1.

`anova2` also displays the standard ANOVA table.

`p = anova2(y,reps,displayopt)` enables the ANOVA table display when displayopt is `'on'` (default) and suppresses the display when displayopt is `'off'`.

`[p,tbl] = anova2( ___ )` returns the ANOVA table (including column and row labels) in cell array `tbl`. To copy a text version of the ANOVA table to the clipboard, select **Edit > Copy Text** menu.

`[p,tbl,stats] = anova2( ___ )` returns a `stats` structure, which you can use to perform a multiple comparison test. A multiple comparison test enables you to

determine which pairs of group means are significantly different. To perform this test, use `multcompare`, providing the stats structure as input.

Examples

Two-Way ANOVA

Load the sample data.

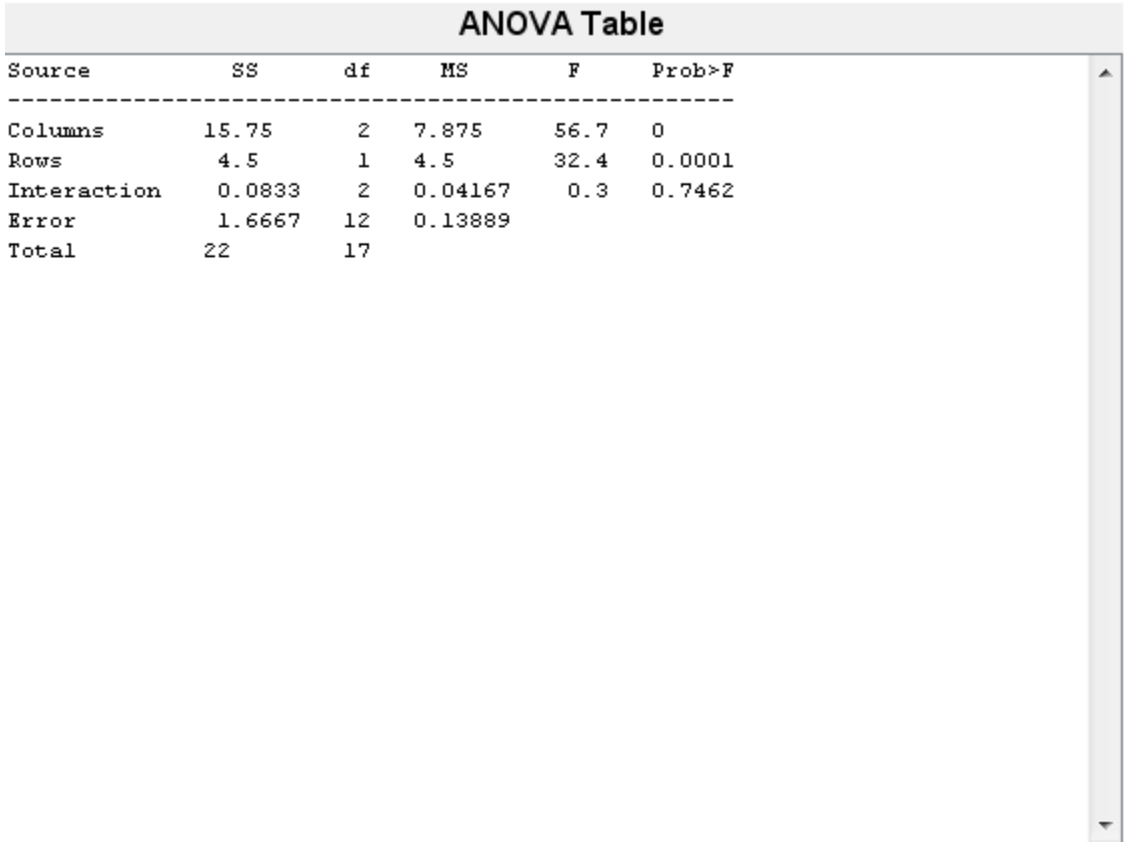
```
load popcorn
popcorn
```

```
popcorn =

    5.5000    4.5000    3.5000
    5.5000    4.5000    4.0000
    6.0000    4.0000    3.0000
    6.5000    5.0000    4.0000
    7.0000    5.5000    5.0000
    7.0000    5.0000    4.5000
```

The data is from a study of popcorn brands and popper types (Hogg 1987). The columns of the matrix `popcorn` are brands, Gourmet, National, and Generic, respectively. The rows are popper types, oil and air. In the study, researchers popped a batch of each brand three times with each popper, that is, the number of replications is 3. The first three rows correspond to the oil popper, and the last three rows correspond to the air popper. The response values are the yield in cups of popped popcorn.

Perform a two-way ANOVA. Save the ANOVA table in the cell array `tbl` for easy access to results.

```
[p,tbl] = anova2(popcorn,3);
```



The column `Prob>F` shows the *p*-values for the three brands of popcorn (0.0000), the two popper types (0.0001), and the interaction between brand and popper type (0.7462). These values indicate that popcorn brand and popper type affect the yield of popcorn, but there is no evidence of an interaction effect of the two.

Display the cell array containing the ANOVA table.

```
tbl
```

```
tbl =

    'Source'         'SS'         'df'    'MS'        'F'           'Prob>F'
    'Columns'        [15.7500]    [ 2]    [7.8750]    [56.7000]     [7.6790e-07]
```

```
    'Rows'           [ 4.5000]    [ 1]    [4.5000]    [32.4000]    [1.0037e-04]
    'Interaction'    [ 0.0833]    [ 2]    [0.0417]    [ 0.3000]    [    0.7462]
    'Error'          [ 1.6667]    [12]    [0.1389]          []             []
    'Total'          [     22]    [17]          []          []             []
```

Store the *F*-statistic for the factors and factor interaction in separate variables.

```
Fbrands = tbl{2,5}
Fpoppertype = tbl{3,5}
Finteraction = tbl{4,5}
```

```
Fbrands =

   56.7000


Fpoppertype =

   32.4000


Finteraction =

    0.3000
```

Multiple Comparisons for Two-Way ANOVA

Load the sample data.

```
load popcorn
popcorn
```

```
popcorn =

    5.5000    4.5000    3.5000
    5.5000    4.5000    4.0000
    6.0000    4.0000    3.0000
    6.5000    5.0000    4.0000
    7.0000    5.5000    5.0000
    7.0000    5.0000    4.5000
```

The data is from a study of popcorn brands and popper types (Hogg 1987). The columns of the matrix `popcorn` are brands (Gourmet, National, and Generic). The rows are popper types oil and air. In the study, researchers popped a batch of each brand three times with each popper. The values are the yield in cups of popped popcorn.

Perform a two-way ANOVA. Also compute the statistics that you need to perform a multiple comparison test on the main effects.

```
[~,~,stats] = anova2(popcorn,3,'off')
```

```
stats =

      source: 'anova2'
     sigmasq: 0.1389
    colmeans: [6.2500 4.7500 4]
        coln: 6
    rowmeans: [4.5000 5.5000]
        rown: 9
       inter: 1
        pval: 0.7462
          df: 12
```

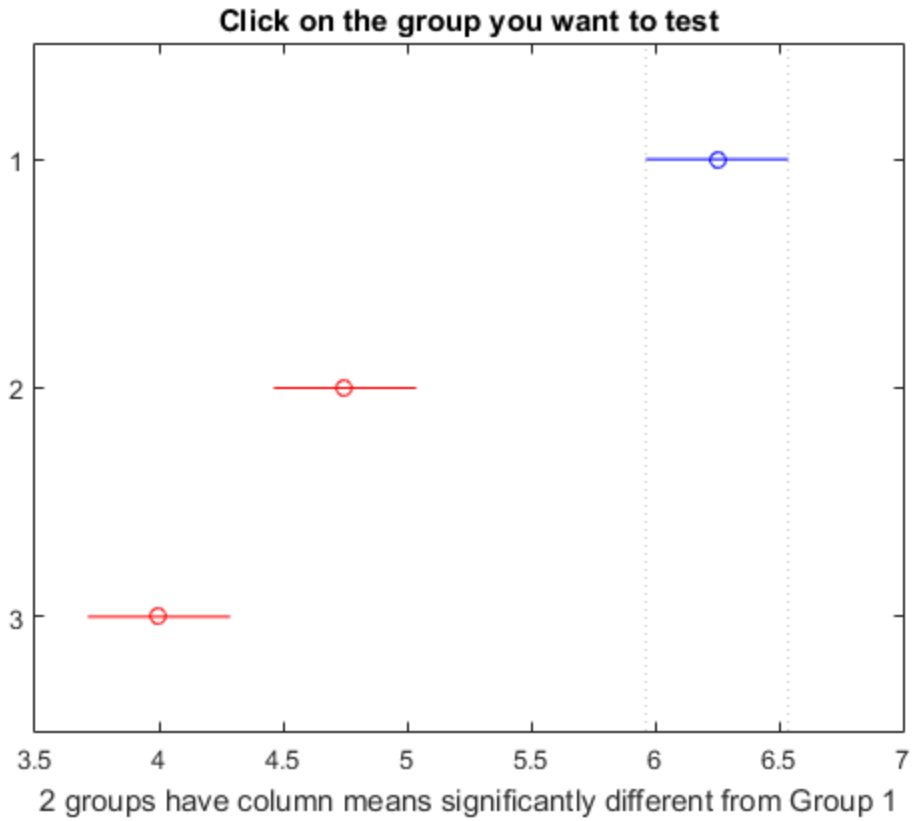
The `stats` structure includes

- The mean squared error (`sigmasq`)
- The estimates of the mean yield for each popcorn brand (`colmeans`)
- The number of observations for each popcorn brand (`coln`)
- The estimate of the mean yield for each popper type (`rowmeans`)
- The number of observations for each popper type (`rown`)
- The number of interactions (`inter`)
- The *p*-value that shows the significance level of the interaction term (`pval`)
- The error degrees of freedom (`df`).

Perform a multiple comparison test to see if the popcorn yield differs between pairs of popcorn brands (columns).

```
c = multcompare(stats)
```

```
Note: Your model includes an interaction term.  A test of main effects can be
difficult to interpret when the model includes interactions.

c =

    1.0000    2.0000    0.9260    1.5000    2.0740    0.0000
    1.0000    3.0000    1.6760    2.2500    2.8240    0.0000
    2.0000    3.0000    0.1760    0.7500    1.3240    0.0116
```



The first two columns of `c` show the groups that are compared. The fourth column shows the difference between the estimated group means. The third and fifth columns show the lower and upper limits for 95% confidence intervals for the true mean difference.

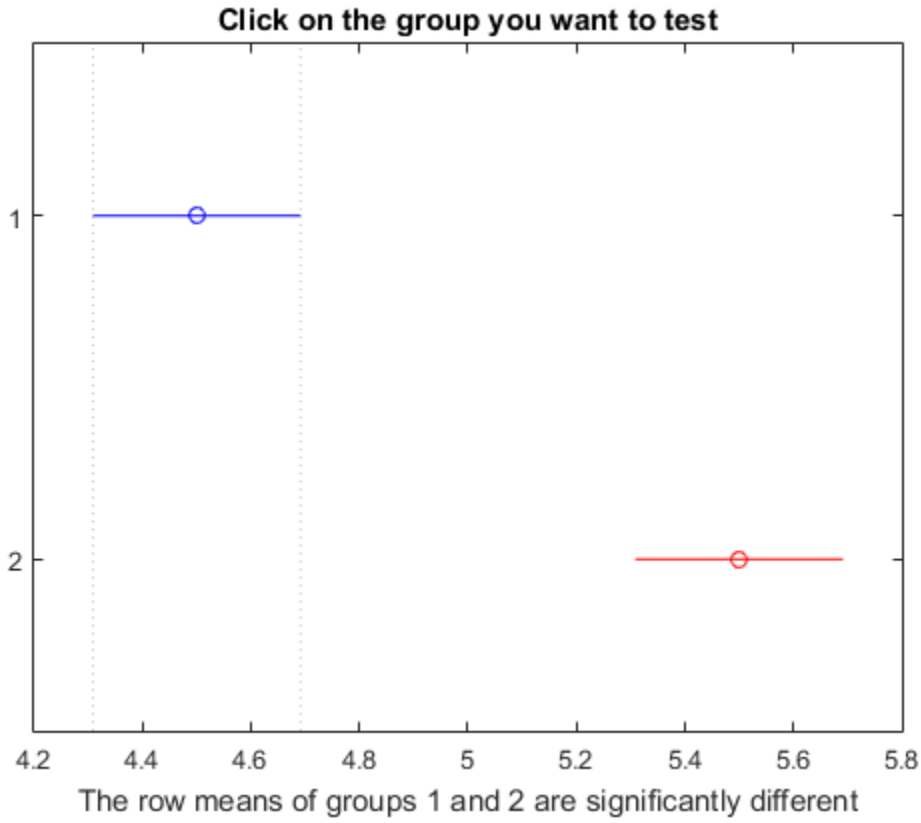
The sixth column contains the *p*-value for a hypothesis test that the corresponding mean difference is equal to zero. All *p*-values (0, 0, and 0.0116) are very small, which indicates that the popcorn yield differs across all three brands.

The figure shows the multiple comparison of the means. By default, the group 1 mean is highlighted and the comparison interval is in blue. Because the comparison intervals for the other two groups do not intersect with the intervals for the group 1 mean, they are highlighted in red. This lack of intersection indicates that both means are different than group 1 mean. Select other group means to confirm that all group means are significantly different from each other.

Perform a multiple comparison test to see the popcorn yield differs between the two popper types (rows).

```
c = multcompare(stats,'Estimate','row')
```

```
Note: Your model includes an interaction term.  A test of main effects can be
difficult to interpret when the model includes interactions.

c =

    1.0000    2.0000   -1.3828   -1.0000   -0.6172    0.0001
```



The small *p*-value of 0.0001 indicates that the popcorn yield differs between the two popper types (air and oil). The figure shows the same results. The disjoint comparison intervals indicate that the group means are significantly different from each other.

- "Perform Two-Way ANOVA" on page 8-18

Input Arguments

y — Sample data

matrix

Sample data, specified as a matrix. The columns correspond to groups of one factor, and the rows correspond to the groups of the other factor and the replications. Replications are the measurements or observations for each combination of groups (levels) of the row and column factor. For example, in the following data the row factor *A* has three levels, column factor *B* has two levels, and there are two replications (`reps = 2`). The subscripts indicate row, column, and replication, respectively.

$$\begin{matrix} B=1 & B=2 \\ \left[\begin{matrix} y_{111} & y_{121} \\ y_{112} & y_{122} \end{matrix}\right. & \left.\begin{matrix} \\ \\ \end{matrix}\right\} A=1 \\ \left[\begin{matrix} y_{211} & y_{221} \\ y_{212} & y_{222} \end{matrix}\right. & \left.\begin{matrix} \\ \\ \end{matrix}\right\} A=2 \\ \left[\begin{matrix} y_{311} & y_{321} \\ y_{312} & y_{322} \end{matrix}\right. & \left.\begin{matrix} \\ \\ \end{matrix}\right\} A=3 \end{matrix}$$

Data Types: `single` | `double`

`reps` — Number of replications

1 (default) | an integer number

Number of replications for each combination of groups, specified as an integer number. For example, the following data has two replications (`reps = 2`) for each group combination of row factor *A* and column factor *B*.

$$\begin{matrix} B=1 & B=2 \\ \left[\begin{matrix} y_{111} & y_{121} \\ y_{112} & y_{122} \end{matrix}\right. & \left.\begin{matrix} \\ \\ \end{matrix}\right\} A=1 \\ \left[\begin{matrix} y_{211} & y_{221} \\ y_{212} & y_{222} \end{matrix}\right. & \left.\begin{matrix} \\ \\ \end{matrix}\right\} A=2 \\ \left[\begin{matrix} y_{311} & y_{321} \\ y_{312} & y_{322} \end{matrix}\right. & \left.\begin{matrix} \\ \\ \end{matrix}\right\} A=3 \end{matrix}$$

- When `reps` is `1` (default), `anova2` returns two *p*-values in vector `p`:
  - The *p*-value for the null hypothesis that all samples from factor *B* (i.e., all column samples in `y`) are drawn from the same population.

  - The p-value for the null hypothesis, that all samples from factor A (i.e., all row samples in `y`) are drawn from the same population.
- When `reps` is greater than `1`, `anova2` also returns the p-value for the null hypothesis that factors A and B have no interaction (i.e., the effects due to factors A and B are *additive*).

Example: `p = anova(y,3)` specifies that each combination of groups (levels) has three replications.

Data Types: `single | double`

`displayopt` — Indicator to display the ANOVA table

`'on'` (default) | `'off'`

Indicator to display the ANOVA table as a figure, specified as `'on'` or `'off'`.

Data Types: `logical`

Output Arguments

`p` — *p*-value

scalar value

p-value for the F-test, returned as a scalar value. A small p-value indicates that the results are statistically significant. Common significance levels are 0.05 or 0.01. For example:

- A sufficiently small p-value for the null hypothesis for group means of row factor A suggests that at least one row-sample mean is significantly different from the other row-sample means; i.e., there is a main effect due to factor A
- A sufficiently small p-value for the null hypothesis for group (level) means of column factor B suggests that at least one column-sample mean is significantly different from the other column-sample means; i.e., there is a main effect due to factor B.
- A sufficiently small p-value for combinations of groups (levels) of factors A and B suggests that there is an interaction between factors A and B.

`tbl` — ANOVA table

cell array

ANOVA table, returned as a cell array. `tbl` has six columns.

Column name	Definition
`source`	Source of the variability.
`SS`	Sum of squares due to each source.
`df`	Degrees of freedom associated with each source.
`MS`	Mean squares for each source, which is the ratio `SS/df`.
`F`	*F*-statistic, which is the ratio of the mean squares.
`Prob>F`	*p*-value, which is the probability that the *F*-statistic can take a value larger than the computed test-statistic value. `anova1` derives this probability from the cdf of the *F*-distribution.

The rows of the ANOVA table show the variability in the data, divided by the source into three or four parts, depending on the value of `reps`.

Row	Definition
`Columns`	Variability due to the differences among the column means
`Rows`	Variability due to the differences among the row means
`Interaction`	Variability due to the interaction between rows and columns (if reps is greater than its default value of 1)
`Error`	Remaining variability not explained by any systematic source

Data Types: `cell`

`stats` — Statistics for multiple comparison test

structure

Statistics for multiple comparisons tests, returned as a structure. Use `multcompare` to perform multiple comparison tests, supplying stats as an input argument. stats has nine fields.

Field	Definition
`source`	Source of the stats output
`sigmasq`	Mean squared error
`colmeans`	Estimated values of the column means
`coln`	Number of observations for each group in columns
`rowmeans`	Estimated values of the row means
`rown`	Number of observations for each group in rows
`inter`	Number of interactions
`pval`	*p*-value for the interaction term
`df`	Error degrees of freedom (*reps* — 1)**r***c* where *reps* is the number of replications and *c* and *r* are the number of groups in factors, respectively.

Data Types: `struct`

More About

- "Two-Way ANOVA" on page 8-15
- "Multiple Comparisons" on page 8-26

References

[1] Hogg, R. V., and J. Ledolter. *Engineering Statistics*. New York: MacMillan, 1987.

See Also

`anova1` | `anovan` | `multcompare`

anovan

N-way analysis of variance

Syntax

```
p = anovan(y,group)
p = anovan(y,group,Name,Value)
[p,tbl] = anovan( ___ )
[p,tbl,stats] = anovan( ___ )
[p,tbl,stats,terms] = anovan( ___ )
```

Description

`p = anovan(y,group)` returns a vector of *p*-values, one per term, for multiway (*n*-way) analysis of variance (ANOVA) for testing the effects of multiple factors on the mean of the vector `y`.

`anovan` also displays a figure showing the standard ANOVA table.

`p = anovan(y,group,Name,Value)` returns a vector of *p*-values for multiway (*n*-way) ANOVA using additional options specified by one or more Name,Value pair arguments.

For example, you can specify which predictor variable is continuous, if any, or the type of sum of squares to use.

`[p,tbl] = anovan( ___ )` returns the ANOVA table (including factor labels) in cell array `tbl` for any of the input arguments specified in the previous syntaxes. Copy a text version of the ANOVA table to the clipboard by using the `Copy Text` item on the **Edit** menu.

`[p,tbl,stats] = anovan( ___ )` returns a stats structure that you can use to perform a multiple comparison test, which enables you to determine which pairs of group means are significantly different. You can perform such a test using the `multcompare` function by providing the stats structure as input.

`[p,tbl,stats,terms] = anovan( ___ )` returns the main and interaction terms used in the ANOVA computations in terms.

Examples

Three-Way ANOVA

Load the sample data.

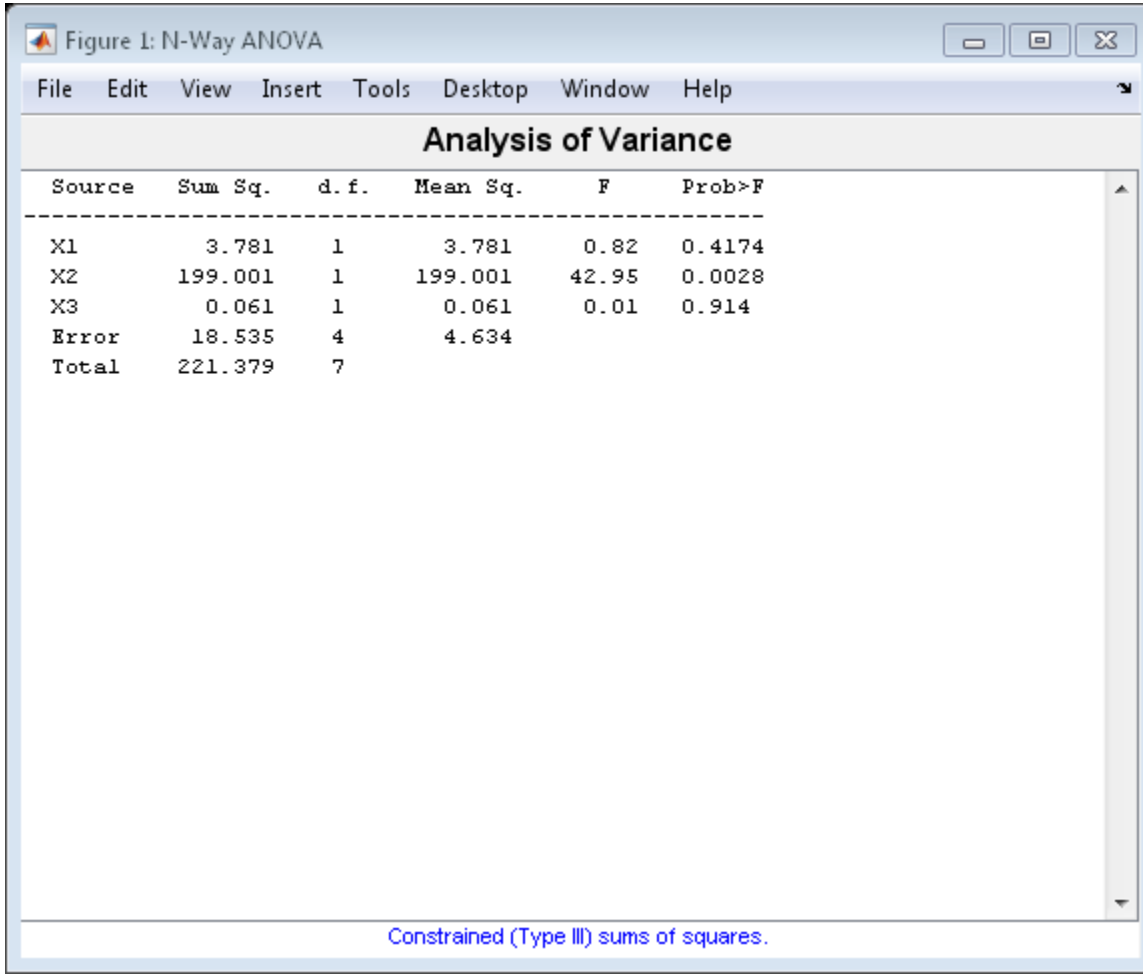
```
y = [52.7 57.5 45.9 44.5 53.0 57.0 45.9 44.0]';
g1 = [1 2 1 2 1 2 1 2];
g2 = {'hi';'hi';'lo';'lo';'hi';'hi';'lo';'lo'};
g3 = {'may';'may';'may';'may';'june';'june';'june';'june'};
```

`y` is the response vector and `g1`, `g2`, and `g3` are the grouping variables (factors). Each factor has two levels ,and every observation in `y` is identified by a combination of factor levels. For example, observation `y(1)` is associated with level 1 of factor `g1`, level `'hi'` of factor `g2`, and level `'may'` of factor `g3`. Similarly, observation `y(6)` is associated with level 2 of factor `g1`, level `'hi'` of factor `g2`, and level `'june'` of factor `g3`.

Test if the response is the same for all factor levels.

```
p = anovan(y,{g1,g2,g3})
```

```
p =

    0.4174
    0.0028
    0.9140
```

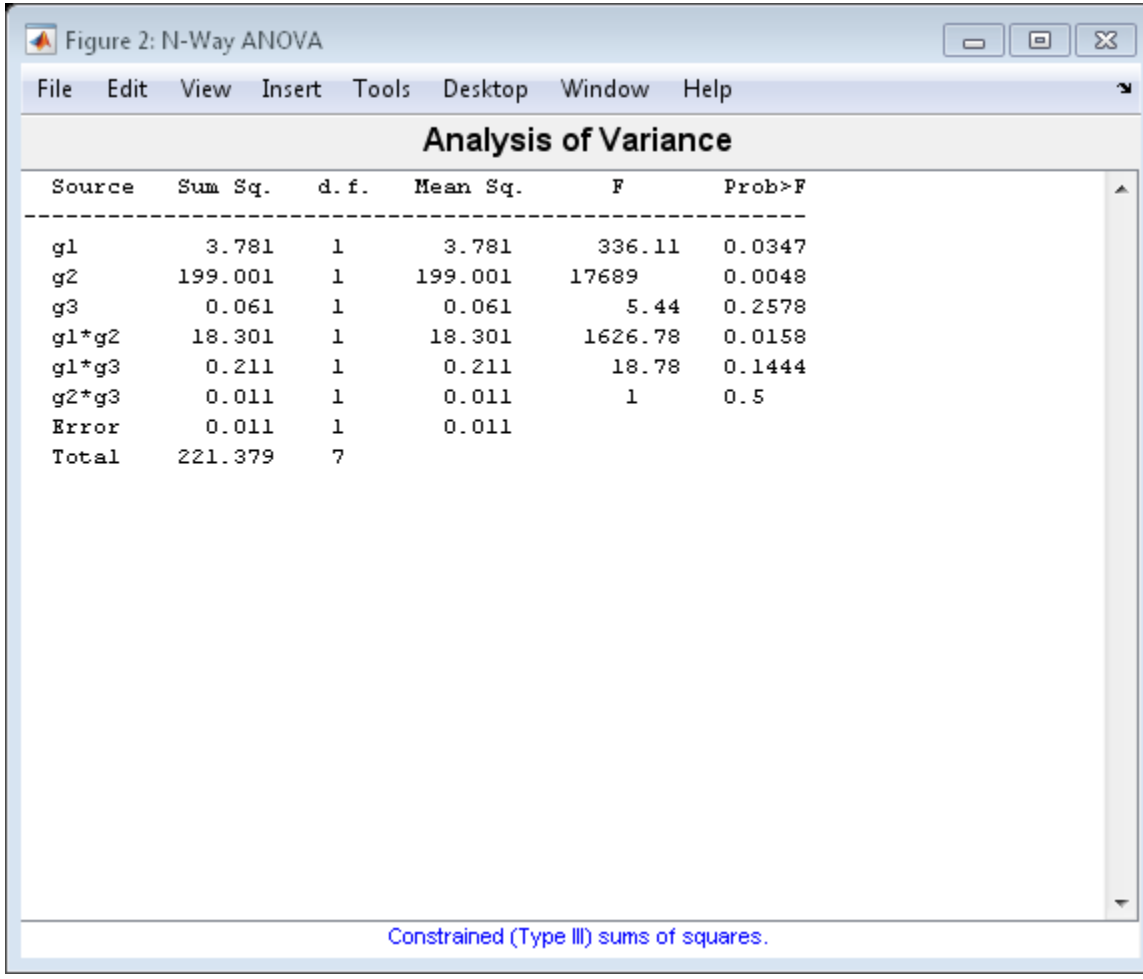


In the ANOVA table, `X1`, `X2`, and `X3` correspond to the factors `g1`, `g2`, and `g3`, respectively. The *p*-value 0.4174 indicates that the mean responses for levels 1 and 2 of the factor `g1` are not significantly different. Similarly, the *p*-value 0.914 indicates that the mean responses for levels `'hi'` and `'lo'` of the factor `g3` are not significantly different. However, the *p*-value 0.0028 is small enough to conclude that the mean responses are significantly different for the two levels, `'may'` and `'june'`, of the factor `g3`. By default, `anovan` computes *p*-values just for the three main effects.

Test the two-factor interactions. This time specify the variable names.

```
p = anovan(y,{g1 g2 g3},'model','interaction','varnames',{'g1','g2','g3'})
```

```
p =

    0.0347
    0.0048
    0.2578
    0.0158
    0.1444
    0.5000
```



The interaction terms are represented by `g1*g2`, `g1*g3`, and `g2*g3` in the ANOVA table. The first three entries of `p` are the *p*-values for the main effects. The last three entries are the *p*-values for the two-way interactions. The *p*-value of 0.0158 indicates that the interaction between `g1` and `g2` is significant. The *p*-values of 0.1444 and 0.5 indicate that the corresponding interactions are not significant.

Two-Way ANOVA for Unbalanced Design

Load the sample data.

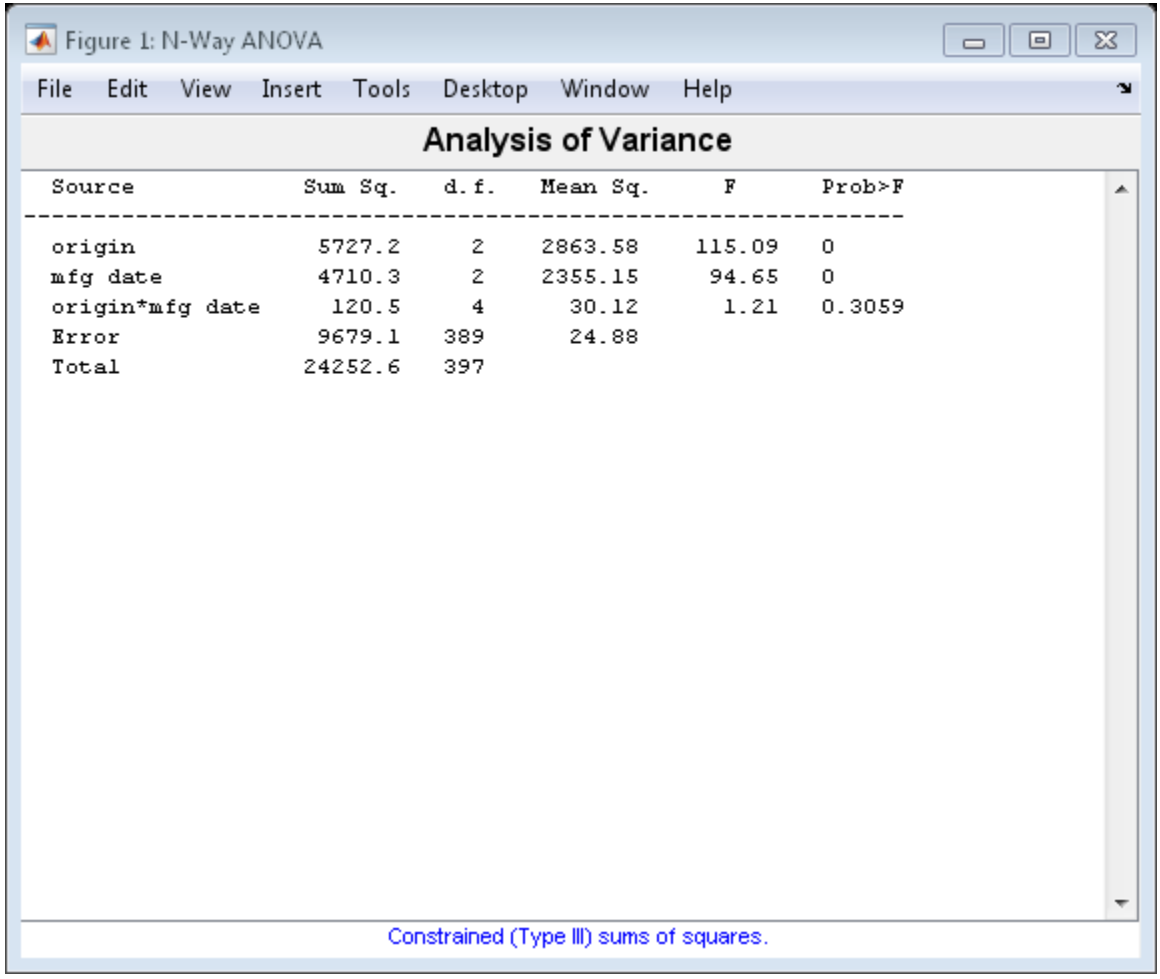
```
load carbig
```

The data has measurements on 406 cars. The variable `org` shows where the cars were made and `when` shows when in the year the cars were manufactured.

Study how the mileage depends on when and where the cars were made. Also include the two-way interactions in the model.

```
p = anovan(MPG,{org when},'model',2,'varnames',{'origin','mfg date'})
```

```
p =

    0.0000
    0.0000
    0.3059
```



The `'model',2` name-value pair argument represents the two-way interactions. The *p*-value for the interaction term, 0.3059, is not small, indicating little evidence that the effect of the time of manufacture (`mfg date`) depends on where the car was made (`origin`). The main effects of origin and manufacturing date, however, are significant, both *p*-values are 0.

Multiple Comparisons for Three-Way ANOVA

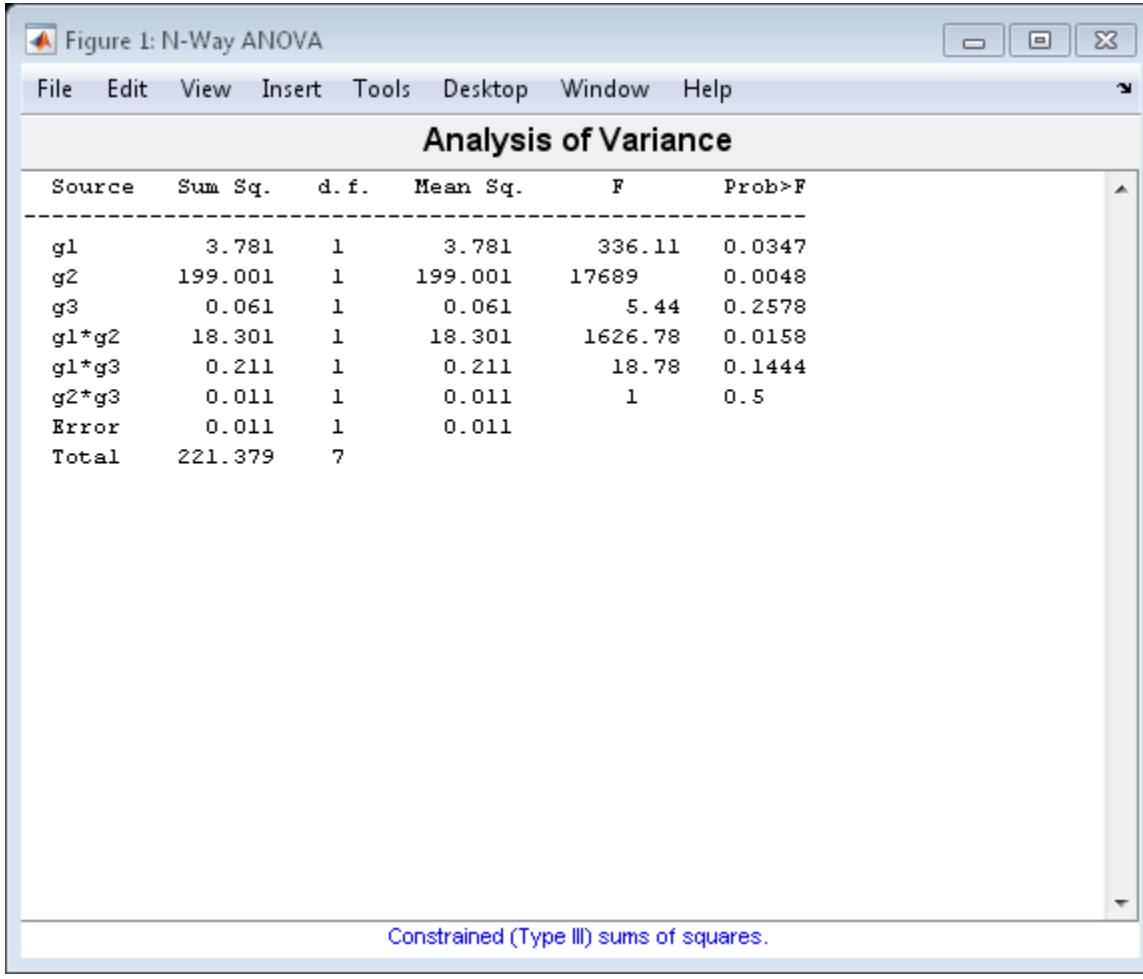
Load the sample data.

```
y = [52.7 57.5 45.9 44.5 53.0 57.0 45.9 44.0]';
g1 = [1 2 1 2 1 2 1 2];
g2 = {'hi';'hi';'lo';'lo';'hi';'hi';'lo';'lo'};
g3 = {'may';'may';'may';'may';'june';'june';'june';'june'};
```

`y` is the response vector and `g1`, `g2`, and `g3` are the grouping variables (factors). Each factor has two levels, and every observation in `y` is identified by a combination of factor levels. For example, observation `y(1)` is associated with level 1 of factor `g1`, level `'hi'` of factor `g2`, and level `'may'` of factor `g3`. Similarly, observation `y(6)` is associated with level 2 of factor `g1`, level `'hi'` of factor `g2`, and level `'june'` of factor `g3`.

Test if the response is the same for all factor levels. Also compute the statistics required for multiple comparison tests.

```
[~,~,stats] = anovan(y,{g1 g2 g3},'model','interaction',...
    'varnames',{'g1','g2','g3'});
```

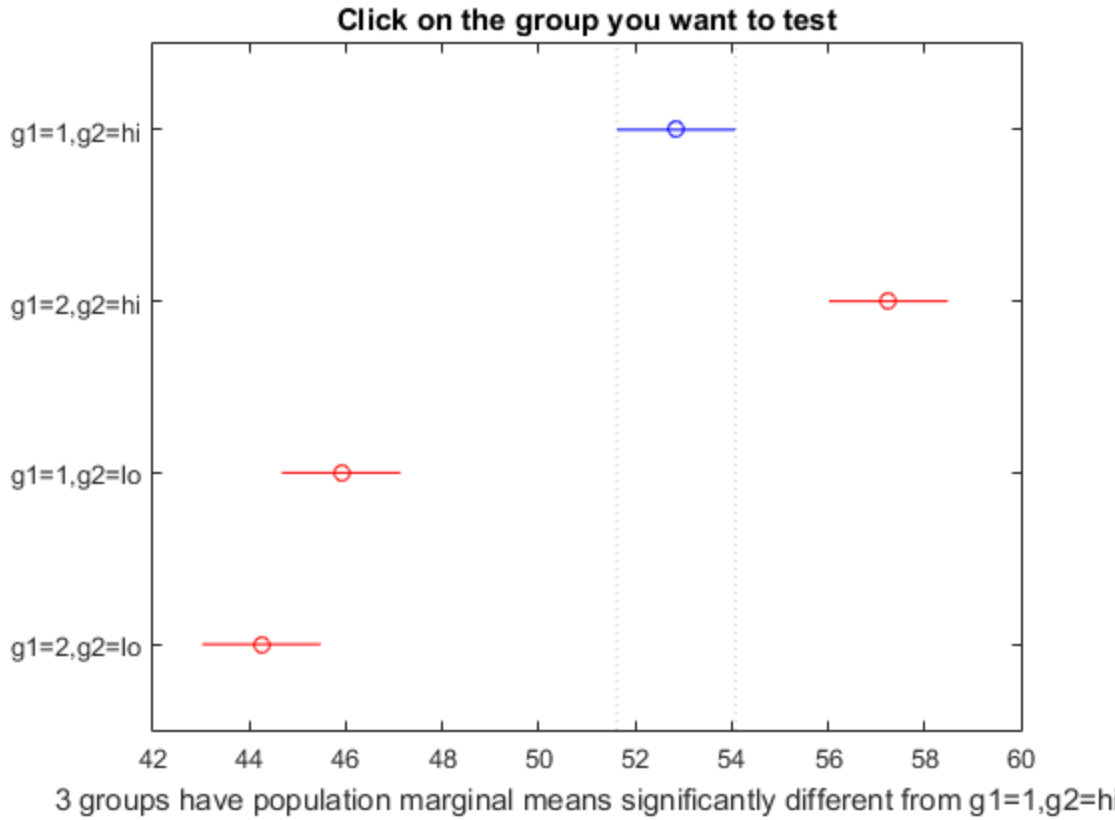


The *p*-value of 0.2578 indicates that the mean responses for levels `'may'` and `'june'` of factor `g3` are not significantly different. The *p*-value of 0.0347 indicates that the mean responses for levels `1` and `2` of factor `g1` are significantly different. Similarly, the *p*-value of 0.0048 indicates that the mean responses for levels `'hi'` and `'lo'` of factor `g2` are significantly different.

Perform multiple comparison tests to find out which groups of the factors `g1` and `g2` are significantly different.

```
results = multcompare(stats,'Dimension',[1 2])
```

```
results =

    1.0000    2.0000   -6.8604   -4.4000   -1.9396    0.0280
    1.0000    3.0000    4.4896    6.9500    9.4104    0.0177
    1.0000    4.0000    6.1396    8.6000   11.0604    0.0143
    2.0000    3.0000    8.8896   11.3500   13.8104    0.0108
    2.0000    4.0000   10.5396   13.0000   15.4604    0.0095
    3.0000    4.0000   -0.8104    1.6500    4.1104    0.0745
```



multcompare compares the combinations of groups (levels) of the two grouping variables, `g1` and `g2`. In the `results` matrix, the number 1 corresponds to the combination of level `1` of `g1` and level `hi` of `g2`, the number 2 corresponds to the combination of level `2` of `g1` and level `hi` of `g2`. Similarly, the number 3 corresponds to the combination of level `1` of `g1` and level `lo` of `g2`, and the number 4 corresponds to the combination of level `2` of `g1` and level `lo` of `g2`. The last column of the matrix contains the *p*-values.

For example, the first row of the matrix shows that the combination of level `1` of `g1` and level `hi` of `g2` has the same mean response values as the combination of level `2` of `g1` and level `hi` of `g2`. The *p*-value corresponding to this test is 0.0280, which indicates that the mean responses are significantly different. You can also see this result in the figure. The blue bar shows the comparison interval for the mean response for the combination of level `1` of `g1` and level `hi` of `g2`. The red bars are the comparison intervals for the mean response for other group combinations. None of the red bars overlap with the blue bar, which means the mean response for the combination of level `1` of `g1` and level `hi` of `g2` is significantly different from the mean response for other group combinations.

You can test the other groups by clicking on the corresponding comparison interval for the group. The bar you click on turns to blue. The bars for the groups that are significantly different are red. The bars for the groups that are not significantly different are gray. For example, if you click on the comparison interval for the combination of level `1` of `g1` and level `lo` of `g2`, the comparison interval for the combination of level `2` of `g1` and level `lo` of `g2` overlaps, and is therefore gray. Conversely, the other comparison intervals are red, indicating significant difference.

- “Perform N-Way ANOVA” on page 8-39
- “ANOVA with Random Effects” on page 8-48
- “Multiple Comparisons” on page 8-26

Input Arguments

y — Sample data

numeric vector

Sample data, specified as a numeric vector.

Data Types: `single | double`

group — Grouping variables

cell array

Grouping variables, i.e. the factors and factor levels of the observations in y, specified as a cell array. Each of the cells in group contains a list of factor levels identifying the observations in `y` with respect to one of the factors. The list within each cell can be a categorical array, numeric vector, character matrix, or single-column cell array of strings, and must have the same number of elements as `y`.

$$
\begin{array}{lcl}
y & = & [\ \underset{\uparrow}{y_1},\ \underset{\uparrow}{y_2},\ \underset{\uparrow}{y_3},\ \underset{\uparrow}{y_4},\ \underset{\uparrow}{y_5},\ \cdots,\ \underset{\uparrow}{y_N}\ ]' \\
g1 & = & \{\ 'A',\ 'A',\ 'C',\ 'B',\ 'B',\ \cdots,\ 'D'\ \} \\
g2 & = & [\ 1\ \ 2\ \ 1\ \ 3\ \ 1\ \ \cdots,\ 2\ ] \\
g3 & = & \{\ \text{'hi'},\ \text{'mid'},\ \text{'low'},\ \text{'mid'},\ \text{'hi'},\ \cdots,\ \text{'low'}\ \}
\end{array}
$$

By default, `anovan` treats all grouping variables as fixed effects.

For example, in a study you want to investigate the effects of gender, school, and the education method on the academic success of elementary school students, then you can specify the grouping variables as follows.

Example: `{'Gender','School','Method'}`

Data Types: `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'alpha',0.01,'model','interaction','sstype',2` specifies `anovan` to compute the 99% confidence bounds and p-values for the main effects and two-way interactions using type II sum of squares.

`'alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 to 1

Confidence level for confidence bounds, specified as the comma-separated pair consisting of`'alpha'` and a scalar value in the range 0 to 1. For a value α, the confidence level is 100*(1–α)%.

Example: `'alpha',0.01` corresponds to 99% confidence intervals

Data Types: `single` | `double`

`'continuous'` — Indicator for continuous predictors

vector of indices

Indicator for continuous predictors, representing which grouping variables should be treated as continuous predictors rather than as categorical predictors, specified as the comma-separated pair consisting of`'continuous'` and a vector of indices.

For example, if there are three grouping variables and second one is continuous, then you can specify as follows.

Example: `continuous',[2]`

Data Types: `single` | `double`

`'display'` — Indicator to display ANOVA table

`'on'` (default) | `'off'`

Indicator to display ANOVA table, specified as the comma-separated pair consisting of `'display'` and `'on'` or `'off'`. When `displayopt` is `'off'`, `anova1` only returns the output arguments, and does not display the standard ANOVA table as a figure.

Example: `'display','off'`

`'model'` — Type of the model

`'linear'` (default) | `'interaction'` | `'full'` | integer value | terms matrix

Type of the model, specified as the comma-separated pair consisting of `'model'` and one of the following:

- `'linear'` — The default `'linear'` model computes only the p-values for the null hypotheses on the N main effects.
- `'interaction'` — The `'interaction'` model computes the p-values for null hypotheses on the N main effects and the $\binom{N}{2}$ two-factor interactions.
- `'full'` — The `'full'` model computes the p-values for null hypotheses on the N main effects and interactions at all levels.
- An integer — For an integer value of k, ($k \le N$) for model type, `anovan` computes all interaction levels through the kth level. For example, the value 3 means main effects

plus two- and three-factor interactions. The values $k = 1$ and $k = 2$ are equivalent to the `'linear'` and `'interaction'` specifications, respectively. The value $k = N$ is equivalent to the `'full'` specification.

- Terms matrix — A matrix of term definitions having the same form as the input to the `x2fx` function. All entries must be `0` or `1` (no higher powers).

  For more precise control over the main and interaction terms that `anovan` computes, you can specify a matrix containing one row for each main or interaction term to include in the ANOVA model. Each row defines one term using a vector of N zeros and ones. The table below illustrates the coding for a 3-factor ANOVA for factors A, B, and C.

Matrix Row	ANOVA Term
`[1 0 0]`	Main term A
`[0 1 0]`	Main term B
`[0 0 1]`	Main term C
`[1 1 0]`	Interaction term AB
`[1 0 1]`	Interaction term AC
`[0 1 1]`	Interaction term BC
`[1 1 1]`	Interaction term ABC

  For example, if there are three factors A, B, and C, and `'model',[0 1 0;0 0 1;0 1 1]`, then `anovan` tests for the main effects B and C, and the interaction effect BC, respectively.

  A simple way to generate the terms matrix is to modify the terms output, which codes the terms in the current model using the format described above. If `anovan` returns `[0 1 0;0 0 1;0 1 1]` for terms, for example, and there is no significant interaction BC, then you can recompute ANOVA on just the main effects B and C by specifying `[0 1 0;0 0 1]` for model.

Example: `'model',[0 1 0;0 0 1;0 1 1]`

Example: `'model','interaction'`

`'nested'` — Nesting relationships

matrix of 0's and 1's

Nesting relationships among the grouping variables, specified as the comma-separated pair consisting of `'nested'` and a matrix M of 0's and 1's, i.e.$M(i,j) = 1$ if variable i is nested in variable j.

For example, if there are two grouping variables District and School, where School is nested in District, then you can express this relationship as follows.

Example: `'nested',[0,0;1 0]`

Data Types: `single | double`

`'random'` — Indicator for random variables

vector of indices

Indicator for random variables, representing which grouping variables are random, specified as the comma-separated pair consisting of `'random'` and a vector of indices. By default, `anovan` treats all grouping variables as fixed.

`anovan` treats an interaction term as random if any of the variables in the interaction term is random.

Example: `'random',[3]`

Data Types: `single | double`

`'sstype'` — Type of sum of squares

3 (default) | 1 | 2 | h

Type of sum squares, specified as the comma-separated pair consisting of `'sstype'` and the following:

- 1 — Type I sum of squares. The reduction in residual sum of squares obtained by adding that term to a fit that already includes the terms listed before it.
- 2 — Type II sum of squares. The reduction in residual sum of squares obtained by adding that term to a model consisting of all other terms that do not contain the term in question.
- 3 — Type III sum of squares. The reduction in residual sum of squares obtained by adding that term to a model containing all other terms, but with their effects constrained to obey the usual "sigma restrictions" that make models estimable.
- h — Hierarchical model. Similar to type 2, but with continuous as well as categorical factors used to determine the hierarchy of terms.

The sum of squares for any term is determined by comparing two models. For a model containing main effects but no interactions, the value of sstype only influences computations on unbalanced data.

Suppose you are fitting a model with two factors and their interaction, and that the terms appear in the order A, B, AB. Let $R(\cdot)$ represent the residual sum of squares for a model, so for example $R(A, B, AB)$ is the residual sum of squares fitting the whole model, $R(A)$ is the residual sum of squares fitting just the main effect of A, and $R(1)$ is the residual sum of squares fitting just the mean. The three types of sums of squares are as follows:

Term	Type 1 Sum of Squares	Type 2 Sum of Squares	Type 3 Sum of Squares
A	$R(1)–R(A)$	$R(B)– R(A, B)$	$R(B, AB) – R(A, B, AB)$
B	$R(A)– R(A, B)$	$R(A)– R(A, B)$	$R(A, AB) – R(A, B, AB)$
AB	$R(A, B) – R(A, B, AB)$	$R(A, B) – R(A, B, AB)$	$R(A, B) – R(A, B, AB)$

The models for Type 3 sum of squares have sigma restrictions imposed. This means, for example, that in fitting $R(B, AB)$, the array of AB effects is constrained to sum to 0 over A for each value of B, and over B for each value of A.

Example: `'sstype','h'`

Data Types: `single` | `double`

`'varnames'` — Names of grouping variables

`X1,X2,...,XN` (default) | character matrix | cell array of strings

Names of grouping variables, specified as the comma-separating pair consisting of `'varnames'` and a character matrix or a cell array of strings.

Example: `'varnames',{'Gender','City'}`

Data Types: `char` | `cell`

Output Arguments

p — *p*-values

vector

p-values, returned as a vector.

Output vector `p` contains *p*-values for the null hypotheses on the *N* main effectsand any interaction terms specified. Element `p(1)` contains the *p*-value for the null hypotheses that samples at all levels of factor *A* are drawn from the same population; element `p(2)` contains the *p*-value for the null hypotheses that samples at all levels of factor *B* are drawn from the same population; and so on.

For example, if there are three factors *A*, *B*, and *C*, and `'model',[0 1 0;0 0 1;0 1 1]`, then the output vector p contains the *p*-values for the null hypotheses on the main effects *B* and *C* and the interaction effect *BC*, respectively.

A sufficiently small *p*-value corresponding to a factor suggests that at least one group mean is significantly different from the other group means; that is, there is a main effect due to that factor. It is common to declare a result significant if the *p*-value is less than 0.05 or 0.01.

`tbl` — ANOVA table

cell array

ANOVA table, returned as a cell array. The ANOVA table has seven columns:

Column name	Definition
`source`	The source of the variability.
`SS`	The sum of squares due to each source.
`df`	The degrees of freedom associated with each source.
`MS`	The mean squares for each source, which is the ratio `SS/df`.
`F`	*F*-statistic, which is the ratio of the mean squares.
`Prob>F`	The *p*-values , which is the probability that the *F*-statistic can take a value larger than a computed test-statistic value. `anovan` derives these probabilities from the cdf of *F*-distribution.

`stats` — Statistics

structure

Statistics to use in a multiple comparison test using the `multcompare` function, returned as a structure.

`anovan` evaluates the hypothesis that the different groups (levels) of a factor (or more generally, a term) have the same effect, against the alternative that they do not all have the same effect. Sometimes it is preferable to perform a test to determine which pairs of levels are significantly different, and which are not. Use the `multcompare` function to perform such tests by supplying the `stats` structure as input.

The `stats` structure contains the fields listed below, in addition to a number of other fields required for doing multiple comparisons using the `multcompare` function:

Field	Description
`coeffs`	Estimated coefficients
`coeffnames`	Name of term for each coefficient
`vars`	Matrix of grouping variable values for each term
`resid`	Residuals from the fitted model

The `stats` structure also contains the following fields if there are random effects:

Field	Description
`ems`	Expected mean squares
`denom`	Denominator definition
`rtnames`	Names of random terms
`varest`	Variance component estimates (one per random term)
`varci`	Confidence intervals for variance components

`terms` — Main and interaction terms

matrix

Main and interaction terms, returned as a matrix. The terms are encoded in the output matrix terms using the same format described above for input model. When you specify model itself in this format, the matrix returned in terms is identical.

More About

- “N-Way ANOVA” on page 8-36

See Also

`anova1` | `anova2` | `multcompare`

anova

Class: RepeatedMeasuresModel

Analysis of variance for between-subject effects

Syntax

```
anovatbl = anova(rm)
anovatbl = anova(rm,'WithinModel',WM)
```

Description

`anovatbl = anova(rm)` returns the analysis of variance results for the repeated measures model rm.

`anovatbl = anova(rm,'WithinModel',WM)` returns the analysis of variance results it performs using the response or responses specified by the within-subject model WM.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`WM` — Within-subject model

`'separatemeans'` (default) | `'orthogonalcontrasts'` | string defining a model specification | *r*-by-*nc* matrix specifying *nc* contrasts

Within-subject model, specified as one of the following:

- `'separatemeans'` — The response is the average of the repeated measures (average across the within-subject model).

- `'orthogonalcontrasts'` — This is valid when the within-subject model has a single numeric factor T. Responses are the average, the slope of centered T, and, in general, all orthogonal contrasts for a polynomial up to T^(p – 1), where p is the number of rows in the within-subject model. `anova` multiplies `Y`, the response you use in the repeated measures model `rm` by the orthogonal contrasts, and uses the columns of the resulting product matrix as the responses.

  `anova` computes the orthogonal contrasts for T using the Q factor of a QR factorization of the Vandermonde matrix.
- A string that defines a model specification in the within-subject factors. Responses are defined by the terms in that model. `anova` multiplies Y, the response matrix you use in the repeated measures model `rm` by the terms of the model, and uses the columns of the result as the responses.

  For example, if there is a Time factor and `'Time'` is the model specification, then `anova` uses two terms, the constant and the uncentered Time term. The default is `'1'` to perform on the average response.
- An r-by-nc matrix, C, specifying nc contrasts among the r repeated measures. If Y represents the matrix of repeated measures you use in the repeated measures model `rm`, then the output `tbl` contains a separate analysis of variance for each column of Y*C.

The `anova` table contains a separate univariate analysis of variance results for each response.

Example: `'WithinModel','Time'`

Example: `'WithinModel','orthogonalcontrasts'`

Output Arguments

`anovatbl` — Results of analysis of variance

table

Results of analysis of variance for between-subject effects, returned as a table. This includes all terms on the between-subjects model and the following columns.

Column Name	Definition
`Within`	Within-subject factors

Column Name	Definition
`Between`	Between-subject factors
`SumSq`	Sum of squares
`DF`	Degrees of freedom
`MeanSq`	Mean squared error
`F`	F-statistic
`pValue`	p-value corresponding to the F-statistic

Definitions

Vandermonde Matrix

Vandermonde matrix is the matrix where columns are the powers of the vector a, that is, $V(i,j) = a(i)^{(n-j)}$, where n is the length of a.

QR Factorization

QR factorization of an m-by-n matrix A is the factorization that matrix into the product $A = Q*R$, where R is an m-by-n upper triangular matrix and Q is an m-by-m unitary matrix.

Examples

Analysis of Variance for Average Response

Load the sample data.

```
load fisheriris
```

The column vector `species` consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
```

```
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform analysis of variance.

```
anova(rm)
```

```
ans =

    Within      Between      SumSq      DF      MeanSq        F          pValue
    ________    ________     ______     ___     _______     ______     ___________

    Constant    constant     7201.7       1      7201.7      19650    2.0735e-158
    Constant    species      309.61       2       154.8     422.39     1.1517e-61
    Constant    Error        53.875     147     0.36649
```

There are 150 observations and 3 species. The degrees of freedom for species is 3 – 1 = 2, and for error it is 150 – 3 = 147. The small *p*-value of 1.1517e-61 indicates that the measurements differ significantly according to species.

Panel Data

Navigate to the folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample panel data.

```
load('panelData')
```

The dataset array, `panelData`, contains yearly observations on eight cities for 6 years. The first variable, `Growth`, measures economic growth (the response variable). The second and third variables are city and year indicators, respectively. The last variable, `Employ`, measures employment (the predictor variable). This is simulated data.

Store the data in a table array and define city as a nominal variable.

```
t = table(panelData.Growth,panelData.City,panelData.Year,...
 'VariableNames',{'Growth','City','Year'});
```

Convert the data in a proper format to do repeated measures analysis.

```
t = unstack(t,'Growth','Year','NewDataVariableNames',...
 {'year1','year2','year3','year4','year5','year6'});
```

Add the mean employment level over the years as a predictor variable to the table `t`.

```
t(:,8) = table(grpstats(panelData.Employ,panelData.City));
t.Properties.VariableNames{'Var8'} = 'meanEmploy';
```

Define the within-subjects variable.

```
Year = [1 2 3 4 5 6]';
```

Fit a repeated measures model, where the growth figures over the 6 years are the responses and the mean employment is the predictor variable.

```
rm = fitrm(t,'year1-year6 ~ meanEmploy','WithinDesign',Year);
```

Perform analysis of variance.

```
anovatbl = anova(rm,'WithinModel',Year)
```

```
anovatbl =

    Within      Between       SumSq       DF      MeanSq         F          pValue
    _________   __________   _________   __   __________   ________   _____________

    Contrast1   constant          588.17   1        588.17   0.038495       0.85093
    Contrast1   meanEmploy    3.7064e+05   1    3.7064e+05     24.258    0.0026428
    Contrast1   Error              91675   6         15279
```

Longitudinal Data

Navigate to the folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load('longitudinalData')
```

The matrix `Y` contains response data for 16 individuals. The response is the blood level of a drug measured at five time points (time = 0, 2, 4, 6, and 8). Each row of `Y` corresponds

to an individual, and each column corresponds to a time point. The first eight subjects are female, and the second eight subjects are male. This is simulated data.

Define a variable that stores gender information.

```
Gender = ['F' 'F' 'F' 'F' 'F' 'F' 'F' 'F' 'M' 'M' 'M' 'M' 'M' 'M' 'M' 'M']';
```

Store the data in a proper table array format to do repeated measures analysis.

```
t = table(Gender,Y(:,1),Y(:,2),Y(:,3),Y(:,4),Y(:,5),...
'VariableNames',{'Gender','t0','t2','t4','t6','t8'});
```

Define the within-subjects variable.

```
Time = [0 2 4 6 8]';
```

Fit a repeated measures model, where blood levels are the responses and gender is the predictor variable.

```
rm = fitrm(t,'t0-t8 ~ Gender','WithinDesign',Time);
```

Perform analysis of variance.

```
anovatbl = anova(rm)
```

```
anovatbl =

    Within     Between     SumSq     DF     MeanSq       F          pValue
    _______    _______     _____     __     ______     ______     __________

    Constant   constant      54702    1      54702    1079.2    1.1897e-14
    Constant   Gender       2251.7    1     2251.7    44.425    1.0693e-05
    Constant   Error         709.6   14     50.685
```

There are 2 genders and 16 observations, so the degrees of freedom for gender is (2 –1) = 1 and for error it is (16 – 2)*(2 – 1) = 14. The small *p*-value of 1.0693e-05 indicates that there is a significant effect of gender on blood pressure.

Repeat analysis of variance using orthogonal contrasts.

```
anovatbl = anova(rm,'WithinModel','orthogonalcontrasts')
```

```
anovatbl =

    Within     Between       SumSq       DF      MeanSq          F           pValue
```

Constant	constant	54702	1	54702	1079.2	1.1897e-14
Constant	Gender	2251.7	1	2251.7	44.425	1.0693e-05
Constant	Error	709.6	14	50.685		
Time	constant	310.83	1	310.83	31.023	6.9065e-05
Time	Gender	13.341	1	13.341	1.3315	0.26785
Time	Error	140.27	14	10.019		
Time^2	constant	565.42	1	565.42	98.901	1.0003e-07
Time^2	Gender	1.4076	1	1.4076	0.24621	0.62746
Time^2	Error	80.039	14	5.7171		
Time^3	constant	2.6127	1	2.6127	1.4318	0.25134
Time^3	Gender	7.8853e-06	1	7.8853e-06	4.3214e-06	0.99837
Time^3	Error	25.546	14	1.8247		
Time^4	constant	2.8404	1	2.8404	0.47924	0.50009
Time^4	Gender	2.9016	1	2.9016	0.48956	0.49559
Time^4	Error	82.977	14	5.9269		

See Also

`fitrm` | `manova` | `qr` | `ranova` | `vander`

More About

- "Model Specification for Repeated Measures Models" on page 8-77

ansaribradley

Ansari-Bradley test

Syntax

```
h = ansaribradley(x,y)
h = ansaribradley(x,y,Name,Value)
[h,p] = ansaribradley(___)
[h,p,stats] = ansaribradley(___)
```

Description

`h = ansaribradley(x,y)` returns a test decision for the null hypothesis that the data in vectors x and y comes from the same distribution, using the Ansari-Bradley test. The alternative hypothesis is that the data in x and y comes from distributions with the same median and shape but different dispersions (e.g., variances). The result h is `1` if the test rejects the null hypothesis at the 5% significance level, or `0` otherwise.

`h = ansaribradley(x,y,Name,Value)` returns a test decision for the Ansari-Bradley test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level, conduct a one-sided test, or use a normal approximation to calculate the value of the test statistic.

`[h,p] = ansaribradley(___)` also returns the *p*-value, p, of the test, using any of the input arguments in the previous syntaxes.

`[h,p,stats] = ansaribradley(___)` also returns the structure stats containing information about the test statistic.

Examples

Test for Equal Variances

Load the sample data. Create data vectors of miles per gallon (`MPG`) measurements for the model years 1982 and 1976.

```
load carsmall;
x = MPG(Model_Year==82);
y = MPG(Model_Year==76);
```

Test the null hypothesis that the miles per gallon measured in cars from 1982 and 1976 have equal variances.

```
[h,p,stats] = ansaribradley(x,y)
```

```
h =
     0

p =
    0.8426

stats =
        W: 526.9000
    Wstar: 0.1986
```

The returned value of `h = 0` indicates that `ansaribradley` does not reject the null hypothesis at the default 5% significance level.

One-Sided Hypothesis Test

Load the sample data. Create data vectors of miles per gallon (`MPG`) measurements for the model years 1982 and 1976.

```
load carsmall;
x = MPG(Model_Year==82);
y = MPG(Model_Year==76);
```

Test the null hypothesis that the miles per gallon measured in cars from 1982 and 1976 have equal variances, against the alternative hypothesis that the variance of cars from 1982 is greater than that of cars from 1976.

```
[h,p,stats] = ansaribradley(x,y,'Tail','right')
```

```
h =
     0

p =
    0.5787

stats =
```

```
     W: 526.9000
 Wstar: 0.1986
```

The returned value of `h = 0` indicates that `ansaribradley` does not reject the null hypothesis that the variance in miles per gallon is the same for the two model years, when the alternative is that the variance of cars from 1982 is greater than that of cars from 1976.

Input Arguments

x — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array.

- If x and y are specified as vectors, they do not need to be the same length.
- If x and y are specified as matrices, they must have the same number of columns. `ansaribradley` performs separate tests along each column and returns a vector of results.
- If x and y are specified as multidimensional arrays, `ansaribradley` works along the first nonsingleton dimension. x and y must have the same size along all remaining dimensions.

Data Types: `single` | `double`

y — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array.

- If x and y are specified as vectors, they do not need to be the same length.
- If x and y are specified as matrices, they must have the same number of columns. `ansaribradley` performs separate tests along each column and returns a vector of results.
- If x and y are specified as multidimensional arrays, `ansaribradley` works along the first nonsingleton dimension. x and y must have the same size along all remaining dimensions.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Alpha',0.01` specifies a right-tailed hypothesis test at the 1% significance level.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Dim'` — Dimension

first nonsingleton dimension (default) | positive integer value

Dimension of the input matrix along which to test the means, specified as the comma-separated pair consisting of `'Dim'` and a positive integer value. For example, specifying `'Dim',1` tests the column means, while `'Dim',2` tests the row means.

Example: `'Dim',2`

Data Types: `single` | `double`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'left'` | `'right'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the dispersion parameters of x and y are not equal.
`'right'`	Test the alternative hypothesis that the dispersion parameter of x is greater than that of y.
`'left'`	Test the alternative hypothesis that the dispersion parameter of x is less than that of y.

Example: `'Tail','right'`

`'Method'` — Computation method

`'exact' | 'approximate'`

Computation method for the test statistic, specified as the comma-separated pair consisting of `'Method'` and one of the following.

`'exact'`	Compute p using an exact calculation of the distribution of the test statistic `W`. This is the default if n, the total number of rows in x and y, is 25 or less. Note that n is computed before any `NaN` values (representing missing data) are removed.
`'approximate'`	Compute p using a normal approximation for the statistic `W*`. This is the default if n, the total number of rows in x and y, is greater than 25.

Example: `'Method','exact'`

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

- If h = `1`, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = `0`, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

`stats` — Test statistics

structure

Test statistics for the Ansari-Bradley test, returned as a structure containing:

- `W` — Value of the test statistic, which is the sum of the Ansari-Bradley ranks for the x sample.
- `Wstar` — Approximate normal statistic `W*`.

More About

Ansari-Bradley Test

The Ansari-Bradley test is a nonparametric alternative to the two-sample *F*-test of equal variances. It does not require the assumption that x and y come from normal distributions. The dispersion of a distribution is generally measured by its variance or standard deviation, but the Ansari-Bradley test can be used with samples from distributions that do not have finite variances.

This test requires that the samples have equal medians. Under that assumption, and if the distributions of the samples are continuous and identical, the test is independent of the distributions. If the samples do not have the same medians, the results can be misleading. In that case, Ansari and Bradley recommend subtracting the median, but then the distribution of the resulting test under the null hypothesis is no longer independent of the common distribution of x and y. If you want to perform the tests with medians subtracted, you should subtract the medians from x and y before calling `ansaribradley`.

Multidimensional Array

A multidimensional array has more than two dimensions. For example, if `x` is a 1-by-3-by-4 array, then `x` is a three-dimensional array.

First Nonsingleton Dimension

The first nonsingleton dimension is the first dimension of an array whose size is not equal to 1. For example, if `x` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `x`.

See Also

`ttest2` | `vartest2` | `vartestn`

aoctool

Interactive analysis of covariance

Syntax

```
aoctool(x,y,group)
aoctool(x,y,group,alpha)
aoctool(x,y,group,alpha,xname,yname,gname)
aoctool(x,y,group,alpha,xname,yname,gname,displayopt)
aoctool(x,y,group,alpha,xname,yname,gname,displayopt,model)
h = aoctool(...)
[h,atab,ctab] = aoctool(...)
[h,atab,ctab,stats] = aoctool(...)
```

Description

`aoctool(x,y,group)` fits a separate line to the column vectors, `x` and `y`, for each group defined by the values in the array `group`. `group` may be a categorical variable, vector, character array, or cell array of strings. These types of models are known as one-way analysis of covariance (ANOCOVA) models. The output consists of three figures:

- An interactive graph of the data and prediction curves
- An ANOVA table
- A table of parameter estimates

You can use the figures to change models and to test different parts of the model. More information about interactive use of the `aoctool` function appears in “Analysis of Covariance Tool” on page 8-58.

`aoctool(x,y,group,alpha)` determines the confidence levels of the prediction intervals. The confidence level is `100(1-alpha)`%. The default value of `alpha` is 0.05.

`aoctool(x,y,group,alpha,xname,yname,gname)` specifies the name to use for the `x`, `y`, and `g` variables in the graph and tables. If you enter simple variable names for the `x`, `y`, and `g` arguments, the aoctool function uses those names. If you enter an expression for one of these arguments, you can specify a name to use in place of that expression by

supplying these arguments. For example, if you enter `m(:,2)` as the `x` argument, you might choose to enter `'Col 2'` as the `xname` argument.

`aoctool(x,y,group,alpha,xname,yname,gname,displayopt)` enables the graph and table displays when *`displayopt`* is `'on'` (default) and suppresses those displays when *`displayopt`* is `'off'`.

`aoctool(x,y,group,alpha,xname,yname,gname,displayopt,model)` specifies the initial model to fit. The value of *`model`* can be any of the following:

- `'same mean'` — Fit a single mean, ignoring grouping
- `'separate means'` — Fit a separate mean to each group
- `'same line'` — Fit a single line, ignoring grouping
- `'parallel lines'` — Fit a separate line to each group, but constrain the lines to be parallel
- `'separate lines'` — Fit a separate line to each group, with no constraints

`h = aoctool(...)` returns a vector of handles to the line objects in the plot.

`[h,atab,ctab] = aoctool(...)` returns cell arrays containing the entries in ANOVA table (`atab`) and the table of coefficient estimates (`ctab`). (You can copy a text version of either table to the clipboard by using the `Copy Text` item on the **Edit** menu.)

`[h,atab,ctab,stats] = aoctool(...)` returns a `stats` structure that you can use to perform a follow-up multiple comparison test. The ANOVA table output includes tests of the hypotheses that the slopes or intercepts are all the same, against a general alternative that they are not all the same. Sometimes it is preferable to perform a test to determine which pairs of values are significantly different, and which are not. You can use the `multcompare` function to perform such tests by supplying the `stats` structure as input. You can test either the slopes, the intercepts, or population marginal means (the heights of the curves at the mean `x` value).

Examples

This example illustrates how to fit different models non-interactively. After loading the smaller car data set and fitting a separate-slopes model, you can examine the coefficient estimates.

```
load carsmall
```

```
[h,a,c,s] = aoctool(Weight,MPG,Model_Year,0.05,...
                    '','','','off','separate lines');
c(:,1:2)
ans =
  'Term'       'Estimate'
  'Intercept'  [45.97983716833132]
  ' 70'        [-8.58050531454973]
  ' 76'        [-3.89017396094922]
  ' 82'        [12.47067927549897]
  'Slope'      [-0.00780212907455]
  ' 70'        [ 0.00195840368824]
  ' 76'        [ 0.00113831038418]
  ' 82'        [-0.00309671407243]
```

Roughly speaking, the lines relating `MPG` to `Weight` have an intercept close to 45.98 and a slope close to -0.0078. Each group's coefficients are offset from these values somewhat. For instance, the intercept for the cars made in 1970 is 45.98-8.58 = 37.40.

Next, try a fit using parallel lines. (The ANOVA table shows that the parallel-lines fit is significantly worse than the separate-lines fit.)

```
[h,a,c,s] = aoctool(Weight,MPG,Model_Year,0.05,...
                    '','','','off','parallel lines');

c(:,1:2)

ans =

  'Term'       'Estimate'
  'Intercept'  [43.38984085130596]
  ' 70'        [-3.27948192983761]
  ' 76'        [-1.35036234809006]
  ' 82'        [ 4.62984427792768]
  'Slope'      [-0.00664751826198]
```

Again, there are different intercepts for each group, but this time the slopes are constrained to be the same.

See Also

`anova1` | `multcompare` | `polytool`

append

Class: TreeBagger

Append new trees to ensemble

Syntax

```
B = append(B,other)
```

Description

`B = append(B,other)` appends the trees from the `other` ensemble to those in `B`. This method checks for consistency of the `X` and `Y` properties of the two ensembles, as well as consistency of their compact objects and out-of-bag indices, before appending the trees. The output ensemble `B` takes training parameters such as `FBoot`, `Prior`, `Cost`, and `other` from the `B` input. There is no attempt to check if these training parameters are consistent between the two objects.

See Also

`CompactTreeBagger.combine`

BandWidth property

Class: ProbDistKernel

Read-only value specifying bandwidth of kernel smoothing function for ProbDistKernel object

Description

`BandWidth` is a read-only property of the `ProbDistKernel` class. `BandWidth` is a value specifying the width of the kernel smoothing function used to compute a nonparametric estimate of the probability distribution when creating a ProbDistKernel object.

Values

For a distribution specified to cover only the positive numbers or only a finite interval, the data are transformed before the kernel density is applied, and the bandwidth is on the scale of the transformed data.

Use this information to view and compare the width of the kernel smoothing function used to create distributions.

See Also

`ksdensity`

barttest

Bartlett's test

Syntax

```
ndim = barttest(x,alpha)
[ndim,prob,chisquare] = barttest(x,alpha)
```

Description

`ndim = barttest(x,alpha)` returns the number of dimensions necessary to explain the nonrandom variation in the data matrix x at the alpha significance level.

`[ndim,prob,chisquare] = barttest(x,alpha)` also returns the significance values for the hypothesis tests prob, and the χ^2 values associated with the tests chisquare.

Examples

Determine Dimensions Needed to Explain Nonrandom Data Variation

Generate a 20-by-6 matrix of random numbers from a multivariate normal distribution with mean `mu = [0 0]` and covariance `sigma = [1 0.99; 0.99 1]`.

```
rng default  % for reproducibility
mu = [0 0];
sigma = [1 0.99; 0.99 1];
X = mvnrnd(mu,sigma,20);  % columns 1 and 2
X(:,3:4) = mvnrnd(mu,sigma,20);  % columns 3 and 4
X(:,5:6) = mvnrnd(mu,sigma,20);  % columns 5 and 6
```

Determine the number of dimensions necessary to explain the nonrandom variation in data matrix `X`. Report the significance values for the hypothesis tests.

```
[ndim, prob] = barttest(X,0.05)
```

```
ndim =
```

```
     3


prob =

    0.0000
    0.0000
    0.0000
    0.5148
    0.3370
```

The returned value of `ndim` indicates that three dimensions are necessary to explain the nonrandom variation in `X`.

Input Arguments

`x` — Input data

matrix of scalar values

Input data, specified as a matrix of scalar values.

Data Types: `single` | `double`

`alpha` — Significance level

`0.05` (default) | scalar value in the range `(0,1)`

Significance level of the hypothesis test, specified as a scalar value in the range `(0,1)`.

Example: `0.1`

Data Types: `single` | `double`

Output Arguments

`ndim` — Number of dimensions

positive integer value

Number of dimensions, returned as a positive integer value. The dimension is determined by a series of hypothesis tests. The test for `ndim = 1` tests the hypothesis

that the variances of the data values along each principal component are equal, the test for `ndim = 2` tests the hypothesis that the variances along the second through last components are equal, and so on. The null hypothesis is that the number of dimensions is equal to the number of the largest unequal eigenvalues of the covariance matrix of x.

`prob` — Significance value

vector of scalar values in the range `(0,1)`

Significance value for the hypothesis tests, returned as a vector of scalar values in the range `(0,1)`. Each element in prob corresponds to an element of chisquare.

`chisquare` — Test statistics

vector of scalar values

Test statistics for each dimension's hypothesis test, returned as a vector of scalar values.

bbdesign

Box-Behnken design

Syntax

```
dBB = bbdesign(n)
[dBB,blocks] = bbdesign(n)
[...] = bbdesign(n,param,val)
```

Description

`dBB = bbdesign(n)` generates a Box-Behnken design for `n` factors. `n` must be an integer `3` or larger. The output matrix `dBB` is *m*-by-`n`, where *m* is the number of runs in the design. Each row represents one run, with settings for all factors represented in the columns. Factor values are normalized so that the cube points take values between `-1` and `1`.

`[dBB,blocks] = bbdesign(n)` requests a blocked design. The output `blocks` is an *m*-by-1 vector of block numbers for each run. Blocks indicate runs that are to be measured under similar conditions to minimize the effect of inter-block differences on the parameter estimates.

`[...] = bbdesign(n,param,val)` specifies one or more optional parameter/value pairs for the design. The following table lists valid parameter/value pairs.

Parameter	Description	Values
`'center'`	Number of center points.	Integer. The default depends on `n`.
`'blocksize'`	Maximum number of points per block.	Integer. The default is `Inf`.

Examples

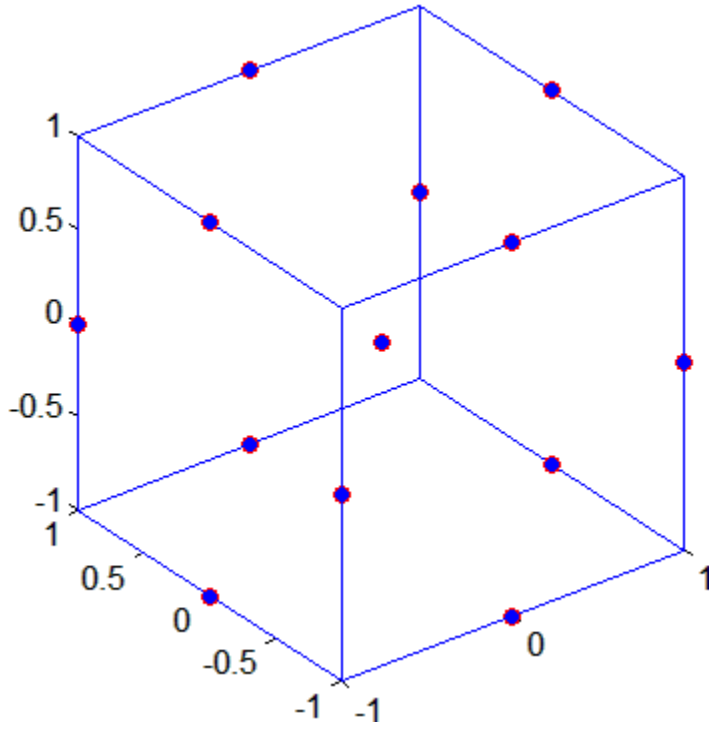
The following creates a 3-factor Box-Behnken design:

```
dBB = bbdesign(3)
dBB =
     -1     -1      0
     -1      1      0
      1     -1      0
      1      1      0
     -1      0     -1
     -1      0      1
      1      0     -1
      1      0      1
      0     -1     -1
      0     -1      1
      0      1     -1
      0      1      1
      0      0      0
      0      0      0
      0      0      0
```

The center point is run 3 times to allow for a more uniform estimate of the prediction variance over the entire design space.

Visualize the design as follows:

```
plot3(dBB(:,1),dBB(:,2),dBB(:,3),'ro',...
          'MarkerFaceColor','b')
X = [1 -1 -1 -1 1 -1 -1 -1 1 1 -1 -1; ...
     1 1 1 -1 1 1 1 -1 1 1 -1 -1];
Y = [-1 -1 1 -1 -1 -1 1 -1 1 -1 1 -1; ...
     1 -1 1 1 1 -1 1 1 1 -1 1 -1];
Z = [1 1 1 1 -1 -1 -1 -1 -1 -1 -1 -1; ...
     1 1 1 1 -1 -1 -1 -1 1 1 1 1];
line(X,Y,Z,'Color','b')
axis square equal
```



See Also

`ccdesign`

prob.BetaDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Beta probability distribution object

Description

`prob.BetaDistribution` is an object consisting of parameters, a model description, and sample data for a beta probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Beta')` creates a beta probability distribution object using the default parameter values.

`pd = makedist('Beta','a',a,'b',b)` creates a beta probability distribution object using the specified parameter values.

Input Arguments

a — First shape parameter

1 (default) | positive scalar value

First shape parameter of the beta distribution, specified as a positive scalar value.

Data Types: `single` | `double`

b — Second shape parameter

1 (default) | positive scalar value

Second shape parameter of the beta distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

a — First shape parameter

positive scalar value

First shape parameter of the beta distribution, stored as a positive scalar value.

Data Types: `single | double`

b — Second shape parameter

positive scalar value

Second shape parameter of the beta distribution, stored as a positive scalar value.

Data Types: `single | double`

DistributionName — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

InputData — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

IsTruncated — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Beta Distribution

The beta distribution describes a family of curves that are unique in that they are nonzero only on the interval (0,1). A more general version of the distribution assigns parameters to the endpoints of the interval.

The beta distribution uses the following parameters.

Parameter	Description	Support
a	First shape parameter	$a > 0$
b	Second shape parameter	$b > 0$

The probability density function (pdf) is

$$f(x \mid a,b) = \frac{1}{B(a,b)} x^{a-1}(1-x)^{b-1} \quad ; \quad 0 < x < 1,$$

where $B(\cdot)$ is the beta function.

Examples

Create a Beta Distribution Object Using Default Parameters

Create a beta distribution object using the default parameter values.

```
pd = makedist('Beta')
```

```
pd =

  BetaDistribution

  Beta distribution
    a = 1
    b = 1
```

Create a Beta Distribution Object Using Specified Parameters

Create a beta distribution object by specifying the parameter values.

```
pd = makedist('Beta','a',2,'b',4)
```

```
pd =

  BetaDistribution

  Beta distribution
    a = 2
    b = 4
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =
```

```
    0.3333
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Beta Distribution"
- Class Attributes
- Property Attributes

betacdf

Beta cumulative distribution function

Syntax

```
p = betacdf(x,a,b)
p = betacdf(x,a,b,'upper')
```

Description

`p = betacdf(x,a,b)` returns the beta cdf at each of the values in `x` using the corresponding parameters in `a` and `b`. `x`, `a`, and `b` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `a` and `b` must all be positive, and the values in `x` must lie on the interval [0,1].

`p = betacdf(x,a,b,'upper')` returns the complement of the beta cdf at each of the values in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The beta cdf for a given value `x` and given pair of parameters `a` and `b` is

$$p = F(x \mid a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1}\,dt$$

where $B(\cdot)$ is the Beta function.

Examples

Compute Beta Distribution CDF

Compute the cdf for a beta distribution with parmaters `a = 2` and `b = 2`.

```
x = 0.1:0.2:0.9;
```

```
a = 2;
b = 2;
p = betacdf(x,a,b)

p =
    0.0280  0.2160  0.5000  0.7840  0.9720

a = [1 2 3];
p = betacdf(0.5,a,a)

p =
    0.5000  0.5000  0.5000
```

More About

- "Beta Distribution" on page B-4

See Also

cdf | betapdf | betainv | betastat | betalike | betarnd | betafit

betafit

Beta parameter estimates

Syntax

```
phat = betafit(data)
[phat,pci] = betafit(data,alpha)
```

Description

`phat = betafit(data)` computes the maximum likelihood estimates of the beta distribution parameters a and b from the data in the vector `data` and returns a column vector containing the a and b estimates, where the beta cdf is given by

$$F(x \mid a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1} dt$$

and $B(\cdot)$ is the Beta function. The elements of `data` must lie in the open interval (0, 1), where the beta distribution is defined. However, it is sometimes also necessary to fit a beta distribution to data that include exact zeros or ones. For such data, the beta likelihood function is unbounded, and standard maximum likelihood estimation is not possible. In that case, `betafit` maximizes a modified likelihood that incorporates the zeros or ones by treating them as if they were values that have been left-censored at `sqrt(realmin)` or right-censored at 1-`eps`/2, respectively.

`[phat,pci] = betafit(data,alpha)` returns confidence intervals on the a and b parameters in the 2-by-2 matrix `pci`. The first column of the matrix contains the lower and upper confidence bounds for parameter a, and the second column contains the confidence bounds for parameter b. The optional input argument `alpha` is a value in the range [0, 1] specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals. The confidence intervals are based on a normal approximation for the distribution of the logs of the parameter estimates.

Examples

This example generates 100 beta distributed observations. The true a and b parameters are 4 and 3, respectively. Compare these to the values returned in `p` by the beta fit. Note that the columns of `ci` both bracket the true parameters.

```
data = betarnd(4,3,100,1);
[p,ci] = betafit(data,0.01)
p =
    5.5328    3.8097
ci =
    3.6538    2.6197
    8.3781    5.5402
```

More About

- "Beta Distribution" on page B-4

References

[1] Hahn, Gerald J., and S. S. Shapiro. *Statistical Models in Engineering*. Hoboken, NJ: John Wiley & Sons, Inc., 1994, p. 95.

See Also

`mle` | `betapdf` | `betainv` | `betastat` | `betalike` | `betarnd` | `betacdf`

betainv

Beta inverse cumulative distribution function

Syntax

```
X = betainv(P,A,B)
```

Description

`X = betainv(P,A,B)` computes the inverse of the beta cdf with parameters specified by `A` and `B` for the corresponding probabilities in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that are all the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must all be positive, and the values in `P` must lie on the interval [0, 1].

The inverse beta cdf for a given probability p and a given pair of parameters a and b is

$$x = F^{-1}(p \mid a,b) = \{x : F(x \mid a,b) = p\}$$

where

$$p = F(x \mid a,b) = \frac{1}{B(a,b)} \int_0^x t^{a-1}(1-t)^{b-1}\,dt$$

and $B(\cdot)$ is the Beta function. Each element of output `X` is the value whose cumulative probability under the beta cdf defined by the corresponding parameters in `A` and `B` is specified by the corresponding value in `P`.

Examples

```
p = [0.01 0.5 0.99];
x = betainv(p,10,5)
x =
```

```
  0.3726   0.6742   0.8981
```

According to this result, for a beta cdf with $a = 10$ and $b = 5$, a value less than or equal to 0.3726 occurs with probability 0.01. Similarly, values less than or equal to 0.6742 and 0.8981 occur with respective probabilities 0.5 and 0.99.

More About

Algorithms

The `betainv` function uses Newton's method with modifications to constrain steps to the allowable range for x, i.e., [0 1].

- "Beta Distribution" on page B-4

See Also

`icdf` | `betapdf` | `betafit` | `betainv` | `betastat` | `betalike` | `betarnd` | `betacdf`

betalike

Beta negative log-likelihood

Syntax

```
nlogL = betalike(params,data)
[nlogL,AVAR] = betalike(params,data)
```

Description

`nlogL = betalike(params,data)` returns the negative of the beta log-likelihood function for the beta parameters a and b specified in vector `params` and the observations specified in the column vector `data`.

The elements of `data` must lie in the open interval (0, 1), where the beta distribution is defined. However, it is sometimes also necessary to fit a beta distribution to data that include exact zeros or ones. For such data, the beta likelihood function is unbounded, and standard maximum likelihood estimation is not possible. In that case, `betalike` computes a modified likelihood that incorporates the zeros or ones by treating them as if they were values that have been left-censored at `sqrt(realmin)` or right-censored at 1-`eps`/2, respectively.

`[nlogL,AVAR] = betalike(params,data)` also returns `AVAR`, which is the asymptotic variance-covariance matrix of the parameter estimates if the values in `params` are the maximum likelihood estimates. `AVAR` is the inverse of Fisher's information matrix. The diagonal elements of `AVAR` are the asymptotic variances of their respective parameters.

`betalike` is a utility function for maximum likelihood estimation of the beta distribution. The likelihood assumes that all the elements in the data sample are mutually independent. Since `betalike` returns the negative beta log-likelihood function, minimizing `betalike` using `fminsearch` is the same as maximizing the likelihood.

Examples

This example continues the `betafit` example, which calculates estimates of the beta parameters for some randomly generated beta distributed data.

```
r = betarnd(4,3,100,1);
[nlogl,AVAR] = betalike(betafit(r),r)
nlogl =

  -27.5996


AVAR =

    0.2783    0.1316
    0.1316    0.0867
```

More About

- "Beta Distribution" on page B-4

See Also

`betapdf` | `betafit` | `betainv` | `betastat` | `betarnd` | `betacdf`

betapdf

Beta probability density function

Syntax

```
Y = betapdf(X,A,B)
```

Description

`Y = betapdf(X,A,B)` computes the beta pdf at each of the values in `X` using the corresponding parameters in `A` and `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions of the other inputs. The parameters in `A` and `B` must all be positive, and the values in `X` must lie on the interval `[0, 1]`.

The beta probability density function for a given value x and given pair of parameters a and b is

$$y = f(x \mid a,b) = \frac{1}{B(a,b)} x^{a-1}(1-x)^{b-1} I_{(0,1)}(x)$$

where $B(\cdot)$ is the Beta function. The indicator function $I_{(0,1)}(x)$ ensures that only values of x in the range (0 1) have nonzero probability. The uniform distribution on (0 1) is a degenerate case of the beta pdf where $a = 1$ and $b = 1$.

A *likelihood function* is the pdf viewed as a function of the parameters. Maximum likelihood estimators (MLEs) are the values of the parameters that maximize the likelihood function for a fixed value of x.

Examples

```
a = [0.5 1; 2 4]
a =
  0.5000  1.0000
```

```
  2.0000  4.0000
y = betapdf(0.5,a,a)
y =
  0.6366  1.0000
  1.5000  2.1875
```

More About

- "Beta Distribution" on page B-4

See Also

pdf | betafit | betainv | betastat | betalike | betarnd | betacdf

betarnd

Beta random numbers

Syntax

```
R = betarnd(A,B)
R = betarnd(A,B,m,n,...)
R = betarnd(A,B,[m,n,...])
```

Description

`R = betarnd(A,B)` generates random numbers from the beta distribution with parameters specified by `A` and `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

`R = betarnd(A,B,m,n,...)` or `R = betarnd(A,B,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the beta distribution with parameters `A` and `B`. `A` and `B` can each be scalars or arrays of the same size as `R`.

Examples

```
a = [1 1;2 2];
b = [1 2;1 2];

r = betarnd(a,b)
r =
  0.6987  0.6139
  0.9102  0.8067

r = betarnd(10,10,[1 5])
r =
  0.5974  0.4777  0.5538  0.5465  0.6327

r = betarnd(4,2,2,3)
r =
```

```
  0.3943   0.6101   0.5768
  0.5990   0.2760   0.5474
```

More About

- "Beta Distribution" on page B-4

See Also

`random` | `betapdf` | `betafit` | `betainv` | `betastat` | `betalike` | `betacdf`

betastat

Beta mean and variance

Syntax

```
[M,V] = betastat(A,B)
```

Description

`[M,V] = betastat(A,B)`, with `A>0` and `B>0`, returns the mean of and variance for the beta distribution with parameters specified by `A` and `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

The mean of the beta distribution with parameters a and b is $a/(a+b)$ and the variance is

$$\frac{ab}{(a+b+1)(a+b)^2}$$

Examples

If parameters a and b are equal, the mean is 1/2.

```
a = 1:6;
[m,v] = betastat(a,a)
m =
  0.5000  0.5000  0.5000  0.5000  0.5000  0.5000
v =
  0.0833  0.0500  0.0357  0.0278  0.0227  0.0192
```

More About

- “Beta Distribution” on page B-4

See Also

betapdf | betafit | betainv | betalike | betarnd | betacdf

BIC property

Class: gmdistribution

Bayes Information Criterion

Description

The Bayes Information Criterion: `2*NlogL + m*log(n)`, where `NlogL` is the negative loglikelihood, `n` is the number of observations, and `m` is the number of estimated parameters.

prob.BinomialDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Binomial probability distribution object

Description

`prob.BinomialDistribution` is an object consisting of parameters, a model description, and sample data for a binomial probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Binomial')` creates a binomial probability distribution object using the default parameter values.

`pd = makedist('Binomial','N',N,'p',p)` creates a binomial probability distribution object using the specified parameter values.

Input Arguments

`N` — Number of trials

`1` (default) | positive integer value

Number of trials for the binomial distribution, specified as a positive integer value.

Data Types: `single` | `double`

`p` — Probability of success

`0.5` (default) | positive scalar value in the range `[0,1]`

Probability of success of any individual trial for the binomial distribution, specified as a positive scalar value in the range `[0,1]`.

Data Types: `single` | `double`

Properties

`N` — Number of trials

positive integer value

Number of trials for the binomial distribution, stored as a positive integer value.

Data Types: `single` | `double`

`p` — Probability of success

positive scalar value in the range `[0,1]`

Probability of success of any individual trial for the binomial distribution, stored as a positive scalar value in the range `[0,1]`.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object

pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Binomial Distribution

The binomial distribution models the total number of successes in repeated trials from an infinite population under the following conditions:

- Only two outcomes are possible for each of n trials.
- The probability of success for each trial is constant.

- All trials are independent of each other.

The binomial distribution uses the following parameters.

Parameter	Description	Support
N	Number of trials	positive integer
p	Probability of success	$0 \le p \le 1$

The probability density function (pdf) is

$$f(x \mid N, p) = \binom{N}{x} p^x (1-p)^{N-x} \quad ; \quad x = 0, 1, 2, \ldots, N,$$

where x is the number of successes in N trials of a Bernoulli process with probability of success p.

Examples

Create a Binomial Distribution Object Using Default Parameters

Create a binomial distribution object using the default parameter values.

```
pd = makedist('Binomial')
```

```
pd =

  BinomialDistribution

  Binomial distribution
    N =   1
    p = 0.5
```

Create a Binomial Distribution Object Using Specified Parameters

Create a binomial distribution object by specifying the parameter values.

```
pd = makedist('Binomial','N',30,'p',0.25)
```

```
pd =
```

```
  BinomialDistribution

  Binomial distribution
    N =   30
    p = 0.25
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    7.5000
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Binomial Distribution"
- "Bernoulli Distribution"
- Class Attributes
- Property Attributes

binocdf

Binomial cumulative distribution function

Syntax

```
y = binocdf(x,N,p)
y = binocdf(x,N,p,'upper')
```

Description

`y = binocdf(x,N,p)` computes a binomial cdf at each of the values in `x` using the corresponding number of trials in `N` and probability of success for each trial in `p`. `x`, `N`, and `p` can be vectors, matrices, or multidimensional arrays that are all the same size. A scalar input is expanded to a constant array with the same dimensions of the other inputs. The values in `N` must all be positive integers, the values in `x` must lie on the interval `[0,N]`, and the values in `p` must lie on the interval [0, 1].

`y = binocdf(x,N,p,'upper')` returns the complement of the binomial cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The binomial cdf for a given value x and a given pair of parameters n and p is

$$y = F(x \mid n,p) = \sum_{i=0}^{x} \binom{n}{i} p^i (1-p)^{(n-i)} I_{(0,1,\ldots,n)}(i).$$

The result, y, is the probability of observing up to x successes in n independent trials, where the probability of success in any given trial is p. The indicator function $I_{(0,1,\ldots,n)}(i)$ ensures that x only adopts values of $0,1,\ldots,n$.

Examples

Compute Binomial CDF

If a baseball team plays 162 games in a season and has a 50-50 chance of winning any game, then the probability of that team winning more than 100 games in a season is:

```
1 - binocdf(100,162,0.5)
```

```
ans =

    0.0010
```

The result is `0.001` (i.e., `1-0.999`). If a team wins 100 or more games in a season, this result suggests that it is likely that the team's true probability of winning any game is greater than 0.5.

More About

- "Binomial Distribution" on page B-9

See Also

`cdf` | `binopdf` | `binoinv` | `binostat` | `binofit` | `binornd`

binofit

Binomial parameter estimates

Syntax

```
phat = binofit(x,n)
[phat,pci] = binofit(x,n)
[phat,pci] = binofit(x,n,alpha)
```

Description

`phat = binofit(x,n)` returns a maximum likelihood estimate of the probability of success in a given binomial trial based on the number of successes, `x`, observed in `n` independent trials. If `x = (x(1), x(2), ... x(k))` is a vector, `binofit` returns a vector of the same size as `x` whose ith entry is the parameter estimate for `x(i)`. All `k` estimates are independent of each other. If `n = (n(1), n(2), ..., n(k))` is a vector of the same size as `x`, the binomial fit, `binofit`, returns a vector whose ith entry is the parameter estimate based on the number of successes `x(i)` in `n(i)` independent trials. A scalar value for `x` or `n` is expanded to the same size as the other input.

`[phat,pci] = binofit(x,n)` returns the probability estimate, `phat`, and the 95% confidence intervals, `pci`. `binofit` uses the Clopper-Pearson method to calculate confidence intervals.

`[phat,pci] = binofit(x,n,alpha)` returns the `100(1 - alpha)`% confidence intervals. For example, `alpha = 0.01` yields 99% confidence intervals.

Note `binofit` behaves differently than other Statistics and Machine Learning Toolbox functions that compute parameter estimates, in that it returns independent estimates for each entry of `x`. By comparison, `expfit` returns a single parameter estimate based on all the entries of `x`.

Unlike most other distribution fitting functions, the `binofit` function treats its input `x` vector as a collection of measurements from separate samples. If you want to treat

`x` as a single sample and compute a single parameter estimate for it, you can use `binofit(sum(x),sum(n))` when `n` is a vector, and `binofit(sum(X),N*length(X))` when `n` is a scalar.

Examples

This example generates a binomial sample of 100 elements, where the probability of success in a given trial is 0.6, and then estimates this probability from the outcomes in the sample.

```
r = binornd(100,0.6);
[phat,pci] = binofit(r,100)
phat =
  0.5800
pci =
  0.4771  0.6780
```

The 95% confidence interval, `pci`, contains the true value, 0.6.

More About

- "Binomial Distribution" on page B-9

References

[1] Johnson, N. L., S. Kotz, and A. W. Kemp. *Univariate Discrete Distributions*. Hoboken, NJ: Wiley-Interscience, 1993.

See Also

`mle` | `binopdf` | `binocdf` | `binoinv` | `binostat` | `binornd`

binoinv

Binomial inverse cumulative distribution function

Syntax

```
X = binoinv(Y,N,P)
```

Description

`X = binoinv(Y,N,P)` returns the smallest integer `X` such that the binomial cdf evaluated at `X` is equal to or exceeds `Y`. You can think of `Y` as the probability of observing `X` successes in `N` independent trials where `P` is the probability of success in each trial. Each `X` is a positive integer less than or equal to `N`.

`Y`, `N`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `N` must be positive integers, and the values in both `P` and `Y` must lie on the interval [0 1].

Examples

If a baseball team has a 50-50 chance of winning any game, what is a reasonable range of games this team might win over a season of 162 games?

```
binoinv([0.05 0.95],162,0.5)
ans =
    71    91
```

This result means that in 90% of baseball seasons, a .500 team should win between 71 and 91 games.

More About

- “Binomial Distribution” on page B-9

See Also

icdf | binopdf | binocdf | binofit | binostat | binornd

binopdf

Binomial probability density function

Syntax

```
Y = binopdf(X,N,P)
```

Description

`Y = binopdf(X,N,P)` computes the binomial pdf at each of the values in `X` using the corresponding number of trials in `N` and probability of success for each trial in `P`. `Y`, `N`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions of the other inputs.

The parameters in `N` must be positive integers, and the values in `P` must lie on the interval [0, 1].

The binomial probability density function for a given value x and given pair of parameters n and p is

$$y = f(x \mid n, p) = \binom{n}{x} p^x q^{(n-x)} I_{(0,1,\ldots,n)}(x)$$

where $q = 1 - p$. The result, y, is the probability of observing x successes in n independent trials, where the probability of success in any *given* trial is p. The indicator function $I_{(0,1,\ldots,n)}(x)$ ensures that x only adopts values of 0, 1, ..., n.

Examples

A Quality Assurance inspector tests 200 circuit boards a day. If 2% of the boards have defects, what is the probability that the inspector will find no defective boards on any given day?

```
binopdf(0,200,0.02)
```

```
ans =
  0.0176
```

What is the most likely number of defective boards the inspector will find?

```
defects=0:200;
y = binopdf(defects,200,.02);
[x,i]=max(y);
defects(i)
ans =
  4
```

More About

- "Binomial Distribution" on page B-9

See Also

`pdf` | `binoinv` | `binocdf` | `binofit` | `binostat` | `binornd`

binornd

Binomial random numbers

Syntax

```
R = binornd(N,P)
R = binornd(N,P,m,n,...)
R = binornd(N,P,[m,n,...])
```

Description

`R = binornd(N,P)` generates random numbers from the binomial distribution with parameters specified by the number of trials, `N`, and probability of success for each trial, `P`. `N` and `P` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `N` or `P` is expanded to a constant array with the same dimensions as the other input.

`R = binornd(N,P,m,n,...)` or `R = binornd(N,P,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the binomial distribution with parameters `N` and `P`. `N` and `P` can each be scalars or arrays of the same size as `R`.

Examples

```
n = 10:10:60;

r1 = binornd(n,1./n)
r1 =
   2   1   0   1   1   2

r2 = binornd(n,1./n,[1 6])
r2 =
   0   1   2   1   3   1

r3 = binornd(n,1./n,1,6)
r3 =
   0   1   1   1   0   3
```

More About

Algorithms

The `binornd` function uses the direct method using the definition of the binomial distribution as a sum of Bernoulli random variables.

- "Binomial Distribution" on page B-9

See Also

`random` | `binoinv` | `binocdf` | `binofit` | `binostat` | `binopdf`

binostat

Binomial mean and variance

Syntax

```
[M,V] = binostat(N,P)
```

Description

`[M,V] = binostat(N,P)` returns the mean of and variance for the binomial distribution with parameters specified by the number of trials, `N`, and probability of success for each trial, `P`. `N` and `P` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `M` and `V`. A scalar input for `N` or `P` is expanded to a constant array with the same dimensions as the other input.

The mean of the binomial distribution with parameters n and p is np. The variance is npq, where $q = 1 - p$.

Examples

```
n = logspace(1,5,5)
n =
     10     100    1000    10000   100000

[m,v] = binostat(n,1./n)
m =
   1   1   1   1   1
v =
  0.9000  0.9900  0.9990  0.9999  1.0000

[m,v] = binostat(n,1/2)
m =
      5     50     500    5000    50000
v =
  1.0e+04 *
  0.0003  0.0025  0.0250  0.2500  2.5000
```

More About

- “Binomial Distribution” on page B-9

See Also

`binoinv` | `binocdf` | `binofit` | `binornd` | `binopdf`

biplot

Biplot

Syntax

```
biplot(coefs)
h = biplot(coefs,'Name',Value)
```

Description

`biplot(coefs)` creates a biplot of the coefficients in the matrix `coefs`. The biplot is 2-D if `coefs` has two columns or 3-D if it has three columns. `coefs` usually contains principal component coefficients created with `pca`, `pcacov`, or factor loadings estimated with `factoran`. The axes in the biplot represent the principal components or latent factors (columns of `coefs`), and the observed variables (rows of `coefs`) are represented as vectors.

A biplot allows you to visualize the magnitude and sign of each variable's contribution to the first two or three principal components, and how each observation is represented in terms of those components.

`biplot` imposes a sign convention, forcing the element with largest magnitude in each column of `coefs` to be positive. This flips some of the vectors in `coefs` to the opposite direction, but often makes the plot easier to read. Interpretation of the plot is unaffected, because changing the sign of a coefficient vector does not change its meaning.

`biplot` scales the scores so that they fit on the plot: It divides each score by the maximum absolute value of all scores, and multiplies by the maximum coefficient length of `coefs`. Then `biplot` changes the sign of score coordinates according to the sign convention for the `coefs`.

`h = biplot(coefs,'Name',Value)` specifies one or more name/value input pairs and returns a column vector of handles to the graphics objects created by `biplot`. The `h` contains, in order, handles corresponding to variables (line handles, followed by marker handles, followed by text handles), to observations (if present, marker handles followed by text handles), and to the axis lines.

Input Arguments

Name-Value Pair Arguments

`'Scores'`

Plots both `coefs` and the `scores` in the matrix `scores` in the biplot. `scores` usually contains principal component scores created with `pca` or factor scores estimated with `factoran`. Each observation (row of scores) is represented as a point in the biplot.

`'VarLabels'`

Labels each vector (variable) with the text in the character array or cell array `varlabels`.

`'ObsLabels'`

Uses the text in the character array or cell array `obslabels` as observation names when displaying data cursors.

`'Positive'`

- `'true'` — restricts the biplot to the positive quadrant (in 2-D) or octant (in 3-D).
- `'false'` — makes the biplot over the range `+/- max(coefs(:))` for all coordinates.

Default: `false`

`'PropertyName'`

Specifies optional property name/value pairs for all Primitive Line Properties graphics objects created by `biplot`.

Examples

Biplot of Coefficients and Scores

Load the sample data.

```
load carsmall
```

Define the variable matrix and delete the rows with missing values.

```
x = [Acceleration Displacement Horsepower MPG Weight];
```

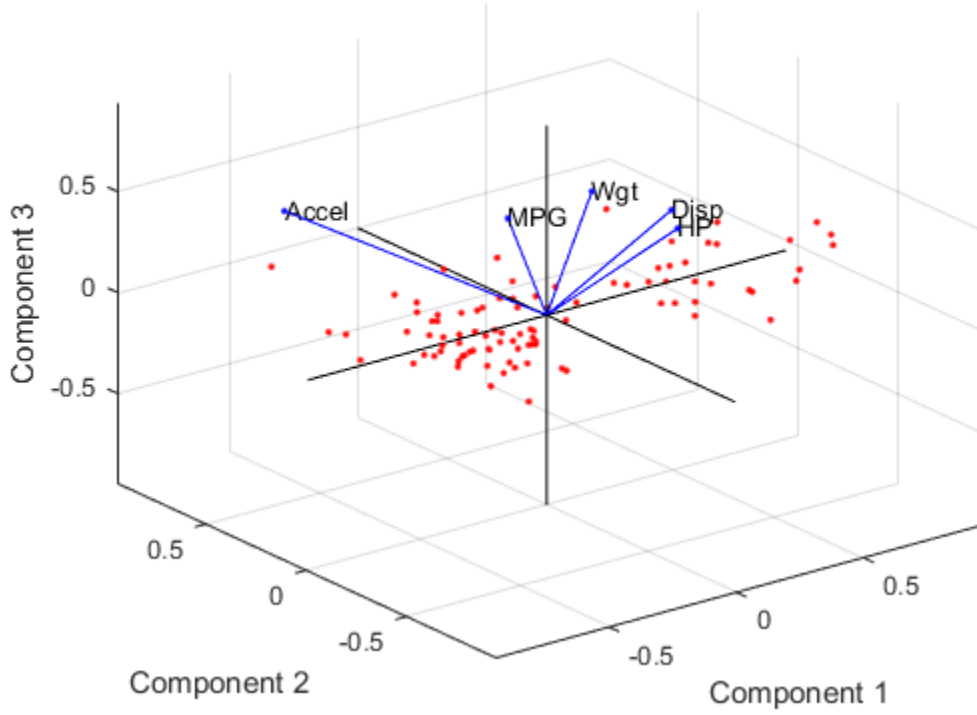
```
x = x(all(~isnan(x),2),:);
```

Perform a principal component analysis of the data.

```
[coefs,score] = pca(zscore(x));
```

View the data and the original variables in the space of the first three principal components.

```
vbls = {'Accel','Disp','HP','MPG','Wgt'};
biplot(coefs(:,1:3),'scores',score(:,1:3),'varlabels',vbls);
```



See Also

`factoran` | `nnmf` | `pca` | `pcacov` | `rotatefactors`

prob.BirnbaumSaundersDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Birnbaum-Saunders probability distribution object

Description

`prob.BirnbaumSaundersDistribution` is an object consisting of parameters, a model description, and sample data for a Birnbaum-Saunders probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('BirnbaumSaunders')` creates a Birnbaum-Saunders probability distribution object using the default parameter values.

`pd = makedist('BirnbaumSaunders','beta',beta,'gamma',gamma)` creates a Birnbaum-Saunders distribution object using the specified parameter values.

Input Arguments

`beta` — Scale parameter

1 (default) | positive scalar value

Scale parameter of the Birnbaum-Saunders distribution, specified as a positive scalar value.

Data Types: `single` | `double`

`gamma` — Shape parameter

1 (default) | nonnegative scalar value

Shape parameter of the Birnbaum-Saunders distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

Properties

`beta` — Scale parameter

positive scalar value

Scale parameter of the Birnbaum-Saunders distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`gamma` — Shape parameter

nonnegative scalar value

Shape parameter of the Birnbaum-Saunders distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object

pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Birnbaum-Saunders Distribution

The Birnbaum-Saunders distribution was originally proposed as a lifetime model for materials subject to cyclic patterns of stress and strain, where the ultimate failure of the material comes from the growth of a prominent flaw. It is also called the fatigue life distribution.

The Birnbaum-Saunders distribution uses the following parameters.

Parameter	Description	Support
`beta`	Scale parameter	$\beta > 0$
`gamma`	Shape parameter	$\gamma \geq 0$

The probability density function (pdf) is

$$f(x \mid \beta, \gamma) = \frac{1}{\sqrt{2\pi}} \exp\left\{ -\frac{\left(\sqrt{\frac{x}{\beta}} - \sqrt{\frac{\beta}{x}} \right)^2}{2\gamma^2} \right\} \left(\frac{\left(\sqrt{\frac{x}{\beta}} - \sqrt{\frac{\beta}{x}} \right)}{2\gamma x} \right) \quad ; \quad x > 0.$$

Examples

Create a Birnbaum-Saunders Distribution Object Using Default Parameters

Create a Birnbaum-Saunders distribution object using the default parameter values.

```
pd = makedist('BirnbaumSaunders')
```

```
pd =

  BirnbaumSaundersDistribution

  Birnbaum-Saunders distribution
     beta = 1
    gamma = 1
```

Create a Birnbaum-Saunders Distribution Object Using Specified Parameter Values

Create a Birnbaum-Saunders distribution object by specifying the parameter values.

```
pd = makedist('BirnbaumSaunders','beta',2,'gamma',5)
```

```
pd =

  BirnbaumSaundersDistribution

  Birnbaum-Saunders distribution
     beta = 2
```

```
    gamma = 5
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    27
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Birnbaum-Saunders Distribution"
- Class Attributes
- Property Attributes

bootci

Bootstrap confidence interval

Syntax

```
ci = bootci(nboot,bootfun,...)
ci = bootci(nboot,{bootfun,...},'alpha',alpha)
ci = bootci(nboot,{bootfun,...},...,'type',type)
ci = bootci(nboot,
{bootfun,...},...,'type','student','nbootstd',nbootstd)
ci = bootci(nboot,
{bootfun,...},...,'type','student','stderr',stderr)
ci = bootci(nboot,{bootfun,...},...,'Weights',weights)
ci = bootci(nboot,{bootfun,...},...,'Options',options)
[ci,bootstat] = bootci(...)
```

Description

`ci = bootci(nboot,bootfun,...)` computes the 95% bootstrap confidence interval of the statistic computed by the function `bootfun`. `nboot` is a positive integer indicating the number of bootstrap samples used in the computation. `bootfun` is a function handle specified with `@`. The third and later input arguments to `bootci` are data (scalars, column vectors, or matrices) that are used to create inputs to `bootfun`. `bootci` creates each bootstrap sample by sampling with replacement from the rows of the non-scalar data arguments (these must have the same number of rows). Scalar data are passed to `bootfun` unchanged.

If `bootfun` returns a scalar, `ci` is a vector containing the lower and upper bounds of the confidence interval. If `bootfun` returns a vector of length *m*, `ci` is an array of size 2-by-*m*, where `ci(1,:)` are lower bounds and `ci(2,:)` are upper bounds. If `bootfun` returns an array of size *m*-by-*n*-by-*p*-by-..., `ci` is an array of size 2-by-*m*-by-*n*-by-*p*-by-..., where `ci(1,:,:,:,...)` is an array of lower bounds and `ci(2,:,:,:,...)` is an array of upper bounds.

`ci = bootci(nboot,{bootfun,...},'alpha',alpha)` computes the `100*(1-alpha)` bootstrap confidence interval of the statistic defined by the function `bootfun`.

`bootfun` and the data that `bootci` passes to it are contained in a single cell array. `alpha` is a scalar between `0` and `1`. The default value of `alpha` is `0.05`.

`ci = bootci(nboot,{bootfun,...},...,'type',type)` computes the bootstrap confidence interval of the statistic defined by the function `bootfun`. *`type`* is the confidence interval type, chosen from among the following strings:

- `'norm'` or `'normal'` — Normal approximated interval with bootstrapped bias and standard error.
- `'per'` or `'percentile'` — Basic percentile method.
- `'cper'` or `'corrected percentile'` — Bias corrected percentile method.
- `'bca'` — Bias corrected and accelerated percentile method. This is the default.
- `'stud'` or `'student'` — Studentized confidence interval.

`ci = bootci(nboot,{bootfun,...},...,'type','student','nbootstd',nbootstd)` computes the studentized bootstrap confidence interval of the statistic defined by the function `bootfun`. The standard error of the bootstrap statistics is estimated using bootstrap, with `nbootstd` bootstrap data samples. `nbootstd` is a positive integer value. The default value of `nbootstd` is `100`.

`ci = bootci(nboot,{bootfun,...},...,'type','student','stderr',stderr)` computes the studentized bootstrap confidence interval of statistics defined by the function `bootfun`. The standard error of the bootstrap statistics is evaluated by the function `stderr`. `stderr` is a function handle. `stderr` takes the same arguments as `bootfun` and returns the standard error of the statistic computed by `bootfun`.

`ci = bootci(nboot,{bootfun,...},...,'Weights',weights)` specifies observation weights. `weights` must be a vector of non-negative numbers with at least one positive element. The number of elements in `weights` must be equal to the number of rows in non-scalar input arguments to `bootfun`. To obtain one bootstrap replicate, `bootstrp` samples N out of N with replacement using these weights as multinomial sampling probabilities.

`ci = bootci(nboot,{bootfun,...},...,'Options',options)` specifies options that govern the computation of bootstrap iterations. One option requests that `bootci` perform bootstrap iterations using multiple processors, if the Parallel Computing Toolbox is available. Two options specify the random number streams to be used in bootstrap

resampling. This argument is a struct that you can create with a call to `statset`. You can retrieve values of the individual fields with a call to `statget`. Applicable `statset` parameters are:

- `'UseParallel'` — If `true` and if a `parpool` of the Parallel Computing Toolbox is open, compute bootstrap iterations in parallel. If the Parallel Computing Toolbox is not installed, or a `parpool` is not open, computation occurs in serial mode. Default is `false`, or serial computation.
- `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
- `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `bootci` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case

  - You have an open Parallel pool
  - `UseParallel` is `true`
  - `UseSubstreams` is `false`

  In that case, use a cell array the same size as the Parallel pool.

`[ci,bootstat] = bootci(...)` also returns the bootstrapped statistic computed for each of the `nboot` bootstrap replicate samples. Each row of `bootstat` contains the results of applying `bootfun` to one bootstrap sample. If `bootfun` returns a matrix or array, then this output is converted to a row vector for storage in `bootstat`.

Examples

Compute the confidence interval for the capability index in statistical process control:

```
y = normrnd(1,1,30,1);                % Simulated process data
LSL = -3; USL = 3;                    % Process specifications
capable = @(x)(USL-LSL)./(6* std(x));  % Process capability
ci = bootci(2000,capable,y)           % BCa confidence interval
ci =
    0.8122
    1.2657

sci = bootci(2000,{capable,y},'type','student') % Studentized ci
sci =
    0.7739
    1.2707
```

See Also

`bootstrp` | `jackknife` | `parfor` | `statget` | `statset` | `randsample`

bootstrp

Bootstrap sampling

Syntax

```
bootstat = bootstrp(nboot,bootfun,d1,...)
[bootstat,bootsam] = bootstrp(...)
bootstat = bootstrp(...,'Name',Value)
```

Description

`bootstat = bootstrp(nboot,bootfun,d1,...)` draws `nboot` bootstrap data samples, computes statistics on each sample using `bootfun`, and returns the results in the matrix `bootstat`. `nboot` must be a positive integer. `bootfun` is a function handle specified with `@`. Each row of `bootstat` contains the results of applying `bootfun` to one bootstrap sample. If `bootfun` returns a matrix or array, then this output is converted to a row vector for storage in `bootstat`.

The third and later input arguments (`d1,...`) are data (scalars, column vectors, or matrices) used to create inputs to `bootfun`. `bootstrp` creates each bootstrap sample by sampling with replacement from the rows of the non-scalar data arguments (these must have the same number of rows). `bootfun` accepts scalar data unchanged.

`[bootstat,bootsam] = bootstrp(...)` returns an `n`-by-`nboot` matrix of bootstrap indices, `bootsam`. Each column in `bootsam` contains indices of the values that were drawn from the original data sets to constitute the corresponding bootstrap sample. For example, if `d1,...` each contain 16 values, and `nboot = 4`, then `bootsam` is a 16-by-4 matrix. The first column contains the indices of the 16 values drawn from `d1,...`, for the first of the four bootstrap samples, the second column contains the indices for the second of the four bootstrap samples, and so on. (The bootstrap indices are the same for all input data sets.) To get the output samples `bootsam` without applying a function, set `bootfun` to empty (`[]`).

`bootstat = bootstrp(...,'Name',Value)` uses additional arguments specified by one or more Name,Value pair arguments. The name-value pairs must appear after the data arguments. The available name-value pairs:

- `'Weights'` — Observation weights. The `weights` value must be a vector of nonnegative numbers with at least one positive element. The number of elements in `weights` must be equal to the number of rows in non-scalar input arguments to `bootstrp`. To obtain one bootstrap replicate, `bootstrp` samples *N* out of *N* with replacement using these weights as multinomial sampling probabilities.
- `'Options'` — The value is a structure that contains options specifying whether to compute bootstrap iterations in parallel, and specifying how to use random numbers during the bootstrap sampling. Create the options structure with `statset`. Applicable `statset` parameters are:
  - `'UseParallel'` — If `true` and if a `parpool` of the Parallel Computing Toolbox is open, compute bootstrap iterations in parallel. If the Parallel Computing Toolbox is not installed, or a `parpool` is not open, computation occurs in serial mode. Default is `false`, meaning serial computation.
  - `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
  - `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `bootstrp` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
    - You have an open Parallel pool
    - `UseParallel` is `true`
    - `UseSubstreams` is `false`

    In that case, use a cell array the same size as the Parallel pool.

Examples

Bootstrapping a Correlation Coefficient Standard Error

This example shows how to compute a correlation coefficient standard error using bootstrap resampling of the sample data.

Load a data set containing the LSAT scores and law-school GPA for 15 students. These 15 data points are resampled to create 1000 different data sets, and the correlation between the two variables is computed for each data set.

```
load lawdata
```

```
rng default  % For reproducibility
[bootstat,bootsam] = bootstrp(1000,@corr,lsat,gpa);
```

Display the first 5 bootstrapped correlation coefficients.

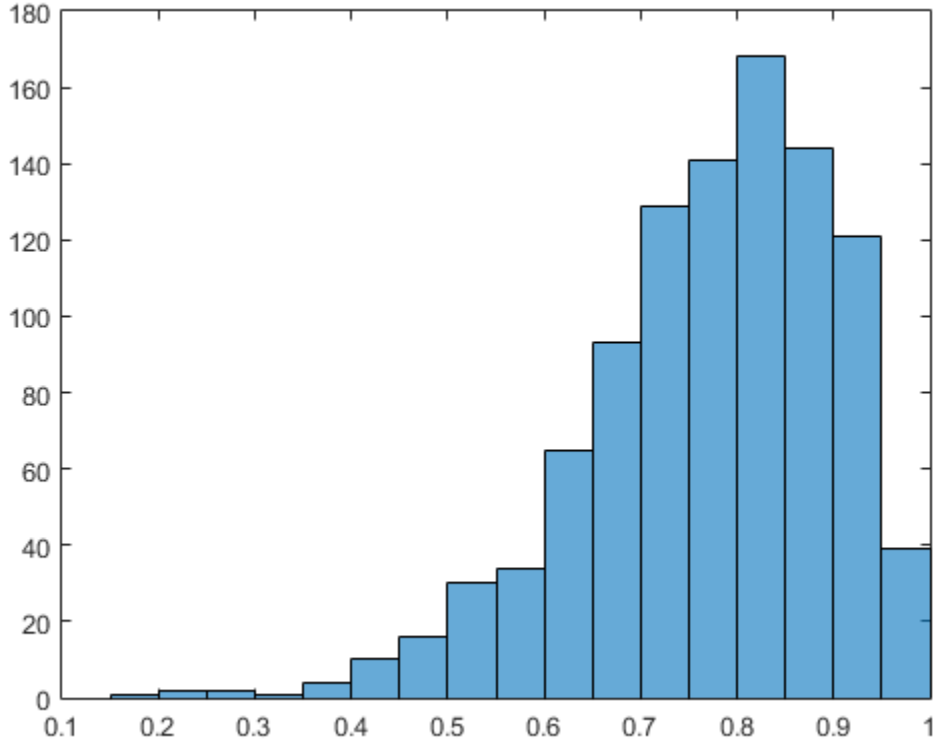
```
bootstat(1:5,:)
```

```
ans =

    0.9874
    0.4918
    0.5459
    0.8458
    0.8959
```

Display the indices of the data selected for the first 5 bootstrap samples.

```
bootsam(:,1:5)
figure
histogram(bootstat)
```

```
ans =

    13     3    11     8    12
    14     7     1     7     4
     2    14     5    10     8
    14    12     1    11    11
    10    15     2    12    14
     2    10    13     5    15
     5     1    11    11     9
     9    13     5    10     3
    15    15    15     3     3
    15    11     1     2     4
     3    12     7     8    13
    15    12     6    15     4
    15     6    12     6    13
     8    10    12     9     4
    13     3     3     4    14
```



The histogram shows the variation of the correlation coefficient across all the bootstrap samples. The sample minimum is positive, indicating that the relationship between LSAT score and GPA is not accidental.

Finally, compute a bootstrap standard of error for the estimated correlation coefficient.

```
se = std(bootstat)
```

```
se =

    0.1285
```

Estimate the Density of Bootstrapped Statistic

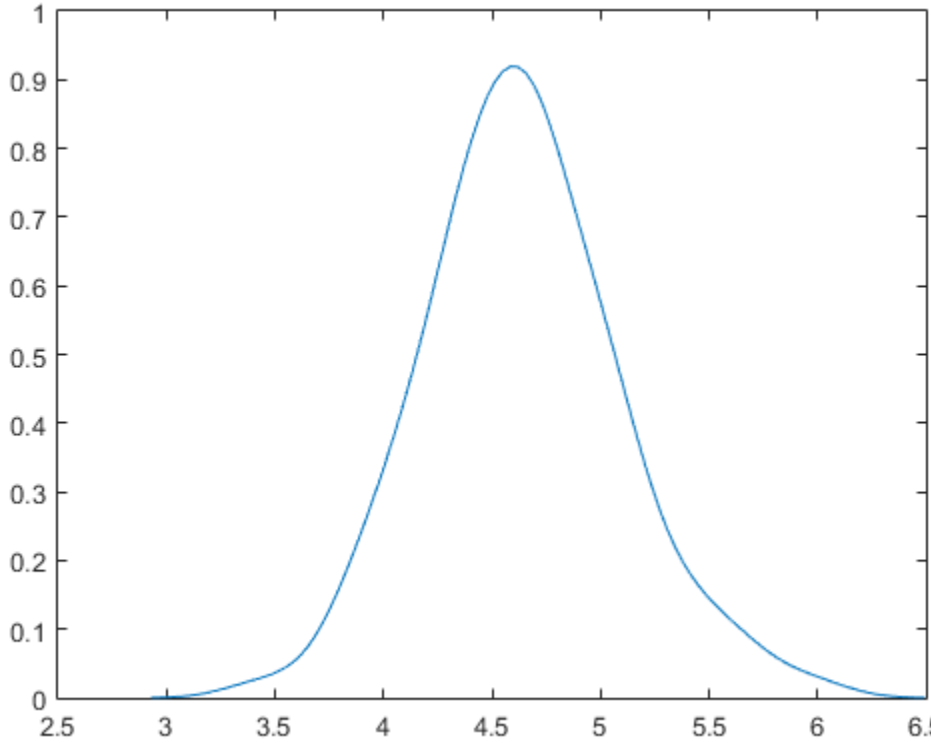
This example shows how to estimate the kernel density of bootstrapped means.

Compute a sample of 100 bootstrapped means of random samples taken from the vector Y.

```
rng default;  % For reproducibility
y = exprnd(5,100,1);
m = bootstrp(100,@mean,y);
```

Plot an estimate of the density of these bootstrapped means.

```
figure;
[fi,xi] = ksdensity(m);
plot(xi,fi);
```



Bootstrapping Multiple Statistics

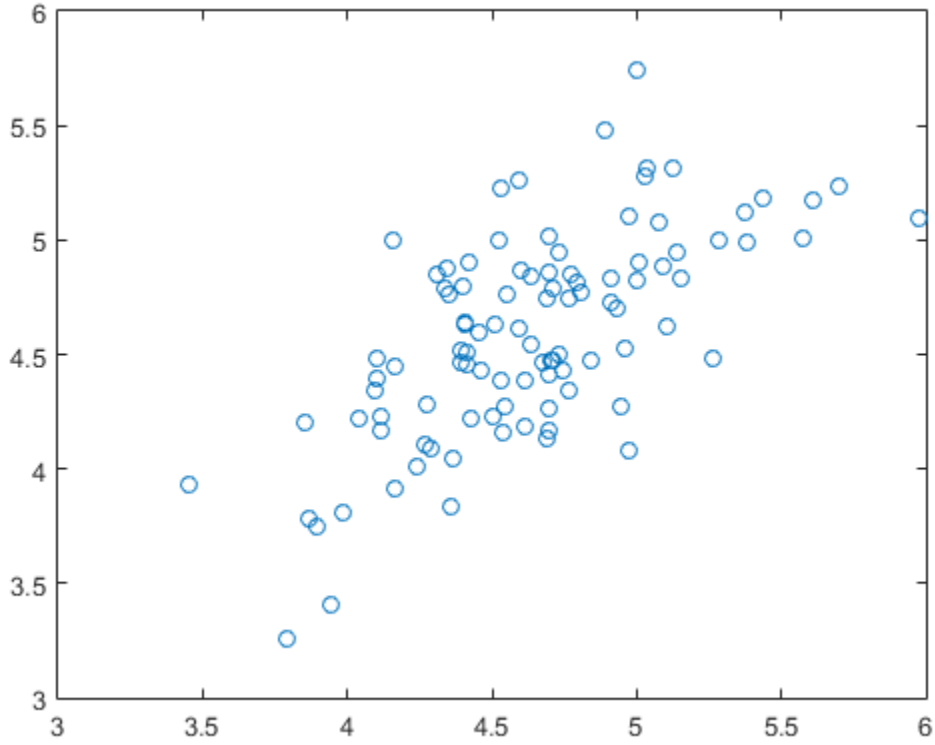
This example shows how to compute and plot the means and standard deviations of bootstraped 100 samples from a data vector.

Compute a sample of 100 bootstrapped means and standard deviations of random samples taken from the vector `y`.

```
rng default  % For reproducibility
y = exprnd(5,100,1);
stats = bootstrp(100,@(x)[mean(x) std(x)],y);
```

Plot the bootstrap estimate pairs.

```
plot(stats(:,1),stats(:,2),'o')
```



Bootstrapping a Regression Model

This example shows how to estimate the standard errors for a coefficient vector in a linear regression by bootstrapping the residuals.

Load the sample data.

```
load hald
```

Perform a linear regression and compute the residuals.

```
x = [ones(size(heat)),ingredients];
y = heat;
b = regress(y,x);
```

```
yfit = x*b;
resid = y - yfit;
```

Estimate the standard errors by bootstrapping the residuals.

```
se = std(bootstrp(...
         1000,@(bootr)regress(yfit+bootr,x),resid))
```

```
se =

   56.1752    0.5940    0.5815    0.5989    0.5691
```

See Also

histogram | parfor | random | bootci | ksdensity | randsample | RandStream | statget | statset

boxplot

Box plot

Syntax

```
boxplot(X)
boxplot(X,G)
boxplot(axes,X,...)
boxplot(...,'Name',value)
```

Description

`boxplot(X)` produces a box plot of the data in `X`. If `X` is a matrix, there is one box per column; if `X` is a vector, there is just one box. On each box, the central mark is the median, the edges of the box are the 25th and 75th percentiles, the whiskers extend to the most extreme data points not considered outliers, and outliers are plotted individually. For controlling how much the whiskers extend, see the `'whiskers'` name-value pair argument.

`boxplot(X,G)` specifies one or more grouping variables `G`, producing a separate box for each set of `X` values sharing the same `G` value or values. Grouping variables must have one row per element of `X`, or one row per column of `X`. Specify a single grouping variable in `G` using a vector, a character array, a cell array of strings, or a vector categorical array; specify multiple grouping variables in `G` using a cell array of these variable types, such as `{G1 G2 G3}`, or by using a matrix. If multiple grouping variables are used, they must all be the same length. Groups that contain a `NaN` value or an empty string in a grouping variable are omitted, and are not counted in the number of groups considered by other parameters.

By default, character and string grouping variables are sorted in the order they initially appear in the data, categorical grouping variables are sorted by the order of their levels, and numeric grouping variables are sorted in numeric order. To control the order of groups, do one of the following:

- Use categorical variables in `G` and specify the order of their levels.
- Use the `'grouporder'` parameter described below.

- Pre-sort your data.

`boxplot(axes,X,...)` creates the plot in the axes with handle `axes`.

`boxplot(...,'Name',value)` specifies one or more optional parameter name/value pairs, as described in the following table. Specify *`Name`* in single quotes.

Name	Value
`'plotstyle'`	• `'traditional'` — Traditional box style. This is the default. • `'compact'` — Box style designed for plots with many groups. This style changes the defaults for some other parameters, as described in the following table.
`'boxstyle'`	• `'outline'` — Draws an unfilled box with dashed whiskers. This is the default. • `'filled'` — Draws a narrow filled box with lines for whiskers.
`'colorgroup'`	One or more grouping variables, of the same type as permitted for `G`, specifying that the box color should change when the specified variables change. The default is `[]` for no box color change.
`'colors'`	Colors for boxes, specified as a single color (such as `'r'` or `[1 0 0]`) or multiple colors (such as `'rgbm'` or a three-column matrix of RGB values). The sequence is replicated or truncated as required, so for example `'rb'` gives boxes that alternate in color. The default when no `'colorgroup'` is specified is to use the same color scheme for all boxes. The default when `'colorgroup'` is specified is a modified `hsv colormap`.
`'datalim'`	A two-element vector containing lower and upper limits, used by `'extrememode'` to determine which points are extreme. The default is `[-Inf Inf]`.
`'extrememode'`	• `'clip'` — Moves data outside the `datalim` limits to the limit. This is the default. • `'compress'` — Evenly distributes data outside the `datalim` limits in a region just outside the limit, retaining the relative order of the points.

Name	Value
	A dotted line marks the limit if any points are outside it, and two gray lines mark the compression region if any points are compressed. Values at +/–`Inf` can be clipped or compressed, but `NaN` values still do not appear on the plot. Box notches are drawn to scale and may extend beyond the bounds if the median is inside the limit; they are not drawn if the median is outside the limits.
`'factordirection'`	• `'data'` — Arranges factors with the first value next to the origin. This is the default. • `'list'` — Arranges factors left-to-right if on the *x* axis or top-to-bottom if on the *y* axis. • `'auto'` — Uses `'data'` for numeric grouping variables and `'list'` for strings.
`'fullfactors'`	• `'off'` — One group for each unique row of `G`. This is the default. • `'on'` — Create a group for each possible combination of group variable values, including combinations that do not appear in the data.
`'factorseparator'`	Specifies which factors should have their values separated by a grid line. The value may be `'auto'` or a vector of grouping variable numbers. For example, `[1 2]` adds a separator line when the first or second grouping variable changes value. `'auto'` is `[]` for one grouping variable and `[1]` for two or more grouping variables. The default is `[]`.
`'factorgap'`	Specifies an extra gap to leave between boxes when the corresponding grouping factor changes value, expressed as a percentage of the width of the plot. For example, with `[3 1]`, the gap is 3% of the width of the plot between groups with different values of the first grouping variable, and 1% between groups with the same value of the first grouping variable but different values for the second. `'auto'` specifies that `boxplot` should choose a gap automatically. The default is `[]`.

Name	Value
`'grouporder'`	Order of groups for plotting, specified as a cell array of strings. With multiple grouping variables, separate values within each string with a comma. Using categorical arrays as grouping variables is an easier way to control the order of the boxes. The default is `[]`, which does not reorder the boxes.
`'jitter'`	Maximum distance *d* to displace outliers along the factor axis by a uniform random amount, in order to make duplicate points visible. A *d* of `1` makes the jitter regions just touch between the closest adjacent groups. The default is `0`.
`'labels'`	A character array, cell array of strings, or numeric vector of box labels. There may be one label per group or one label per `X` value. Multiple label variables may be specified via a numeric matrix or a cell array containing any of these types. **Tip** To remove labels from a plot, use the following command: `set(gca,'XTickLabel',{' '})`
`'labelorientation'`	• `'inline'` — Rotates the labels to be vertical. This is the default when `plotstyle` is `'compact'`. • `'horizontal'` — Leaves the labels horizontal. This is the default when `plotstyle` has the default value of `'traditional'`. When the labels are on the *y* axis, both settings leave the labels horizontal.
`'labelverbosity'`	• `'all'` — Displays every label. This is the default. • `'minor'` — Displays a label for a factor only when that factor has a different value from the previous group. • `'majorminor'` — Displays a label for a factor when that factor or any factor major to it has a different value from the previous group.

Name	Value
`'medianstyle'`	• `'line'` — Draws a line for the median. This is the default. • `'target'` — Draws a black dot inside a white circle for the median.
`'notch'`	• `'on'` — Draws comparison intervals using notches when `plotstyle` is `'traditional'`, or triangular markers when `plotstyle` is `'compact'`. • `'marker'` — Draws comparison intervals using triangular markers. • `'off'` — Omits notches. This is the default. Two medians are significantly different at the 5% significance level if their intervals do not overlap. Interval endpoints are the extremes of the notches or the centers of the triangular markers. The extremes correspond to $q_2 - 1.57(q_3 - q_1)/\text{sqrt}(n)$ and $q_2 + 1.57(q_3 - q_1)/\text{sqrt}(n)$, where q_2 is the median (50th percentile), q_1 and q_3 are the 25th and 75th percentiles, respectively, and n is the number of observations without any `NaN` values. When the sample size is small, notches may extend beyond the end of the box.
`'orientation'`	• `'vertical'` — Plots `X` on the y axis. This is the default. • `'horizontal'` — Plots `X` on the x axis.
`'outliersize'`	Size of the marker used for outliers, in points. The default is `6` (6/72 inch).
`'positions'`	Box positions specified as a numeric vector with one entry per group or `X` value. The default is `1:numGroups`, where `numGroups` is the number of groups.
`'symbol'`	Symbol and color to use for outliers, using the same values as the `LineSpec` parameter in `plot`. The default is `'r+'`. If the symbol is omitted then the outliers are invisible; if the color is omitted then the outliers have the same color as their corresponding box.

Name	Value
`'whisker'`	Maximum whisker length w. The default is a w of `1.5`. Points are drawn as outliers if they are larger than $q_3 + w(q_3 - q_1)$ or smaller than $q_1 - w(q_3 - q_1)$, where q_1 and q_3 are the 25th and 75th percentiles, respectively. The default of `1.5` corresponds to approximately +/–2.7σ and 99.3 coverage if the data are normally distributed. The plotted whisker extends to the *adjacent value*, which is the most extreme data value that is not an outlier. Set `whisker` to `0` to give no whiskers and to make every point outside of q_1 and q_3 an outlier.
`'widths'`	A scalar or vector of box widths for when `boxstyle` is `'outline'`. The default is half of the minimum separation between boxes, which is `0.5` when the `positions` argument takes its default value. The list of values is replicated or truncated as necessary.

When the `plotstyle` parameter takes the value `'compact'`, the following default values for other parameters apply.

Parameter	Default when `plotstyle` is `'compact'`
`'boxstyle'`	`'filled'`
`'factorseparator'`	`'auto'`
`'factorgap'`	`'auto'`
`'jitter'`	`0.5`
`'labelorientation'`	`'inline'`
`'labelverbosity'`	`'majorminor'`
`'medianstyle'`	`'target'`
`'outliersize'`	`4`
`'symbol'`	`'o'`

You can see data values and group names using the data cursor in the figure window. The cursor shows the original values of any points affected by the `datalim` parameter. You can label the group to which an outlier belongs using the `gname` function.

To modify graphics properties of a box plot component, use `findobj` with the `Tag` property to find the component's handle. `Tag` values for box plot components depend on parameter settings, and are listed in the table below.

Parameter Settings	Tag Values
All settings	• `'Box'` • `'Outliers'`
When `'plotstyle'` is `'traditional'`	• `'Median'` • `'Upper Whisker'` • `'Lower Whisker'` • `'Upper Adjacent Value'` • `'Lower Adjacent Value'`
When `'plotstyle'` is `'compact'`	• `'Whisker'` • `'MedianOuter'` • `'MedianInner'`
When `'notch'` is `'marker'`	• `'NotchLo'` • `'NotchHi'`

Examples

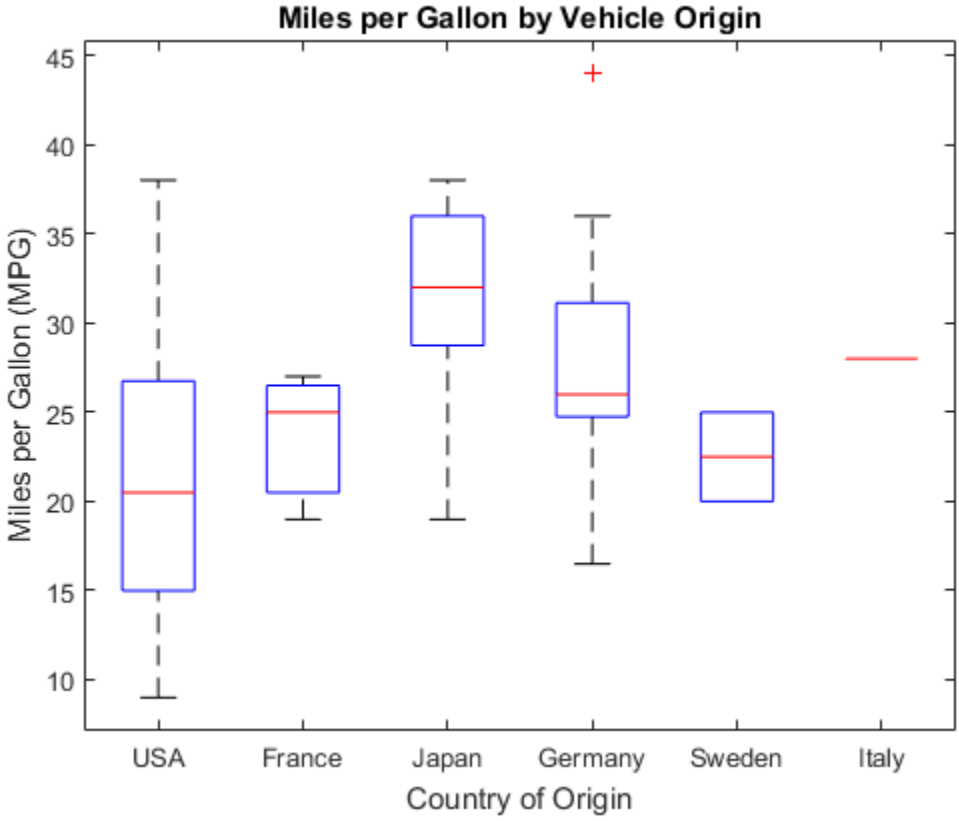
Create Box Plots for Grouped Data

Load the sample data.

```
load carsmall
```

Create a box plot of the miles per gallon (`MPG`) measurements from the sample data, grouped by the vehicles' country of origin, `Origin`. Add a title and label the axes.

```
boxplot(MPG,Origin)
title('Miles per Gallon by Vehicle Origin')
xlabel('Country of Origin')
ylabel('Miles per Gallon (MPG)')
```



Create Notched Box Plots

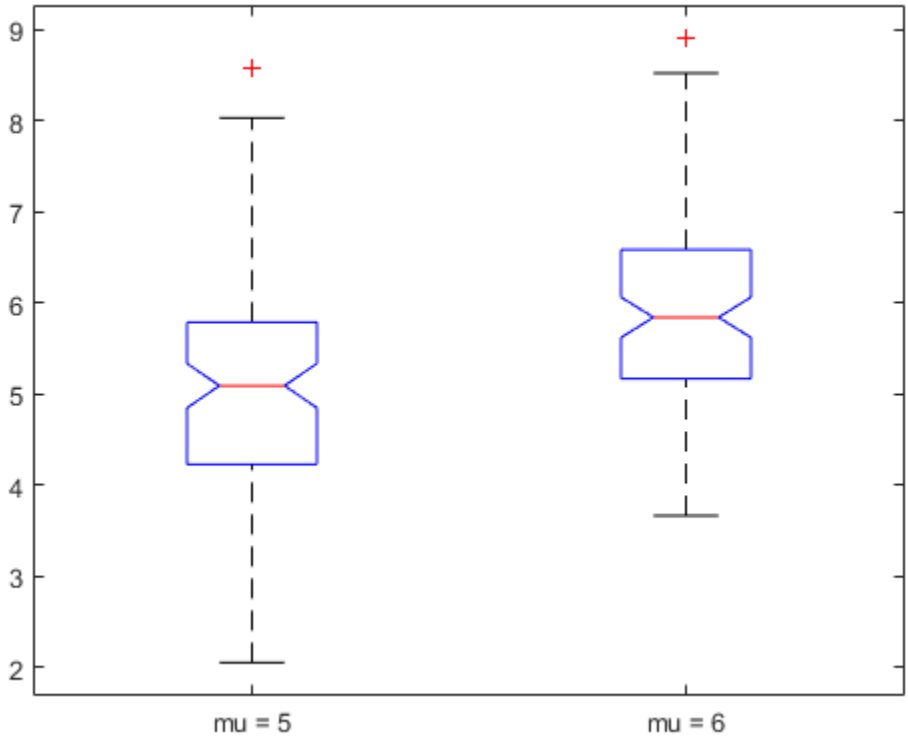
Generate two sets of sample data. The first sample, `x1`, contains random numbers generated from a normal distribution with `mu = 5` and `sigma = 1`. The second sample, `x2`, contains random numbers generated from a normal distribution with `mu = 6` and `sigma = 1`.

```
rng default;  % For reproducibility
x1 = normrnd(5,1,100,1);
x2 = normrnd(6,1,100,1);
```

Create notched box plots of `x1` and `x2`. Label each box with its corresponding `mu` value.

```
figure;
```

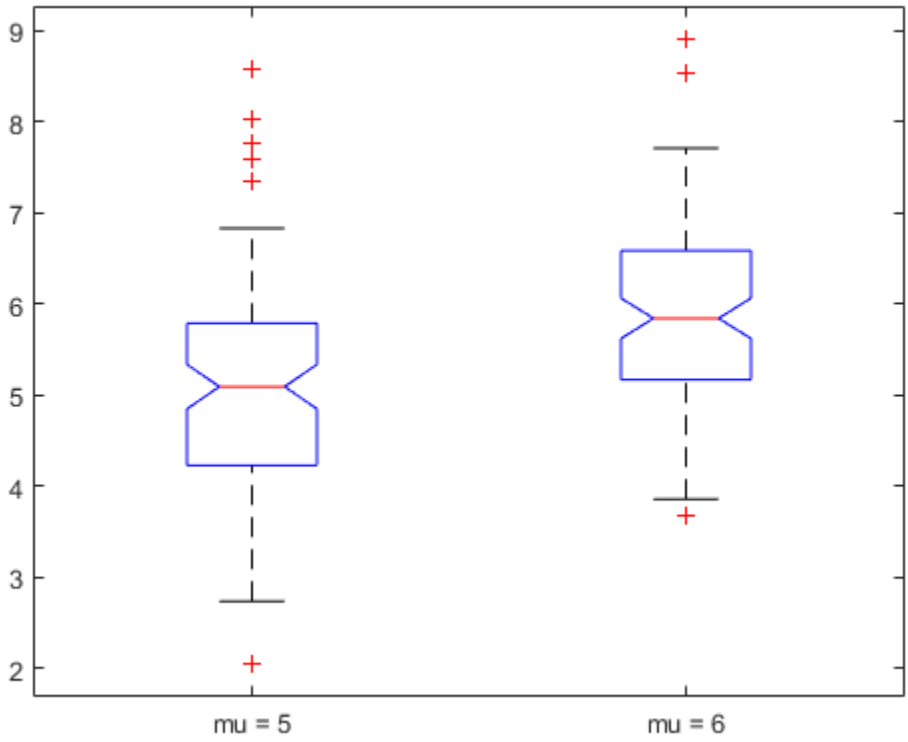
```
boxplot([x1,x2],'notch','on','labels',{'mu = 5','mu = 6'})
```



The difference between the medians of the two groups is approximately 1. Since the notches in the box plot do not overlap, you can conclude, with 95% confidence, that the true medians do differ.

The following figure shows the box plot for the same data with the length of the whiskers specified as 1.0 times the interquartile range. Points beyond the whiskers are displayed using +.

```
figure;
boxplot([x1,x2],'notch','on','labels',{'mu = 5','mu = 6'},'whisker',1)
```



Create Compact Box Plots

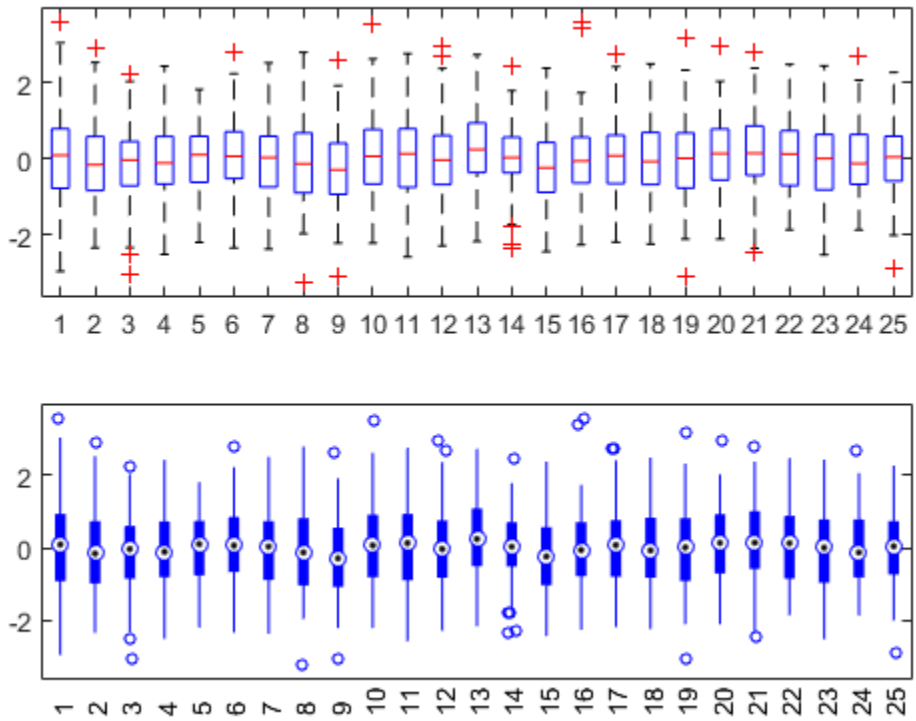
Create a 100-by-25 matrix of random numbers generated from a standard normal distribution to use as sample data.

```
rng('default');  % For reproducibility
X = randn(100,25);
```

Create two box plots for the data in `X` on the same figure. The top plot uses the default box plot formatting. The bottom plot uses compact formatting.

```
figure;

subplot(2,1,1)
```

```
boxplot(X)

subplot(2,1,2)
boxplot(X,'plotstyle','compact')
```



References

[1] McGill, R., J. W. Tukey, and W. A. Larsen. “Variations of Boxplots.” *The American Statistician*. Vol. 32, No. 1, 1978, pp. 12–16.

[2] Velleman, P.F., and D.C. Hoaglin. *Applications, Basics, and Computing of Exploratory Data Analysis*. Pacific Grove, CA: Duxbury Press, 1981.

[3] Nelson, L. S. “Evaluating Overlapping Confidence Intervals.” *Journal of Quality Technology*. Vol. 21, 1989, pp. 140–141.

[4] Langford, E. “Quartiles in Elementary Statistics”, *Journal of Statistics Education*. Vol. 14, No. 3, 2006.

See Also

`anova1` | `kruskalwallis` | `multcompare`

boundary

Class: piecewisedistribution

Piecewise distribution boundaries

Syntax

```
[p,q] = boundary(obj)
[p,q] = boundary(obj,i)
```

Description

`[p,q] = boundary(obj)` returns the boundary points between segments of the piecewise distribution object, `obj`. `p` is a vector of cumulative probabilities at each boundary. `q` is a vector of quantiles at each boundary.

`[p,q] = boundary(obj,i)` returns `p` and `q` for the *i*th boundary.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432
```

See Also

`paretotails` | `icdf` | `cdf` | `nsegments`

prob.BurrDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Burr probability distribution object

Description

`prob.BurrDistribution` is an object consisting of parameters, a model description, and sample data for a Burr probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Burr')` creates a Burr probability distribution object using the default parameter values.

`pd = makedist('Burr','alpha',alpha,'c',c,'k',k)` creates a Burr probability distribution object using the specified parameter values.

Input Arguments

`alpha` — Scale parameter

1 (default) | positive scalar value

Scale parameter of the Burr distribution, specified as a positive scalar value.

Data Types: `single` | `double`

`c` — First shape parameter

1 (default) | positive scalar value

First shape parameter of the Burr distribution, specified as a positive scalar value.

Data Types: `single` | `double`

k — Second shape parameter

1 (default) | positive scalar value

Second shape parameter of the Burr distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

alpha — Scale parameter

positive scalar value

Scale parameter of the Burr distribution, stored as a positive scalar value.

Data Types: `single` | `double`

c — First shape parameter

positive scalar value

First shape parameter of the Burr distribution, stored as a positive scalar value.

Data Types: `single` | `double`

k — Second shape parameter

positive scalar value

Second shape parameter of the Burr distribution, stored as a positive scalar value.

Data Types: `single` | `double`

DistributionName — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

InputData — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.

- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object

iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Burr Distribution

The Burr distribution is a three-parameter family of distributions on the positive real line. It can fit a wide range of empirical data, and is used in various fields such as finance, hydrology, and reliability to model a variety of data types.

The Burr distribution uses the following parameters.

Parameter	Description	Support
`alpha`	Scale parameter	$\alpha > 0$
`c`	First shape parameter	$c > 0$
`k`	Second shape parameter	$k > 0$

The probability density function (pdf) is

$$f(x \mid \alpha, c, k) = \frac{\frac{kc}{\alpha}\left(\frac{x}{\alpha}\right)^{c-1}}{\left(1+\left(\frac{x}{\alpha}\right)^{c}\right)^{k+1}} \quad ; \quad x > 0 .$$

Examples

Create a Burr Distribution Object Using Default Parameters

Create a Burr distribution object using the default parameter values.

```
pd = makedist('Burr')
```

```
pd =

  BurrDistribution

  Burr distribution
```

```
    alpha = 1
        c = 1
        k = 1
```

Create a Burr Distribution Object Using Specified Parameters

Create a Burr distribution object by specifying parameter values.

```
pd = makedist('Burr','alpha',1,'c',2,'k',5)
```

```
pd =

  BurrDistribution

  Burr distribution
    alpha = 1
        c = 2
        k = 5
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    0.4295
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Burr Type XII Distribution"
- Class Attributes
- Property Attributes

clustering.evaluation.CalinskiHarabaszEvaluation class

Package: clustering.evaluation
Superclasses: clustering.evaluation.ClusterCriterion

Calinski-Harabasz criterion clustering evaluation object

Description

`clustering.evaluation.CalinskiHarabaszEvaluation` is an object consisting of sample data, clustering data, and Calinski-Harabasz criterion values used to evaluate the optimal number of clusters. Create a Calinski-Harabasz criterion clustering evaluation object using `evalclusters`.

Construction

`eva = evalclusters(x,clust,'CalinskiHarabasz')` creates a Calinski-Harabasz criterion clustering evaluation object.

`eva = evalclusters(x,clust,'CalinskiHarabasz',Name,Value)` creates a Calinski-Harabasz criterion clustering evaluation object using additional options specified by one or more name-value pair arguments.

Input Arguments

x — Input data

matrix

Input data, specified as an *N*-by-*P* matrix. *N* is the number of observations, and *P* is the number of variables.

Data Types: `single` | `double`

clust — Clustering algorithm

`'kmeans'` | `'linkage'` | `'gmdistribution'` | matrix of clustering solutions | function handle

Clustering algorithm, specified as one of the following.

`'kmeans'`	Cluster the data in x using the `kmeans` clustering algorithm, with `'EmptyAction'` set to `'singleton'` and `'Replicates'` set to `5`.
`'linkage'`	Cluster the data in x using the `clusterdata` agglomerative clustering algorithm, with `'Linkage'` set to `'ward'`.
`'gmdistribution'`	Cluster the data in x using the `gmdistribution` Gaussian mixture distribution algorithm, with `'SharedCov'` set to `true` and `'Replicates'` set to `5`.

If `Criterion` is `'CalinskiHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can specify a clustering algorithm using the `function_handle` (`@`) operator. The function must be of the form `C = clustfun(DATA,K)`, where `DATA` is the data to be clustered, and `K` is the number of clusters. The output of `clustfun` must be one of the following:

- A vector of integers representing the cluster index for each observation in `DATA`. There must be `K` unique values in this vector.
- A numeric n-by-K matrix of score for n observations and K classes. In this case, the cluster index for each observation is determined by taking the largest score value in each row.

If `Criterion` is `'CalinskiHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can also specify `clust` as a n-by-K matrix containing the proposed clustering solutions. n is the number of observations in the sample data, and K is the number of proposed clustering solutions. Column j contains the cluster indices for each of the N points in the jth clustering solution.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'KList',[1:6]` specifies to test 1, 2, 3, 4, 5, and 6 clusters to find the optimal number.

`'KList'` — List of number of clusters to evaluate

vector

List of number of clusters to evaluate, specified as the comma-separated pair consisting of `'KList'` and a vector of positive integer values. You must specify `KList` when clust is a clustering algorithm name string or a function handle. When criterion is `'gap'`, clust must be a string or a function handle, and you must specify KList.

Example: `'KList',[1:6]`

Properties

`ClusteringFunction`

Clustering algorithm used to cluster the input data, stored as a valid clustering algorithm name string or function handle. If the clustering solutions are provided in the input, `ClusteringFunction` is empty.

`CriterionName`

Name of the criterion used for clustering evaluation, stored as a valid criterion name string.

`CriterionValues`

Criterion values corresponding to each proposed number of clusters in `InspectedK`, stored as a vector of numerical values.

`Distance`

Distance measure used for clustering data, stored as a valid distance measure name string.

`InspectedK`

List of the number of proposed clusters for which to compute criterion values, stored as a vector of positive integer values.

`Missing`

Logical flag for excluded data, stored as a column vector of logical values. If `Missing` equals `true`, then the corresponding value in the data matrix `x` is not used in the clustering solution.

`NumObservations`

Number of observations in the data matrix `X`, minus the number of missing (`NaN`) values in `X`, stored as a positive integer value.

`OptimalK`

Optimal number of clusters, stored as a positive integer value.

`OptimalY`

Optimal clustering solution corresponding to `OptimalK`, stored as a column vector of positive integer values. If the clustering solutions are provided in the input, `OptimalY` is empty.

`X`

Data used for clustering, stored as a matrix of numerical values.

Methods

Inherited Methods

addK	Evaluate additional numbers of clusters
plot	Plot clustering evaluation object criterion values
compact	Compact clustering evaluation object

Definitions

Calinski-Harabasz Criterion

The Calinski-Harabasz criterion is sometimes called the variance ratio criterion (VRC). The Calinski-Harabasz index is defined as

$$VRC_k = \frac{SS_B}{SS_W} \times \frac{(N-k)}{(k-1)},$$

, where SS_B is the overall between-cluster variance, SS_W is the overall within-cluster variance, k is the number of clusters, and N is the number of observations.

The overall between-cluster variance SS_B is defined as

$$SS_B = \sum_{i=1}^{k} n_i \left\| m_i - m \right\|^2,$$

where k is the number of clusters, m_i is the centroid of cluster i, m is the overall mean of the sample data, and $\left\| m_i - m \right\|$ is the L^2 norm (Euclidean distance) between the two vectors.

The overall within-cluster variance SS_W is defined as

$$SS_W = \sum_{i=1}^{k} \sum_{x \in c_i} \left\| x - m_i \right\|^2,$$

where k is the number of clusters, x is a data point, c_i is the ith cluster, m_i is the centroid of cluster i, and $\left\| x - m_i \right\|$ is the L^2 norm (Euclidean distance) between the two vectors.

Well-defined clusters have a large between-cluster variance (SS_B) and a small within-cluster variance (SS_W). The larger the VRC_k ratio, the better the data partition. To determine the optimal number of clusters, maximize VRC_k with respect to k. The optimal number of clusters is the solution with the highest Calinski-Harabasz index value.

The Calinski-Harabasz criterion is best suited for k-means clustering solutions with squared Euclidean distances.

Examples

Evaluate the Clustering Solution Using Calinski-Harabasz Criterion

Evaluate the optimal number of clusters using the Calinski-Harabasz clustering evaluation criterion.

Load the sample data.

```
load fisheriris;
```

The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Evaluate the optimal number of clusters using the Calinski-Harabasz criterion. Cluster the data using `kmeans`.

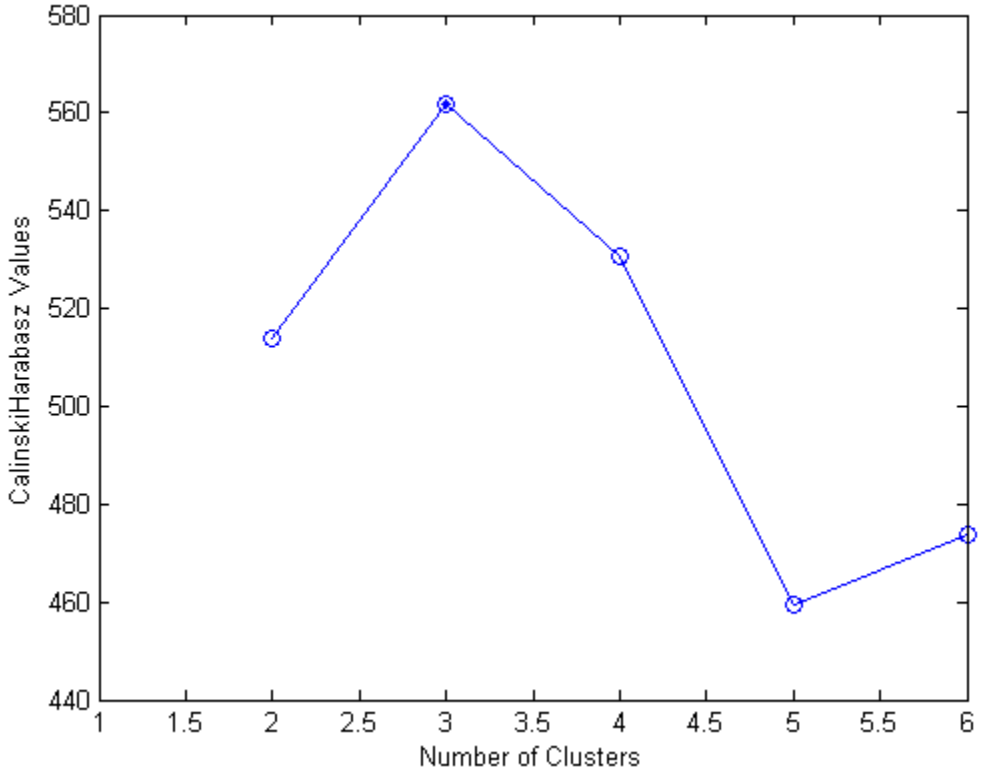
```
rng('default');  % For reproducibility
eva = evalclusters(meas,'kmeans','CalinskiHarabasz','KList',[1:6])
```

```
eva =

  CalinskiHarabaszEvaluation with properties:

    NumObservations: 150
       InspectecedK: [1 2 3 4 5 6]
    CriterionValues: [1x6 double]
           OptimalK: 3
```

The `OptimalK` value indicates that, based on the Calinski-Harabasz criterion, the optimal number of clusters is three.

Plot the Calinski-Harabasz criterion values for each number of clusters tested.

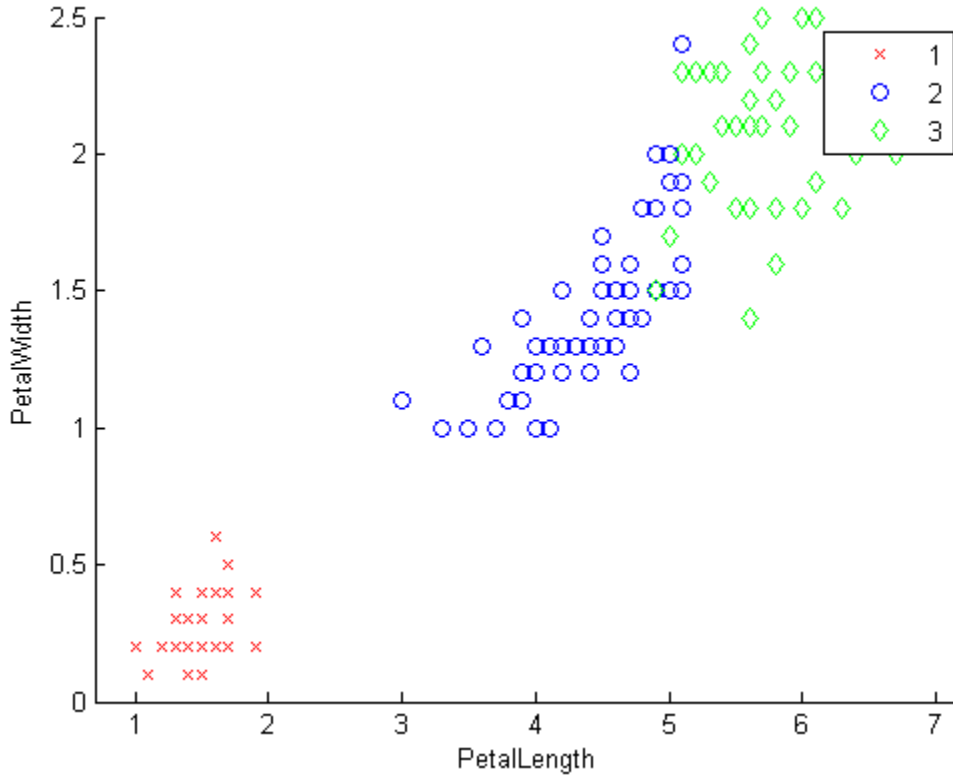
```
figure;
plot(eva);
```



The plot shows that the highest Calinski-Harabasz value occurs at three clusters, suggesting that the optimal number of clusters is three.

Create a grouped scatter plot to examine the relationship between petal length and width. Group the data by suggested clusters.

```
PetalLength = meas(:,3);
PetalWidth = meas(:,4);
ClusterGroup = eva.OptimalY;
figure;
gscatter(PetalLength,PetalWidth,ClusterGroup,'rbg','xod');
```



The plot shows cluster 1 in the lower-left corner, completely separated from the other two clusters. Cluster 1 contains flowers with the smallest petal widths and lengths. Cluster 3 is in the upper-right corner, and contains flowers with the largest petal widths and lengths. Cluster 2 is near the center of the plot, and contains flowers with measurements between these two extremes.

References

[1] Calinski, T., and J. Harabasz. "A dendrite method for cluster analysis." *Communications in Statistics*. Vol. 3, No. 1, 1974, pp. 1–27.

See Also

`clustering.evaluation.DaviesBouldinEvaluation` | `clustering.evaluation.GapEvaluation` | `clustering.evaluation.SilhouetteEvaluation` | `evalclusters`

More About

- Class Attributes
- Property Attributes

candexch

D-optimal design from candidate set using row exchanges

Syntax

```
rlist = candexch(C,nrows)
rlist = candexch(C,nrows,Name,Value)
```

Description

`rlist = candexch(C,nrows)` uses a row-exchange algorithm to select a *D*-optimal design from the candidate set `C`.

`rlist = candexch(C,nrows,Name,Value)` generates a *D*-optimal design with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`C`

`N`-by-`P` matrix containing the values of `P` model terms at each of `N` points.

Default:

`nrows`

The desired number of rows in the design.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

'display'

When 'on', displays iteration number. Disable the display by setting to 'off'.

Default: 'on', except when the UseParallel option is true

'init'

nrows-by-P matrix giving an initial design.

Default: A random subset of the rows of C

'maxiter'

Maximum number of iterations, a positive integer.

Default: 10

'options'

A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the options structure with statset. Option fields:

- UseParallel — Set to true to compute in parallel. Default is false.
- UseSubstreams — Set to true to compute in parallel in a reproducible fashion. Default is false. To compute reproducibly, set Streams to a type allowing substreams: 'mlfg6331_64' or 'mrg32k3a'.
- Streams — A RandStream object or cell array of such objects. If you do not specify Streams, candexch uses the default stream or streams. If you choose to specify Streams, use a single object except in the case

  - You have an open Parallel pool
  - UseParallel is true
  - UseSubstreams is false

  In that case, use a cell array the same size as the Parallel pool.

Default: [ ]

'start'

An nobs-by-*p* matrix of factor settings, specifying a set of nobs fixed design points to include in the design. candexch finds nrows additional rows to add to the start design.

The parameter provides the same functionality as the `daugment` function, using a row-exchange algorithm rather than a coordinate-exchange algorithm.

Default: [ ]

`'tries'`

Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first.

Default: 1

Output Arguments

`rlist`

Vector of length nrows listing the selected rows.

Examples

This example shows how to generate a *D*-optimal design when there is a restriction on the candidate set, so the `rowexch` function isn't appropriate.

```
F = (fullfact([5 5 5])-1)/4; % factor settings in unit cube
T = sum(F,2)<=1.51;          % find rows matching a restriction
F = F(T,:);                  % take only those rows
C = [ones(size(F,1),1) F F.^2];
                             % compute model terms including
                             % a constant and all squared terms
R = candexch(C,12);          % find a D-optimal 12-point subset
X = F(R,:);                  % get factor settings
```

Alternatives

The `rowexch` function also generates *D*-optimal designs using a row-exchange algorithm, but it automatically generates a candidate set that is appropriate for a specified model. The `daugment` function augments a set of fixed design points using a coordinate-exchange algorithm; the `'start'` parameter provides the same functionality using the row exchange algorithm.

More About

Algorithms

`candexch` selects a starting design `X` at random, and uses a row-exchange algorithm to iteratively replace rows of `X` by rows of C in an attempt to improve the determinant of `X'*X`.

- "D-Optimal Designs" on page 19-15

See Also

`candgen` | `rowexch` | `cordexch` | `daugment` | `x2fx`

candgen

Candidate set generation

Syntax

```
dC = candgen(nfactors,'model')
[dC,C] = candgen(nfactors,'model')
[...] = candgen(nfactors,'model','Name',value)
```

Description

`dC = candgen(nfactors,'model')` generates a candidate set `dC` of treatments appropriate for estimating the parameters in the *`model`* with `nfactors` factors. `dC` has `nfactors` columns and one row for each candidate treatment. *`model`* is one of the following strings, specified inside single quotes:

- `linear` — Constant and linear terms. This is the default.
- `interaction` — Constant, linear, and interaction terms
- `quadratic` — Constant, linear, interaction, and squared terms
- `purequadratic` — Constant, linear, and squared terms

Alternatively, *`model`* can be a matrix specifying polynomial terms of arbitrary order. In this case, *`model`* should have one column for each factor and one row for each term in the model. The entries in any row of *`model`* are powers for the factors in the columns. For example, if a model has factors `X1`, `X2`, and `X3`, then a row `[0 1 2]` in *`model`* specifies the term `(X1.^0).*(X2.^1).*(X3.^2)`. A row of all zeros in *`model`* specifies a constant term, which can be omitted.

`[dC,C] = candgen(nfactors,'model')` also returns the design matrix `C` evaluated at the treatments in `dC`. The order of the columns of `C` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n – 1, n)

4 The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Pass `C` to `candexch` to generate a D-optimal design using a coordinate-exchange algorithm.

`[...] = candgen(nfactors,'model','Name',value)` specifies one or more optional name/value pairs for the design. Valid parameters and their values are listed in the following table. Specify *`Name`* inside single quotes.

Name	Value
`bounds`	Lower and upper bounds for each factor, specified as a `2`-by-`nfactors` matrix. Alternatively, this value can be a cell array containing `nfactors` elements, each element specifying the vector of allowable values for the corresponding factor.
`categorical`	Indices of categorical predictors.
`levels`	Vector of number of levels for each factor.

Note The `rowexch` function automatically generates a candidate set using `candgen`, and then creates a D-optimal design from that candidate set using `candexch`. Call `candexch` separately to specify your own candidate set to the row-exchange algorithm.

Examples

The following example uses `rowexch` to generate a five-run design for a two-factor pure quadratic model using a candidate set that is produced internally:

```
dRE1 = rowexch(2,5,'purequadratic','tries',10)
dRE1 =
    -1     1
     0     0
     1    -1
     1     0
     1     1
```

The same thing can be done using `candgen` and `candexch` in sequence:

```
[dC,C] = candgen(2,'purequadratic') % Candidate set, C
```

```
dC =
    -1    -1
     0    -1
     1    -1
    -1     0
     0     0
     1     0
    -1     1
     0     1
     1     1
C =
     1    -1    -1     1     1
     1     0    -1     0     1
     1     1    -1     1     1
     1    -1     0     1     0
     1     0     0     0     0
     1     1     0     1     0
     1    -1     1     1     1
     1     0     1     0     1
     1     1     1     1     1
treatments = candexch(C,5,'tries',10) % Find D-opt subset
treatments =
     2
     1
     7
     3
     4
dRE2 = dC(treatments,:) % Display design
dRE2 =
     0    -1
    -1    -1
    -1     1
     1    -1
    -1     0
```

See Also

candexch | rowexch

canoncorr

Canonical correlation

Syntax

```
[A,B] = canoncorr(X,Y)
[A,B,r] = canoncorr(X,Y)
[A,B,r,U,V] = canoncorr(X,Y)
[A,B,r,U,V,stats] = canoncorr(X,Y)
```

Description

`[A,B] = canoncorr(X,Y)` computes the sample canonical coefficients for the `n`-by-`d1` and `n`-by-`d2` data matrices `X` and `Y`. `X` and `Y` must have the same number of observations (rows) but can have different numbers of variables (columns). `A` and `B` are `d1`-by-`d` and `d2`-by-`d` matrices, where `d = min(rank(X),rank(Y))`. The `j`th columns of `A` and `B` contain the canonical coefficients, i.e., the linear combination of variables making up the `j`th canonical variable for `X` and `Y`, respectively. Columns of `A` and `B` are scaled to make the covariance matrices of the canonical variables the identity matrix (see `U` and `V` below). If `X` or `Y` is less than full rank, `canoncorr` gives a warning and returns zeros in the rows of `A` or `B` corresponding to dependent columns of `X` or `Y`.

`[A,B,r] = canoncorr(X,Y)` also returns a 1-by-`d` vector containing the sample canonical correlations. The `j`th element of `r` is the correlation between the *j*th columns of `U` and `V` (see below).

`[A,B,r,U,V] = canoncorr(X,Y)` also returns the canonical variables, scores. `U` and `V` are `n`-by-`d` matrices computed as

```
U = (X-repmat(mean(X),N,1))*A
V = (Y-repmat(mean(Y),N,1))*B
```

`[A,B,r,U,V,stats] = canoncorr(X,Y)` also returns a structure `stats` containing information relating to the sequence of `d` null hypotheses $H_0^{(k)}$, that the (`k`+1)st through `d`th correlations are all zero, for `k = 0:(d-1)`. `stats` contains seven fields, each a `1`-

by-`d` vector with elements corresponding to the values of `k`, as described in the following table:

Field	Description
`Wilks`	Wilks' lambda (likelihood ratio) statistic
`df1`	Degrees of freedom for the chi-squared statistic, and the numerator degrees of freedom for the F statistic
`df2`	Denominator degrees of freedom for the F statistic
`F`	Rao's approximate F statistic for $H_0^{(k)}$
`pF`	Right-tail significance level for `F`
`chisq`	Bartlett's approximate chi-squared statistic for $H_0^{(k)}$ with Lawley's modification
`pChisq`	Right-tail significance level for `chisq`

`stats` has two other fields (`dfe` and `p`) which are equal to `df1` and `pChisq`, respectively, and exist for historical reasons.

Examples

Compute Sample Canonical Correlation

Load the sample data.

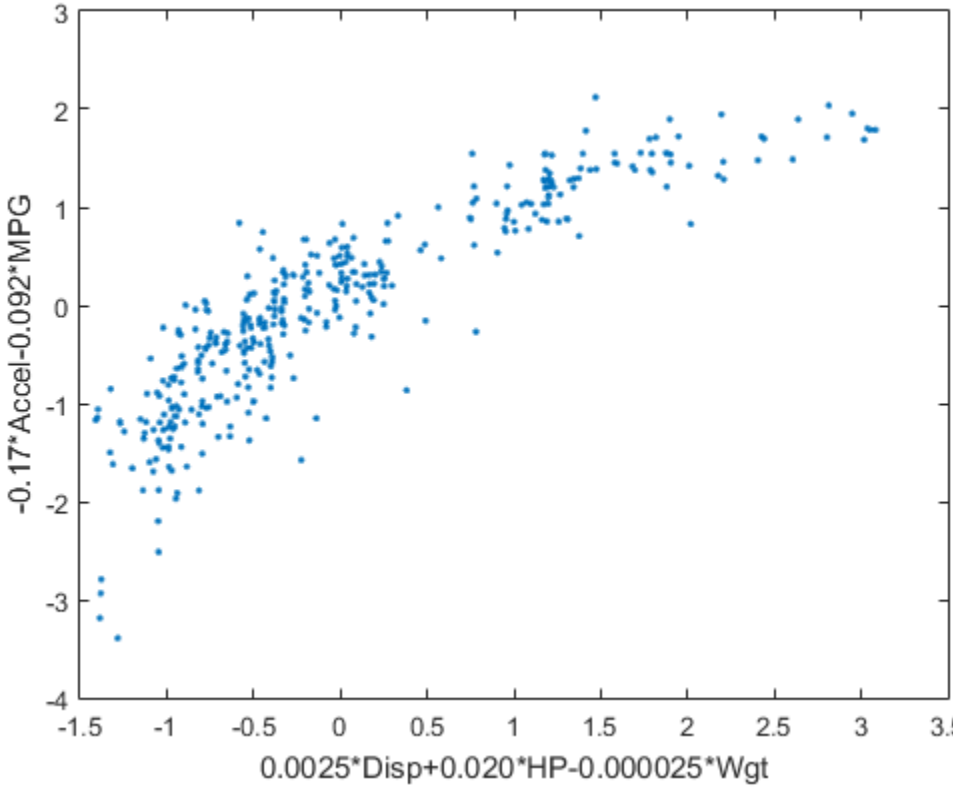
```
load carbig;
X = [Displacement Horsepower Weight Acceleration MPG];
nans = sum(isnan(X),2) > 0;
```

Compute the sample canonical correlation.

```
[A B r U V] = canoncorr(X(~nans,1:3),X(~nans,4:5));
```

Plot the canonical variables scores.

```
plot(U(:,1),V(:,1),'.')
xlabel('0.0025*Disp+0.020*HP-0.000025*Wgt')
ylabel('-0.17*Accel-0.092*MPG')
```



References

[1] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[2] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`manova1` | `pca`

capability

Process capability indices

Syntax

```
S = capability(data,specs)
```

Description

`S = capability(data,specs)` estimates capability indices for measurements in `data` given the specifications in `specs`. `data` can be either a vector or a matrix of measurements. If `data` is a matrix, indices are computed for the columns. `specs` can be either a two-element vector of the form `[L,U]` containing lower and upper specification limits, or (if `data` is a matrix) a two-row matrix with the same number of columns as `data`. If there is no lower bound, use `-Inf` as the first element of `specs`. If there is no upper bound, use `Inf` as the second element of `specs`.

The output `S` is a structure with the following fields:

- `mu` — Sample mean
- `sigma` — Sample standard deviation
- `P` — Estimated probability of being within limits
- `Pl` — Estimated probability of being below `L`
- `Pu` — Estimated probability of being above `U`
- `Cp` — `(U-L)/(6*sigma)`
- `Cpl` — `(mu-L)./(3.*sigma)`
- `Cpu` — `(U-mu)./(3.*sigma)`
- `Cpk` — `min(Cpl,Cpu)`

Indices are computed under the assumption that data values are independent samples from a normal population with constant mean and variance.

Indices divide a “specification width” (between specification limits) by a “process width” (between control limits). Higher ratios indicate a process with fewer measurements outside of specification.

Examples

Compute Capability Indices

Simulate a sample from a process with a mean of 3 and a standard deviation of 0.005.

```
rng default; % for reproducibility
data = normrnd(3,0.005,100,1);
```

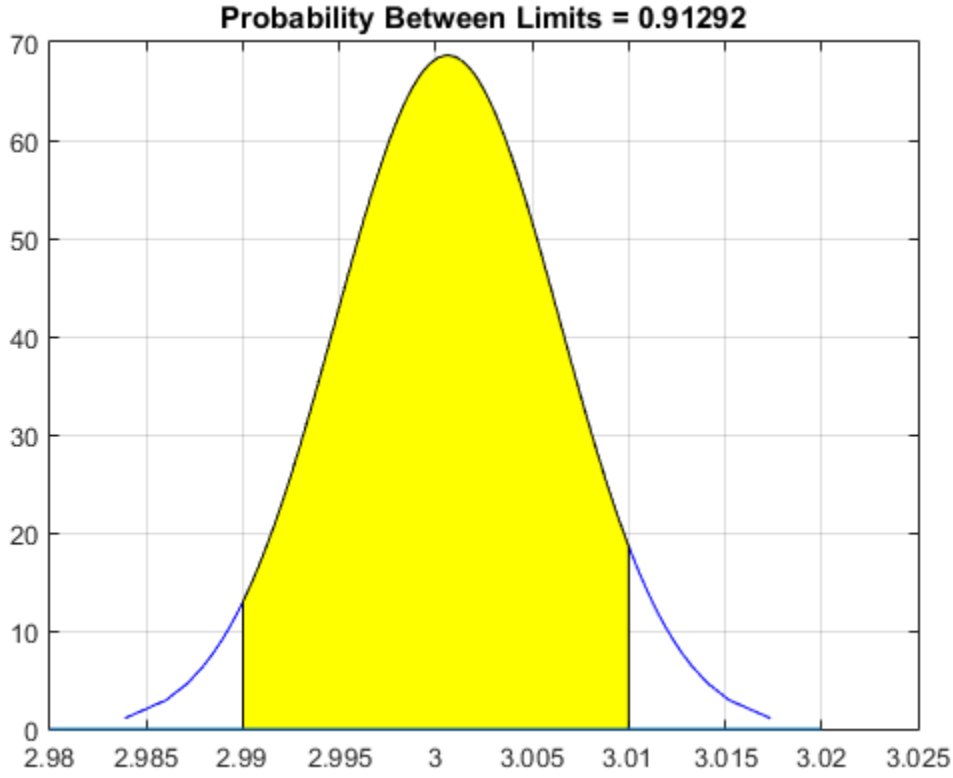
Compute capability indices if the process has an upper specification limit of 3.01 and a lower specification limit of 2.99.

```
S = capability(data,[2.99 3.01])
```

```
S =

       mu: 3.0006
    sigma: 0.0058
        P: 0.9129
       Pl: 0.0339
       Pu: 0.0532
       Cp: 0.5735
      Cpl: 0.6088
      Cpu: 0.5382
      Cpk: 0.5382
```

Visualize the specification and process widths.

```
capaplot(data,[2.99 3.01]);
grid on
```



References

[1] Montgomery, D. *Introduction to Statistical Quality Control*. Hoboken, NJ: John Wiley & Sons, 1991, pp. 369–374.

See Also

`capaplot` | `histfit`

capaplot

Process capability plot

Syntax

```
p = capaplot(data,specs)
[p,h] = capaplot(data,specs)
```

Description

`p = capaplot(data,specs)` estimates the mean of and variance for the observations in input vector `data`, and plots the pdf of the resulting T distribution. The observations in `data` are assumed to be normally distributed. The output, `p`, is the probability that a new observation from the estimated distribution will fall within the range specified by the two-element vector `specs`. The portion of the distribution between the lower and upper bounds specified in `specs` is shaded in the plot.

`[p,h] = capaplot(data,specs)` additionally returns handles to the plot elements in `h`.

`capaplot` treats `NaN` values in `data` as missing, and ignores them.

Examples

Create a Process Capability Plot

Randomly generate sample data from a normal process with a mean of 3 and a standard deviation of 0.005.

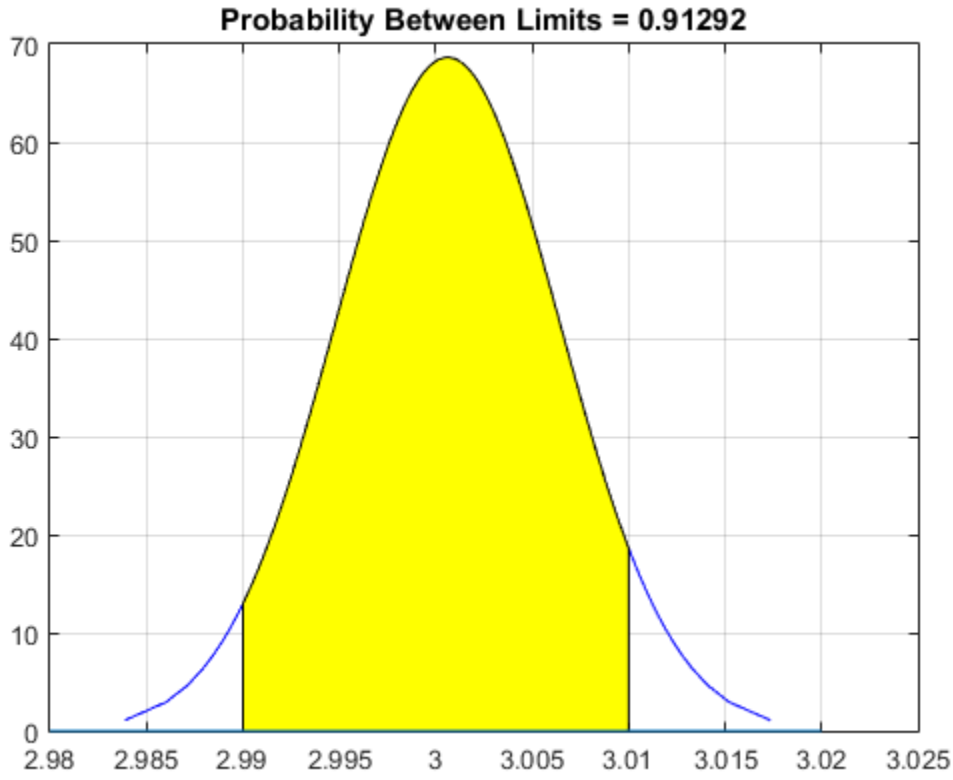
```
rng default; % For reproducibility
data = normrnd(3,0.005,100,1);
```

Compute capability indices if the process has an upper specification limit of 3.01 and a lower specification limit of 2.99.

```
S = capability(data,[2.99 3.01])


S =

       mu: 3.0006
    sigma: 0.0058
        P: 0.9129
       Pl: 0.0339
       Pu: 0.0532
       Cp: 0.5735
      Cpl: 0.6088
      Cpu: 0.5382
      Cpk: 0.5382
```

Visualize the specification and process widths.

```
capaplot(data,[2.99 3.01]);
grid on
```



See Also

`capability` | `histfit`

caseread

Read case names from file

Syntax

```
names = caseread('filename')
names = caseread
```

Description

`names = caseread('filename')` reads the contents of *`filename`* and returns a string matrix of `names`. *`filename`* is the name of a file in the current folder, or the complete path name of any file elsewhere. `caseread` treats each line as a separate case.

`names = caseread` displays the **Select File to Open** dialog box for interactive selection of the input file.

Examples

Read the file `months.dat` created using the `casewrite` function.

```
type months.dat

January
February
March
April
May

names = caseread('months.dat')
names =
January
February
March
April
May
```

See Also

`casewrite` | `gname` | `tdfread` | `tblread`

casewrite

Write case names to file

Syntax

```
casewrite(strmat,'filename')
casewrite(strmat)
```

Description

`casewrite(strmat,'filename')` writes the contents of string matrix `strmat` to *`filename`*. Each row of `strmat` represents one case name. *`filename`* is the name of a file in the current folder, or the complete path name of any file elsewhere. `casewrite` writes each name to a separate line in *`filename`*.

`casewrite(strmat)` displays the **Select File to Write** dialog box for interactive specification of the output file.

Examples

```
strmat = char('January','February',...
                'March','April','May')
strmat =
January
February
March
April
May

casewrite(strmat,'months.dat')
type months.dat

January
February
March
April
```

```
May
```

See Also

`gname` | `caseread` | `tblwrite` | `tdfread`

clustering.evaluation.DaviesBouldinEvaluation class

Package: clustering.evaluation
Superclasses: clustering.evaluation.ClusterCriterion

Davies-Bouldin criterion clustering evaluation object

Description

`clustering.evaluation.DaviesBouldinEvaluation` is an object consisting of sample data, clustering data, and Davies-Bouldin criterion values used to evaluate the optimal number of clusters. Create a Davies-Bouldin criterion clustering evaluation object using `evalclusters`.

Construction

`eva = evalclusters(x,clust,'DaviesBouldin')` creates a Davies-Bouldin criterion clustering evaluation object.

`eva = evalclusters(x,clust,'DaviesBouldin',Name,Value)` creates a Davies-Bouldin criterion clustering evaluation object using additional options specified by one or more name-value pair arguments.

Input Arguments

`x` — Input data

matrix

Input data, specified as an *N*-by-*P* matrix. *N* is the number of observations, and *P* is the number of variables.

Data Types: `single` | `double`

`clust` — Clustering algorithm

`'kmeans'` | `'linkage'` | `'gmdistribution'` | matrix of clustering solutions | function handle

Clustering algorithm, specified as one of the following.

`'kmeans'`	Cluster the data in x using the `kmeans` clustering algorithm, with `'EmptyAction'` set to `'singleton'` and `'Replicates'` set to `5`.
`'linkage'`	Cluster the data in x using the `clusterdata` agglomerative clustering algorithm, with `'Linkage'` set to `'ward'`.
`'gmdistribution'`	Cluster the data in x using the `gmdistribution` Gaussian mixture distribution algorithm, with `'SharedCov'` set to `true` and `'Replicates'` set to `5`.

If `Criterion` is `'CalinskHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can specify a clustering algorithm using the `function_handle` (`@`) operator. The function must be of the form `C = clustfun(DATA,K)`, where `DATA` is the data to be clustered, and `K` is the number of clusters. The output of `clustfun` must be one of the following:

- A vector of integers representing the cluster index for each observation in `DATA`. There must be `K` unique values in this vector.
- A numeric n-by-K matrix of score for n observations and K classes. In this case, the cluster index for each observation is determined by taking the largest score value in each row.

If `Criterion` is `'CalinskHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can also specify `clust` as a n-by-K matrix containing the proposed clustering solutions. n is the number of observations in the sample data, and K is the number of proposed clustering solutions. Column j contains the cluster indices for each of the N points in the jth clustering solution.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'KList',[1:5]` specifies to test 1, 2, 3, 4, and 5 clusters to find the optimal number.

`'KList'` — List of number of clusters to evaluate

vector

List of number of clusters to evaluate, specified as the comma-separated pair consisting of `'KList'` and a vector of positive integer values. You must specify `KList` when clust is a clustering algorithm name string or a function handle. When criterion is `'gap'`, clust must be a string or a function handle, and you must specify KList.

Example: `'KList',[1:6]`

Properties

`ClusteringFunction`

Clustering algorithm used to cluster the input data, stored as a valid clustering algorithm name string or function handle. If the clustering solutions are provided in the input, `ClusteringFunction` is empty.

`CriterionName`

Name of the criterion used for clustering evaluation, stored as a valid criterion name string.

`CriterionValues`

Criterion values corresponding to each proposed number of clusters in `InspectedK`, stored as a vector of numerical values.

`InspectedK`

List of the number of proposed clusters for which to compute criterion values, stored as a vector of positive integer values.

`Missing`

Logical flag for excluded data, stored as a column vector of logical values. If `Missing` equals `true`, then the corresponding value in the data matrix `x` is not used in the clustering solution.

`NumObservations`

Number of observations in the data matrix `X`, minus the number of missing (`NaN`) values in `X`, stored as a positive integer value.

`OptimalK`

Optimal number of clusters, stored as a positive integer value.

`OptimalY`

Optimal clustering solution corresponding to `OptimalK`, stored as a column vector of positive integer values. If the clustering solutions are provided in the input, `OptimalY` is empty.

`X`

Data used for clustering, stored as a matrix of numerical values.

Methods

Inherited Methods

addK	Evaluate additional numbers of clusters
plot	Plot clustering evaluation object criterion values
compact	Compact clustering evaluation object

Definitions

Davies-Bouldin Criterion

The Davies-Bouldin criterion is based on a ratio of within-cluster and between-cluster distances. The Davies-Bouldin index is defined as

$$DB = \frac{1}{k}\sum_{i=1}^{k} \max_{j \neq i}\left\{D_{i,j}\right\},$$

where $D_{i,j}$ is the within-to-between cluster distance ratio for the ith and jth clusters. In mathematical terms,

$$D_{i,j} = \frac{\left(\bar{d}_i + \bar{d}_j\right)}{d_{i,j}}.$$

$\bar{d}_i$ is the average distance between each point in the ith cluster and the centroid of the ith cluster. $\bar{d}_j$ is the average distance between each point in the ith cluster and the centroid of the jth cluster. $d_{i,j}$ is the Euclidean distance between the centroids of the ith and jth clusters.

The maximum value of $D_{i,j}$ represents the worst-case within-to-between cluster ratio for cluster i. The optimal clustering solution has the smallest Davies-Bouldin index value.

Examples

Evaluate the Clustering Solution Using Davies-Bouldin Criterion

Evaluate the optimal number of clusters using the Davies-Bouldin clustering evaluation criterion.

Generate sample data containing random numbers from three multivariate distributions with different parameter values.

```
rng('default');  % For reproducibility
mu1 = [2 2];
sigma1 = [0.9 -0.0255; -0.0255 0.9];

mu2 = [5 5];
sigma2 = [0.5 0 ; 0 0.3];

mu3 = [-2, -2];
sigma3 = [1 0 ; 0 0.9];

N = 200;
```

```
X = [mvnrnd(mu1,sigma1,N);...
     mvnrnd(mu2,sigma2,N);...
     mvnrnd(mu3,sigma3,N)];
```

Evaluate the optimal number of clusters using the Davies-Bouldin criterion. Cluster the data using `kmeans`.

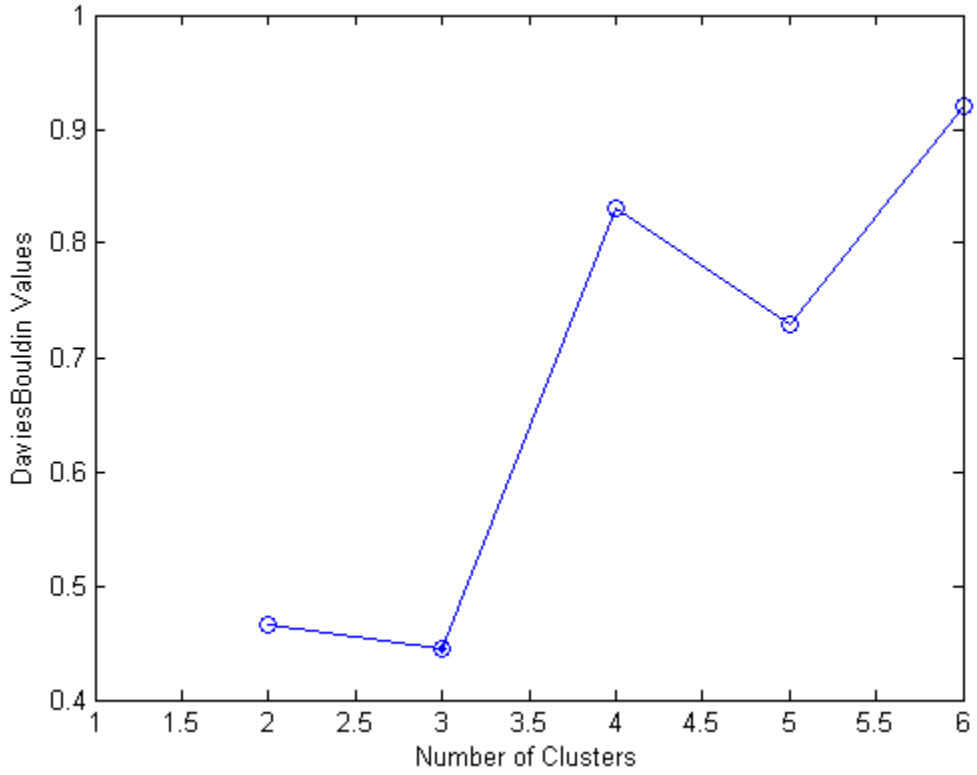
```
E = evalclusters(X,'kmeans','DaviesBouldin','klist',[1:6])
```

```
E =

  DaviesBouldinEvaluation with properties:

    NumObservations: 600
         InspectedK: [1 2 3 4 5 6]
    CriterionValues: [NaN 0.4663 0.4454 0.8300 0.7283 0.9199]
           OptimalK: 3
```

The `OptimalK` value indicates that, based on the Davies-Bouldin criterion, the optimal number of clusters is three.

Plot the Davies-Bouldin criterion values for each number of clusters tested.

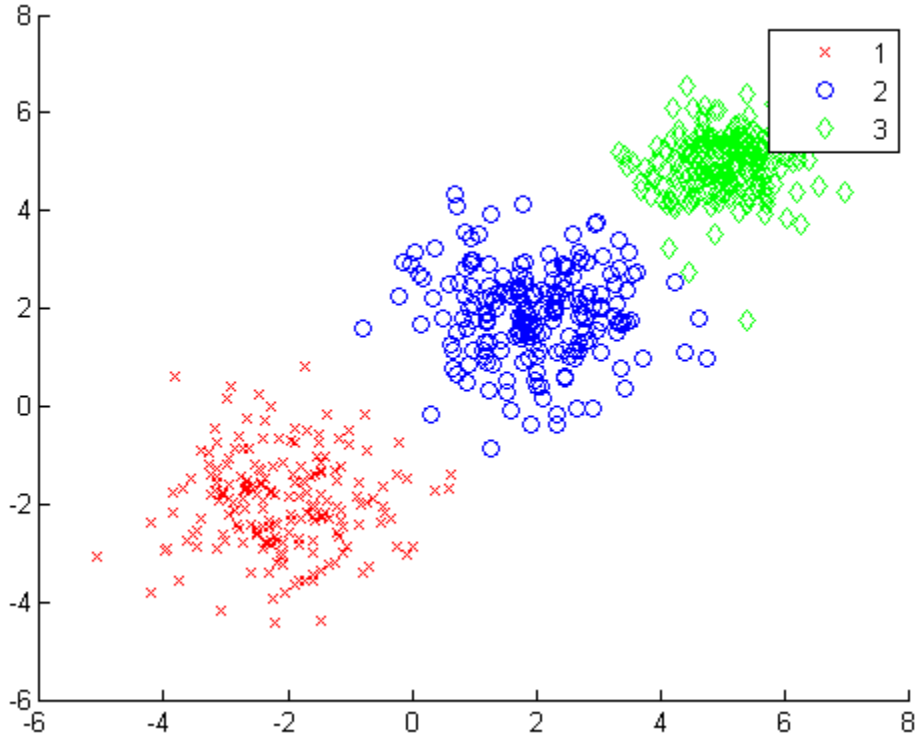
```
figure;
plot(E)
```



The plot shows that the lowest Davies-Bouldin value occurs at three clusters, suggesting that the optimal number of clusters is three.

Create a grouped scatter plot to visually examine the suggested clusters.

```
figure;
gscatter(X(:,1),X(:,2),E.OptimalY,'rbg','xod')
```



The plot shows three distinct clusters within the data: Cluster 1 is in the lower-left corner, cluster 2 is near the center of the plot, and cluster 3 is in the upper-right corner.

References

[1] Davies, D. L., and D. W. Bouldin. “A Cluster Separation Measure.” *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. PAMI-1, No. 2, 1979, pp. 224–227.

See Also

`clustering.evaluation.CalinskiHarabaszEvaluation` | `clustering.evaluation.GapEvaluation` | `clustering.evaluation.SilhouetteEvaluation` | `evalclusters`

More About

- Class Attributes
- Property Attributes

cat

Class: dataset

Concatenate dataset arrays

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds = cat(dim, ds1, ds2, ...)
```

Description

`ds = cat(dim, ds1, ds2, ...)` concatenates the dataset arrays `ds1, ds2, ...` along dimension `dim` by calling the `dataset/horzcat` or `dataset/vertcat` method. `dim` must be 1 or 2.

See Also

`horzcat` | `vertcat`

catsplit

Class: classregtree

Categorical splits used for branches in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
v=catsplit(t)
v=catsplit(t,j)
```

Description

`v=catsplit(t)` returns an `n`-by-2 cell array `v`. Each row in `v` gives left and right values for a categorical split. For each branch node `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `v(j,1)` and the right child is chosen if `z` is in `v(j,2)`. The splits are in the same order as nodes of the tree. Nodes for these splits can be found by running `cuttype` and selecting `'categorical'` cuts from top to bottom.

`v=catsplit(t,j)` takes an array `j` of rows and returns the splits for the specified rows.

See Also

`classregtree`

cdf

Class: gmdistribution

Cumulative distribution function for Gaussian mixture distribution

Syntax

```
y = cdf(obj,X)
```

Description

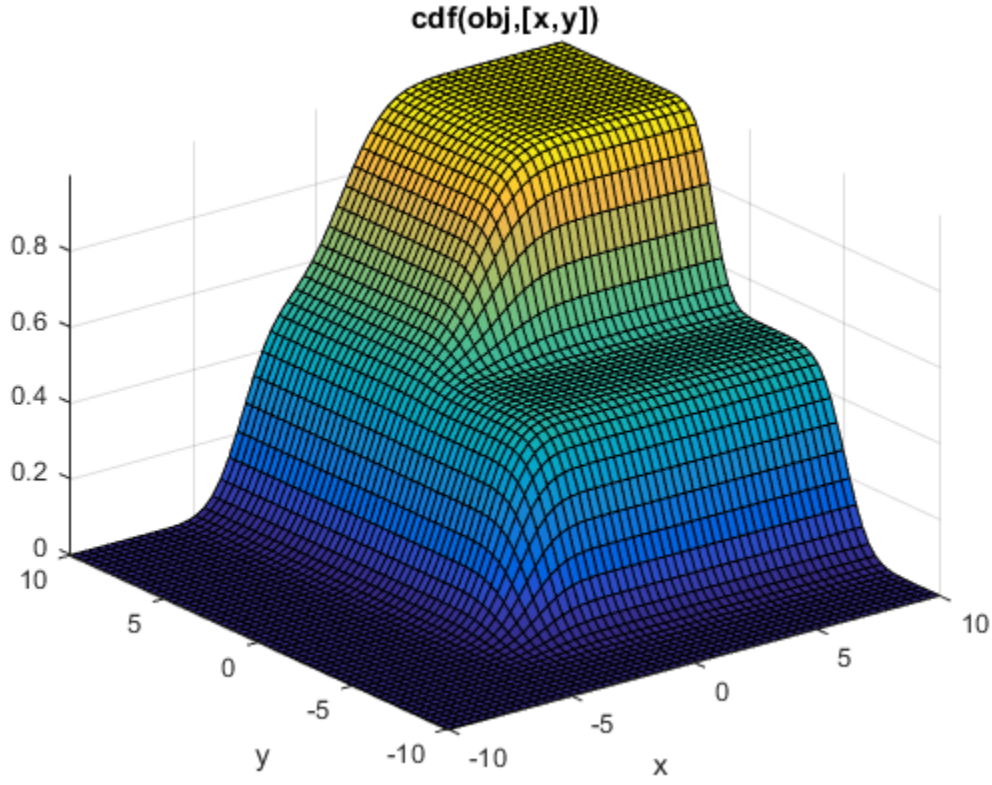
`y = cdf(obj,X)` returns a vector `y` of length n containing the values of the cumulative distribution function (cdf) for the `gmdistribution` object `obj`, evaluated at the n-by-d data matrix `X`, where n is the number of observations and d is the dimension of the data. `obj` is an object created by `gmdistribution` or `fitgmdist`. `y(I)` is the cdf of observation `I`.

Examples

Plot a Gaussian Mixture CDF

Create a `gmdistribution` object defining a two-component mixture of bivariate Gaussian distributions.

```
MU = [1 2;-3 -5];
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(MU,SIGMA,p);

ezsurf(@(x,y)cdf(obj,[x y]),[-10 10],[-10 10])
```



See Also

`gmdistribution` | `fitgmdist` | `pdf` | `mvncdf`

ccdesign

Central composite design

Syntax

```
dCC = ccdesign(n)
[dCC,blocks] = ccdesign(n)
[...] = ccdesign(n,'Name',value)
```

Description

`dCC = ccdesign(n)` generates a central composite design for `n` factors. `n` must be an integer `2` or larger. The output matrix `dCC` is *m*-by-`n`, where *m* is the number of runs in the design. Each row represents one run, with settings for all factors represented in the columns. Factor values are normalized so that the cube points take values between `-1` and `1`.

`[dCC,blocks] = ccdesign(n)` requests a blocked design. The output `blocks` is an *m*-by-1 vector of block numbers for each run. Blocks indicate runs that are to be measured under similar conditions to minimize the effect of inter-block differences on the parameter estimates.

`[...] = ccdesign(n,'Name',value)` specifies one or more optional name/value pairs for the design. Valid parameters and their values are listed in the following table. Specify *`Name`* in single quotes.

Parameter	Description	Values	Value Description
`center`	Number of center points.	Integer	Number of center points to include.
		`'uniform'`	Select number of center points to give uniform precision.
		`'orthogonal'`	Select number of center points to give an

Parameter	Description	Values	Value Description
			orthogonal design. This is the default.
`fraction`	Fraction of full-factorial cube, expressed as an exponent of 1/2.	0	Whole design. Default when $n \le 4$.
		1	1/2 fraction. Default when $4 < n \le 7$ or $n > 11$.
		2	1/4 fraction. Default when $7 < n \le 9$
		3	1/8 fraction. Default when $n = 10$.
		4	1/16 fraction. Default when $n = 11$.
`type`	Type of CCD.	`'circumscribed'`	Circumscribed (CCC). This is the default.
		`'inscribed'`	Inscribed (CCI).
		`'faced'`	Faced (CCF).
`blocksize`	Maximum number of points per block.	Integer	The default is `Inf`.

Examples

Two-Factor Central Composite Design

Create a 2-factor central composite design.

```
dCC = ccdesign(2,'type','circumscribed')
```

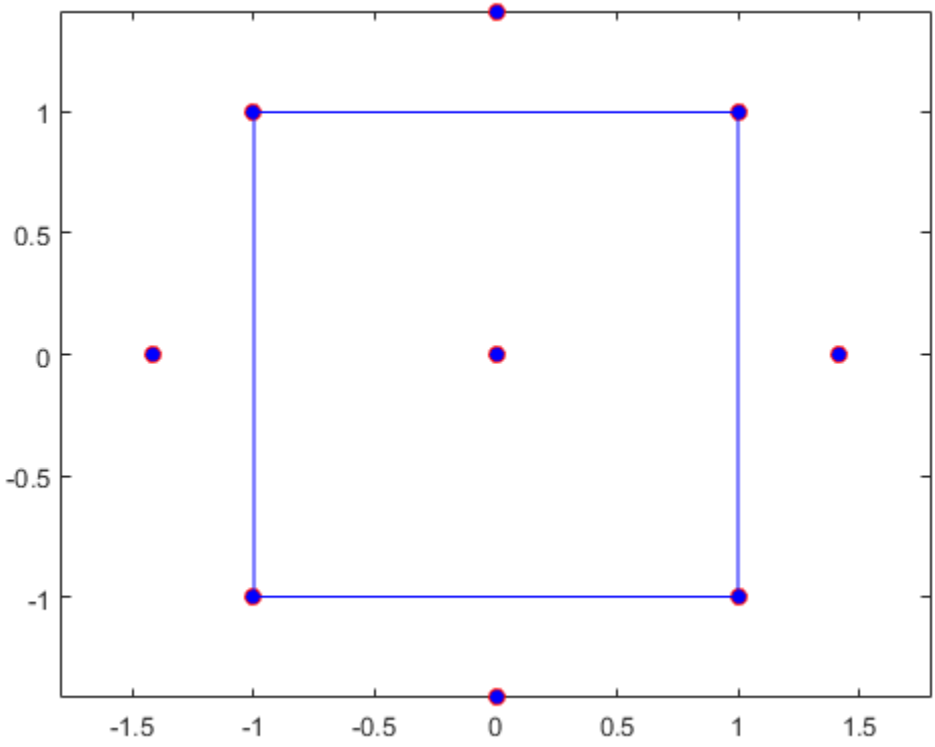
```
dCC =

   -1.0000   -1.0000
   -1.0000    1.0000
```

```
    1.0000   -1.0000
    1.0000    1.0000
   -1.4142         0
    1.4142         0
         0   -1.4142
         0    1.4142
         0         0
         0         0
         0         0
         0         0
         0         0
         0         0
         0         0
         0         0
```

The center point is run 8 times to reduce the correlations among the coefficient estimates.

Visualize the design.

```
plot(dCC(:,1),dCC(:,2),'ro','MarkerFaceColor','b')
X = [1 -1 -1 -1; 1 1 1 -1];
Y = [-1 -1 1 -1; 1 -1 1 1];
line(X,Y,'Color','b')
axis square equal
```



See Also

`bbdesign`

cdf

Cumulative distribution functions

Syntax

```
y = cdf('name',x,A)
y = cdf('name',x,A,B)
y = cdf('name',x,A,B,C)

y = cdf(pd,x)

y = cdf(___,'upper')
```

Description

`y = cdf('name',x,A)` returns the cumulative distribution function (cdf) for the one-parameter distribution family specified by 'name', evaluated at the values in x. `A` contains the parameter value for the distribution.

`y = cdf('name',x,A,B)` returns the cdf for the two-parameter distribution family specified by 'name', evaluated at the values in x. A and B contain the parameter values for the distribution.

`y = cdf('name',x,A,B,C)` returns the cdf for the three-parameter distribution family specified by 'name', evaluated at the values in x. A, B, and C contain the parameter values for the distribution.

`y = cdf(pd,x)` returns the cumulative distribution function of the probability distribution object, pd, evaluated at the values in x.

`y = cdf(___,'upper')` returns the complement of the cumulative distribution function using an algorithm that more accurately computes the extreme upper tail probabilities. You can use the `'upper'` argument with any of the previous syntaxes.

Examples

Compute the Normal Distribution cdf

Create a standard normal distribution object with the mean, μ, equal to 0 and the standard deviation, σ, equal to 1.

```
mu = 0;
sigma = 1;
pd = makedist('Normal',mu,sigma);
```

Define the input vector x to contain the values at which to calculate the cdf.

```
x = [-2,-1,0,1,2];
```

Compute the cdf values for the standard normal distribution at the values in x.

```
y = cdf(pd,x)
```

```
y =

    0.0228    0.1587    0.5000    0.8413    0.9772
```

Each value in y corresponds to a value in the input vector x. For example, at the value x equal to 1, the corresponding cdf value y is equal to 0.8413.

Alternatively, you can compute the same cdf values without creating a probability distribution object. Use the `cdf` function, and specify a standard normal distribution using the same parameter values for μ and σ.

```
y2 = cdf('Normal',x,mu,sigma)
```

```
y2 =

    0.0228    0.1587    0.5000    0.8413    0.9772
```

The cdf values are the same as those computed using the probability distribution object.

Compute the Poisson Distribution cdf

Create a Poisson distribution object with the rate parameter, λ, equal to 2.

```
lambda = 2;
pd = makedist('Poisson',lambda);
```

Define the input vector x to contain the values at which to calculate the cdf.

```
x = [0,1,2,3,4];
```

Compute the cdf values for the Poisson distribution at the values in x.

```
y = cdf(pd,x)
```

```
y =

    0.1353    0.4060    0.6767    0.8571    0.9473
```

Each value in y corresponds to a value in the input vector x. For example, at the value x equal to 3, the corresponding cdf value y is equal to 0.8571.

Alternatively, you can compute the same cdf values without creating a probability distribution object. Use the `cdf` function, and specify a Poisson distribution using the same value for the rate parameter, λ.

```
y2 = cdf('Poisson',x,lambda)
```

```
y2 =

    0.1353    0.4060    0.6767    0.8571    0.9473
```

The cdf values are the same as those computed using the probability distribution object.

Input Arguments

`'name'` — Probability distribution name

probability distribution name string

Probability distribution name, specified as one of the following probability distribution name strings.

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'Beta'	"Beta Distribution" on page B-4	a: first shape parameter	b: second shape parameter	—
'Binomial'	"Binomial Distribution" on page B-9	n: number of trials	p: probability of success for each trial	—
'BirnbaumSaund	"Birnbaum-Saunders Distribution" on page B-13	β: scale parameter	γ: shape parameter	—
'Burr'	"Burr Type XII Distribution" on page B-15	α: scale parameter	c: first shape parameter	k: second shape parameter
'Chisquare'	"Chi-Square Distribution" on page B-29	ν: degrees of freedom	—	—
'Exponential'	"Exponential Distribution" on page B-35	μ: mean	—	—
'Extreme Value'	"Extreme Value Distribution" on page B-39	μ: location parameter	σ: scale parameter	—
'F'	"F Distribution" on page B-45	ν_1: numerator degrees of freedom	ν_2: denominator degrees of freedom	—
'Gamma'	"Gamma Distribution" on page B-48	α: shape parameter	b: scale parameter	—
'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-54	k: shape parameter	σ: scale parameter	μ: location parameter
'Generalized Pareto'	"Generalized Pareto Distribution" on page B-60	k: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter
'Geometric'	"Geometric Distribution" on page B-65	p: probability parameter	—	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'Hypergeometri	"Hypergeometric Distribution" on page B-74	m: size of the population	k: number of items with the desired characteristic in the population	n: number of samples drawn
'InverseGaussi	"Inverse Gaussian Distribution" on page B-77	μ: scale parameter	λ: shape parameter	—
'Logistic'	"Logistic Distribution" on page B-91	μ: mean	σ: scale parameter	—
'LogLogistic'	"Loglogistic Distribution" on page B-93	μ: log mean	σ: log scale parameter	—
'Lognormal'	"Lognormal Distribution" on page B-95	μ: log mean	σ: log standard deviation	—
'Nakagami'	"Nakagami Distribution" on page B-113	μ: shape parameter	ω: scale parameter	—
'Negative Binomial'	"Negative Binomial Distribution" on page B-115	r: number of successes	p: probability of success in a single trial	—
'Noncentral F'	"Noncentral F Distribution" on page B-123	ν_1: numerator degrees of freedom	ν_2: denominator degrees of freedom	δ: noncentrality parameter
'Noncentral t'	"Noncentral t Distribution" on page B-126	ν: degrees of freedom	δ: noncentrality parameter	—
'Noncentral Chi-square'	"Noncentral Chi-Square Distribution" on page B-120	ν: degrees of freedom	δ: noncentrality parameter	—
'Normal'	"Normal Distribution" on page B-130	μ: mean	σ: standard deviation	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'Poisson'	"Poisson Distribution" on page B-138	λ: mean	—	—
'Rayleigh'	"Rayleigh Distribution" on page B-141	b: scale parameter	—	—
'Rician'	"Rician Distribution" on page B-144	s: noncentrality parameter	σ: scale parameter	—
'T'	"Student's t Distribution" on page B-146	ν: degrees of freedom	—	—
'tLocationScal	"t Location-Scale Distribution" on page B-154	μ: location parameter	σ: scale parameter	ν: shape parameter
'Uniform'	"Uniform Distribution (Continuous)" on page B-163	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'Discrete Uniform'	"Uniform Distribution (Discrete)" on page B-169	n: maximum observable value	—	—
'Weibull'	"Weibull Distribution" on page B-172	a: scale parameter	b: shape parameter	—

x — Values at which to evaluate cdf

scalar value | array of scalar values

Values at which to evaluate the cdf, specified as a scalar value, or an array of scalar values.

- If x is a scalar value, and if you specify distribution parameters A, B, or C as arrays, then `cdf` expands x into a constant matrix the same size as `A` and `B`.
- If x is an array, and if you specify distribution parameters A, B, or C as arrays, then x, A, B, and C must all be the same size.

Example: `[0.1,0.25,0.5,0.75,0.9]`

Data Types: `single` | `double`

A — First probability distribution parameter

scalar value | array of scalar values

First probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x and A are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A. If A is a scalar, then `cdf` expands it into a constant matrix the same size as x.

Data Types: `single` | `double`

B — Second probability distribution parameter

scalar value | array of scalar values

Second probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x, A, and B are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A and B. If A or B are scalars, then `cdf` expands them into constant matrices the same size as x

Data Types: `single` | `double`

C — Third probability distribution parameter

scalar value | array of scalar values

Third probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x, A, B, and C are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A, B, and C. If any of A, B or C are scalars, then `cdf` expands them into constant matrices the same size as x.

Data Types: `single` | `double`

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object created using one of the following.

`makedist`	Create a probability distribution object using specified parameter values.

`fitdist`	Fit a probability distribution object to sample data.
`dfittool`	Fit a probability distribution object to sample data using the interactive Distribution Fitting app.
`paretotails`	Create a Pareto tails object.
`gmdistribution`	Create a Gaussian mixture distribution object.

Output Arguments

y — Cumulative distribution function

array

Cumulative distribution function of the specified probability distribution, returned as an array.

- If you specify distribution parameters A, B, or C, then y is the same size as x, A, B, and C, after any necessary scalar expansion.
- If you specify a probability distribution object, pd, then y has the same dimensions as x.

See Also

`ecdf` | `icdf` | `pdf`

cdf

Class: piecewisedistribution

Cumulative distribution function for piecewise distribution

Syntax

```
p= cdf(obj,x)
p= cdf(obj,x,'upper')
```

Description

`p= cdf(obj,x)` returns an array `P` of values of the cumulative distribution function for the piecewise distribution object `obj`, evaluated at the values in the array `X`.

`p= cdf(obj,x,'upper')` returns the complement of the piecewise distribution cdf evaluated at the values in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

Examples

Fit Pareto Tails to *t* Distribution

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9.

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
```

```
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432
```

Compute the cdf at the values in `q`.

```
cdf(obj,q)

ans =
    0.1000
    0.9000
```

See Also

paretotails | icdf | pdf

cdf

Class: ProbDist

Return cumulative distribution function (CDF) for ProbDist object

Syntax

```
Y = cdf(PD, X)
```

Description

`Y = cdf(PD, X)` returns *Y*, an array containing the cumulative distribution function (CDF) for the ProbDist object *PD*, evaluated at values in *X*.

Input Arguments

PD	An object of the class `ProbDistUnivParam` or `ProbDistUnivKernel`.
X	A numeric array of values where you want to evaluate the CDF.

Output Arguments

Y	An array containing the cumulative distribution function (CDF) for the ProbDist object *PD*.

See Also

`cdf`

cdf

Class: prob.TruncatableDistribution
Package: prob

Cumulative distribution function of probability distribution object

Syntax

```
y = cdf(pd,x)
y = cdf(pd,x,'upper')
```

Description

`y = cdf(pd,x)` returns the cumulative distribution function (cdf) of the probability distribution pd at the values in x.

`y = cdf(pd,x,'upper')` returns the complement of the cumulative distribution function (cdf) of the probability distribution pd at the values in x, using an algorithm that more accurately computes the extreme upper tail probabilities.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

`x` — Values at which to calculate cdf

array

Values at which to calculate the cdf, specified as an array.

Data Types: `single` | `double`

`upper` — Upper tail probability flag

`'upper'`

Upper tail probability flag, specified as `'upper'`. If you specify `'upper'`, then cdf returns the complement of the cdf of pd, using an algorithm that more accurately computes the extreme upper tail probabilities.

Output Arguments

y — Cumulative distribution function

array

Cumulative distribution function of the specified probability distribution, evaluated at the values in x, returned as a array. y has the same dimensions as x.

Examples

Plot Standard Normal Distribution cdf

Create a standard normal distribution object.

```
pd = makedist('Normal')
```

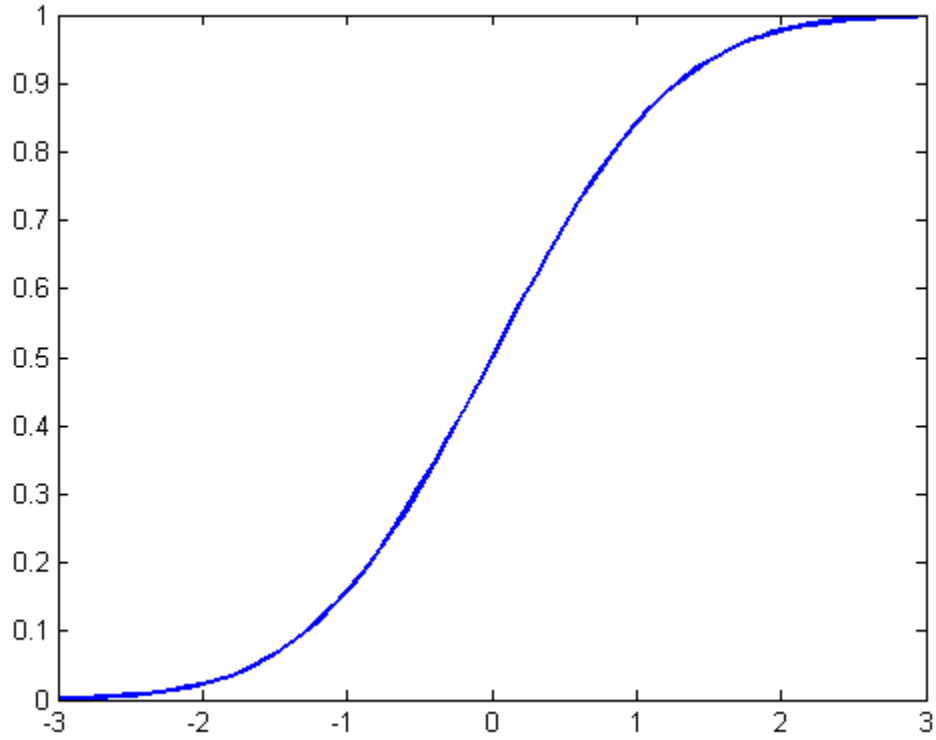
```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Specify the `x` values and compute the cdf.

```
x = -3:.1:3;
cdf_normal = cdf(pd,x);
```

Plot the cdf of the standard normal distribution.

```
plot(x,cdf_normal,'LineWidth',2)
```



Plot Gamma Distribution cdf

Create three gamma distribution objects. The first uses the default parameter values. The second specifies `a = 1` and `b = 2`. The third specifies `a = 2` and `b = 1`.

```
pd_gamma = makedist('Gamma')
```

```
pd_gamma =

  GammaDistribution

  Gamma distribution
    a = 1
    b = 1
```

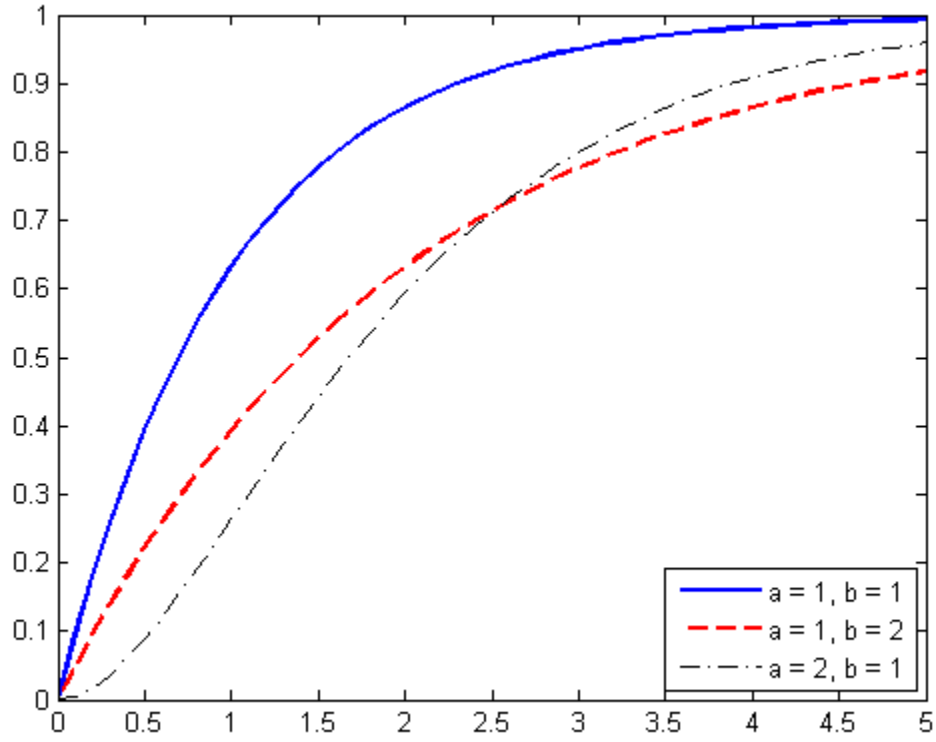
```
pd_12 = makedist('Gamma','a',1,'b',2)

pd_12 =

  GammaDistribution

  Gamma distribution
    a = 1
    b = 2

pd_21 = makedist('Gamma','a',2,'b',1)

pd_21 =

  GammaDistribution

  Gamma distribution
    a = 2
    b = 1
```

Specify the `x` values and compute the cdf for each distribution.

```
x = 0:.1:5;
cdf_gamma = cdf(pd_gamma,x);
cdf_12 = cdf(pd_12,x);
cdf_21 = cdf(pd_21,x);
```

Create a plot to visualize how the cdf of the gamma distribution changes when you specify different values for the shape parameters `a` and `b`.

```
figure;
J = plot(x,cdf_gamma)
hold on;
K = plot(x,cdf_gamma_12,'r--')
L = plot(x,cdf_gamma_21,'k-.')
set(J,'LineWidth',2);
set(K,'LineWidth',2);
legend([J K L],'a = 1, b = 1','a = 1, b = 2','a = 2, b = 1','Location','southeast');
hold off;
```



See Also

`cdf` | `dfittool` | `ecdf` | `fitdist` | `icdf` | `makedist` | `pdf`

cdfplot

Empirical cumulative distribution function plot

Syntax

```
cdfplot(X)
h = cdfplot(X)
[h,stats] = cdfplot(X)
```

Description

`cdfplot(X)` displays a plot of the empirical cumulative distribution function (cdf) for the data in the vector `X`. The empirical cdf *F(x)* is defined as the proportion of `X` values less than or equal to *x*.

This plot is useful for examining the distribution of a sample of data. You can overlay a theoretical cdf on the same plot to compare the empirical distribution of the sample to the theoretical distribution.

The `kstest`, `kstest2`, and `lillietest` functions compute test statistics that are derived from the empirical cdf. You may find the empirical cdf plot produced by `cdfplot` useful in helping you to understand the output from those functions.

`h = cdfplot(X)` returns a handle to the cdf curve.

`[h,stats] = cdfplot(X)` also returns a `stats` structure with the following fields.

Field	Description
`stats.min`	Minimum value
`stats.max`	Maximum value
`stats.mean`	Sample mean
`stats.median`	Sample median (50th percentile)
`stats.std`	Sample standard deviation

Examples

Compare Empirical cdf with Sampling Distribution

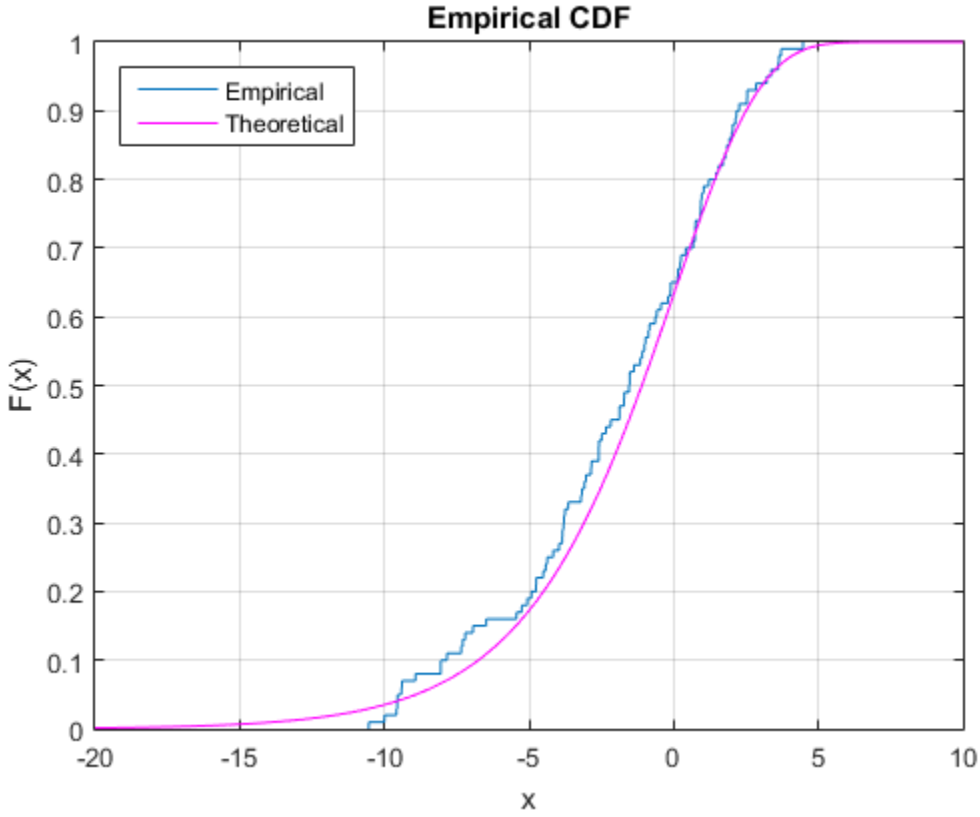
This example shows how to plot the empirical cdf of sample data and compare it with a plot of the cdf for the sampling distribution. In practice, the sampling distribution would be unknown, and would be chosen to match the empirical cdf.

Generate random sample data from an extreme value distribution with a location parameter `mu = 0` and scale parameter `sigma = 3`.

```
rng default;  % For reproducibility
y = evrnd(0,3,100,1);
```

Plot the empirical cdf of the sample data on the same figure as the cdf of the sampling distribution.

```
cdfplot(y)
hold on
x = -20:0.1:10;
f = evcdf(x,0,3);
plot(x,f,'m')
legend('Empirical','Theoretical','Location','NW')
```



See Also

`ecdf`

cell2dataset

Convert cell array to dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds = cell2dataset(C)
ds = cell2dataset(C,Name,Value)
```

Description

`ds = cell2dataset(C)` converts a cell array to a `dataset` array.

`ds = cell2dataset(C,Name,Value)` performs the conversion using additional options specified by one or more Name,Value pair arguments.

Examples

Convert Cell Array to Dataset Array

Convert a cell array to a dataset array using the default options.

Create a cell array to convert.

```
C = {'Name','Gender','SystolicBP','DiastolicBP';
     'CLARK','M',124,93;
     'BROWN','F',122,80;
     'MARTIN','M',130,92}
```

```
C =
```

```
    'Name'      'Gender'    'SystolicBP'    'DiastolicBP'
    'CLARK'     'M'         [       124]    [         93]
    'BROWN'     'F'         [       122]    [         80]
    'MARTIN'    'M'         [       130]    [         92]
```

Convert the cell array to a dataset array.

```
ds = cell2dataset(C)
```

```
ds =

    Name            Gender     SystolicBP    DiastolicBP
    'CLARK'         'M'        124           93
    'BROWN'         'F'        122           80
    'MARTIN'        'M'        130           92
```

The first row of `C` become the variable names in the output dataset array, `ds`.

Create a Dataset Array with Multicolumn Variables

Convert a cell array to a dataset array containing multicolumn variables.

Create a cell array to convert.

```
C = {'Name','Gender','SystolicBP','DiastolicBP';
     'CLARK','M',124,93;
     'BROWN','F',122,80;
     'MARTIN','M',130,92}
```

```
C =

    'Name'      'Gender'    'SystolicBP'    'DiastolicBP'
    'CLARK'     'M'         [       124]    [         93]
    'BROWN'     'F'         [       122]    [         80]
    'MARTIN'    'M'         [       130]    [         92]
```

Convert the cell array to a dataset array, combining the systolic and diastolic blood pressure measurements into one variable named `BloodPressure`.

```
ds = cell2dataset(C,'NumCols',[1,1,2]);
ds.Properties.VarNames{3} = 'BloodPressure';
ds
```

```
ds =
```

```
Name            Gender     BloodPressure
'CLARK'         'M'        124          93
'BROWN'         'F'        122          80
'MARTIN'        'M'        130          92
```

The output dataset array has three observations and three variables.

- "Create a Dataset Array from Workspace Variables" on page 2-63
- "Create a Dataset Array from a File" on page 2-69

Input Arguments

`C` — Input cell array

cell array

Input cell array to convert to a dataset array, specified as an *M*-by-*N* cell array. Each column of `C` becomes a variable in the output dataset array, ds. By default, `cell2dataset` assumes that the first row of `C` contains variable names.

Data Types: `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'ReadVarNames',false,'ReadObsNames',true` specifies that the first row of the cell array does not contain variable names, but the first column contains observation names.

`'ReadVarNames'` — Indicator for whether or not to read variable names

`true` (default) | `false`

Indicator for whether or not to read variable names from the first row of the input cell array, specified as the comma-separated pair consisting of `'ReadVarNames'` and either `true` or `false`. The default value is `true`, unless variable names are specified using the name-value pair argument VarNames. When `ReadVarNames` is `false`, `cell2dataset` creates default variable names if you do not provide any.

Example: `'ReadVarNames',false`

`'VarNames'` — Variable names for output dataset array

cell array of strings

Variable names for the output dataset array, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings. You must provide a variable name for each variable in `ds`. The names must be valid MATLAB identifiers, and must be unique.

Example: `'VarNames',{'myVar1','myVar2','myVar3'}`

`'ReadObsNames'` — Indicator for whether or not to read observation names

`false` (default) | `true`

Indicator for whether or not to read observation names from the input cell array, specified as the comma-separated pair consisting of `'ReadObsNames'` and either `true` or `false`. When `ReadObsNames` has the value `true`, `cell2dataset` creates observation names in ds using the first column of `C`, and sets `ds.Properties.DimNames` equal to `{C{1,1},'Variables'}`.

Example: `'ReadObsNames',true`

`'ObsNames'` — Observation names for output dataset array

cell array of strings

Observation names for the output dataset array, specified as the comma-separated pair consisting of `'ObsNames'` and a cell array of strings. The names do not need to be valid MATLAB identifiers, but they must be unique.

`'NumCols'` — Number of columns for each variable

vector of nonnegative integers

Number of columns for each variable in ds, specified as the comma-separated pair consisting of `'NumCols'` and a vector of nonnegative integers. When the number of columns for a variable is greater than one, `cell2dataset` combines multiple columns in C into a single variable in `ds`. The vector you assign to `NumCols` must sum to `size(C,2)`, or `size(C,1)` of ReadObsNames is equal to `true`.

For example, to convert a cell array with eight columns into a dataset array with five variables, specify a vector with five elements that sum to eight, such as `'NumCols', [1,1,3,1,2]`.

Output Arguments

`ds` — Output dataset array

dataset array

Output dataset array, returned by default with a variable for each column of C, an observation for each row of `C` (except for the first row), and variable names corresponding to the first row of `C`.

- If you set ReadVarNames equal to `false` (or specify `VarNames`), then there is an observation in `ds` for each row of `C`, and `cell2dataset` creates default variable names (or uses the names in `VarNames`).
- If you set ReadObsNames equal to `true`, then `cell2dataset` uses the first column of `C` as observation names.
- If you specify NumCols, then the number of variables in `ds` is equal to the length of the specified vector of column numbers.

More About

- "Dataset Arrays" on page 2-132

See Also

`dataset` | `dataset2cell` | `struct2dataset`

cellstr

Class: dataset

Create cell array of strings from dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
B = cellstr(A)
B = cellstr(A,VARS)
```

Description

`B = cellstr(A)` returns the contents of the dataset `A`, converted to a cell array of strings. The variables in the dataset must support the conversion and must have compatible sizes.

`B = cellstr(A,VARS)` returns the contents of the dataset variables specified by `VARS`. `VARS` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

See Also

`dataset.double` | `dataset.replacedata`

chi2cdf

Chi-square cumulative distribution function

Syntax

```
p = chi2cdf(x,v)
p = chi2cdf(x,v,'upper')
```

Description

`p = chi2cdf(x,v)` computes the chi-square cdf at each of the values in `x` using the corresponding degrees of freedom in `v`. `x` and `v` can be vectors, matrices, or multidimensional arrays that have the same size. The degrees of freedom parameters in `v` must be positive integers, and the values in `x` must lie on the interval `[0 Inf]`. A scalar input is expanded to a constant array with the same dimensions as the other input.

`p = chi2cdf(x,v,'upper')` returns the complement of the chi-square cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The χ^2 cdf for a given value x and degrees-of-freedom ν is

$$p = F(x \mid \nu) = \int_0^x \frac{t^{(\nu-2)/2} e^{-t/2}}{2^{\nu/2}\Gamma(\nu/2)}\,dt$$

where $\Gamma(\cdot)$ is the Gamma function.

The chi-square density function with ν degrees-of-freedom is the same as the gamma density function with parameters $\nu/2$ and 2.

Examples

Compute Chi-Square CDF

```
probability = chi2cdf(5,1:5)
```

```
probability =
  0.9747  0.9179  0.8282  0.7127  0.5841

probability = chi2cdf(1:5,1:5)

probability =
  0.6827  0.6321  0.6084  0.5940  0.5841
```

More About

- "Chi-Square Distribution" on page B-29

See Also

`cdf` | `chi2pdf` | `chi2inv` | `chi2stat` | `chi2rnd`

chi2gof

Chi-square goodness-of-fit test

Syntax

```
h = chi2gof(x)
h = chi2gof(x,Name,Value)
[h,p] = chi2gof(___)
[h,p,stats] = chi2gof(___)
```

Description

`h = chi2gof(x)` returns a test decision for the null hypothesis that the data in vector x comes from a normal distribution with a mean and variance estimated from x, using the chi-square goodness-of-fit test. The alternative hypothesis is that the data does not come from such a distribution. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = chi2gof(x,Name,Value)` returns a test decision for the chi-square goodness-of-fit test with additional options specified by one or more name-value pair arguments. For example, you can test for a distribution other than normal, or change the significance level of the test.

`[h,p] = chi2gof(___)` also returns the *p*-value p of the hypothesis test, using any of the input arguments from the previous syntaxes.

`[h,p,stats] = chi2gof(___)` also returns the structure stats, containing information about the test statistic.

Examples

Test for a Normal Distribution

Create a standard normal probability distribution object. Generate a data vector `x` using random numbers from the distribution.

```
pd = makedist('Normal');
rng default;  % for reproducibility
x = random(pd,100,1);
```

Test the null hypothesis that the data in `x` comes from a population with a normal distribution.

```
h = chi2gof(x)
```

```
h =
     0
```

The returned value `h = 0` indicates that `chi2gof` does not reject the null hypothesis at the default 5% significance level.

Test the Hypothesis at a Different Significance Level

Create a standard normal probability distribution object. Generate a data vector `x` using random numbers from the distribution.

```
pd = makedist('Normal');
rng default;  % for reproducibility
x = random(pd,100,1);
```

Test the null hypothesis that the data in `x` comes from a population with a normal distribution at the 1% significance level.

```
[h,p] = chi2gof(x,'Alpha',0.01)
```

```
h =
     0

p =
    0.3775
```

The returned value `h = 0` indicates that `chi2gof` does not reject the null hypothesis at the 1% significance level.

Test for a Weibull Distribution Using a Probability Distribution Object

Navigate to the appropriate folder and load the lightbulb lifetime sample data.

```
cd(matlabroot);
cd('help/toolbox/stats/examples');
load lightbulb;
```

Create a vector from the first column of the data matrix, which contains the lifetime in hours of the lightbulbs.

```
x = lightbulb(:,1);
```

Test the null hypothesis that the data in `x` comes from a population with a Weibull distribution. Use `fitdist` to create a probability distribution object with `A` and `B` parameters estimated from the data.

```
pd = fitdist(x,'Weibull');
h = chi2gof(x,'CDF',pd)
```

```
h =
     1
```

The returned value `h = 1` indicates that `chi2gof` rejects the null hypothesis at the default 5% significance level.

Test for a Poisson Distribution

Create six bins, numbered 0 through 5, to use for data pooling.

```
bins = 0:5;
```

Create a vector containing the observed counts for each bin and compute the total number of observations.

```
obsCounts = [6 16 10 12 4 2];
n = sum(obsCounts);
```

Fit a Poisson probability distribution object to the data and compute the expected count for each bin. Use the transpose operator `.'` to transform `bins` and `obsCounts` from row vectors to column vectors.

```
pd = fitdist(bins','Poisson','Frequency',obsCounts');
expCounts = n * pdf(pd,bins);
```

Test the null hypothesis that the data in `obsCounts` comes from a Poisson distribution with a lambda parameter equal to `lambdaHat`.

```
[h,p,st] = chi2gof(bins,'Ctrs',bins,...
                        'Frequency',obsCounts, ...
                        'Expected',expCounts,...
                        'NParams',1)
```

```
h =
     0

p =
    0.4654

st =
    chi2stat: 2.5550
          df: 3
       edges: [1x6 double]
           O: [6 16 10 12 6]
           E: [7.0429 13.8041 13.5280 8.8383 6.0284]
```

The returned value `h = 0` indicates that `chi2gof` does not reject the null hypothesis at the default 5% significance level. The vector `E` contains the expected counts for each bin under the null hypothesis, and `O` contains the observed counts for each bin.

Input Arguments

x — Sample data

vector

Sample data for the hypothesis test, specified as a vector.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'NBins',8,'Alpha',0.01` pools the data into eight bins and conducts the hypothesis test at the 1% significance level.

'NBins' — Number of bins

`10` (default) | positive integer value

Number of bins to use for the data pooling, specified as the comma-separated pair consisting of `'NBins'` and a positive integer value. If you specify a value for `NBins`, do not specify a value for `Ctrs` or `Edges`.

Example: `'NBins',8`

Data Types: `single` | `double`

`'Ctrs'` — Bin centers

vector

Bin centers, specified as the comma-separated pair consisting of `'Ctrs'` and a vector of center values for each bin. If you specify a value for `Ctrs`, do not specify a value for `NBins` or `Edges`.

Example: `'Ctrs',[1 2 3 4 5]`

Data Types: `single` | `double`

`'Edges'` — Bin edges

vector

Bin edges, specified as the comma-separated pair consisting of `'Edges'` and a vector of edge values for each bin. If you specify a value for `Edges`, do not specify a value for `NBins` or `Ctrs`.

Example: `'Edges',[-2.5 -1.5 -0.5 0.5 1.5 2.5]`

Data Types: `single` | `double`

`'CDF'` — cdf of hypothesized distribution

probability distribution object | function handle | cell array

The cdf of the hypothesized distribution, specified as the comma-separated pair consisting of `'CDF'` and a probability distribution object, function handle, or cell array.

- If `CDF` is a probability distribution object, the degrees of freedom account for whether you estimate the parameters using `fitdist` or specify them using `makedist`.
- If `CDF` is a function handle, the distribution function must take `x` as its only argument.
- If `CDF` is a cell array, the first element must be a function handle, and the remaining elements must be parameter values, one per cell. The function must take `x` as its first argument, and the other parameters in the array as later arguments.

If you specify a value for `CDF`, do not specify a value for `Expected`.

Example: `'CDF',pd_object`

Data Types: `single` | `double`

`'Expected'` — Expected counts

vector of nonnegative values

Expected counts for each bin, specified as the comma-separated pair of `'Expected'` and a vector of nonnegative values. If `Expected` depends on estimated parameters, use `NParams` to ensure that `chi2gof` correctly calculates the degrees of freedom. If you specify a value for `Expected`, do not specify a value for `CDF`.

Example: `'Expected',[19.1446 18.3789 12.3224 8.2432 4.1378]`

Data Types: `single` | `double`

`'NParams'` — Number of estimated parameters

positive integer value

Number of estimated parameters used to describe the null distribution, specified as the comma-separated pair consisting of `'NParams'` and a positive integer value. This value adjusts the degrees of freedom of the test based on the number of estimated parameters used to compute the cdf or expected counts.

The default value for `NParams` depends on how you specify the null distribution:

- If you specify CDF as a probability distribution object, `NParams` is equal to the number of estimated parameters used to create the object.
- If you specify CDF as a function name or handle, the default value of `NParams` is `0`.
- If you specify CDF as a cell array, the default value of `NParams` is the number of parameters in the array.
- If you specify Expected, the default value of `NParams` is `0`.

Example: `'NParams',1`

Data Types: `single` | `double`

`'EMin'` — Minimum expected count per bin

`5` (default) | nonnegative integer value

Minimum expected count per bin, specified as the comma-separated pair consisting of `'EMin'` and a nonnegative integer value. If the bin at the extreme end of either tail has an expected value less than `EMin`, it is combined with a neighboring bin until the count in each extreme bin is at least 5. If any interior bins have a count less than 5, `chi2gof`

displays a warning, but does not combine the interior bins. In that case, you should use fewer bins, or provide bin centers or edges, to increase the expected counts in all bins. Specify `EMin` as `0` to prevent the combining of bins.

Example: `'EMin',0`

Data Types: `single | double`

`'Frequency'` — Frequency

vector of nonnegative integer values

Frequency of data values, specified as the comma-separated pair consisting of `'Frequency'` and a vector of nonnegative integer values that is the same length as the vector x.

Example: `'Frequency',[20 16 13 10 8]`

Data Types: `single | double`

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single | double`

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

- If h = `1`, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = `0`, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

`stats` — Test statistics
structure

Test statistics, returned as a structure containing the following:

- `chi2stat` — Value of the test statistic.
- `df` — Degrees of freedom of the test.
- `edges` — Vector of bin edges after pooling.
- `O` — Vector of observed counts for each bin.
- `E` — Vector of expected counts for each bin.

More About

Chi-Square Goodness-of-Fit Test

The chi-square goodness-of-fit test determines if a data sample comes from a specified probability distribution, with parameters estimated from the data.

The test groups the data into bins, calculating the observed and expected counts for those bins, and computing the chi-square test statistic

$$\chi^2 = \sum_{i=1}^{N} (O_i - E_i)^2 / E_i ,$$

where O_i are the observed counts and E_i are the expected counts based on the hypothesized distribution. The test statistic has an approximate chi-square distribution when the counts are sufficiently large.

Algorithms

`chi2gof` compares the value of the test statistic to a chi-square distribution with degrees of freedom equal to *nbins* - 1 - *nparams*, where *nbins* is the number of bins used for the data pooling and *nparams* is the number of estimated parameters used to determine the

expected counts. If there are not enough degrees of freedom to conduct the test, `chi2gof` returns the *p*-value as `NaN`.

- "Chi-Square Distribution" on page B-29

See Also

`kstest` | `lillietest`

chi2inv

Chi-square inverse cumulative distribution function

Syntax

```
X = chi2inv(P,V)
```

Description

`X = chi2inv(P,V)` computes the inverse of the chi-square cdf with degrees of freedom specified by `V` for the corresponding probabilities in `P`. `P` and `V` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

The degrees of freedom parameters in `V` must be positive integers, and the values in `P` must lie in the interval [0 1].

The inverse chi-square cdf for a given probability p and v degrees of freedom is

$$x = F^{-1}(p \mid \nu) = \{x : F(x \mid \nu) = p\}$$

where

$$p = F(x \mid \nu) = \int_0^x \frac{t^{(\nu-2)/2} e^{-t/2}}{2^{\nu/2}\Gamma(\nu/2)} dt$$

and $\Gamma(\cdot)$ is the Gamma function. Each element of output `X` is the value whose cumulative probability under the chi-square cdf defined by the corresponding degrees of freedom parameter in `V` is specified by the corresponding value in `P`.

Examples

Find a value that exceeds 95% of the samples from a chi-square distribution with 10 degrees of freedom.

```
x = chi2inv(0.95,10)
x =
  18.3070
```

You would observe values greater than 18.3 only 5% of the time by chance.

More About

- "Chi-Square Distribution" on page B-29

See Also

`icdf` | `chi2cdf` | `chi2pdf` | `chi2stat` | `chi2rnd`

chi2pdf

Chi-square probability density function

Syntax

```
Y = chi2pdf(X,V)
```

Description

`Y = chi2pdf(X,V)` computes the chi-square pdf at each of the values in `X` using the corresponding degrees of freedom in `V`. `X` and `V` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of the output `Y`. A scalar input is expanded to a constant array with the same dimensions as the other input.

The degrees of freedom parameters in `V` must be positive integers, and the values in `X` must lie on the interval `[0 Inf]`.

The chi-square pdf for a given value x and ν degrees of freedom is

$$y = f(x|\nu) = \frac{x^{(\nu-2)/2}e^{-x/2}}{2^{\nu/2}\Gamma(\nu/2)}$$

where $\Gamma(\cdot)$ is the Gamma function.

If x is standard normal, then x^2 is distributed chi-square with one degree of freedom. If x_1, x_2, ..., x_n are n independent standard normal observations, then the sum of the squares of the x's is distributed chi-square with n degrees of freedom (and is equivalent to the gamma density function with parameters $\nu/2$ and 2).

Examples

```
nu = 1:6;
x = nu;
```

```
y = chi2pdf(x,nu)
y =
  0.2420  0.1839  0.1542  0.1353  0.1220  0.1120
```

The mean of the chi-square distribution is the value of the degrees of freedom parameter, `nu`. The above example shows that the probability density of the mean falls as `nu` increases.

More About

- "Chi-Square Distribution" on page B-29

See Also

`pdf` | `chi2cdf` | `chi2inv` | `chi2stat` | `chi2rnd`

chi2rnd

Chi-square random numbers

Syntax

```
R = chi2rnd(V)
R = chi2rnd(V,m,n,...)
R = chi2rnd(V,[m,n,...])
```

Description

`R = chi2rnd(V)` generates random numbers from the chi-square distribution with degrees of freedom parameters specified by `V`. `V` can be a vector, a matrix, or a multidimensional array. `R` is the same size as `V`.

`R = chi2rnd(V,m,n,...)` or `R = chi2rnd(V,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the chi-square distribution with degrees of freedom parameter `V`. `V` can be a scalar or an array of the same size as `R`.

Examples

Note that the first and third commands are the same, but are different from the second command.

```
r = chi2rnd(1:6)
r =
    0.0037  3.0377  7.8142  0.9021  3.2019  9.0729

r = chi2rnd(6,[1 6])
r =
    6.5249  2.6226  12.2497  3.0388  6.3133  5.0388

r = chi2rnd(1:6,1,6)
r =
  0.7638  6.0955  0.8273  3.2506  1.5469  10.9197
```

More About

- "Chi-Square Distribution" on page B-29

See Also

`random` | `chi2cdf` | `chi2pdf` | `chi2inv` | `chi2stat`

chi2stat

Chi-square mean and variance

Syntax

```
[M,V] = chi2stat(NU)
```

Description

`[M,V] = chi2stat(NU)` returns the mean of and variance for the chi-square distribution with degrees of freedom parameters specified by `NU`.

The mean of the chi-square distribution is v, the degrees of freedom parameter, and the variance is 2v.

Examples

```
nu = 1:10;
nu = nu'*nu;
[m,v] = chi2stat(nu)
m =
 1   2   3   4   5   6   7   8   9  10
 2   4   6   8  10  12  14  16  18  20
 3   6   9  12  15  18  21  24  27  30
 4   8  12  16  20  24  28  32  36  40
 5  10  15  20  25  30  35  40  45  50
 6  12  18  24  30  36  42  48  54  60
 7  14  21  28  35  42  49  56  63  70
 8  16  24  32  40  48  56  64  72  80
 9  18  27  36  45  54  63  72  81  90
10  20  30  40  50  60  70  80  90 100

v =
 2   4   6   8  10  12  14  16  18  20
 4   8  12  16  20  24  28  32  36  40
 6  12  18  24  30  36  42  48  54  60
 8  16  24  32  40  48  56  64  72  80
```

```
10   20   30   40   50   60   70   80   90  100
12   24   36   48   60   72   84   96  108  120
14   28   42   56   70   84   98  112  126  140
16   32   48   64   80   96  112  128  144  160
18   36   54   72   90  108  126  144  162  180
20   40   60   80  100  120  140  160  180  200
```

More About

- "Chi-Square Distribution" on page B-29

See Also

`chi2cdf` | `chi2pdf` | `chi2inv` | `chi2rnd`

children

Class: classregtree

Child nodes

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
C = children(t)
C = children(t,nodes)
```

Description

`C = children(t)` returns an n-by-2 array `C` containing the numbers of the child nodes for each node in the tree `t`, where n is the number of nodes. Leaf nodes have child node `0`.

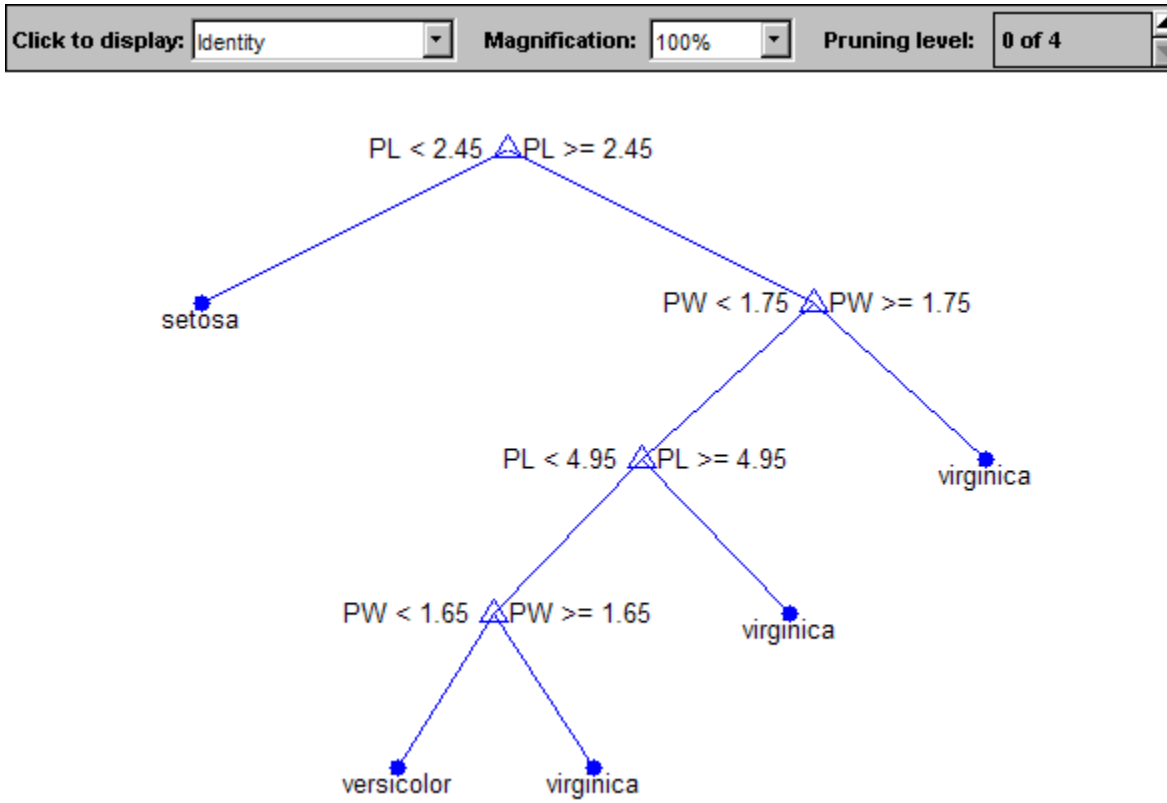
`C = children(t,nodes)` takes a vector `nodes` of node numbers and returns the children for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
```

```
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
C = children(t)
C =
     2     3
     0     0
     4     5
     6     7
     0     0
```

```
     8     9
     0     0
     0     0
     0     0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `parent` | `numnodes`

cholcov

Cholesky-like covariance decomposition

Syntax

```
T = cholcov(SIGMA)
[T,num] = cholcov(SIGMA)
[T,num] = cholcov(SIGMA,0)
```

Description

`T = cholcov(SIGMA)` computes `T` such that `SIGMA = T'*T`. `SIGMA` must be square, symmetric, and positive semi-definite. If `SIGMA` is positive definite, then `T` is the square, upper triangular Cholesky factor. If `SIGMA` is not positive definite, `T` is computed from an eigenvalue decomposition of `SIGMA`. `T` is not necessarily triangular or square in this case. Any eigenvectors whose corresponding eigenvalue is close to zero (within a small tolerance) are omitted. If any remaining eigenvalues are negative, `T` is empty.

`[T,num] = cholcov(SIGMA)` returns the number `num` of negative eigenvalues of `SIGMA`, and `T` is empty if `num` is positive. If `num` is zero, `SIGMA` is positive semi-definite. If `SIGMA` is not square and symmetric, `num` is `NaN` and `T` is empty.

`[T,num] = cholcov(SIGMA,0)` returns `num` equal to zero if `SIGMA` is positive definite, and `T` is the Cholesky factor. If `SIGMA` is not positive definite, `num` is a positive integer and `T` is empty. `[...] = cholcov(SIGMA,1)` is equivalent to `[...] = cholcov(SIGMA)`.

Examples

The following 4-by-4 covariance matrix is rank-deficient:

```
C1 = [2 1 1 2;1 2 1 2;1 1 2 2;2 2 2 3]
C1 =
     2     1     1     2
     1     2     1     2
     1     1     2     2
```

```
     2     2     2     3
rank(C1)
ans =
     3
```

Use `cholcov` to factor `C1`:

```
T = cholcov(C1)
T =
   -0.2113    0.7887   -0.5774         0
    0.7887   -0.2113   -0.5774         0
    1.1547    1.1547    1.1547    1.7321

C2 = T'*T
C2 =
    2.0000   1.0000   1.0000   2.0000
    1.0000   2.0000   1.0000   2.0000
    1.0000   1.0000   2.0000   2.0000
    2.0000   2.0000   2.0000   3.0000
```

Use `T` to generate random data with the specified covariance:

```
C3 = cov(randn(1e6,3)*T)
C3 =
    1.9973    0.9982    0.9995    1.9975
    0.9982    1.9962    0.9969    1.9956
    0.9995    0.9969    1.9980    1.9972
    1.9975    1.9956    1.9972    2.9951
```

See Also

`chol` | `cov`

ClsNonEmpty property

Class: NaiveBayes

Flag for non-empty classes

Description

The `CIsNonEmpty` property is a logical vector of length `NClasses` specifying which classes are not empty. When the grouping variable is categorical, it may contain categorical levels that don't appear in the elements of the grouping variable. Those levels are empty and `NaiveBayes` ignores them for the purposes of training the classifier.

classcount

Class: classregtree

Class counts

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
P = classcount(t)
P = classcount(t,nodes)
```

Description

`P = classcount(t)` returns an *n*-by-*m* array `P` of class counts for the nodes in the classification tree `t`, where *n* is the number of nodes and *m* is the number of classes. For any node number `i`, the class counts `P(i,:)` are counts of observations (from the data used in fitting the tree) from each class satisfying the conditions for node `i`.

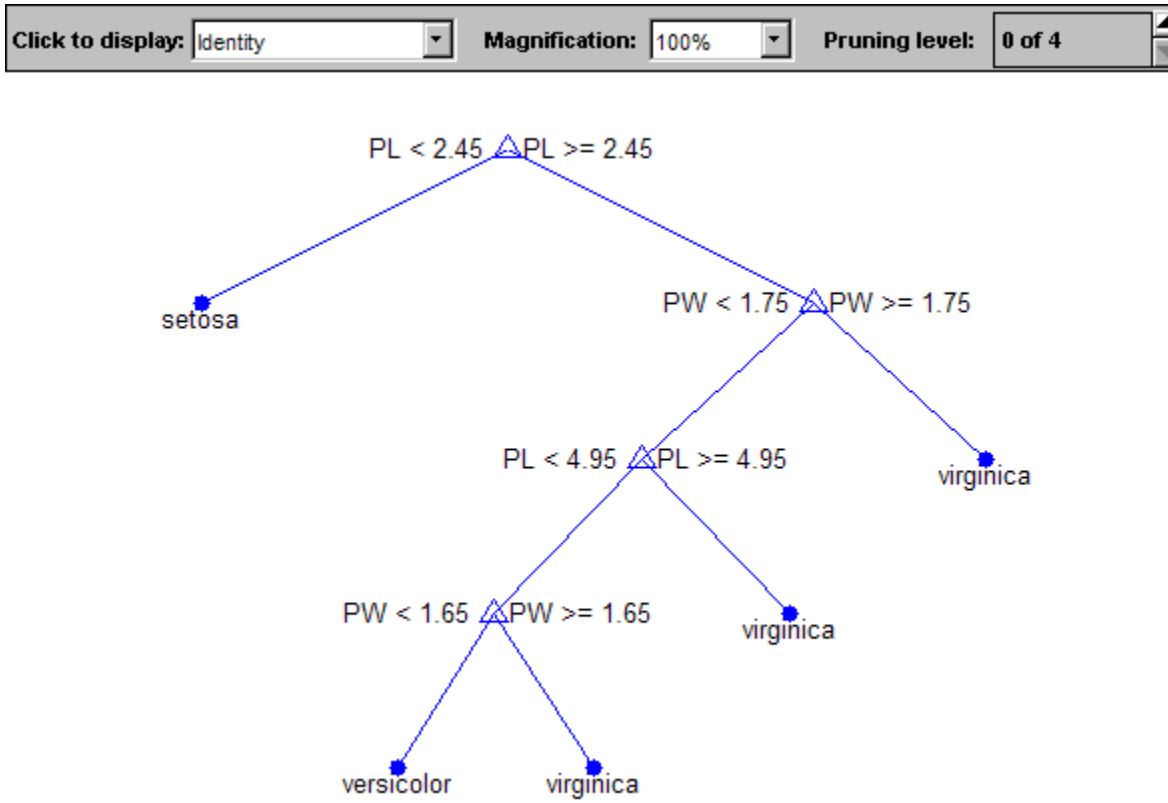
`P = classcount(t,nodes)` takes a vector `nodes` of node numbers and returns the class counts for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
```

```
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
P = classcount(t)
P =
    50    50    50
    50     0     0
     0    50    50
```

```
     0    49     5
     0     1    45
     0    47     1
     0     2     4
     0    47     0
     0     0     1
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes`

ClassificationBaggedEnsemble class

Classification ensemble grown by resampling

Description

`ClassificationBaggedEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners.

Construction

`ens = fitensemble(X,Y,'bag',nlearn,learners,'type','classification')` creates a bagged classification ensemble. For syntax details, see the `fitensemble` reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

String describing how ens combines weak learner weights, either `'WeightedSum'` or `'WeightedAverage'`.

`FitInfo`

Numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

FResample

Numeric scalar between `0` and `1`. `FResample` is the fraction of training data `fitensemble` resampled at random for every weak learner when constructing the ensemble.

Method

String describing the method that creates ens.

ModelParameters

Parameters used in training ens.

NumTrained

Number of trained weak learners in ens, a scalar.

PredictorNames

Cell array of names for the predictor variables, in the order in which they appear in `X`.

ReasonForTermination

String describing the reason `fitensemble` stopped adding weak learners to the ensemble.

Replace

Logical value indicating if the ensemble was trained with replacement (`true`) or without replacement (`false`).

ResponseName

String with the name of the response variable `Y`.

ScoreTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `fitctree`.

Add or change a `ScoreTransform` function using dot notation:

```
ens.ScoreTransform = 'function'
```

or

```
ens.ScoreTransform = @function
```

`Trained`

Trained learners, a cell array of compact classification models.

`TrainedWeights`

Numeric vector of trained weights for the weak learners in ens. `TrainedWeights` has `T` elements, where `T` is the number of weak learners in learners.

`UseObsForLearner`

Logical matrix of size `N`-by-`NumTrained`, where `N` is the number of observations in the training data and `NumTrained` is the number of trained weak learners. `UseObsForLearner(I,J)` is `true` if observation `I` was used for training learner `J`, and is `false` otherwise.

`W`

Scaled weights, a vector with length `n`, the number of rows in X. The sum of the elements of `W` is `1`.

`X`

Matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A categorical array, cell array of strings, character array, logical vector, or a numeric vector with the same number of rows as `X`. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

oobEdge	Out-of-bag classification edge

oobLoss	Out-of-bag classification error
oobMargin	Out-of-bag classification margins
oobPredict	Predict out-of-bag response of ensemble

Inherited Methods

compact	Compact classification ensemble
crossval	Cross validate ensemble
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict ensemble response by resubstitution
resume	Resume training ensemble
compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge
loss	Classification error
margin	Classification margins

predict	Predict classification
predictorImportance	Estimates of predictor importance
removeLearners	Remove members of compact classification ensemble

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a bagged ensemble for the `ionosphere` data, and examine its resubstitution loss:

```
load ionosphere
rng(0,'twister') % for reproducibility
ens = fitensemble(X,Y,'bag',100,'Tree',...
    'type','classification');
L = resubLoss(ens)

L =
     0
```

The ensemble does a perfect job classifying its training data.

See Also

`ClassificationEnsemble` | `fitensemble` | `fitctree`

How To

- “Ensemble Methods” on page 16-68

ClassificationECOC class

Superclasses: CompactClassificationECOC

Multiclass model for support vector machines or other classifiers

Description

`ClassificationECOC` is an error-correcting output codes (ECOC) classifier for multiclass learning by reduction to multiple, binary classifiers such as support vector machines (SVMs). Train a `ClassificationECOC` classifier using `fitcecoc` and the training data.

Trained `ClassificationECOC` classifiers store the training data, parameter values, prior probabilities, and coding matrices. You can use these classifiers to:

- Estimate resubstitution predictions. For details, see `resubPredict`.
- Predict labels or posterior probabilities for new data. For details, see `predict`.

Construction

`Mdl = fitcecoc(X,Y)` returns a trained ECOC multiclass model (`Mdl`) based on the input variables (also known as predictors, features, or attributes) X and output variables (also known as responses or class labels) Y. By default, `fitcecoc` uses the one-versus-one encoding scheme to train multiple, binary support vector machine (SVM) classifiers. For details, see `fitcecoc`.

`Mdl = fitcecoc(X,Y,Name,Value)` returns a trained ECOC classifier with additional options specified by one or more `Name,Value` pair arguments. For name-value pair argument details, e.g., binary learner types or coding design options, see `fitcecoc`.

If you set one of the following five options, then `Mdl` is a `ClassificationPartitionedECOC` model: `'CrossVal'`, `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`. Otherwise, `Mdl` is a `ClassificationECOC` classifier.

Input Arguments

X — Predictor data

matrix of numeric values

Predictor data to which the ECOC classifier is trained, specified as a matrix of numeric values.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one predictor.

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to standardize the predictor variables using the `Standardize` name-value pair argument.

To specify the names of the predictors in the order of their appearance in `X`, use the `PredictorNames` name-value pair argument.

Data Types: `double` | `single`

Y — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels to which the ECOC classifier is trained, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to specify the order of the classes using the `ClassNames` name-value pair argument.

To specify the response variable name, use the `ResponseName` name-value pair argument.

Note: The software treats `NaN`, empty strings (`''`), and `<undefined>` elements as missing data. The software removes rows of `X` corresponding to missing values in `Y`. However, the treatment of missing values in `X` varies among binary learners. For details,

see the training functions for your binary learners: `fitcdiscr`, `fitcknn`, `fitcnb`, `fitcsvm`, `fitctree`, or `fitensemble`. Removing observations decreases the effective training or cross-validation sample size.

Properties

`BinaryLearners` — Trained binary learners

cell vector of model objects

Trained binary learners, specified as a cell vector of model objects. `BinaryLearners` has as many elements as classes in Y.

`BinaryLearner{j}` was trained by the software to solve the binary problem specified by CodingMatrix`(:,j)`. For example, for multiclass learning using SVM learners, each element of `BinaryLearners` is a `CompactClassificationSVM` classifier.

Data Types: `cell`

`BinaryLoss` — Binary learner loss function

string

Binary learner loss function, specified as a string.

If you train using binary learners that use different loss functions, then the software sets `BinaryLoss` to `'hamming'`. To potentially increase accuracy, set a different binary loss function than this default during prediction or loss computation using the `BinaryLoss` name-value pair argument of `predict` or `loss`.

Data Types: `char`

`BinaryY` — Binary learner class labels

numeric matrix

Binary learner class labels, specified as a numeric matrix. `BinaryY` is a NumObservations-by-L matrix, where L is the number of binary learners (`size(`CodingMatrix`,2)`).

Elements of `BinaryY` are `-1`, `0`, or `1`, and the value corresponds to a dichotomous class assignment. This table describes how learner `j` assigns observation `k` to a dichotomous class corresponding to the value of `BinaryY(k,j)`.

Value	Dichotomous Class Assignment
-1	Negative class
0	Before training, learner j removes observations in class i from the data set.
1	Positive class

Data Types: double

CategoricalPredictors — Categorical predictor indices

numeric vector

Categorical predictor indices, specified as a numeric vector. CategoricalPredictors contains indices 1 through p, where p is the number of columns of X (size(X,2)).

Data Types: single | double

ClassNames — Unique class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Unique class labels in the response data (Y), specified as a categorical or character array, logical or numeric vector, or cell array of strings. ClassNames has the same data type as Y.

CodingMatrix — Codes specifying class assignments

numeric matrix

Codes specifying class assignments for the binary learners, specified as a numeric matrix. CodingMatrix is a K-by-L matrix, where K is the number of classes and L is the number of binary learners.

Elements of CodingMatrix are -1, 0, or 1, and the value corresponds to a dichotomous class assignment. This table describes the meaning of CodingMatrix(i,j), that is, the class that learner j assigns to observations in class i.

Value	Dichotomous Class Assignment
-1	Negative class
0	Before training, learner j removes observations in class i from the data set.

Value	Dichotomous Class Assignment
1	Positive class

Data Types: `double` | `single` | `int8` | `int16` | `int32` | `int64`

`CodingName` — Coding design name
string

Coding design name, specified as a string. For more details, see “Coding Design” on page 22-324.

Data Types: `char`

`Cost` — Misclassification costs
square numeric matrix

Misclassification costs, specified as a square numeric matrix. `Cost` has K rows and columns, where K is the number of classes.

`Cost(i,j)` is the cost of misclassifying a point into class `j` if its true class is `i`. The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames.

`fitcecoc` incorporates misclassification costs differently among different types of binary learners.

This property is read-only.

Data Types: `double`

`LearnerWeights` — Binary learner weights
numeric row vector

Binary learner weights, specified as a numeric row vector. `LeanerWeights` has length equal to the number of binary learners (`size(`CodingMatrix`,2)`).

`LearnerWeights(j)` is the sum of the observation weights that binary learner `j` used to train its classifier.

The software uses `LearnerWeights` to fit posterior probabilities by minimizing the Kullback-Leibler divergence.

Data Types: `double` | `single`

`ModelParameters` — Parameter values

object

Parameter values, e.g., the name-value pair argument values, used to train the ECOC classifier, specified as an object. `ModelParameters` does not contain estimated parameters.

Access properties of `ModelParameters` using dot notation. For example, list the templates containing parameters the binary learners using `SVMModel.ModelParameters.BinaryLearner`.

`NumObservations` — Number of observations

positive numeric scalar

Number of observations in the training data, specified as a positive numeric scalar.

Data Types: `double`

`PredictorNames` — Predictors names

cell array of strings

Predictors names in the order that they appear in X, specified as a cell array of strings containing the predictor names. `PredictorNames` has length equal to the number of columns in `X`.

Data Types: `cell`

`Prior` — Prior class probabilities

numeric vector

Prior class probabilities, specified as a numeric vector. `Prior` has as many elements as classes in Y, and the order of the elements corresponds to the elements of `ClassNames`.

`fitcecoc` incorporates misclassification costs differently among different types of binary learners.

This property is read only.

Data Types: `double`

`ResponseName` — Response variable name

string

Response variable name, specified as a string.

Data Types: `char`

`ScoreTransform` — Score transformation function

string | function handle

Score transformation function, specified as a string or function handle. `ScoreTransform` describes how the software transforms raw, predicted classification scores.

To change the score transformation function to, e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

  ```
  SVMModel.ScoreTransform = 'function';
  ```

  This table lists the supported, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  SVMModel.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Data Types: `char` | `function_handle`

`W` — Observation weights

numeric vector

Observation weights used to train the classifier, specified as a numeric vector. `W` has NumObervations elements.

The software normalizes the weights used for training so that `nansum(W)` is `1`.

Data Types: `single` | `double`

`X` — Unstandardized predictor data used to train the classifier

numeric matrix

Unstandardized predictor data used to train the classifier, specified as a numeric matrix. `X` is a NumObservations-by-*p* matrix, where *p* is the number of predictors.

Each row of `X` corresponds to one observation, and each column corresponds to one variable.

Data Types: `single` | `double`

`Y` — Observed class labels

categorical array | character array | logical vector | numeric vector | cell array of strings

Observed class labels used to train the classifier, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` has NumObservations elements, and is the same data type as the input argument Y of `fitcecoc`.

Each row of `Y` represents the observed classification of the corresponding row of `X`.

Methods

compact	Compact error-correcting output codes multiclass model
crossval	Cross-validated, error-correcting output code multiclass model

resubEdge	Classification edge for error-correcting output codes, multiclass models by resubstitution
resubLoss	Classification loss for error-correcting output codes, multiclass models by resubstitution
resubMargin	Classification margins for error-correcting output codes, multiclass models by resubstitution
resubPredict	Predict error-correcting output codes, multiclass model resubstitution responses

Inherited Methods

compareHoldout	Compare accuracies of two classification models using new data
discardSupportVectors	Discard support vectors of linear support vector machine binary learners
edge	Classification edge for error-correcting output code mutliclass classifiers
loss	Classification loss for error-correcting output code multiclass classifiers
margin	Classification margins for error-correcting output code multiclass classifiers
predict	Predict labels for error-correcting output code multiclass classifiers

Definitions

Error-Correcting Output Code Multiclass Model

An *error-correcting output code multiclass model* (ECOC) reduces the problem of classification with three or more classes to a set of binary classifiers.

ECOC classification requires a coding design, which determines the classes that the binary learners train on, and a decoding scheme, which determines how the results (predictions) of the binary classifiers are aggregated. Suppose that there are three classes, the coding design is one-versus-one, the decoding scheme uses loss *g*, and the learners are SVMs. To build this classification model, ECOC follows these steps.

1

A one-versus-one coding design is

	Learner 1	Learner 2	Learner 3
Class 1	1	1	0
Class 2	–1	0	1
Class 3	0	–1	–1

Learner 1 trains on observations having Class 1 and Class 2, and treats Class 1 as the positive class and Class 2 as the negative class. The other learners are trained similarly. Let M be the coding design matrix with elements m_{kl}, and s_l be the predicted classification score for the positive class of learner l.

2

A new observation is assigned to the class ($\hat{k}$) that minimizes the aggregation of the losses for the L binary learners. That is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{l=1}^{L} |m_{kl}| g(m_{kl}, s_l)}{\sum_{l=1}^{L} |m_{kl}|}.$$

ECOC models can improve classification accuracy, even compared to other multiclass models [2].

Coding Design

A *coding design* is a matrix where elements direct which classes are trained by each binary learner, that is, how the multiclass problem is reduced to a series of binary problems.

Each row of the coding design corresponds to a distinct class, and each column corresponds to a binary learner. In a ternary coding design (adopted by the software), for a particular column (or binary learner):

- Rows containing a 1 indicate to the binary learner to group all observations in the corresponding classes into a positive class.
- Rows containing a -1 indicate to the binary learner to group all observations in the corresponding classes into a negative class.
- Rows containing a 0 indicate to the binary learner to ignore all observations in the corresponding classes.

Coding matrices with large, minimal, pair-wise row distances based on the Hamming measure are desirable. For details on the pair-wise row distance measure, see "Random Coding Design Matrices" on page 22-1542 and [4].

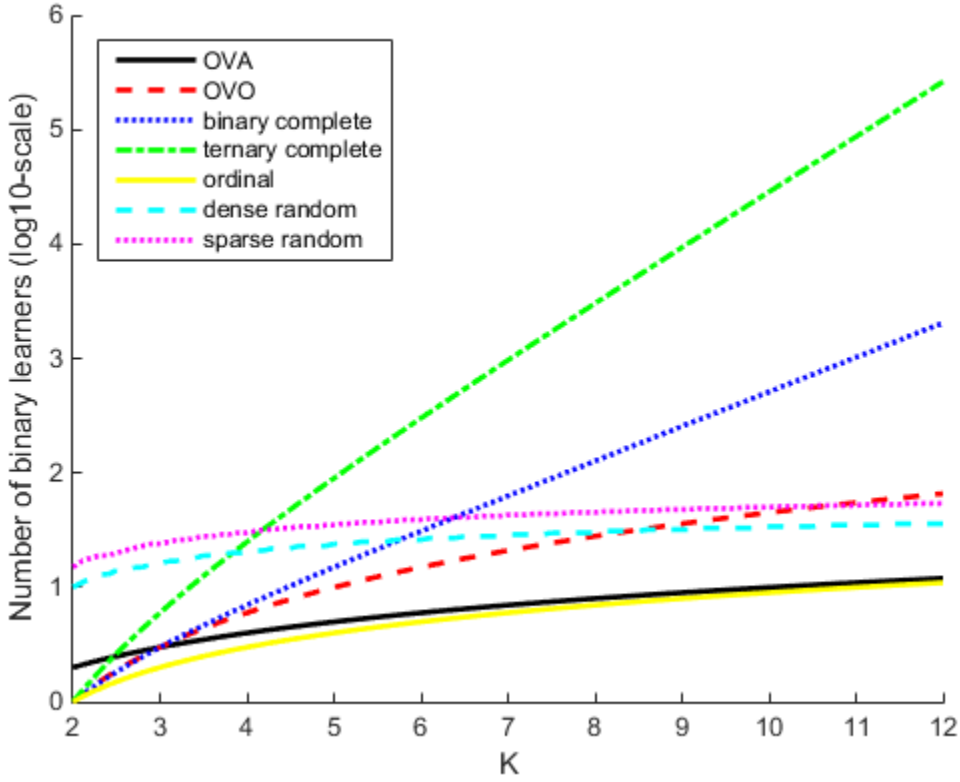
This table describes popular coding designs. For the example, suppose K (the number of distinct classes) is 3.

Coding Design	Description	Number of Learners	Minimal Pair-Wise Row Distance
one-versus-all (OVA)	For each binary learner, one class is positive and the rest are negative. This design exhausts all combinations of positive class assignments.	K	2
one-versus-one (OVO)	For each binary learner, one class is positive, another is negative, and the rest are ignored. This design exhausts	$K(K-1)/2$	1

Coding Design	Description	Number of Learners	Minimal Pair-Wise Row Distance
	all combinations of class pair assignments.		
binary complete	This design partitions the classes into all binary combinations, and does not ignore any classes. That is, all class assignments are `-1` and `1` with at least one positive and negative class in the assignment for each binary learner.	$2^{K-1}-1$	2^{K-2}
ternary complete	This design partitions the classes into all ternary combinations. That is, all class assignments are `0`, `-1`, and `1` with at least one positive and negative class in the assignment for each binary learner.	$(3^K-2^{K+1}+1)/2$	3^{K-2}
ordinal	For the first binary learner, the first class is negative, and the rest positive. For the second binary learner, the first two classes are negative, and the rest positive, and so on.	$K-1$	1

Coding Design	Description	Number of Learners	Minimal Pair-Wise Row Distance
dense random	For each binary learner, the software randomly assigns classes into positive or negative classes, with at least one of each type. For more details, see "Random Coding Design Matrices" on page 22-1542.	Random, but approximately 10 $\log_2 K$	Variable
sparse random	For each binary learner, the software randomly assigns classes as positive or negative with probability 0.25 for each, and ignores classes with probability 0.5. For more details, see "Random Coding Design Matrices" on page 22-1542.	Random, but approximately 15 $\log_2 K$	Variable

This plot compares the number of binary learners for the coding designs with increasing K.



Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Train a Multiclass Model Using SVM Learners

Train an error-correcting output codes (ECOC) multiclass model using support vector machine (SVM) binary learners.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

Train an ECOC multiclass model using the default options.

```
Mdl = fitcecoc(X,Y)
```

```
Mdl =

  ClassificationECOC
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
    BinaryLearners: {3x1 cell}
        CodingName: 'onevsone'
```

`Mdl` is a `ClassificationECOC` model. By default, `fitcecoc` uses SVM binary learners, and uses a one-versus-one coding design. You can access `Mdl` properties using dot notation.

Display the coding design matrix.

```
Mdl.ClassNames
CodingMat = Mdl.CodingMatrix
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


CodingMat =

     1     1     0
    -1     0     1
```

```
     0    -1    -1
```

A one-versus-one coding design on three classes yields three binary learners. Columns of `CodingMat` correspond to learners and rows correspond to classes. The class order corresponds to the order in `Mdl.ClassNames`. For example, `CodingMat(:,1)` is `[1; -1; 0]`, and indicates that the software trains the first SVM binary learner using all observations classified as `'setosa'` and `'versicolor'`. Since `'setosa'` corresponds to `1`, it is the positive class, and since `'versicolor'` corresponds to `-1`, it is the negative class.

You can access each binary learner using cell indexing and dot notation.

```
Mdl.BinaryLearners{1}                % The first binary learner
Mdl.BinaryLearners{1}.SupportVectors % Support vector indices
```

```
ans =

  classreg.learning.classif.CompactClassificationSVM
      PredictorNames: {'x1'  'x2'  'x3'  'x4'}
        ResponseName: 'Y'
          ClassNames: [-1 1]
      ScoreTransform: 'none'
                Beta: [4x1 double]
                Bias: 1.4505
    KernelParameters: [1x1 struct]



ans =

     []
```

Compute the in-sample classification error.

```
isLoss = resubLoss(Mdl)
```

```
isLoss =

    0.0067
```

The classification error is small, but the classifier might have been overfit. You can cross validate the classifier using `crossval`.

Inspect Binary Leaner Properties of ECOC Classifiers

You can access properties of binary learners, such as estimated parameters, using dot notation.

Load Fisher's iris data set. Use the petal dimensions as predictors.

```
load fisheriris
X = meas(:,3:4);
Y = species;
```

Train an ECOC classifier using the SVM binary learners (SVM) and the default coding design (one-versus-one). Specify to standardize the predictors, and to use the default linear kernel.

```
t = templateSVM('Standardize',1,'SaveSupportVectors',true);
predictorNames = {'petalLength','petalWidth'};
responseName = 'irisSpecies';
classNames = {'setosa','versicolor','virginica'}; % Specify class order
Mdl = fitcecoc(X,Y,'Learners',t,'ResponseName',responseName,...
    'PredictorNames',predictorNames,'ClassNames',classNames)
```

`t` is a template object that contains options for SVM classification. All properties are empty (`[ ]`), except for `Method`, `StandardizeData`, and `Type`. `fitcecoc` uses the default values of the empty properties. `Mdl` is a `ClassificationECOC` classifier. You can access its properties using dot notation.

Display the class names and coding design matrix.

```
Mdl.ClassNames
Mdl.CodingMatrix
L = size(Mdl.CodingMatrix,2); % Number of SVMs
```

The columns correspond to SVM binary learners, and the rows to the distinct classes. The row order corresponds to the order of the `ClassNames` property of `Mdl`. For each column:

- A `1` indicates that `fitcecoc` trained the SVM using observations in the corresponding class as members of the positive group.
- A `-1` indicates that `fitcecoc` trained the SVM using observations in the corresponding class as members of the negative group.
- A `0` indicates that the SVM did not use observations in the corresponding class.

For example, `fitcecoc` assigns all observations to `'setosa'` or `'versicolor'`, but not `'virginica'` in the first SVM.

You can access properties of the SVMs using cell subscripting and dot notation. Store the standardized support vectors of each SVM. Unstandardize the support vectors.

```
sv = cell(L,1); % Preallocate for support vector indices
for j = 1:L;
    SVM = Mdl.BinaryLearners{j};
    sv{j} = SVM.SupportVectors;
    sv{j} = bsxfun(@plus,bsxfun(@times,sv{j},SVM.Sigma),SVM.Mu);
end
```

`sv` is a cell array of matrices containing the unstandardized support vectors for the SVMs.

Plot the data, and identify the support vectors.

```
figure;
h = zeros(3 + L,1); % Preallocate for handles
h(1:3) = gscatter(X(:,1),X(:,2),Y);
hold on;
markers = {'ko','ro','bo'};
for j = 1:L;
    svs = sv{j};
    h(j + 3) = plot(svs(:,1),svs(:,2),markers{j},...
        'MarkerSize',10 + (j - 1)*3);
end
title 'Fisher''s Iris -- ECOC Support Vectors';
xlabel(predictorNames{1});
ylabel(predictorNames{2});
legend(h,[classNames,{'Support vectors - SVM 1',...
    'Support vectors - SVM 2','Support vectors - SVM 3'}],...
    'Location','Best')
hold off
```

You can pass `Mdl` to:

- `predict` to classify new observations
- `resubLoss` to estimate the in-sample classification error
- `crossval` to perform 10-fold cross validation.

Cross Validate an ECOC Classifier

Train a one-versus-one ECOC classifier using binary SVM learners.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
rng(1); % For reproducibility
```

Create an SVM template. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1)
```

```
t =

Fit template for classification SVM.

                    Alpha: [0x1 double]
             BoxConstraint: []
                 CacheSize: []
             CachingMethod: ''
    DeltaGradientTolerance: []
              GapTolerance: []
              KKTTolerance: []
            IterationLimit: []
            KernelFunction: ''
               KernelScale: []
              KernelOffset: []
     KernelPolynomialOrder: []
                 NumPrint: []
                       Nu: []
          OutlierFraction: []
          ShrinkagePeriod: []
                   Solver: ''
          StandardizeData: 1
       SaveSupportVectors: []
           VerbosityLevel: []
                   Method: 'SVM'
                     Type: 'classification'
```

`t` is an SVM template. All of its properties are empty, except for `StandardizeData`, `Method`, and `Type`. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier. It is good practice to specify the class order.

```
Mdl = fitcecoc(X,Y,'Learners',t,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationECOC` classifier. You can access its properties using dot notation.

Cross validate `Mdl` using 10-fold cross validation.

```
CVMdl = crossval(Mdl);
```

`CVMdl` is a `ClassificationPartitionedECOC` cross-validated ECOC classifier.

Estimate the generalization error.

```
oosLoss = kfoldLoss(CVMdl)
```

```
oosLoss =

    0.0400
```

The out-of-sample classification error is 4%, which indicates that the ECOC classifier generalizes fairly well.

Algorithms

Random Coding Design Matrices

For a given number of classes, e.g., K, the software generates random coding design matrices as follows.

1. The software generates one of the following:
   a. Dense random — The software sets each element of the K-by-L_d coding design matrix with a 1 or a -1 with equal probability, where $L_d \approx \lceil 10 \log_2 K \rceil$.
   b. Sparse random — The software sets each element of the K-by-L_s coding design matrix with a 1, with probability 0.25, a -1 with probability 0.25, and a 0 with probability 0.5, where $L_s \approx \lceil 15 \log_2 K \rceil$.

2 If a column does not contain at least one 1 and at least one -1, then the software removes that column.

3 For distinct columns u and v, if $u = v$ or $u \neq -v$, then the software removes v from the coding design matrix.

The software randomly generates 10,000 matrices by default, and retains the matrix with the largest, minimal pair-wise row distance based on the Hamming measure ([4]) given by

$$\Delta(k_1,k_2) = 0.5\sum_{l=1}^{L}\left|m_{k_1 l}\right|\left|m_{k_2 l}\right|\left|m_{k_1 l} - m_{k_2 l}\right|,$$

where $m_{k_j l}$ is an element of coding design matrix j.

Support Vector Storage

For linear, SVM binary learners, and for efficiency, `fitcecoc` empties the properties `Alpha`, `SupportVectorLabels`, and `SupportVectors`. `fitcecoc` lists `Beta`, rather than `Alpha`, in the model display.

To store `Alpha`, `SupportVectorLabels`, and `SupportVectors`, pass a linear, SVM template that specifies storing support vectors to `fitcecoc`. For example, enter:

```
t = templateSVM('SaveSupportVectors','on')
Mdl = fitcecoc(X,Y,'Learners',t);
```

You can subsequently remove the support vectors and related values by passing the resulting `ClassificationECOC` model to `discardSupportVectors`.

References

[1] Fürnkranz, Johannes. “Round Robin Classification.” *J. Mach. Learn. Res.*, Vol. 2, 2002, pp. 721–747.

[2] Escalera, S., O. Pujol, and P. Radeva. “Separability of ternary codes for sparse designs of error-correcting output codes.” *Pattern Recog. Lett.*, Vol. 30, Issue 3, 2009, pp. 285–297.

Alternatives

You can use these alternative algorithms to train a multiclass model:

- Classification ensembles; see `fitensemble` and `ClassificationEnsemble`
- Classification trees; see `fitctree` and `ClassificationTree`
- Discriminant analysis classifiers; see `fitcdiscr` and `ClassificationDiscriminant`
- *k*-nearest neighbor classifiers; see `fitcknn` and `ClassificationKNN`
- Naive Bayes classifiers; see `fitcnb` and `ClassificationNaiveBayes`

See Also

`ClassificationDiscriminant` | `ClassificationEnsemble` | `ClassificationKNN` | `ClassificationNaiveBayes` | `ClassificationPartitonedECOC` | `ClassificationTree` | `CompactClassificationECOC` | `fitcdiscr` | `fitcecoc` | `fitcknn` | `fitcnb` | `fitcsvm` | `fitctree` | `fitensemble`

ClassificationDiscriminant class

Superclasses: CompactClassificationDiscriminant

Discriminant analysis classification

Description

A `ClassificationDiscriminant` object encapsulates a discriminant analysis classifier, which is a Gaussian mixture model for data generation. A `ClassificationDiscriminant` object can predict responses for new data using the `predict` method. The object contains the data used for training, so can compute resubstitution predictions.

Construction

`obj = fitcdiscr(x,y)` creates a discriminant classification object based on the input variables (also known as predictors, features, or attributes) x and output (response) y. For syntax details, see `fitcdiscr`.

`obj = fitcdiscr(x,y,Name,Value)` creates a classifier with additional options specified by one or more Name,Value pair arguments. If you use one of the following five options, `obj` is of class `ClassificationPartitionedModel`: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. Otherwise, `obj` is of class `ClassificationDiscriminant`.

Input Arguments

x

Matrix of numeric predictor values. Each column of x represents one variable, and each row represents one observation.

`NaN` values in x are considered missing values. Observations with missing values for x are not used in the fit.

`y`

A categorical array, cell array of strings, character array, logical vector, or a numeric vector with the same number of rows as `x`. Each row of y represents the classification of the corresponding row of x. `NaN` values in y are considered missing values. Observations with missing values for y are not used in the fit.

Properties

`BetweenSigma`

`p`-by-`p` matrix, the between-class covariance, where `p` is the number of predictors.

`CategoricalPredictors`

List of categorical predictors, which is always empty (`[ ]`) for SVM and discriminant analysis classifiers.

`ClassNames`

List of the elements in the training data `Y` with duplicates removed. `ClassNames` can be a categorical array, cell array of strings, character array, logical vector, or a numeric vector. `ClassNames` has the same data type as the data in the argument `Y`.

`Coeffs`

`k`-by-`k` structure of coefficient matrices, where `k` is the number of classes. `Coeffs(i,j)` contains coefficients of the linear or quadratic boundaries between classes `i` and `j`. Fields in `Coeffs(i,j)`:

- DiscrimType
- `Class1` — ClassNames`(i)`
- `Class2` — ClassNames`(j)`
- `Const` — A scalar
- `Linear` — A vector with `p` components, where `p` is the number of columns in `X`
- `Quadratic` — `p`-by-`p` matrix, exists for quadratic DiscrimType

The equation of the boundary between class `i` and class `j` is

`Const + Linear * x + x' * Quadratic * x = 0`,

where `x` is a column vector of length `p`.

If `fitcdiscr` had the `FillCoeffs` name-value pair set to `'off'` when constructing the classifier, `Coeffs` is empty (`[]`).

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames. The number of rows and columns in `Cost` is the number of unique classes in the response.

Change a `Cost` matrix using dot notation: `obj.Cost = costMatrix`.

`Delta`

Value of the Delta threshold for a linear discriminant model, a nonnegative scalar. If a coefficient of `obj` has magnitude smaller than `Delta`, `obj` sets this coefficient to `0`, and so you can eliminate the corresponding predictor from the model. Set `Delta` to a higher value to eliminate more predictors.

`Delta` must be `0` for quadratic discriminant models.

Change `Delta` using dot notation: `obj.Delta = newDelta`.

`DeltaPredictor`

Row vector of length equal to the number of predictors in `obj`. If `DeltaPredictor(i) < Delta` then coefficient `i` of the model is `0`.

If `obj` is a quadratic discriminant model, all elements of `DeltaPredictor` are `0`.

`DiscrimType`

String specifying the discriminant type. One of:

- `'linear'`
- `'quadratic'`

- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

Change `DiscrimType` using dot notation: `obj.DiscrimType = newDiscrimType`.

You can change between linear types, or between quadratic types, but cannot change between linear and quadratic types.

`Gamma`

Value of the Gamma regularization parameter, a scalar from `0` to `1`. Change `Gamma` using dot notation: `obj.Gamma = newGamma`.

- If you set `1` for linear discriminant, the discriminant sets its type to `'diagLinear'`.
- If you set a value between `MinGamma` and `1` for linear discriminant, the discriminant sets its type to `'linear'`.
- You cannot set values below the value of the `MinGamma` property.
- For quadratic discriminant, you can set either `0` (for `DiscrimType 'quadratic'`) or `1` (for `DiscrimType 'diagQuadratic'`).

`LogDetSigma`

Logarithm of the determinant of the within-class covariance matrix. The type of `LogDetSigma` depends on the discriminant type:

- Scalar for linear discriminant analysis
- Vector of length `K` for quadratic discriminant analysis, where `K` is the number of classes

`MinGamma`

Nonnegative scalar, the minimal value of the Gamma parameter so that the correlation matrix is invertible. If the correlation matrix is not singular, `MinGamma` is `0`.

`ModelParameters`

Parameters used in training obj.

Mu

Class means, specified as a K-by-p matrix of scalar values class means of size. K is the number of classes, and p is the number of predictors. Each row of Mu represents the mean of the multivariate normal distribution of the corresponding class. The class indices are in the ClassNames attribute.

NumObservations

Number of observations in the training data, a numeric scalar. NumObservations can be less than the number of rows of input data X when there are missing values in X or response Y.

PredictorNames

Cell array of names for the predictor variables, in the order in which they appear in the training data X.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of Prior corresponds to the order of the classes in ClassNames.

Add or change a Prior vector using dot notation: obj.Prior = priorVector.

ResponseName

String describing the response variable Y.

ScoreTransform

Function handle for transforming scores, or string representing a built-in transformation function. 'none' means no transformation; equivalently, 'none' means @(x)x. For a list of built-in transformation functions and the syntax of custom transformation functions, see fitcdiscr.

Implement dot notation to add or change a ScoreTransform function using one of the following:

- cobj.ScoreTransform = '*function*'
- cobj.ScoreTransform = @*function*

`Sigma`

Within-class covariance matrix or matrices. The dimensions depend on DiscrimType:

- `'linear'` (default) — Matrix of size `p`-by-`p`, where `p` is the number of predictors
- `'quadratic'` — Array of size `p`-by-`p`-by-`K`, where `K` is the number of classes
- `'diagLinear'` — Row vector of length `p`
- `'diagQuadratic'` — Array of size `1`-by-`p`-by-`K`
- `'pseudoLinear'` — Matrix of size `p`-by-`p`
- `'pseudoQuadratic'` — Array of size `p`-by-`p`-by-`K`

`W`

Scaled weights, a vector with length `n`, the number of rows in `X`.

`X`

Matrix of predictor values. Each column of `X` represents one predictor (variable), and each row represents one observation.

`Xcentered`

`X` data with class means subtracted. If `Y(i)` is of class `j`, `Xcentered(i,:)` = `X(i,:)` – `Mu(j,:)`,

where Mu is the class mean property.

`Y`

A categorical array, cell array of strings, character array, logical vector, or a numeric vector with the same number of rows as `X`. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

compact

Compact discriminant analysis classifier

crossval	Cross-validated discriminant analysis classifier
cvshrink	Cross-validate regularization of linear discriminant
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict resubstitution response of classifier

Inherited Methods

compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge
logP	Log unconditional probability density for discriminant analysis classifier
loss	Classification error
mahal	Mahalanobis distance to class means
margin	Classification margins
nLinearCoeffs	Number of nonzero linear coefficients
predict	Predict classification

Definitions

Discriminant Classification

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. That is, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class, only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \arg\min_{y=1,\ldots,K} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

For details, see “How the predict Method Classifies” on page 15-6.

Regularization

Regularization is the process of finding a small set of predictors that yield an effective predictive model. For linear discriminant analysis, there are two parameters, γ and δ, that control regularization as follows. `cvshrink` helps you select appropriate values of the parameters.

Let Σ represent the covariance matrix of the data X, and let $\hat{X}$ be the centered data (the data X minus the mean by class). Define

$$D = \mathrm{diag}\left(\hat{X}^T * \hat{X}\right).$$

The regularized covariance matrix $\tilde{\Sigma}$ is

$$\tilde{\Sigma} = (1-\gamma)\Sigma + \gamma D.$$

Whenever $\gamma \geq$ `MinGamma`, $\tilde{\Sigma}$ is nonsingular.

Let μ_k be the mean vector for those elements of X in class k, and let μ_0 be the global mean vector (the mean of the rows of X). Let C be the correlation matrix of the data X, and let $\tilde{C}$ be the regularized correlation matrix:

$$\tilde{C} = (1-\gamma)C + \gamma I,$$

where I is the identity matrix.

The linear term in the regularized discriminant analysis classifier for a data point x is

$$(x-\mu_0)^T \tilde{\Sigma}^{-1}(\mu_k - \mu_0) = \left[(x-\mu_0)^T D^{-1/2}\right]\left[\tilde{C}^{-1}D^{-1/2}(\mu_k-\mu_0)\right].$$

The parameter δ enters into this equation as a threshold on the final term in square brackets. Each component of the vector $\left[\tilde{C}^{-1}D^{-1/2}(\mu_k-\mu_0)\right]$ is set to zero if it is smaller in magnitude than the threshold δ. Therefore, for class k, if component j is thresholded to zero, component j of x does not enter into the evaluation of the posterior probability.

The `DeltaPredictor` property is a vector related to this threshold. When $\delta \geq$ `DeltaPredictor(i)`, all classes k have

$$\left|\tilde{C}^{-1}D^{-1/2}(\mu_k-\mu_0)\right| \leq \delta.$$

Therefore, when $\delta \geq$ `DeltaPredictor(i)`, the regularized classifier does not use predictor `i`.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Create a discriminant analysis classifier for the Fisher iris data:

```
load fisheriris
obj = fitcdiscr(meas,species)

obj =
ClassificationDiscriminant:
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
     NumObservations: 150
       DiscrimType: 'linear'
                Mu: [3x4 double]
            Coeffs: [3x3 struct]
```

References

[1] Guo, Y., T. Hastie, and R. Tibshirani. *Regularized linear discriminant analysis and its application in microarrays.* Biostatistics, Vol. 8, No. 1, pp. 86–100, 2007.

See Also

`CompactClassificationDiscriminant` | `fitcdiscr`

How To

- “Discriminant Analysis” on page 15-3

ClassificationEnsemble class

Superclasses: CompactClassificationEnsemble

Ensemble classifier

Description

`ClassificationEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners. It also stores data used for training and can compute resubstitution predictions. It can resume training if desired.

Construction

`ens = fitensemble(X,Y,method,nlearn,learners)` returns an ensemble model that can predict responses to data. The ensemble consists of models listed in learners. For more information on the syntax, see the `fitensemble` function reference page.

`ens = fitensemble(X,Y,method,nlearn,learners,Name,Value)` returns an ensemble model with additional options specified by one or more Name,Value pair arguments. For more information on the syntax, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`ClassNames`

List of the elements in Y with duplicates removed. `ClassNames` can be a numeric vector, categorical vector, logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument Y.

`CombineWeights`

String describing how ens combines weak learner weights, either `'WeightedSum'` or `'WeightedAverage'`.

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames. The number of rows and columns in `Cost` is the number of unique classes in the response. This property is read-only.

`FitInfo`

Numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

`LearnerNames`

Cell array of strings with names of weak learners in the ensemble. The name of each learner appears just once. For example, if you have an ensemble of 100 trees, `LearnerNames` is `{'Tree'}`.

`Method`

String describing the method that creates ens.

`ModelParameters`

Parameters used in training ens.

`NumObservations`

Numeric scalar containing the number of observations in the training data.

`NumTrained`

Number of trained weak learners in ens, a scalar.

PredictorNames

Cell array of names for the predictor variables, in the order in which they appear in `X`.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames. The number of elements of `Prior` is the number of unique classes in the response. This property is read-only.

ReasonForTermination

String describing the reason `fitensemble` stopped adding weak learners to the ensemble.

ResponseName

String with the name of the response variable `Y`.

ScoreTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `fitctree`.

Add or change a `ScoreTransform` function using dot notation:

```
ens.ScoreTransform = 'function'
```

or

```
ens.ScoreTransform = @function
```

Trained

Trained learners, a cell array of compact classification models.

TrainedWeights

Numeric vector of trained weights for the weak learners in ens. `TrainedWeights` has `T` elements, where `T` is the number of weak learners in learners.

`UsePredForLearner`

Logical matrix of size `P`-by-`NumTrained`, where `P` is the number of predictors (columns) in the training data `X`. `UsePredForLearner(i,j)` is `true` when learner `j` uses predictor `i`, and is `false` otherwise. For each learner, the predictors have the same order as the columns in the training data `X`.

If the ensemble is not of type `Subspace`, all entries in `UsePredForLearner` are `true`.

`W`

Scaled weights, a vector with length `n`, the number of rows in X. The sum of the elements of `W` is `1`.

`X`

Matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

`Y`

Numeric vector, categorical vector, logical vector, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

compact	Compact classification ensemble
crossval	Cross validate ensemble
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict ensemble response by resubstitution

resume	Resume training ensemble

Inherited Methods

compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge
loss	Classification error
margin	Classification margins
predict	Predict classification
predictorImportance	Estimates of predictor importance
removeLearners	Remove members of compact classification ensemble

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a boosted classification ensemble for the `ionosphere` data, using the `AdaBoostM1` method:

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree')
```

```
ens =
```

```
  classreg.learning.classif.ClassificationEnsemble
          PredictorNames: {1x34 cell}
            ResponseName: 'Y'
              ClassNames: {'b'  'g'}
          ScoreTransform: 'none'
         NumObservations: 351
              NumTrained: 100
                  Method: 'AdaBoostM1'
           LearnerNames: {'Tree'}
    ReasonForTermination: 'Terminated normally after comp...'
                 FitInfo: [100x1 double]
      FitInfoDescription: {2x1 cell}


  Properties, Methods
```

Predict the classification of the mean of `X`:

```
ypredict = predict(ens,mean(X))
```

```
ypredict =
    'g'
```

See Also

`RegressionEnsemble` | `ClassificationTree` | `fitensemble` | `CompactClassificationEnsemble`

ClassificationKNN class

k-nearest neighbor classification

Description

A nearest-neighbor classification object, where both distance metric ("nearest") and number of neighbors can be altered. The object classifies new observations using the `predict` method. The object contains the data used for training, so can compute resubstitution predictions.

Construction

`mdl = fitcknn(X,y)` creates a k-nearest neighbor classification model.

`mdl = fitcknn(X,y,Name,Value)` creates a classifier with additional options specified by one or more Name,Value pair arguments. For details, see `fitcknn`.

Input Arguments

`X` — Predictor values

numeric matrix

Predictor values, specified as a numeric matrix. Each column of X represents one variable, and each row represents one observation.

Data Types: `single` | `double`

`y` — Classification values

numeric vector | categorical vector | logical vector | character array | cell array of strings

Classification values, specified as a numeric vector, categorical vector, logical vector, character array, or cell array of strings, with the same number of rows as X. Each row of y represents the classification of the corresponding row of X.

Data Types: `single` | `double` | `cell` | `logical` | `char`

Properties

`BreakTies`

String specifying the method `predict` uses to break ties if multiple classes have the same smallest cost. By default, ties occur when multiple classes have the same number of nearest points among the `K` nearest neighbors.

- `'nearest'` — Use the class with the nearest neighbor among tied groups.
- `'random'` — Use a random tiebreaker among tied groups.
- `'smallest'` — Use the smallest index among tied groups.

`'BreakTies'` applies when `'IncludeTies'` is `false`.

Change `BreakTies` using dot notation: `mdl.BreakTies = newBreakTies`.

`CategoricalPredictors`

Specification of which predictors are categorical.

- `'all'` — All predictors are categorical.
- `[ ]` — No predictors are categorical.

`ClassNames`

List of elements in the training data Y with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables, logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument Y.

Change `ClassNames` using dot notation: `mdl.ClassNames = newClassNames`

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of

the classes in ClassNames. The number of rows and columns in `Cost` is the number of unique classes in the response.

Change a `Cost` matrix using dot notation: `obj.Cost = costMatrix`.

`Distance`

String or function handle specifying the distance metric. The allowable strings depend on the `NSMethod` parameter, which you set in `fitcknn`, and which exists as a field in `ModelParameters`.

NSMethod	Distance Metric Names
`exhaustive`	Any distance metric of `ExhaustiveSearcher`
`kdtree`	`'cityblock'`, `'chebychev'`, `'euclidean'`, or `'minkowski'`

For definitions, see “Distance Metrics”.

The distance metrics of `ExhaustiveSearcher`:

Value	Description
`'cityblock'`	City block distance.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values).
`'cosine'`	One minus the cosine of the included angle between observations (treated as vectors).
`'euclidean'`	Euclidean distance.
`'hamming'`	Hamming distance, percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of `X`, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair.
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'P'` name-value pair.

Value	Description
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between X and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from `X`, `S = nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair.
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@distfun`	Distance function handle. *`distfun`* has the form
	`function D2 = DISTFUN(ZI,ZJ)`
	`% calculation of  distance`
	`...`
	where
	• `ZI` is a `1`-by-`N` vector containing one row of X or Y.
	• `ZJ` is an `M2`-by-`N` matrix containing multiple rows of X or Y.
	• `D2` is an `M2`-by-`1` vector of distances, and `D2(k)` is the distance between observations `ZI` and `ZJ(J,:)`.

Change `Distance` using dot notation: `mdl.Distance = newDistance`.

If `NSMethod` is `kdtree`, you can use dot notation to change `Distance` only among the types `'cityblock'`, `'chebychev'`, `'euclidean'`, or `'minkowski'`.

`DistanceWeight`

String or function handle specifying the distance weighting function.

DistanceWeight	Meaning
`'equal'`	No weighting
`'inverse'`	Weight is 1/distance
`'inversesquared'`	Weight is $1/\text{distance}^2$
`@fcn`	*`fcn`* is a function that accepts a matrix of nonnegative distances, and returns a matrix the same size containing nonnegative distance weights. For example, `'inversesquared'` is equivalent to `@(d)d.^(-2)`.

Change `DistanceWeight` using dot notation: `mdl.DistanceWeight = newDistanceWeight`.

`DistParameter`

Additional parameter for the distance metric.

Distance Metric	Parameter
`'mahalanobis'`	Positive definite covariance matrix `C`.
`'minkowski'`	Minkowski distance exponent, a positive scalar.
`'seuclidean'`	Vector of positive scale values with length equal to the number of columns of `X`.

For values of the distance metric other than those in the table, `DistParameter` must be `[]`.

You can alter `DistParameter` using dot notation: `mdl.DistParameter = newDistParameter`. However, if `Distance` is `mahalanobis` or `seuclidean`, then you cannot alter `DistParameter`.

`IncludeTies`

Logical value indicating whether `predict` includes all the neighbors whose distance values are equal to the `K`th smallest distance. If `IncludeTies` is `true`, `predict` includes all these neighbors. Otherwise, `predict` uses exactly `K` neighbors (see `'BreakTies'`).

Change `IncludeTies` using dot notation: `mdl.IncludeTies = newIncludeTies`.

`ModelParameters`

Parameters used in training `mdl`.

`Mu`

Numeric vector of predictor means with length `numel(`PredictorNames`)`.

If you did not standardize `mdl` when you trained it using `fitcknn`, then `Mu` is empty (`[]`).

`NumNeighbors`

Positive integer specifying the number of nearest neighbors in `X` to find for classifying each point when predicting. Change `NumNeighbors` using dot notation: `mdl.NumNeighbors = newNumNeighbors`.

`NumObservations`

Number of observations used in training `mdl`. This can be less than the number of rows in the training data, because data rows containing `NaN` values are not part of the fit.

`PredictorNames`

Cell array of names for the predictor variables, in the order in which they appear in the training data `X`. Change `PredictorNames` using dot notation: `mdl.PredictorNames = newPredictorNames`.

`Prior`

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames.

Add or change a `Prior` vector using dot notation: `obj.Prior = priorVector`.

`ResponseName`

String describing the response variable Y. Change `ResponseName` using dot notation: `mdl.ResponseName = newResponseName`.

`Sigma`

Numeric vector of predictor standard deviations with length `numel(`PredictorNames`)`.

If you did not standardize `mdl` when you trained it using `fitcknn`, then `Sigma` is empty (`[]`).

`W`

Numeric vector of nonnegative weights with the same number of rows as `Y`. Each entry in `W` specifies the relative importance of the corresponding observation in `Y`.

`X`

Numeric matrix of unstandardized predictor values. Each column of `X` represents one predictor (variable), and each row represents one observation.

Y

A numeric vector, vector of categorical variables, logical vector, character array, or cell array of strings, with the same number of rows as X.

Y is of the same type as the passed-in Y data.

Methods

compareHoldout	Compare accuracies of two models using new data
crossval	Cross-validated *k*-nearest neighbor classifier
edge	Edge of *k*-nearest neighbor classifier
loss	Loss of *k*-nearest neighbor classifier
margin	Margin of *k*-nearest neighbor classifier
predict	Predict *k*-nearest neighbor classification
resubEdge	Edge of *k*-nearest neighbor classifier by resubstitution
resubLoss	Loss of *k*-nearest neighbor classifier by resubstitution
resubMargin	Margin of *k*-nearest neighbor classifier by resubstitution
resubPredict	Predict resubstitution response of *k*-nearest neighbor classifier

Definitions

Prediction

`ClassificationKNN` predicts the classification of a point `Xnew` using a procedure equivalent to this:

1. Find the `NumNeighbors` points in the training set `X` that are nearest to `Xnew`.
2. Find the `NumNeighbors` response values `Y` to those nearest points.
3. Assign the classification label `Ynew` that has smallest expected misclassification cost among the values in `Y`.

For details, see “Posterior Probability” on page 22-3654 and “Expected Cost” on page 22-3655 in the `predict` documentation.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Train a *k*-Nearest Neighbor Classifier

Construct a *k*-nearest neighbor classifier for Fisher's iris data, where *k*, the number of nearest neighbors in the predictors, is 5.

Load Fisher's iris data.

```
load fisheriris
X = meas;
Y = species;
```

`X` is a numeric matrix that contains four petal measurements for 150 irises. `Y` is a cell array of strings that contains the corresponding iris species.

Train a 5-nearest neighbors classifier. It is good practice to standardize noncategorical predictor data.

```
Mdl = fitcknn(X,Y,'NumNeighbors',5,'Standardize',1)


Mdl =

  ClassificationKNN
     PredictorNames: {'x1'  'x2'  'x3'  'x4'}
       ResponseName: 'Y'
         ClassNames: {'setosa'  'versicolor'  'virginica'}
     ScoreTransform: 'none'
    NumObservations: 150
           Distance: 'euclidean'
       NumNeighbors: 5
```

`Mdl` is a trained `ClassificationKNN` classifier, and some of its properties display in the Command Window.

To access the properties of `Mdl`, use dot notation.

```
Mdl.ClassNames
Mdl.Prior


ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

    0.3333    0.3333    0.3333
```

`Mdl.Prior` contains the class prior probabilities, which are settable using the name-value pair argument `'Prior'` in `fitcknn`. The order of the class prior probabilities corresponds to the order of the classes in `Mdl.ClassNames`. By default, the prior probabilities are the respective relative frequencies of the classes in the data.

You can also reset the prior probabilities after training. For example, set the prior probabilities to 0.5, 0.2, and 0.3 respectively.

```
Mdl.Prior = [0.5 0.2 0.3];
```

You can pass `Mdl` to, for example, predict (ClassificationKNN) to label new measurements, or crossval (ClassificationKNN) to cross validate the classifier.

- "Construct a KNN Classifier" on page 16-28
- "Examine the Quality of a KNN Classifier" on page 16-29
- "Predict Classification Based on a KNN Classifier" on page 16-30
- "Modify a KNN Classifier" on page 16-30

Alternatives

`knnsearch` finds the k-nearest neighbors of points. `rangesearch` finds all the points within a fixed distance. You can use these functions for classification, as shown in "Classify Query Data" on page 16-16. If you want to perform classification, `ClassificationKNN` can be more convenient, in that you can construct a classifier in one step and classify in other steps. Also, `ClassificationKNN` has cross-validation options.

See Also

`fitcknn` | `predict`

More About

- "Classification Using Nearest Neighbors" on page 16-8

ClassificationNaiveBayes class

Superclasses: CompactClassificationNaiveBayes

Naive Bayes classification

Description

`ClassificationNaiveBayes` is a naive Bayes classifier for multiclass learning. Use `fitcnb` and the training data to train a `ClassificationNaiveBayes` classifier.

Trained `ClassificationNaiveBayes` classifiers store the training data, parameter values, data distribution, and prior probabilities. You can use these classifiers to:

- Estimate resubstitution predictions. For details, see `resubPredict`.
- Predict labels or posterior probabilities for new data. For details, see `predict`.

Construction

`Mdl = fitcnb(X,Y)` returns a trained naive Bayes classifier (Mdl), based on the input variables X (also known as predictors, features, or attributes) and output variable Y (also known as responses or class labels) for multiclass classification. `Mdl` stores the training data.

Predict labels for new data by passing the data and `Mdl` to `predict`.

`Mdl = fitcnb(X,Y,Name,Value)` returns a trained naive Bayes classifier with additional options specified by one or more Name,Value pair arguments.

If you set one of the following five options, then `Mdl` is a `ClassificationPartitionedModel` model: `'CrossVal'`, `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`. Otherwise, `Mdl` is a `ClassificationNaiveBayes` classifier.

Input Arguments

X — Predictor data

matrix of numeric values

Predictor data to which the naive Bayes classifier is trained, specified as a matrix of numeric values.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature).

The length of `Y` and the number of rows of `X` must be equivalent.

Data Types: `double`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels to which the naive Bayes classifier is trained, specified as a categorical or character array, logical or numeric vector, or cell array of strings. Each element of `Y` defines the class membership of the corresponding row of `X`. `Y` supports K class levels.

If `Y` is a character array, then each row must correspond to one class label.

The length of `Y` and the number of rows of `X` must be equivalent.

Data Types: `cell` | `char` | `double` | `logical`

Note: The software treats `NaN`, empty string (`''`), and `<undefined>` elements as missing values.

- If `Y` contains missing values, then the software removes them and the corresponding rows of `X`.
- If `X` contains any rows composed entirely of missing values, then the software removes those rows and the corresponding elements of `Y`.
- If `X` contains missing values and you set `'Distribution','mn'`, then the software removes those rows of `X` and the corresponding elements of `Y`.
- If a predictor is not represented in a class, that is, if all of its values are `NaN` within a class, then the software returns an error.

Removing rows of `X` and corresponding elements of `Y` decreases the effective training or cross-validation sample size.

Properties

`CategoricalPredictors` — Categorical predictor indices

numeric vector

Categorical predictor indices, specified as a numeric vector.

Data Types: `double`

`CategoricalLevels` — Multivariate multinomial levels

cell vector of numeric vectors

Multivariate multinomial levels, specified as a cell vector of numeric vectors. `CategoricalLevels` has length equal to the number of predictors (`size(X,2)`).

The cells of `CategoricalLevels` correspond to predictors that you specified as `'mvmn'` (i.e., having a multivariate multinomial distribution) during training. Cells that do not correspond to a multivariate multinomial distribution are empty (`[]`).

If predictor *j* is multivariate multinomial, then `CategoricalLevels{`*j*`}` is a list of all distinct values of predictor *j* in the sample (`NaN`s removed from `unique(X(:,j))`).

Data Types: `cell`

`ClassNames` — Distinct class names

categorical array | character array | logical vector | numeric vector | cell array of strings

Distinct class names, specified as a categorical or character array, logical or numeric vector, or cell vector of strings.

`ClassNames` is the same data type as Y, and has as *K* elements or rows for character arrays.

`Cost` — Misclassification cost

square matrix

Misclassification cost, specified as a *K*-by-*K* square matrix.

The value of `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. The order of the rows and columns of `Cost` correspond to the order of the classes in `ClassNames`.

The value of `Cost` does not influence training. You can reset `Cost` after training `Mdl` using dot notation, e.g., `Mdl.Cost = [0 0.5; 1 0];`.

Data Types: `double` | `single`

`DistributionNames` — Predictor distributions

`'normal'` (default) | `'kernel'` | `'mn'` | `'mvmn'` | cell array of strings

Predictor distributions `fitcnb` uses to model the predictors, specified as a string or cell array of strings.

This table summarizes the available distributions.

Value	Description
`'kernel'`	Kernel smoothing density estimate.
`'mn'`	Multinomial bag-of-tokens model. Indicates that all predictors have this distribution.
`'mvmn'`	Multivariate multinomial distribution.
`'normal'`	Normal (Gaussian) distribution.

If `Distribution` is a 1-by-P cell array of strings, then the software models feature j using the distribution in element j of the cell array.

Data Types: `cell` | `char`

`DistributionParameters` — Distribution parameter estimates

cell array

Distribution parameter estimates, specified as a cell array. `DistributionParameters` is a K-by-P cell array, where cell (k,d) contains the distribution parameter estimates for instances of predictor d in class k. The order of the rows follows the order of the classes in the property ClassNames, and the order of the predictors follows the order of the columns of X.

If class k has no observations for predictor j, then `Distribution{`k`,`j`}` is empty (`[]`).

The elements of `DistributionParameters` depends on the distributions of the predictors. This table describes the values in `DistributionParameters{`k`,`j`}`.

Value	\Distribution of Predictor *j*
`kernel`	A `prob.KernelDistribution` model. Display properties using cell indexing and dot notation. For example, to display the estimated bandwidth of the kernel density for predictor 2 in the third class, use `Mdl.DistributionParameters{3,2}.BandWidth`.
`mn`	A scalar representing the probability that token *j* appears in class *k*. For details, see "Algorithms".
`mvmn`	A numeric vector containing the probabilities for each possible level of predictor *j* in class *k*. The software orders the probabilities by the sorted order of all unique levels of predictor *j* (stored in the property CategoricalLevels). For more details, see "Algorithms".
`normal`	A 2-by-1 numeric vector. The first element is the sample mean and the second element is the sample standard deviation.

`Kernel` — Kernel smoother types

`'normal'` (default) | `'box'` | `'epanechnikov'` | `'triangle'` | cell array of strings

Kernel smoother types, specified as a string or cell array of strings. `Kernel` has length equal to the number of predictors (`size(X,2)`). `Kernel{j}` corresponds to predictor *j*, and contains a string describing the type of kernel smoother. This table describes the supported kernel smoother types. Let $I\{u\}$ denote the indictor function.

Value	Kernel	Formula
`'box'`	Box (uniform)	$f(x) = 0.5I\{\lvert x\rvert \le 1\}$
`'epanechni`	Epanechnikov	$f(x) = 0.75\left(1 - x^2\right)I\{\lvert x\rvert \le 1\}$
`'normal'`	Gaussian	$f(x) = \frac{1}{\sqrt{2\pi}}\exp\left(-0.5x^2\right)$

Value	Kernel	Formula
`'triangle'`	Triangular	$f(x) = (1 - \lvert x \rvert) I\{\lvert x \rvert \le 1\}$

If a cell is empty ([ ]), then the software did not fit a kernel distribution to the corresponding predictor.

`ModelParameters` — Parameter values used to train

object

Parameter values used to train the classifier (such as the name-value pair argument values), specified as an object. This table summarizes the properties of `ModelParameters`. The properties correspond to the name-value pair argument values set for training the classifier.

Property	Purpose
`DistributionNames`	Data distribution or distributions. This is the same value as the property `DistributionNames`.
`Kernel`	Kernel smoother type. This is the same as the property `Kernel`.
`Method`	Training method. For naive Bayes, the value is `'NaiveBayes'`.
`Support`	Kernel-smoothing density support. This is the same as the property `Support`.
`Type`	Learning type. For classification, the value is `'classification'`.
`Width`	Kernel smoothing window width. This is the same as the property `Width`.

Access fields of `ModelParameters` using dot notation. For example, access the kernel support using `Mdl.ModelParameters.Support`.

`NumObservations` — Number of training observations

numeric scalar

Number of training observations, specified as a numeric scalar.

If X or Y contain missing values, then `NumObservations` might be less than the length of `Y`.

Data Types: `double`

`PredictorNames` — Predictor names
string

Predictor names, specified as a cell vector of strings. The order of the elements in `PredictorNames` corresponds to the order in X.

Data Types: `cell`

`Prior` — Class prior probabilities
numeric vector

Class prior probabilities, specified as a numeric row vector. `Prior` is a 1-by-*K* vector, and the order of its elements correspond to the elements of `ClassNames`.

`fitcnb` normalizes the prior probabilities you set using the name-value pair parameter `'Prior'` so that `sum(Prior) = 1`.

The value of `Prior` does not change the best-fitting model. Therefore, you can reset `Prior` after training `Mdl` using dot notation, e.g., `Mdl.Prior = [0.2 0.8];`.

Data Types: `double | single`

`ResponseName` — Response name
string

Response name, specified as a string.

Data Types: `char`

`ScoreTransform` — Classification score transformation function
function handle | string

Classification score transformation function, specified as a function handle or a string.

To change the score transformation function to e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

  ```
  Mdl.ScoreTransform = 'function';
  ```

  This table lists available, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  Mdl.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Data Types: `char` | `function_handle`

`Support` — Kernel smoother density support

cell vector

Kernel smoother density support, specified as a cell vector. `Support` has length equal to the number of predictors (`size(X,2)`). The cells represent the regions to apply the kernel density.

This table describes the supported options.

Value	Description
1-by-2 numeric row vector	For example, `[L,U]`, where `L` and `U` are the finite lower and upper bounds, respectively, for the density support.

Value	Description
`'positive'`	The density support is all positive real values.
`'unbounded'`	The density support is all real values.

If a cell is empty (`[]`), then the software did not fit a kernel distribution to the corresponding predictor.

`W` — Observation weights

numeric vector

Observation weights, specified as a numeric vector.

The length of `W` is `NumObservations`.

`fitcnb` normalizes the value you set for the name-value pair parameter `'Weights'` so that the weights within a particular class sum to the prior probability for that class.

Data Types: `double`

`Width` — Kernel smoother window width

numeric matrix

Kernel smoother window width, specified as a numeric matrix. `Width` is a K-by-P matrix, where K is the number of classes in the data, and P is the number of predictors (`size(X,2)`).

`Width(`k`,`j`)` is the kernel smoother window width for the kernel smoothing density of predictor j within class k. `NaN`s in column j indicate that the software did not fit predictor j using a kernel density.

`X` — Unstandardized predictor data

numeric matrix

Unstandardized predictor data, specified as a numeric matrix. `X` has `NumObservations` rows and P columns.

Each row of `X` corresponds to one observation, and each column corresponds to one variable.

The software excludes rows removed due to missing values from `X`.

Data Types: `double`

Y — Observed class labels

categorical array | character array | logical vector | numeric vector | cell array of strings

Observed class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` is the same data type as the input argument `Y` of `fitcnb`.

Each row of `Y` represents the observed classification of the corresponding row of `X`.

The software excludes elements removed due to missing values from `Y`.

Methods

compact	Compact naive Bayes classifier
crossval	Cross-validated naive Bayes classifier
resubEdge	Classification edge for naive Bayes classifiers by resubstitution
resubLoss	Classification loss for naive Bayes classifiers by resubstitution
resubMargin	Classification margins for naive Bayes classifiers by resubstitution
resubPredict	Predict naive Bayes classifier resubstitution response

Inherited Methods

compareHoldout	Compare accuracies of two classification models using new data

edge	Classification edge for naive Bayes classifiers
logP	Log unconditional probability density for naive Bayes classifier
loss	Classification error for naive Bayes classifier
margin	Classification margins for naive Bayes classifiers
predict	Predict classification for naive Bayes models

Definitions

Bag-of-Tokens Model

In the bag-of-tokens model, the value of predictor *j* is the nonnegative number of occurrences of token *j* in this observation. The number of categories (bins) in this multinomial model is the number of distinct tokens, that is, the number of predictors.

Naive Bayes

Naive Bayes is a classification algorithm that applies density estimation to the data.

The algorithm leverages Bayes theorem, and (naively) assumes that the predictors are conditionally independent, given the class. Though the assumption is usually violated in practice, naive Bayes classifiers tend to yield posterior distributions that are robust to biased class density estimates, particularly where the posterior is 0.5 (the decision boundary) [1].

Naive Bayes classifiers assign observations to the most probable class (in other words, the *maximum a posteriori* decision rule). Explicitly, the algorithm:

1 Estimates the densities of the predictors within each class.

2 Models posterior probabilities according to Bayes rule. That is, for all $k = 1,...,K$,

$$\hat{P}(Y = k \mid X_1,..,X_P) = \frac{\pi(Y = k)\prod_{j=1}^{P} P(X_j \mid Y = k)}{\sum_{k=1}^{K}\pi(Y = k)\prod_{j=1}^{P} P(X_j \mid Y = k)},$$

where:

- Y is the random variable corresponding to the class index of an observation.
- $X_1,...,X_P$ are the random predictors of an observation.
- $\pi(Y = k)$ is the prior probability that a class index is k.

3 Classifies an observation by estimating the posterior probability for each class, and then assigns the observation to the class yielding the maximum posterior probability.

If the predictors compose a multinomial distribution, then the posterior probability $\hat{P}(Y = k \mid X_1,..,X_P) \propto \pi(Y = k)P_{mn}(X_1,...,X_P \mid Y = k)$, where $P_{mn}(X_1,...,X_P \mid Y = k)$ is the probability mass function of a multinomial distribution.

Algorithms

- If you specify `'Distribution','mn'` when training Mdl using `fitcnb`, then the software fits a multinomial distribution using the bag-of-tokens model. The software stores the probability that token j appears in class k in the property `DistributionParameters{`k`,`j`}`. Using additive smoothing [2], the estimated probability is

$$P(\text{token } j \mid \text{class } k) = \frac{1 + c_{j|k}}{P + c_k},$$

where:

- $c_{j|k} = n_k \frac{\sum_{i:y_i \in \text{class } k} x_{ij} w_i}{\sum_{i:y_i \in \text{class } k} w_i}$; which is the weighted number of occurrences of token j in class k.
- n_k is the number of observations in class k.
- w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.
- $c_k = \sum_{j=1}^{P} c_{j|k}$; which is the total weighted number of occurrences of all tokens in class k.

- If you specify `'Distribution','mvmn'` when training Mdl using `fitcnb`, then:

  1. For each predictor, the software collects a list of the unique levels, stores the sorted list in `CategoricalLevels`, and considers each level a bin. Each predictor/class combination is a separate, independent multinomial random variable.
  2. For predictor j in class k, the software counts instances of each categorical level using the list stored in `CategoricalLevels{`j`}`.
  3. The software stores the probability that predictor j, in class k, has level L in the property `DistributionParameters{`k`,`j`}`, for all levels in `CategoricalLevels{`j`}`. Using additive smoothing [2], the estimated probability is

$$P(\text{predictor } j = L \mid \text{class } k) = \frac{1 + m_{j|k}(L)}{m_j + m_k},$$

     where:

- $m_{j|k}(L) = n_k \frac{\sum_{i:y_i \in \text{ class } k} I\{x_{ij} = L\} w_i}{\sum_{i:y_i \in \text{ class } k} w_i}$; which is the weighted number of observations for which predictor j equals L in class k.
- n_k is the number of observations in class k.
- $I\{x_{ij} = L\} = 1$ if $x_{ij} = L$, 0 otherwise.
- w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.
- m_j is the number of distinct levels in predictor j.
- m_k is the weighted number of observations in class k.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Train a Naive Bayes Classifier

Construct a naive Bayes classifier for Fisher's iris data. Also, specify prior probabilites after training.

Load Fisher's iris data.

```
load fisheriris
X = meas;
Y = species;
```

`X` is a numeric matrix that contains four petal measurements for 150 irises. `Y` is a cell array of strings that contains the corresponding iris species.

Train a naive Bayes classifier.

```
Mdl = fitcnb(X,Y)
```

```
Mdl =

  ClassificationNaiveBayes
           PredictorNames: {'x1'  'x2'  'x3'  'x4'}
             ResponseName: 'Y'
                ClassNames: {'setosa'  'versicolor'  'virginica'}
           ScoreTransform: 'none'
          NumObservations: 150
        DistributionNames: {'normal'  'normal'  'normal'  'normal'}
    DistributionParameters: {3x4 cell}
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier, and some of its properties display in the Command Window. By default, the software treats each predictor as independent, and fits them using normal distributions.

To access the properties of `Mdl`, use dot notation.

```
Mdl.ClassNames
Mdl.Prior
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

    0.3333    0.3333    0.3333
```

`Mdl.Prior` contains the class prior probabilities, which are settable using the name-value pair argument `'Prior'` in `fitcnb`. The order of the class prior probabilities corresponds to the order of the classes in `Mdl.ClassNames`. By default, the prior probabilities are the respective relative frequencies of the classes in the data.

You can also reset the prior probabilities after training. For example, set the prior probabilities to 0.5, 0.2, and 0.3 respectively.

```
Mdl.Prior = [0.5 0.2 0.3];
```

You can pass `Mdl` to e.g., `predict` to label new measurements, or `crossval` to cross validate the classifier.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[2] Manning, C. D., P. Raghavan, and M. Schütze. *Introduction to Information Retrieval*, NY: Cambridge University Press, 2008.

See Also

`CompactClassificationNaiveBayes` | `fitcnb` | `loss` | `predict`

More About

- “Naive Bayes Classification” on page 15-31
- “Grouping Variables” on page 2-52

ClassificationPartitionedECOC class

Superclasses: ClassificationPartitionedModel

Cross-validated multiclass model for support vector machines or other classifiers

Description

`ClassificationPartitionedECOC` is a set of error-correcting output codes (ECOC) models trained on cross-validated folds. Estimate the quality of classification by cross validation using one or more "kfold" functions: `kfoldPredict`, `kfoldLoss`, `kfoldMargin`, `kfoldEdge`, and `kfoldfun`.

Every "kfold" method uses models trained on in-fold observations to predict the response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, the software randomly assigns each observation into five roughly equal-sized groups. The *training fold* contains four of the groups (i.e., roughly 4/5 of the data) and the *test fold* contains the other group (i.e., roughly 1/5 of the data). In this case, cross validation proceeds as follows.

- The software trains the first model (stored in `CVMdl.Trained{1}`) using the observations in the last four groups and reserves the observations in the first group for validation.
- The software trains the second model (stored in `CVMdl.Trained{2}`) using the observations in the first group and last three groups, and reserves the observations in the second group for validation.
- The software proceeds in a similar fashion for the third, fourth, and fifth models.

If you validate by calling `kfoldPredict`, it computes predictions for the observations in group 1 using the first model, group 2 for the second model, and so on. In short, the software estimates a response for every observation using the model trained without that observation.

Construction

`CVMdl = crossval(Mdl)` returns a cross-validated ECOC model from `Mdl`, an ECOC model. For details, see `crossval`.

Alternatively, `CVMdl = fitcecoc(X,Y,Name,Value)` returns a cross-validated ECOC model when `Name` is one of `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. For syntax details, see `fitcecoc`.

Properties

`BinaryLoss` — Binary learner loss function

string

Binary learner loss function, specified as a string.

If you train using binary learners that use different loss functions, then the software sets `BinaryLoss` to `'hamming'`. To potentially increase accuracy, set a different binary loss function than this default during prediction or loss computation using the `BinaryLoss` name-value pair argument of `predict` or `loss`.

Data Types: `char`

`BinaryY` — Binary learner class labels

numeric matrix | `[]`

Binary learner class labels, specified as a numeric matrix or `[]`.

- If the coding matrix is the same across folds, then `BinaryY` is a NumObservations-by-L matrix, where L is the number of binary learners (`size(`CodingMatrix`,2)`).

  Elements of `BinaryY` are `-1`, `0`, or `1`, and the value corresponds to a dichotomous class assignment. This table describes how learner `j` assigns observation `k` to a dichotomous class corresponding to the value of `BinaryY(k,j)`.

Value	Dichotomous Class Assignment
`-1`	Negative class
`0`	Before training, learner `j` removes observations in class `i` from the data set.
`1`	Positive class

- If the coding matrix varies across folds, then `BinaryY` is empty (`[]`).

Data Types: `double`

`CategoricalPredictors` — Categorical predictor indices

numeric vector

Categorical predictor indices, specified as a numeric vector. `CategoricalPredictors` contains indices `1` through `p`, where `p` is the number of columns of `X` (`size(X,2)`).

Data Types: `single` | `double`

`ClassNames` — Unique class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Unique class labels in the response data (Y), specified as a categorical or character array, logical or numeric vector, or cell array of strings. `ClassNames` has the same data type as `Y`.

`CodingMatrix` — Codes specifying class assignments

numeric matrix | `[]`

Codes specifying class assignments for the binary learners, specified as a numeric matrix or `[]`.

- If the coding matrix is the same across folds, then `CodingMatrix` is a K-by-L matrix, where K is the number of classes and L is the number of binary learners.

  Elements of `CodingMatrix` are `-1`, `0`, or `1`, and the value corresponds to a dichotomous class assignment. This table describes how learner `j` assigns observations in class `k` to a dichotomous class corresponding to the value of `CodingMatrix(k,j)`.

Value	Dichotomous Class Assignment
`-1`	Negative class
`0`	Before training, learner `j` removes observations in class `i` from the data set.
`1`	Positive class

- If the coding matrix varies across folds, then `CodingMatrix` is empty (`[]`). Obtain the coding matrix for each fold using the Trained property. For example, `CVMdl.Trained{1}.CodingMatrix` is the coding matrix in the first fold of the cross-validated ECOC model `CVMdl`.

Data Types: `char` | `double` | `single` | `int8` | `int16` | `int32` | `int64`

`Cost` — Misclassification costs

square numeric matrix

Misclassification costs, specified as a square numeric matrix. `Cost` has K rows and columns, where K is the number of classes.

`Cost(i,j)` is the cost of misclassifying a point into class `j` if its true class is `i`. The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames.

`fitcecoc` incorporates misclassification costs differently among different types of binary learners.

This property is read-only.

Data Types: `double`

`CrossValidatedModel` — Cross-validated model name

string

Cross-validated model name, specified as a string.

For example, `ECOC` specifies a cross-validated ECOC model.

Data Types: `char`

`Kfold` — Number of cross-validated folds

positive integer

Number of cross-validated folds, specified as a positive integer.

Data Types: `double`

`ModelParameters` — Cross-validation parameter values

object

Cross-validation parameter values, e.g., the name-value pair argument values used to cross-validate the ECOC classifier, specified as an object. `ModelParameters` does not contain estimated parameters.

Access properties of `ModelParameters` using dot notation.

`NumObservations` — Number of observations

positive numeric scalar

Number of observations in the training data, specified as a positive numeric scalar.

Data Types: `double`

`Partition` — Data partition
`cvpartition` model

Data partition indicating how the software splits the data into cross-validation folds, specified as a `cvpartition` model.

`PredictorNames` — Predictors names
cell array of strings

Predictors names in the order that they appear in X, specified as a cell array of strings containing the predictor names. `PredictorNames` has length equal to the number of columns in `X`.

Data Types: `cell`

`Prior` — Prior class probabilities
numeric vector

Prior class probabilities, specified as a numeric vector. `Prior` has as many elements as classes in Y, and the order of the elements corresponds to the elements of `ClassNames`.

`fitcecoc` incorporates misclassification costs differently among different types of binary learners.

This property is read only.

Data Types: `double`

`ResponseName` — Response variable name
string

Response variable name, specified as a string.

Data Types: `char`

`ScoreTransform` — Score transformation function
string | function handle

Score transformation function, specified as a string or function handle. `ScoreTransform` describes how the software transforms raw, predicted classification scores.

To change the score transformation function to, e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

  ```
  SVMModel.ScoreTransform = 'function';
  ```

  This table lists the supported, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  SVMModel.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Data Types: `char | function_handle`

`Trained` — Compact classifiers trained on cross-validation folds

cell array of `CompactClassificationECOC` models

Compact classifiers trained on cross-validation folds, specified cell as a array of `CompactClassificationECOC` models. `Trained` has k cells, where k is the number of folds.

Data Types: `cell`

`W` — Observation weights

numeric vector

Observation weights used to cross validate the classifier, specified as a numeric vector. `W` has NumObervations elements.

The software normalizes the weights used for training so that `nansum(W)` is `1`.

Data Types: `single` | `double`

`X` — Unstandardized predictor data used to cross validate the classifier

numeric matrix

Unstandardized predictor data used to cross validate the classifier, specified as a numeric matrix. `X` is a NumObervations-by-p matrix, where p is the number of predictors.

Each row of `X` corresponds to one observation, and each column corresponds to one variable.

Data Types: `single` | `double`

`Y` — Observed class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Observed class labels used to train the classifier, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` has NumObervations elements, and is the same data type as the input argument Y of `fitcecoc`.

Each row of `Y` represents the observed classification of the corresponding row of `X`.

Methods

kfoldEdge	Classification edge for observations not used for training

kfoldfun	Cross validate function
kfoldLoss	Classification loss for observations not used for training
kfoldMargin	Classification margins for observations not used for training
kfoldPredict	Predict responses for observations not used for training

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Cross Validate an ECOC Classifier

Train a one-versus-one ECOC classifier using binary SVM learners.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
rng(1); % For reproducibility
```

Create an SVM template. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1)
```

```
t =

Fit template for classification SVM.
```

```
                    Alpha: [0x1 double]
          BoxConstraint: []
              CacheSize: []
          CachingMethod: ''
    DeltaGradientTolerance: []
           GapTolerance: []
           KKTTolerance: []
         IterationLimit: []
         KernelFunction: ''
            KernelScale: []
           KernelOffset: []
     KernelPolynomialOrder: []
               NumPrint: []
                     Nu: []
        OutlierFraction: []
        ShrinkagePeriod: []
                 Solver: ''
        StandardizeData: 1
    SaveSupportVectors: []
        VerbosityLevel: []
                 Method: 'SVM'
                   Type: 'classification'
```

`t` is an SVM template. All of its properties are empty, except for `StandardizeData`, `Method`, and `Type`. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier. It is good practice to specify the class order.

```
Mdl = fitcecoc(X,Y,'Learners',t,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationECOC` classifier. You can access its properties using dot notation.

Cross validate `Mdl` using 10-fold cross validation.

```
CVMdl = crossval(Mdl);
```

`CVMdl` is a `ClassificationPartitionedECOC` cross-validated ECOC classifier.

Estimate the generalization error.

```
oosLoss = kfoldLoss(CVMdl)
```

```
oosLoss =

    0.0400
```

The out-of-sample classification error is 4%, which indicates that the ECOC classifier generalizes fairly well.

Train ECOC Classifiers Using Ensembles and Parallel Computing

Train a one-versus-all ECOC classifier using a GentleBoost ensemble of decision trees with surrogate splits. Estimate the classification error using 10-fold cross validation.

Load and inspect the `arrhythmia` data set.

```
load arrhythmia
[n,p] = size(X)
isLabels = unique(Y);
nLabels = numel(isLabels)
tabulate(categorical(Y))
```

```
n =

   452


p =

   279


nLabels =

    13

    Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
```

```
     6        25       5.53%
     7         3       0.66%
     8         2       0.44%
     9         9       1.99%
    10        50      11.06%
    14         4       0.88%
    15         5       1.11%
    16        22       4.87%
```

There are 279 predictors, and a relatively small sample size of 452. There are 16 distinct labels, but only 13 are represented in the response (Y), and each label describes various degrees of arrhythmia. 54.20% of the observations are in class 1.

Create an ensemble template. You must specify at least three arguments: a method, a number of learners, and the type of learner. For this example, specify `'GentleBoost'` for the method, `100` for the number of learners, and a decision tree template that uses surrogate splits since there are missing observations.

```
tTree = templateTree('surrogate','on');
tEnsemble = templateEnsemble('GentleBoost',100,tTree);
```

`tEnsemble` is a template object. Most of its properties are empty, but the software fills them with their default values during training.

Train a one-versus-all ECOC classifier using the ensembles of decision trees as binary learners. If you have a Parallel Computing Toolbox license, then you can speed up the computation by specifying to use parallel computing. This sends each binary learner to a worker in the pool (the number of workers depends on your system configuration). Also, specify that the prior probabilities are $1/K$, where $K = 13$, which is the number of distinct classes.

```
pool = parpool; % Invoke workers
options = statset('UseParallel',1);
Mdl = fitcecoc(X,Y,'Coding','onevsall','Learners',tEnsemble,...
               'Prior','uniform','Options',options);
```

```
Starting parallel pool (parpool) using the 'local' profile ... connected to 2 workers.
```

`Mdl` is a `ClassificationECOC` model.

Cross validate the ECOC classifier using 10-fold cross validation.

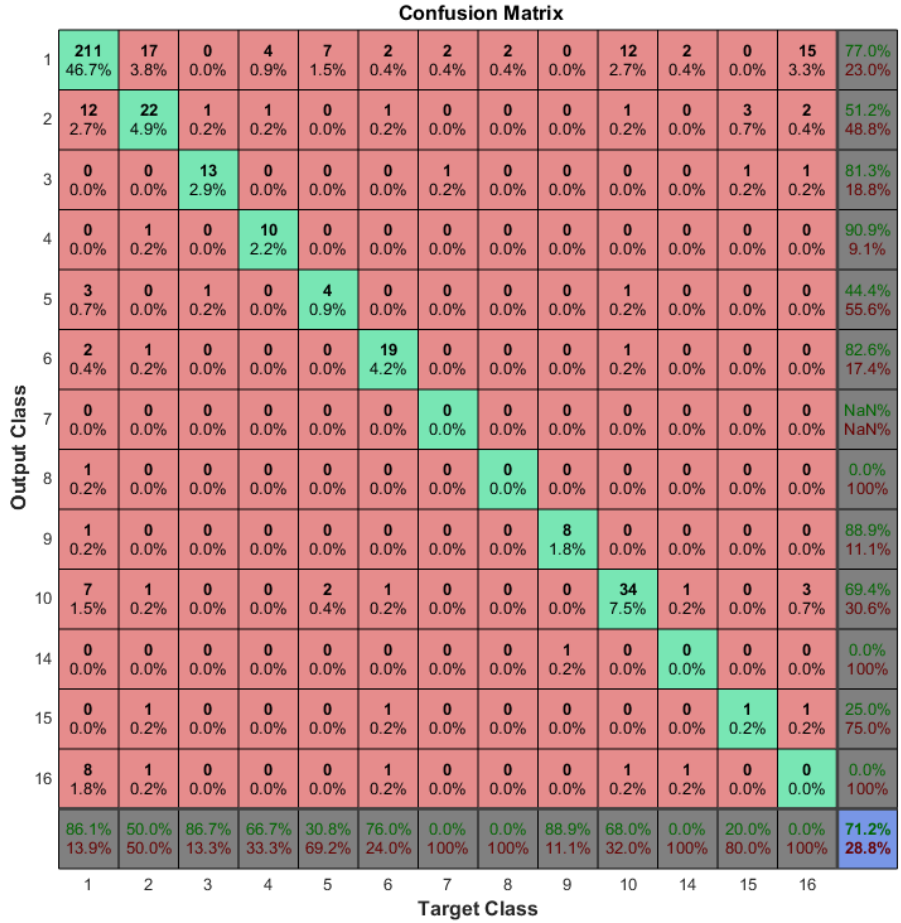
```
CVMdl = crossval(Mdl,'Options',options);
```

```
Warning: One or more folds do not contain points from all the groups.
```

`CVMdl` is a `ClassificationPartitionedECOC` model. The warning indicates that some classes are not represented while the software trains at least one fold. Therefore, those folds cannot predict labels for the missing classes. You can inspect the results of a fold using cell indexing and dot notation, e.g., access the results of the first fold by entering `CVMdl.Trained{1}`. Your results might vary.

Use the cross-validated ECOC classifier to predict out-of-fold labels. You can compute the confusion matrix using `confusionmat`. However, if you have a Neural Network Toolbox™ license, you can plot the confusion matrix using `plotconfusion`. The input arguments of `plotconfusion` are not vectors of the true and predicted labels like `confusionmat`, but indicator matrices of the true and predicted labels. Both start as K-by-n matrices of 0s. If observation j has label index k (or has predicted label k), then element (k,j) of the true label indicator matrix (or predicted label indicator matrix) is `1`. You can convert label indices returned by `predict`, `resubPredict`, or `kfoldPredict` to label indicator matrices using linear indexing. For details on linear indexing, see `sub2ind` and `ind2sub`.

```
oofLabel = kfoldPredict(CVMdl,'Options',options);
ConfMat = confusionmat(Y,oofLabel);

% Convert the integer label vector to a class-identifier matrix.
[~,grp] = ismember(oofLabel,isLabels);
oofLabelMat = zeros(nLabels,n);
idxLinear = sub2ind([nLabels n],grp,(1:n)');
oofLabelMat(idxLinear) = 1; % Flags the row corresponding to the class
YMat = zeros(nLabels,n);
idxLinearY = sub2ind([nLabels n],grp,(1:n)');
YMat(idxLinearY) = 1;

figure;
plotconfusion(YMat,oofLabelMat);
h = gca;
h.XTickLabel = [num2cell(isLabels); {''}];
h.YTickLabel = [num2cell(isLabels); {''}];
```



Algorithms

For linear, SVM binary learners, and for efficiency, `fitcecoc` empties the properties `Alpha`, `SupportVectorLabels`, and `SupportVectors`. `fitcecoc` lists `Beta`, rather than `Alpha`, in the model display.

To store `Alpha`, `SupportVectorLabels`, and `SupportVectors`, pass a linear, SVM template that specifies storing support vectors to `fitcecoc`. For example, enter:

```
t = templateSVM('SaveSupportVectors','on')
Mdl = fitcecoc(X,Y,'Learners',t);
```

You can subsequently remove the support vectors and related values by passing the resulting `ClassificationECOC` model to `discardSupportVectors`.

See Also

`ClassificationECOC` | `CompactClassificationECOC` | `cvpartiton` | `fitcecoc`

ClassificationPartitionedEnsemble class

Cross-validated classification ensemble

Description

`ClassificationPartitionedEnsemble` is a set of classification ensembles trained on cross-validated folds. Estimate the quality of classification by cross validation using one or more "kfold" methods: `kfoldPredict`, `kfoldLoss`, `kfoldMargin`, `kfoldEdge`, and `kfoldfun`.

Every "kfold" method uses models trained on in-fold observations to predict response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, every training fold contains roughly 4/5 of the data and every test fold contains roughly 1/5 of the data. The first model stored in `Trained{1}` was trained on `X` and `Y` with the first 1/5 excluded, the second model stored in `Trained{2}` was trained on `X` and `Y` with the second 1/5 excluded, and so on. When you call `kfoldPredict`, it computes predictions for the first 1/5 of the data using the first model, for the second 1/5 of data using the second model, and so on. In short, response for every observation is computed by `kfoldPredict` using the model trained without this observation.

Construction

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a classification ensemble. For syntax details, see the `crossval` method reference page.

`cvens = fitensemble(X,Y,method,nlearn,learners,name,value)` creates a cross-validated ensemble when `name` is one of `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. For syntax details, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

ClassNames

List of the elements in Y with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables, logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument Y.

Combiner

Cell array of combiners across all folds.

Cost

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames. The number of rows and columns in `Cost` is the number of unique classes in the response. This property is read-only.

CrossValidatedModel

Name of the cross-validated model, a string.

Kfold

Number of folds used in a cross-validated ensemble, a positive integer.

ModelParameters

Object holding parameters of `cvens`.

NumObservations

Number of data points used in training the ensemble, a positive integer.

NTrainedPerFold

Number of data points used in training each fold of the ensemble, a positive integer.

Partition

Partition of class `cvpartition` used in creating the cross-validated ensemble.

PredictorNames

Cell array of names for the predictor variables, in the order in which they appear in `X`.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames. The number of elements of `Prior` is the number of unique classes in the response. This property is read-only.

ResponseName

Name of the response variable Y, a string.

ScoreTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `fitctree`.

Add or change a `ScoreTransform` function using dot notation:

```
ens.ScoreTransform = 'function'
```

or

```
ens.ScoreTransform = @function
```

Trainable

Cell array of ensembles trained on cross-validation folds. Every ensemble is full, meaning it contains its training data and weights.

Trained

Cell array of compact ensembles trained on cross-validation folds.

W

Scaled weights, a vector with length `n`, the number of rows in X.

X

A matrix of predictor values. Each column of X represents one variable, and each row represents one observation.

Y

A numeric column vector with the same number of rows as X. Each entry in Y is the response to the data in the corresponding row of X.

Methods

kfoldEdge	Classification edge for observations not used for training
kfoldLoss	Classification loss for observations not used for training
resume	Resume training learners on cross-validation folds

Inherited Methods

kfoldEdge	Classification edge for observations not used for training
kfoldfun	Cross validate function
kfoldLoss	Classification loss for observations not used for training
kfoldMargin	Classification margins for observations not used for training

kfoldPredict	Predict response for observations not used for training

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Evaluate the k-fold cross-validation error for a classification ensemble that models the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)

L =
    0.0533
```

See Also

`RegressionPartitionedEnsemble` | `ClassificationPartitionedModel` | `ClassificationEnsemble` | `fitctree`

ClassificationPartitionedModel class

Cross-validated classification model

Description

`ClassificationPartitionedModel` is a set of classification models trained on cross-validated folds. Estimate the quality of classification by cross validation using one or more "kfold" methods: `kfoldPredict`, `kfoldLoss`, `kfoldMargin`, `kfoldEdge`, and `kfoldfun`.

Every "kfold" method uses models trained on in-fold observations to predict the response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, the software randomly assigns each observation into five roughly equally sized groups. The *training fold* contains four of the groups (i.e., roughly 4/5 of the data) and the *test fold* contains the other group (i.e., roughly 1/5 of the data). In this case, cross validation proceeds as follows:

- The software trains the first model (stored in `CVMdl.Trained{1}`) using the observations in the last four groups and reserves the observations in the first group for validation.
- The software trains the second model (stored in `CVMdl.Trained{2}`) using the observations in the first group and last three groups, and reserves the observations in the second group for validation.
- The software proceeds in a similar fashion for the third to fifth models.

If you validate by calling `kfoldPredict`, it computes predictions for the observations in group 1 using the first model, group 2 for the second model, and so on. In short, the software estimates a response for every observation using the model trained without that observation.

Construction

`CVMdl = crossval(Mdl)` creates a cross-validated classification model from a classification model (`Mdl`).

Alternatively:

- `CVDiscrMdl = fitcdiscr(X,Y,Name,Value)`
- `CVEnsMdl = fitensemble(X,Y,Name,Value)`
- `CVKNNMdl = fitcknn(X,Y,Name,Value)`
- `CVNBMdl = fitcnb(X,Y,Name,Value)`
- `CVSVMMdl = fitcsvm(X,Y,Name,Value)`
- `CVTreeMdl = fitctree(X,Y,Name,Value)`

create a cross-validated model when `name` is either `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. For syntax details, see `fitcdiscr`, `fitensemble`, `fitcknn`, `fitcnb`, `fitcsvm`, and `fitctree`.

For a cross-validated, error-correcting output code multiclass model, see `ClassificationPartitionedECOC` and `fitcecoc`.

Input Arguments

`Mdl`

A classification model. `Mdl` can be any of the following:

- A classification tree trained using `fitctree`
- A classification ensemble trained using `fitensemble`
- A discriminant analysis classifier trained using `fitcdiscr`
- A naive Bayes classifier trained using `fitcnb`
- A nearest-neighbor classifier trained using `fitcknn`
- A support vector machine classifier trained using `fitcsvm`

Properties

`CategoricalPredictors`

List of categorical predictors.

If `Model` is a trained classification tree, then `CategoricalPredictors` is a numeric vector with indices from `1` through `p`, where `p` is the number of columns of `X`.

If `Model` is a trained discriminant analysis or support vector machine classifier, then `CategoricalPredictors` is an empty vector (`[]`).

`ClassNames`

List of elements in Y with duplicates removed. `ClassNames` has the same data type as the data in the argument Y, and therefore can be a categorical or character array, logical or numeric vector, or cell array of strings.

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames. The number of rows and columns in `Cost` is the number of unique classes in the response.

If CVModel is a cross-validated `ClassificationDiscriminant`, `ClassificationKNN`, or `ClassificationNaiveBayes` model, then you can change its cost matrix to e.g., `CostMatrix`, using dot notation.

```
CVModel.Cost = CostMatrix;
```

`CrossValidatedModel`

Name of the cross-validated model, which is a string.

`KFold`

Number of folds used in cross-validated model, which is a positive integer.

`ModelParameters`

Object holding parameters of CVModel.

`Partition`

The partition of class `CVPartition` used in creating the cross-validated model.

`PredictorNames`

Cell array of strings containing the predictor names, in the order that they appear in `X`.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames.

If CVModel is a cross-validated `ClassificationDiscriminant` or `ClassificationNaiveBayes` model, then you can change its vector of priors to e.g., `priorVector`, using dot notation.

```
CVModel.Prior = priorVector;
```

ResponseName

String describing the response variable `Y`.

ScoreTransform

String representing a built-in transformation function, or a function handle for transforming predicted classification scores.

To change the score transformation function to, e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

  ```
  SVMModel.ScoreTransform = 'function';
  ```

  This table contains the available, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$

String	Formula
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  SVMModel.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

`Trained`

The trained learners, which is a cell array of compact classification models.

`W`

The scaled weights, which is a vector with length `n`, the number of rows in X.

`X`

Numeric matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

Categorical or character array, logical or numeric vector, or cell array of strings specifying the class labels for each observation. `Y` has the same number of rows as `X`, and each entry of `Y` is the response to the data in the corresponding row of `X`.

Methods

kfoldEdge	Classification edge for observations not used for training
kfoldfun	Cross validate function

kfoldLoss	Classification loss for observations not used for training
kfoldMargin	Classification margins for observations not used for training
kfoldPredict	Predict response for observations not used for training

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Tips

To estimate posterior probabilities of trained, cross-validated SVM classifiers, use `fitSVMPosterior`.

Examples

Evaluate the Classification Error of a Classification Tree Classifier

Evaluate the *k*-fold cross-validation error for a classification tree model.

Load Fisher's iris data set.

```
load fisheriris
```

Train a classification tree using default options.

```
Mdl = fitctree(meas,species);
```

Cross validate the classification tree model.

```
CVMdl = crossval(Mdl);
```

Estimate the 10-fold cross-validation loss.

```
L = kfoldLoss(CVMdl)
```

```
L =

    0.0533
```

Estimate Posterior Probabilities for Test Samples

Estimate positive class posterior probabilities for the test set of an SVM algorithm.

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. Specify a 20% holdout sample. It is good practice to standardize the predictors and specify the class order.

```
rng(1) % For reproducibility
CVSVMModel = fitcsvm(X,Y,'Holdout',0.2,'Standardize',true,...
    'ClassNames',{'b','g'});
```

`CVSVMModel` is a trained `ClassificationPartitionedModel` cross-validated classifier.

Estimate the optimal score function for mapping observation scores to posterior probabilities of an observation being classified as `'g'`.

```
ScoreCVSVMModel = fitSVMPosterior(CVSVMModel);
```

`ScoreSVMModel` is a trained `ClassificationPartitionedModel` cross-validated classifier containing the optimal score transformation function estimated from the training data.

Estimate the out-of-sample positive class posterior probabilities. Display the results for the first 10 out-of-sample observations.

```
[~,OOSPostProbs] = kfoldPredict(ScoreCVSVMModel);
indx = ~isnan(OOSPostProbs(:,2));
hoObs = find(indx); % Holdout observation numbers
OOSPostProbs = [hoObs, OOSPostProbs(indx,2)];
table(OOSPostProbs(1:10,1),OOSPostProbs(1:10,2),...
```

```
    'VariableNames',{'ObservationIndex','PosteriorProbability'})

ans =

    ObservationIndex    PosteriorProbability
    ________________    ____________________

     6                     0.17378
     7                     0.89637
     8                    0.0076609
     9                     0.91602
    16                    0.026718
    22                   4.6081e-06
    23                       0.9024
    24                   2.4129e-06
    38                   0.00042697
    41                      0.86427
```

- “Cross Validating a Discriminant Analysis Classifier” on page 15-18

See Also

`ClassificationSVM` | `ClassificationTree` | `ClassificationDiscriminant` | `CompactClassificationSVM` | `CompactClassificationTree` | `CompactClassificationDiscriminant` | `ClassificationKNN` | `ClassificationEnsemble` | `CompactClassificationEnsemble` | `ClassificationECOC` | `ClassificationNaiveBayes` | `ClassificationPartitionedEnsemble` | `CompactClassificationNaiveBayes` | `fitcdiscr` | `fitcecoc` | `fitcknn` | `fitcnb` | `fitcsvm` | `fitctree` | `fitensemble` | `fitSVMPosterior` | `RegressionPartitionedModel`

ClassificationSVM class

Superclasses: CompactClassificationSVM

Support vector machine for binary classification

Description

`ClassificationSVM` is a support vector machine classifier for one- or two-class learning. Use `fitcsvm` and the training data to train a `ClassificationSVM` classifier.

Trained `ClassificationSVM` classifiers store the training data, parameter values, prior probabilities, support vectors, and algorithmic implementation information. You can use these classifiers to:

- Estimate resubstitution predictions. For details, see `resubPredict`.
- Predict labels or posterior probabilities for new data. For details, see `predict`.

Construction

`SVMModel = fitcsvm(X,Y)` returns a trained SVM classifier (`SVMModel`) based on the input variables (also known as predictors, features, or attributes) X and output variables (also known as responses or class labels) Y. For details, see `fitcsvm`.

`SVMModel = fitcsvm(X,Y,Name,Value)` returns a trained SVM classifier with additional options specified by one or more `Name,Value` pair arguments. For name-value pair argument details, see `fitcsvm`.

If you set one of the following five options, then `SVMModel` is a `ClassificationPartitionedModel` model: `'CrossVal'`, `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`. Otherwise, `SVMModel` is a `ClassificationSVM` classifier.

Input Arguments

`X` — Predictor data

matrix of numeric values

Predictor data to which the SVM classifier is trained, specified as a matrix of numeric values.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one predictor.

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to:

- Cross validate using the `KFold` name-value pair argument. The cross-validation results determine how well the SVM classifier generalizes.
- Standardize the predictor variables using the `Standardize` name-value pair argument.

To specify the names of the predictors in the order of their appearance in `X`, use the `PredictorNames` name-value pair argument.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels to which the SVM classifier is trained, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to specify the order of the classes using the `ClassNames` name-value pair argument.

To specify the response variable name, use the `ResponseName` name-value pair argument.

Note: The software treats `NaN`, empty string (`''`), and `<undefined>` elements as missing values. If a row of `X` or an element of `Y` contains at least one `NaN`, then the software removes those rows and elements from both arguments. Such deletion decreases the effective training or cross-validation sample size.

Properties

`Alpha`

Numeric vector of trained classifier coefficients from the dual problem (i.e., the estimated Lagrange multipliers). `Alpha` has length equal to the number of support vectors in the trained classifier (i.e., `sum(SVMModel.IsSupportVector)`).

`Beta`

Numeric vector of linear predictor coefficients. `Beta` has length equal to the number of predictors (i.e., `size(SVMModel.X,2)`).

If KernelParameters`.Function` is `'linear'`, then the software estimates the classification score for the observation x using

$$f(x) = (x / s)'\beta + b.$$

SVMModel stores β, b, and s in the properties Beta, Bias, and KernelParameters`.Scale`, respectively.

If KernelParameters`.Function` is not `'linear'`, then `Beta` is empty (`[]`).

`Bias`

Scalar corresponding to the trained classifier bias term.

`BoxConstraints`

Numeric vector of box constraints.

`BoxConstraints` has length equal to the number of observations (i.e., `size(SVMModel.X,1)`).

`CacheInfo`

Structure array containing:

- The cache size (in MB) that the software reserves to train the SVM classifier (`SVMModel.CacheInfo.Size`). To set the cache size to *`CacheSize`* MB, set the `fitcsvm` name-value pair argument to `'CacheSize',`*`CacheSize`*.
- The caching algorithm that the software uses during optimization (`SVMModel.CacheInfo.Algorithm`). Currently, the only available caching algorithm is `Queue`. You cannot set the caching algorithm.

`CategoricalPredictors`

List of categorical predictors, which is always empty ([ ]) for SVM and discriminant analysis classifiers.

`ClassNames`

List of elements in Y with duplicates removed. `ClassNames` has the same data type as the data in the argument Y, and therefore can be a categorical or character array, logical or numeric vector, or cell array of strings.

`ConvergenceInfo`

Structure array containing convergence information.

Field	Description
`Converged`	Logical flag indicating whether the algorithm converged (`1` indicates convergence)
`ReasonForConvergence`	String indicating the criterion the software uses to detect convergence
`Gap`	Scalar feasibility gap between the dual and primal objective functions
`GapTolerance`	Scalar feasibility gap tolerance. Set this tolerance to, e.g., *`gt`*, using the name-value pair argument `'GapTolerance',`*`gt`* of `fitcsvm`.
`DeltaGradient`	Scalar-attained gradient difference between upper and lower violators
`DeltaGradientTolerance`	Scalar tolerance for gradient difference between upper and lower violators. Set this tolerance to, e.g., *`dgt`*, using the name-value pair argument `'DeltaGradientTolerance',`*`dgt`* of `fitcsvm`.
`LargestKKTViolation`	Maximal, scalar Karush-Kuhn-Tucker (KKT) violation value
`KKTTolerance`	Scalar tolerance for the largest KKT violation. Set this tolerance to, e.g., *`kktt`*,

Field	Description
	using the name-value pair argument `'KKTTolerance',kktt` of `fitcsvm`.
`History`	Structure array containing convergence information at set optimization iterations. The fields are: • `NumIterations`: numeric vector of iteration indices for which the software records convergence information • `Gap`: numeric vector of `Gap` values at the iterations • `DeltaGradient` numeric vector of `DeltaGradient` values at the iterations • `LargestKKTViolation`: numeric vector of `LargestKKTViolation` values at the iterations • `NumSupportVectors`: numeric vector indicating the number of support vectors at the iterations • `Objective`: numeric vector of `Objective` values at the iterations
`Objective`	Scalar value of the dual objective function

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

During training, the software updates the prior probabilities by incorporating the penalties described in the cost matrix. Therefore,

- For two-class learning, `Cost` always has this form: `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames.
- For one-class learning, `Cost = 0`.

This property is read-only. For more details, see Algorithms.

`Gradient`

Numeric vector of training data gradient values. `Gradient` has length equal to the number of observations (i.e., `size(SVMModel.X,1)`).

`IsSupportVector`

Logical vector indicating whether a corresponding row in the predictor data matrix is a support vector. `IsSupportVector` has length equal to the number of observations (i.e., `size(SVMModel.X,1)`).

`KernelParameters`

Structure array containing the kernel name and parameter values.

To display the values of `KernelParameters`, use dot notation, e.g., `SVMModel.KernelParameters.Scale` displays the scale parameter value.

The software accepts `KernelParameters` as inputs, and does not modify them. Alter `KernelParameters` by setting the appropriate name-value pair arguments when you train the SVM classifier using `fitcsvm`.

`ModelParameters`

Object containing parameter values, e.g., the name-value pair argument values, used to train the SVM classifier. `ModelParameters` does not contain estimated parameters.

Access fields of `ModelParameters` using dot notation. For example, access the initial values for estimating `Alpha` using `SVMModel.ModelParameters.Alpha`.

`Mu`

Numeric vector of predictor means.

If you specify `'Standardize',1` or `'Standardize',true` when you train an SVM classifier using `fitcsvm`, then `Mu` has length equal to the number of predictors (i.e., `size(SVMModel.X,2)`). Otherwise, `Mu` is an empty vector (`[]`).

`NumIterations`

Positive integer indicating the number of iterations required by the optimization routine to attain convergence.

To set a limit on the number of iterations to, e.g., *k*, specify the name-value pair argument `'IterationLimit',k` of `fitcsvm`.

`Nu`

Positive scalar representing the *ν* parameter for one-class learning.

`NumObservations`

Numeric scalar representing the number of observations in the training data. If the input arguments `X` or `Y` contain missing values, then `NumObservations` is less than the length of `Y`.

`OutlierFraction`

Scalar indicating the expected proportion of outliers in the training data.

`PredictorNames`

Cell array of strings containing the predictor names, in the order that they appear in `X`.

`Prior`

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the elements of `SVMModel.ClassNames`.

For two-class learning, if you specify a cost matrix, then the software updates the prior probabilities by incorporating the penalties described in the cost matrix.

This property is read-only. For more details, see Algorithms.

`ResponseName`

String describing the response variable `Y`.

`ScoreTransform`

String representing a built-in transformation function, or a function handle for transforming predicted classification scores.

To change the score transformation function to, e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

```
SVMModel.ScoreTransform = 'function';
```

This table contains the available, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  SVMModel.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

`ShrinkagePeriod`

Nonnegative integer indicating the shrinkage period, i.e., number of iterations between reductions of the active set.

To set the shrinkage period to, e.g., *`sp`*, specify the name-value pair argument `'ShrinkagePeriod',sp` of `fitcsvm`.

`Sigma`

Numeric vector of predictor standard deviations.

If you specify `'Standardize',1` or `'Standardize',true` when you train the SVM classifier, then `Sigma` has length equal to the number of predictors (i.e., `size(SVMModel.X,2)`). Otherwise, `Sigma` is an empty vector (`[]`).

`Solver`

String indicating the solving routine that the software used to train the SVM classifier.

To set the solver to, e.g., *`solver`*, specify the name-value pair argument `'Solver',`*`solver`* of `fitcsvm`.

`SupportVectors`

Matrix containing rows of `X` that the software considers the support vectors.

If you specify `'Standardize',1` or `'Standardize',true`, then `SupportVectors` are the standardized rows of `X`.

`SupportVectorLabels`

Numeric vector of support vector class labels. `SupportVectorLabels` has length equal to the number of support vectors (i.e., `sum(SVMModel.IsSupportVector)`).

`+1` indicates that the corresponding support vector is in the positive class (`SVMModel.ClassNames{2}`). `-1` indicates that the corresponding support vector is in the negative class (`SVMModel.ClassNames{1}`).

`W`

Numeric vector of observation weights that the software used to train the SVM classifier.

The length of `W` is `SVMModel.NumObservations`.

`fitcsvm` normalizes `Weights` so that the elements of `W` within a particular class sum up to the prior probability of that class.

`X`

Numeric matrix of unstandardized predictor values that the software used to train the SVM classifier.

Each row of `X` corresponds to one observation, and each column corresponds to one variable.

The software excludes predictor data rows removed due to `NaN`s from `X`.

`Y`

Categorical or character array, logical or numeric vector, or cell array of strings representing the observed class labels that the software used to train the SVM classifier. `Y` is the same data type as the input argument Y of `fitcsvm`.

Each row of `Y` represents the observed classification of the corresponding row of `X`.

The software excludes elements removed due to `NaN`s from `Y`.

Methods

compact	Compact support vector machine classifier
crossval	Cross-validated support vector machine classifier
fitPosterior	Fit posterior probabilities
resubEdge	Classification edge for support vector machine classifiers by resubstitution
resubLoss	Classification loss for support vector machine classifiers by resubstitution
resubMargin	Classification margins for support vector machine classifiers by resubstitution
resubPredict	Predict support vector machine classifier resubstitution responses
resume	Resume training support vector machine classifier

Inherited Methods

compareHoldout	Compare accuracies of two classification models using new data
discardSupportVectors	Discard support vectors for linear support vector machine models
edge	Classification edge for support vector machine classifiers
fitPosterior	Fit posterior probabilities
loss	Classification error for support vector machine classifiers
margin	Classification margins for support vector machine classifiers
predict	Predict labels for support vector machine classifiers

Definitions

Box Constraint

A parameter that controls the maximum penalty imposed on margin-violating observations, and aids in preventing overfitting (regularization).

If you increase the box constraint, then the SVM classifier assigns fewer support vectors. However, increasing the box constraint can lead to longer training times.

Gram Matrix

The Gram matrix of a set of n vectors $\{x_1,..,x_n; x_j \in R^p\}$ is an n-by-n matrix with element (j,k) defined as $G(x_j,x_k) = <\phi(x_j),\phi(x_k)>$, an inner product of the transformed predictors using the kernel function ϕ.

For nonlinear SVM, the algorithm forms a Gram matrix using the predictor matrix columns. The dual formalization replaces the inner product of the predictors with corresponding elements of the resulting Gram matrix (called the "kernel trick"). Subsequently, nonlinear SVM operates in the transformed predictor space to find a separating hyperplane.

Karush-Kuhn-Tucker Complementarity Conditions

KKT complementarity conditions are optimization constraints required for optimal nonlinear programming solutions.

In SVM, the KKT complementarity conditions are

$$\begin{cases} \alpha_j \left[y_j \left(w'\phi\left(x_j\right) + b \right) - 1 + \xi_j \right] = 0 \\ \xi_j \left(C - \alpha_j \right) = 0 \end{cases}$$

for all $j = 1,...,n$, where w_j is a weight, ϕ is a kernel function (see Gram matrix), and ξ_j is a slack variable. If the classes are perfectly separable, then $\xi_j = 0$ for all $j = 1,...,n$.

One-Class Learning

One-class learning, or unsupervised SVM, aims at separating data from the origin in the high-dimensional, predictor space (not the original predictor space), and is an algorithm used for outlier detection.

The algorithm resembles that of SVM for binary classification. The objective is to minimize dual expression

$$0.5\sum_{jk}\alpha_j\alpha_k G(x_j,x_k)$$

with respect to $\alpha_1,...,\alpha_n$, subject to

$$\sum \alpha_j = n\nu$$

and $0 \le \alpha_j \le 1$ for all $j = 1,...,n$. $G(x_j,x_k,)$ is element (j,k) of the Gram matrix.

A small value of ν leads to fewer support vectors, and, therefore, a smooth, crude decision boundary. A large value of ν leads to more support vectors, and therefore, a curvy, flexible decision boundary. The optimal value of ν should be large enough to capture the data complexity and small enough to avoid overtraining. Also, $0 < \nu \le 1$.

For more details, see [5].

Support Vector

Support vectors are observations corresponding to strictly positive estimates of $\alpha_1,...,\alpha_n$.

SVM classifiers that yield fewer support vectors for a given training set are more desirable.

Support Vector Machines for Binary Classification

The SVM binary classification algorithm searches for an optimal hyperplane that separates the data into two classes. For separable classes, the optimal hyperplane maximizes a *margin* (space that does not contain any observations) surrounding itself, which creates boundaries for the positive and negative classes. For inseparable classes, the objective is the same, but the algorithm imposes a penalty on the length of the margin for every observation that is on the wrong side of its class boundary.

The linear SVM score function is

$$f(x) = x'\beta + \beta_0,$$

where:

- x is an observation (corresponding to a row of `X`).
- The vector β contains the coefficients that define an orthogonal vector to the hyperplane (corresponding to `SVMModel.Beta`). For separable data, the optimal margin length is $2 / \|\beta\|$.
- β_0 is the bias term (corresponding to `SVMModel.Bias`).

The root of $f(x)$ for particular coefficients defines a hyperplane. For a particular hyperplane, $f(z)$ is the distance from point z to the hyperplane.

An SVM classifier searches for the maximum margin length, while keeping observations in the positive ($y = 1$) and negative ($y = -1$) classes separate. Therefore:

- For separable classes, the objective is to minimize $\|\beta\|$ with respect to the β and β_0 subject to $y_j f(x_j) \geq 1$, for all $j = 1,..,n$. This is the *primal* formalization for separable classes.
- For inseparable classes, SVM uses slack variables (ξ_j) to penalize the objective function for observations that cross the margin boundary for their class. $\xi_j = 0$ for observations that do not cross the margin boundary for their class, otherwise $\xi_j \geq 0$.

  The objective is to minimize $0.5\|\beta\|^2 + C\sum \xi_j$ with respect to the β, β_0, and ξ_j subject to $y_j f(x_j) \geq 1 - \xi_j$ and $\xi_j \geq 0$ for all $j = 1,..,n$, and for a positive scalar box constraint C. This is the primal formalization for inseparable classes.

SVM uses the Lagrange multipliers method to optimize the objective. This introduces n coefficients $\alpha_1,...,\alpha_n$ (corresponding to `SVMModel.Alpha`). The dual formalizations for linear SVM are:

- For separable classes, minimize

  $$0.5\sum_{j=1}^{n}\sum_{k=1}^{n}\alpha_j\alpha_k y_j y_k x_j' x_k - \sum_{j=1}^{n}\alpha_j$$

  with respect to $\alpha_1,...,\alpha_n$, subject to $\sum \alpha_j y_j = 0$, $\alpha_j \geq 0$ for all $j = 1,...,n$, and Karush-Kuhn-Tucker (KKT) complementarity conditions.
- For inseparable classes, the objective is the same as for separable classes, except for the additional condition $0 \leq \alpha_j \leq C$ for all $j = 1,..,n$.

The resulting score function is

$$f(x) = \sum_{j=1}^{n}\alpha_j y_j x' x_j + b.$$

The score function is free of the estimate of β as a result of the primal formalization.

In some cases, there is a nonlinear boundary separating the classes. *Nonlinear SVM* works in a transformed predictor space to find an optimal, separating hyperplane.

The dual formalization for nonlinear SVM is

$$0.5\sum_{j=1}^{n}\sum_{k=1}^{n}\alpha_j\alpha_k y_j y_k G(x_j,x_k)-\sum_{j=1}^{n}\alpha_j$$

with respect to $\alpha_1,...,\alpha_n$, subject to $\sum\alpha_j y_j=0$, $0\le\alpha_j\le C$ for all $j = 1,..,n$, and the KKT complementarity conditions.$G(x_k,x_j)$ are elements of the Gram matrix. The resulting score function is

$$f(x)=\sum_{j=1}^{n}\alpha_j y_j G(x,x_j)+b.$$

For more details, see Understanding Support Vector Machines, [1], and [3].

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Train a Support Vector Machine Classifier

Load Fisher's iris data set. Remove the sepal lengths and widths, and all observed setosa irises.

```
load fisheriris
inds = ~strcmp(species,'setosa');
X = meas(inds,3:4);
y = species(inds);
```

Train an SVM classifier using the processed data set.

```
SVMModel = fitcsvm(X,y)
```

```
SVMModel =

  ClassificationSVM
      PredictorNames: {'x1'  'x2'}
        ResponseName: 'Y'
          ClassNames: {'versicolor'  'virginica'}
      ScoreTransform: 'none'
     NumObservations: 100
               Alpha: [24x1 double]
                Bias: -14.4149
    KernelParameters: [1x1 struct]
      BoxConstraints: [100x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [100x1 logical]
              Solver: 'SMO'
```

The Command Window shows that `SVMModel` is a trained `ClassificationSVM` classifier and a property list. Display the properties of `SVMModel`, for example, to determine the class order, by using dot notation.

```
classOrder = SVMModel.ClassNames
```

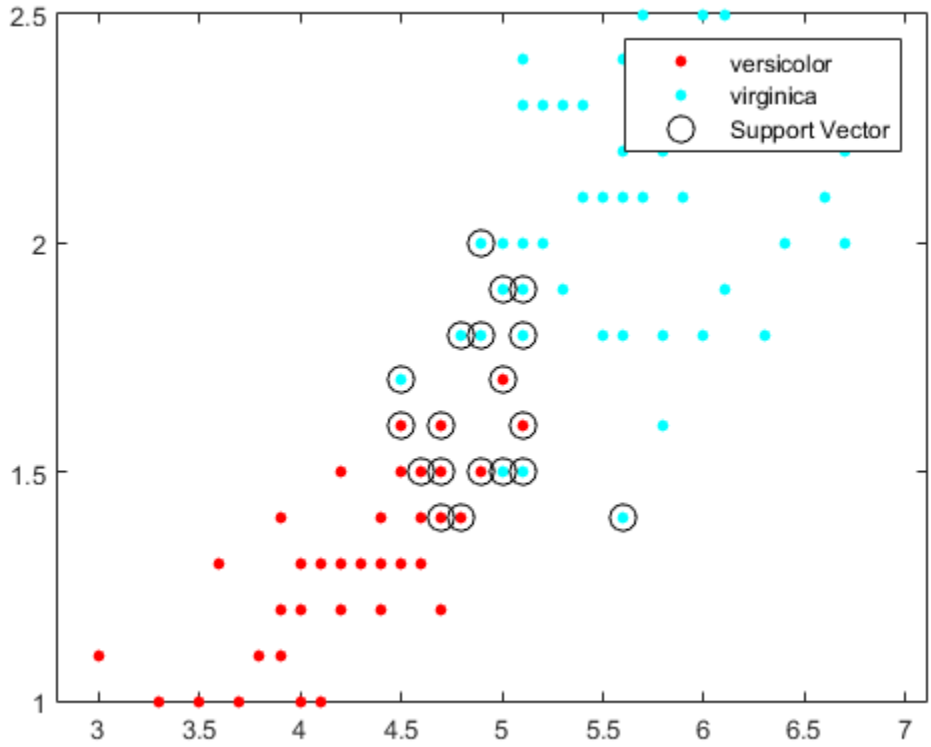
```
classOrder =

    'versicolor'
    'virginica'
```

The first class (`'versicolor'`) is the negative class, and the second (`'virginica'`) is the positive class. You can change the class order during training by using the `'ClassNames'` name-value pair argument.

Plot a scatter diagram of the data and circle the support vectors.

```
sv = SVMModel.SupportVectors;
figure
gscatter(X(:,1),X(:,2),y)
```

```
hold on
plot(sv(:,1),sv(:,2),'ko','MarkerSize',10)
legend('versicolor','virginica','Support Vector')
hold off
```



The support vectors are observations that occur on or beyond their estimated class boundaries.

You can adjust the boundaries (and therefore the number of support vectors) by setting a box constraint during training using the `'BoxConstraint'` name-value pair argument.

Train and Cross Validate Support Vector Machine Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train and cross validate an SVM classifier. It is good practice to standardize the predictors and specify the order of the classes.

```
rng(1);  % For reproducibility
CVSVMModel = fitcsvm(X,Y,'Standardize',true,...
    'ClassNames',{'b','g'},'CrossVal','on')
```

```
CVSVMModel =

  classreg.learning.partition.ClassificationPartitionedModel
    CrossValidatedModel: 'SVM'
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
        NumObservations: 351
                  KFold: 10
              Partition: [1x1 cvpartition]
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
```

`CVSVMModel` is not a `ClassificationSVM` classifier, but a `ClassificationPartitionedModel` cross-validated, SVM classifier. By default, the software implements 10-fold cross validation.

Alternatively, you can cross validate a trained `ClassificationSVM` classifier by passing it to `crossval`.

Inspect one of the trained folds using dot notation.

```
CVSVMModel.Trained{1}
```

```
ans =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
                  Alpha: [78x1 double]
```

```
                Bias: -0.2209
    KernelParameters: [1x1 struct]
                  Mu: [1x34 double]
               Sigma: [1x34 double]
      SupportVectors: [78x34 double]
SupportVectorLabels: [78x1 double]
```

Each fold is a `CompactClassificationSVM` classifier trained on 90% of the data.

Estimate the generalization error.

```
genError = kfoldLoss(CVSVMModel)
```

```
genError =

    0.1168
```

On average, the generalization error is approximately 12%.

- Using Support Vector Machines

Algorithms

- All solvers implement $L1$ soft-margin minimization.
- `fitcsvm` and `svmtrain` use, among other algorithms, SMO for optimization. The software implements SMO differently between the two functions, but numerical studies show that there is sensible agreement in the results.
- For one-class learning, the software estimates the Lagrange multipliers, $\alpha_1,...,\alpha_n$, such that

  $$\sum_{j=1}^{n}\alpha_j = n\nu.$$

- For two-class learning, if you specify a cost matrix C, then the software updates the class prior probabilities (p) to p_c by incorporating the penalties described in C. The formula for the updated prior probability vector is

$$p_c = \frac{p'C}{\sum p'C}.$$

Subsequently, the software resets the cost matrix to the default:

$$C = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}.$$

- If you set `'Standardize',true` when you train the SVM classifier using `fitcsvm`, then the software trains the classifier using the standardized predictor matrix, but stores the unstandardized data in the classifier property `X`. However, if you standardize the data, then the data size in memory doubles until optimization ends.
- If you set `'Standardize',true` and any of `'Cost'`, `'Prior'`, or `'Weights'`, then the software standardizes the predictors using their corresponding weighted means and weighted standard deviations.
- Let `p` be the proportion of outliers you expect in the training data. If you use `'OutlierFraction',p` when you train the SVM classifier using `fitcsvm`, then:
  - For one-class learning, the software trains the bias term such that 100`p`% of the observations in the training data have negative scores.
  - The software implements *robust learning* for two-class learning. In other words, the software attempts to remove 100`p`% of the observations when the optimization algorithm converges. The removed observations correspond to gradients that are large in magnitude.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[2] Scholkopf, B., J. C. Platt, J. C. Shawe-Taylor, A. J. Smola, and R. C. Williamson. "Estimating the Support of a High-Dimensional Distribution." *Neural Comput.*, Vol. 13, Number 7, 2001, pp. 1443–1471.

[3] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[4] Scholkopf, B. and A. Smola. *Learning with Kernels: Support Vector Machines, Regularization, Optimization and Beyond, Adaptive Computation and Machine Learning* Cambridge, MA: The MIT Press, 2002.

See Also

`ClassificationPartitionedModel` | `CompactClassificationSVM` | `fitcsvm`

More About

- Understanding Support Vector Machines

ClassificationTree class

Superclasses: CompactClassificationTree

Binary decision tree for classification

Description

A decision tree with binary splits for classification. An object of class `ClassificationTree` can predict responses for new data with the `predict` method. The object contains the data used for training, so can compute resubstitution predictions.

Construction

`tree = fitctree(X,Y)` returns a classification tree based on the input variables (also known as predictors, features, or attributes) X and output (response) Y. tree is a binary tree, where each branching node is split based on the values of a column of X.

`tree = fitctree(X,Y,Name,Value)` fits a tree with additional options specified by one or more Name,Value pair arguments. If you use one of the following five options, `tree` is of class `ClassificationPartitionedModel`: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. Otherwise, `tree` is of class `ClassificationTree`.

Input Arguments

X

A matrix of numeric predictor values. Each column of X represents one variable, and each row represents one observation.

`NaN` values in X are taken to be missing values. Observations with all missing values for X are not used in the fit. Observations with some missing values for X are used to find splits on variables for which these observations have valid values.

Y

A categorical array, cell array of strings, character array, logical vector, or a numeric vector with the same number of rows as `X`. Each row of y represents the classification

of the corresponding row of X. For numeric Y, consider using `fitrtree` instead of `fitctree`.

`NaN` values in Y are taken to be missing values. Observations with missing values for Y are not used in the fit.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'AlgorithmForCategorical'` — Algorithm for best categorical predictor split

`'Exact' | 'PullLeft' | 'PCA' | 'OVAbyClass'`

Algorithm to find the best split on a categorical predictor with C categories for data and $K \geq 3$ classes, specified as the comma-separated pair consisting of `'AlgorithmForCategorical'` and one of the following.

`'Exact'`	Consider all $2^{C-1} - 1$ combinations.
`'PullLeft'`	Start with all C categories on the right branch. Consider moving each category to the left branch as it achieves the minimum impurity for the K classes among the remaining categories. From this sequence, choose the split that has the lowest impurity.
`'PCA'`	Compute a score for each category using the inner product between the first principal component of a weighted covariance matrix (of the centered class probability matrix) and the vector of class probabilities for that category. Sort the scores in ascending order, and consider all $C - 1$ splits.
`'OVAbyClass'`	Start with all C categories on the right branch. For each class, order the categories based on their probability for that class. For the first class, consider moving each

category to the left branch in order, recording the impurity criterion at each move. Repeat for the remaining classes. From this sequence, choose the split that has the minimum impurity.

`fitctree` automatically selects the optimal subset of algorithms for each split using the known number of classes and levels of a categorical predictor. For $K = 2$ classes, `fitctree` always performs the exact search. Use the `'AlgorithmForCategorical'` name-value pair argument to specify a particular algorithm.

Example: `'AlgorithmForCategorical','PCA'`

`'CategoricalPredictors'` — Categorical predictors list

numeric or logical vector | cell array of strings | character matrix | `'all'`

Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following:

- A numeric vector with indices from `1` through `p`, where `p` is the number of columns of X.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of X is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in `PredictorNames` values.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in `PredictorNames` values. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

Example: `'CategoricalPredictors','all'`

Data Types: `single` | `double` | `char`

`'ClassNames'` — Class names

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and an array representing the class names. Use the same data type as the values that exist in Y.

Use `ClassNames` to order the classes or to select a subset of classes for training. The default is the class names that exist in Y.

Data Types: `single` | `double` | `char` | `logical` | `cell`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification of a point, specified as the comma-separated pair consisting of `'Cost'` and one of the following:

- Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.
- Structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same data type as Y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Data Types: `single` | `double` | `struct`

`'CrossVal'` — Flag to grow cross-validated decision tree

`'off'` (default) | `'on'`

Flag to grow a cross-validated decision tree, specified as the comma-separated pair consisting of `'CrossVal'` and `'on'` or `'off'`.

If `'on'`, `fitctree` grows a cross-validated decision tree with 10 folds. You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments. Note that you can only use one of these four arguments at a time when creating a cross-validated tree.

Alternatively, cross validate tree later using the `crossval` method.

Example: `'CrossVal','on'`

`'CVPartition'` — Partition for cross-validated tree

`cvpartition` object

Partition to use in a cross-validated tree, specified as the comma-separated pair consisting of `'CVPartition'` and an object created using `cvpartition`.

If you use `'CVPartition'`, you cannot use any of the `'KFold'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

`'Holdout'` — Fraction of data for holdout validation
`0` (default) | scalar value in the range `[0,1]`

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the rest of the data for training.

If you use `'Holdout'`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single` | `double`

`'KFold'` — Number of folds
`10` (default) | positive integer value

Number of folds to use in a cross-validated tree, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

If you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag
`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and `'on'` or `'off'`. Specify `'on'` to use leave-one-out cross-validation.

If you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

`'MaxNumCategories'` — Maximum category levels
`10` (default) | nonnegative scalar value

Maximum category levels, specified as the comma-separated pair consisting of `'MaxNumCategories'` and a nonnegative scalar value. `fitctree` splits a

categorical predictor using the exact search algorithm if the predictor has at most `MaxNumCategories` levels in the split node. Otherwise, `fitctree` finds the best categorical split using one of the inexact algorithms.

Passing a small value can lead to loss of accuracy and passing a large value can increase computation time and memory overload.

Example: `'MaxNumCategories',8`

`'MaxNumSplits'` — Maximal number of decision splits

`size(X,1) - 1` (default) | positive integer

Maximal number of decision splits (or branch nodes), specified as the comma-separated pair consisting of `'MaxNumSplits'` and a positive integer. `ClassificationTree` splits `MaxNumSplits` or fewer branch nodes. For more details on splitting behavior, see Algorithms.

Example: `'MaxNumSplits',5`

Data Types: `single` | `double`

`'MergeLeaves'` — Leaf merge flag

`'on'` (default) | `'off'`

Leaf merge flag, specified as the comma-separated pair consisting of `'MergeLeaves'` and `'on'` or `'off'`.

If `MergeLeaves` is `'on'`, then `ClassificationTree`:

- Merges leaves that originate from the same parent node, and that yields a sum of risk values greater or equal to the risk associated with the parent node
- Estimates the optimal sequence of pruned subtrees, but does not prune the classification tree

Otherwise, `ClassificationTree` does not merge leaves.

Example: `'MergeLeaves','off'`

`'MinLeafSize'` — Minimum number of leaf node observations

1 (default) | positive integer value

Minimum number of leaf node observations, specified as the comma-separated pair consisting of `'MinLeafSize'` and a positive integer value. Each leaf has at least `MinLeafSize` observations per tree leaf. If you supply both `MinParentSize` and

`MinLeafSize`, `fitctree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinLeafSize',3`

Data Types: `single | double`

`'MinParentSize'` — Minimum number of branch node observations
`10` (default) | positive integer value

Minimum number of branch node observations, specified as the comma-separated pair consisting of `'MinParentSize'` and a positive integer value. Each branch node in the tree has at least `MinParentSize` observations. If you supply both `MinParentSize` and `MinLeafSize`, `fitctree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinParentSize',8`

Data Types: `single | double`

`'NumVariablesToSample'` — Number of predictors to select at random for each split
`'all'` | positive integer value

Number of predictors to select at random for each split, specified as the comma-separated pair consisting of `'NumVariablesToSample'` and a positive integer value. You can also specify `'all'` to use all available predictors.

Example: `'NumVariablesToSample',3`

Data Types: `single | double`

`'PredictorNames'` — Predictor variable names
`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in X.

`'Prior'` — Prior probabilities
`'empirical'` (default) | `'uniform'` | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- A string:

  - `'empirical'` determines class probabilities from class frequencies in Y. If you pass observation weights, `fitctree` uses the weights to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class). To specify the class order for the corresponding elements of `Prior`, additionally specify the ClassNames name-value pair argument.
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as Y
  - `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `weights` and `prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Example: `'Prior','uniform'`

`'Prune'` — Flag to estimate optimal sequence of pruned subtrees
`'on'` (default) | `'off'`

Flag to estimate the optimal sequence of pruned subtrees, specified as the comma-separated pair consisting of `'Prune'` and `'on'` or `'off'`.

If `Prune` is `'on'`, then `ClassificationTree` grows the classification tree without pruning it, but estimates the optimal sequence of pruned subtrees. Otherwise, `ClassificationTree` grows the classification tree without estimating the optimal sequence of pruned subtrees.

To prune a trained `ClassificationTree` model, pass it to `prune`.

Example: `'Prune','off'`

`'PruneCriterion'` — Pruning criterion
`'error'` (default) | `'impurity'`

Pruning criterion, specified as the comma-separated pair consisting of `'PruneCriterion'` and `'error'` or `'impurity'`.

Example: `'PruneCriterion','impurity'`

`'ResponseName'` — Response variable name
`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string representing the name of the response variable Y.

Example: `'ResponseName','Response'`

`'ScoreTransform'` — Score transform function

`'none'` | `'symmetric'` | `'invlogit'` | `'ismax'` | function handle | ...

Score transform function, specified as the comma-separated pair consisting of `'ScoreTransform'` and a function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Alternatively, you can specify one of the following strings representing a built-in transformation function.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to 0.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to -1.

Example: `'ScoreTransform','logit'`

`'SplitCriterion'` — Split criterion

`'gdi'` (default) | `'twoing'` | `'deviance'`

Split criterion, specified as the comma-separated pair consisting of `'SplitCriterion'` and `'gdi'` (Gini's diversity index), `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction (also known as cross entropy).

Example: `'SplitCriterion','deviance'`

`'Surrogate'` — Surrogate decision splits flag

`'off'` | `'on'` | `'all'` | positive integer value

Surrogate decision splits flag, specified as the comma-separated pair consisting of `'Surrogate'` and `'on'`, `'off'`, `'all'`, or a positive integer value.

- When set to `'on'`, `fitctree` finds at most 10 surrogate splits at each branch node.
- When set to `'all'`, `fitctree` finds all surrogate splits at each branch node. The `'all'` setting can use considerable time and memory.
- When set to a positive integer value, `fitctree` finds at most the specified number of surrogate splits at each branch node.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also lets you compute measures of predictive association between predictors.

Example: `'Surrogate','on'`

`'Weights'` — Observation weights

`ones(size(x,1),1)` (default) | vector of scalar values

Vector of observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` equals the number of rows in `X`. `fitctree` normalizes the weights in each class to add up to the value of the prior probability of the class.

Data Types: `single` | `double`

Properties

`CategoricalPredictors`

List of categorical predictors, a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CategoricalSplits`

An n-by-2 cell array, where n is the number of categorical splits in tree. Each row in `CategoricalSplits` gives left and right values for a categorical split. For each branch node with categorical split `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `CategoricalSplits(j,1)` and the right child is chosen if `z` is in

`CategoricalSplits(j,2)`. The splits are in the same order as nodes of the tree. Find the nodes for these splits by selecting `'categorical'` cuts from top to bottom in the `CutType` property.

`Children`

An *n*-by-2 array containing the numbers of the child nodes for each node in tree, where *n* is the number of nodes. Leaf nodes have child node `0`.

`ClassCount`

An *n*-by-*k* array of class counts for the nodes in tree, where *n* is the number of nodes and *k* is the number of classes. For any node number `i`, the class counts `ClassCount(i,:)` are counts of observations (from the data used in fitting the tree) from each class satisfying the conditions for node `i`.

`ClassNames`

List of the elements in Y with duplicates removed. `ClassNames` can be a categorical array, cell array of strings, character array, logical vector, or a numeric vector. `ClassNames` has the same data type as the data in the argument Y.

`ClassProbability`

An *n*-by-*k* array of class probabilities for the nodes in tree, where *n* is the number of nodes and *k* is the number of classes. For any node number `i`, the class probabilities `ClassProbability(i,:)` are the estimated probabilities for each class for a point satisfying the conditions for node `i`.

`Cost`

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames. The number of rows and columns in `Cost` is the number of unique classes in the response. This property is read-only.

`CutCategories`

An *n*-by-2 cell array of the categories used at branches in tree, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `X`, the left child is chosen if `X` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `X` is among those listed in `CutCategories{i,2}`. Both columns of

`CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutPoint`

An n-element vector of the values used as cut points in tree, where n is the number of nodes. For each branch node `i` based on a continuous predictor variable `X`, the left child is chosen if `X<CutPoint(i)` and the right child is chosen if `X>=CutPoint(i)`. `CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutType`

An n-element cell array indicating the type of cut at each node in tree, where n is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `X < v` for a variable `X` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `X` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutPredictor`

An n-element cell array of the names of the variables used for branching in each node in tree, where n is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `CutPredictor` contains an empty string.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`IsBranchNode`

An n-element logical vector that is `true` for each branch node and `false` for each leaf node of tree.

`ModelParameters`

Parameters used in training tree. To display all parameter values, enter `tree.ModelParameters`. To access a particular parameter, use dot notation.

`NumObservations`

Number of observations in the training data, a numeric scalar. `NumObservations` can be less than the number of rows of input data X when there are missing values in X or response Y.

`NodeClass`

An n-element cell array with the names of the most probable classes in each node of tree, where n is the number of nodes in the tree. Every element of this array is a string equal to one of the class names in ClassNames.

`NodeError`

An n-element vector of the errors of the nodes in tree, where n is the number of nodes. `NodeError(i)` is the misclassification probability for node `i`.

`NodeProbability`

An n-element vector of the probabilities of the nodes in tree, where n is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

`NodeRisk`

An n-element vector of the risk of the nodes in the tree, where n is the number of nodes. The risk for each node is the measure of impurity (Gini index or deviance) for this node weighted by the node probability. If the tree is grown by twoing, the risk for each node is zero.

`NodeSize`

An n-element vector of the sizes of the nodes in tree, where n is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

`NumNodes`

The number of nodes in tree.

Parent

An n-element vector containing the number of the parent node for each node in tree, where n is the number of nodes. The parent of the root node is `0`.

PredictorNames

Cell array of strings containing the predictor names, in the order which they appear in `X`.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames. The number of elements of `Prior` is the number of unique classes in the response. This property is read-only.

PruneAlpha

Numeric vector with one element per pruning level. If the pruning level ranges from 0 to M, then `PruneAlpha` has $M + 1$ elements sorted in ascending order. `PruneAlpha(1)` is for pruning level 0 (no pruning), `PruneAlpha(2)` is for pruning level 1, and so on.

PruneList

An n-element numeric vector with the pruning levels in each node of tree, where n is the number of nodes. The pruning levels range from 0 (no pruning) to M, where M is the distance between the deepest leaf and the root node.

ResponseNames

String describing the response variable `Y`.

ScoreTransform

Function handle for transforming predicted classification scores, or string representing a built-in transformation function.

`none` means no transformation, or `@(x)x`.

To change the score transformation function to, e.g., *`function`*, use dot notation.

- For available functions (see `fitctree`), enter

  ```
  Mdl.ScoreTransform = 'function';
  ```

- You can set a function handle for an available function, or a function you define yourself by entering

  ```
  tree.ScoreTransform = @function;
  ```

SurrogateCutCategories

An n-element cell array of the categories used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutCategories{k}` is a cell array. The length of `SurrogateCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutCategories{k}` is either an empty string for a continuous surrogate predictor, or is a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split, and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutCategories` contains an empty cell.

SurrogateCutFlip

An n-element cell array of the numeric cut assignments used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutFlip{k}` is a numeric vector. The length of `SurrogateCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and the cut assignment for this surrogate split is +1, or if $Z\geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and the cut assignment for this surrogate split is +1, or if $Z<C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutFlip` contains an empty array.

SurrogateCutPoint

An n-element cell array of the numeric values used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutPoint{k}` is a numeric vector. The length of `SurrogateCutPoint{k}` is equal to the number of surrogate

predictors found at this node. Every element of `SurrogateCutPoint{k}` is either `NaN` for a categorical surrogate predictor, or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `SurrogateCutFlip` for this surrogate split is +1, or if $Z\geq C$ and `SurrogateCutFlip` for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and `SurrogateCutFlip` for this surrogate split is +1, or if $Z<C$ and `SurrogateCutFlip` for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutPoint` contains an empty cell.

SurrogateCutType

An n-element cell array indicating types of surrogate splits at each node in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutType{k}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutType` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cut point `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

SurrogateCutPredictor

An n-element cell array of the names of the variables used for surrogate splits in each node in tree, where n is the number of nodes in tree. Every element of `SurrogateCutPredictor` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutPredictor` contains an empty cell.

SurrogatePredictorAssociation

An n-element cell array of the predictive measures of association for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogatePredictorAssociation{k}` is a numeric vector. The length of `SurrogatePredictorAssociation{k}` is equal to the number of surrogate predictors

found at this node. Every element of `SurrogatePredictorAssociation{k}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogatePredictorAssociation` contains an empty cell.

`W`

The scaled weights, a vector with length `n`, the number of rows in X.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A categorical array, cell array of strings, character array, logical vector, or a numeric vector. Each row of `Y` represents the classification of the corresponding row of `X`.

Methods

compact	Compact tree
crossval	Cross-validated decision tree
cvloss	Classification error by cross validation
prune	Produce sequence of subtrees by pruning
resubEdge	Classification edge by resubstitution
resubLoss	Classification error by resubstitution
resubMargin	Classification margins by resubstitution
resubPredict	Predict resubstitution response of tree

Inherited Methods

compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge
loss	Classification error
margin	Classification margins
surrogateAssociation	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict classification
predictorImportance	Estimates of predictor importance
view	View tree

Definitions

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*.

Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair argument:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

$$1 - \sum_i p^2(i),$$

where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined the same as for the Gini index, the deviance of a node is

$$-\sum_i p(i)\log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

$$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

  where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with the largest number of training samples at a node, the node error is $1 - p(j)$.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a Classification Tree

Construct a classification tree for the data in `ionosphere.mat`.

```
load ionosphere
tc = fitctree(X,Y)
```

```
tc =

  ClassificationTree
             PredictorNames: {1x34 cell}
               ResponseName: 'Y'
                 ClassNames: {'b'  'g'}
             ScoreTransform: 'none'
    CategoricalPredictors: []
             NumObservations: 351


  Properties, Methods
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`ClassificationEnsemble` | `fitctree` | `predict` | `RegressionTree` | `CompactClassificationTree`

How To

- “Classification Trees and Regression Trees” on page 16-33

classify

Discriminant analysis

Compatibility

`classify` will be removed in a future release. Use `fitcdiscr` instead.

Syntax

```
class = classify(sample,training,group)
class = classify(sample,training,group,'type')
class = classify(sample,training,group,'type',prior)
[class,err] = classify(...)
[class,err,POSTERIOR] = classify(...)
[class,err,POSTERIOR,logp] = classify(...)
[class,err,POSTERIOR,logp,coeff] = classify(...)
```

Description

`class = classify(sample,training,group)` classifies each row of the data in `sample` into one of the groups in `training`. `sample` and `training` must be matrices with the same number of columns. `group` is a grouping variable for `training`. Its unique values define groups; each element defines the group to which the corresponding row of `training` belongs. `group` can be a categorical variable, a numeric vector, a string array, or a cell array of strings. `training` and `group` must have the same number of rows. `classify` treats `NaN`s or empty strings in `group` as missing values, and ignores the corresponding rows of `training`. The output `class` indicates the group to which each row of `sample` has been assigned, and is of the same type as `group`.

`class = classify(sample,training,group,'type')` allows you to specify the type of discriminant function. Specify *`type`* inside single quotes. *`type`* is one of:

- `linear` — Fits a multivariate normal density to each group, with a pooled estimate of covariance. This is the default.
- `diaglinear` — Similar to `linear`, but with a diagonal covariance matrix estimate (naive Bayes classifiers).

- `quadratic` — Fits multivariate normal densities with covariance estimates stratified by group.
- `diagquadratic` — Similar to `quadratic`, but with a diagonal covariance matrix estimate (naive Bayes classifiers).
- `mahalanobis` — Uses Mahalanobis distances with stratified covariance estimates.

`class = classify(sample,training,group,'type',prior)` allows you to specify prior probabilities for the groups. *`prior`* is one of:

- A numeric vector the same length as the number of unique values in `group` (or the number of levels defined for `group`, if `group` is categorical). If `group` is numeric or categorical, the order of *`prior`* must correspond to the ordered values in `group`, or, if `group` contains strings, to the order of first occurrence of the values in `group`.
- A 1-by-1 structure with fields:
  - `prob` — A numeric vector.
  - `group` — Of the same type as `group`, containing unique values indicating the groups to which the elements of `prob` correspond.

  As a structure, *`prior`* can contain groups that do not appear in `group`. This can be useful if `training` is a subset a larger training set. `classify` ignores any groups that appear in the structure but not in the `group` array.
- The string `'empirical'`, indicating that group prior probabilities should be estimated from the group relative frequencies in `training`.

`prior` defaults to a numeric vector of equal probabilities, i.e., a uniform distribution. *`prior`* is not used for discrimination by Mahalanobis distance, except for error rate calculation.

`[class,err] = classify(...)` also returns an estimate `err` of the misclassification error rate based on the `training` data. `classify` returns the apparent error rate, i.e., the percentage of observations in `training` that are misclassified, weighted by the prior probabilities for the groups.

`[class,err,POSTERIOR] = classify(...)` also returns a matrix `POSTERIOR` of estimates of the posterior probabilities that the *j*th training group was the source of the *i*th sample observation, i.e., *Pr*(*group j*|*obs i*). `POSTERIOR` is not computed for Mahalanobis discrimination.

`[class,err,POSTERIOR,logp] = classify(...)` also returns a vector `logp` containing estimates of the logarithms of the unconditional predictive probability density of the sample observations, $p(obs\ i) = \sum p(obs\ i \mid group\ j) Pr(group\ j)$ over all groups. `logp` is not computed for Mahalanobis discrimination.

`[class,err,POSTERIOR,logp,coeff] = classify(...)` also returns a structure array `coeff` containing coefficients of the boundary curves between pairs of groups. Each element `coeff(I,J)` contains information for comparing group `I` to group `J` in the following fields:

- `type` — Type of discriminant function, from the *`type`* input.
- `name1` — Name of the first group.
- `name2` — Name of the second group.
- `const` — Constant term of the boundary equation (K)
- `linear` — Linear coefficients of the boundary equation (L)
- `quadratic` — Quadratic coefficient matrix of the boundary equation (Q)

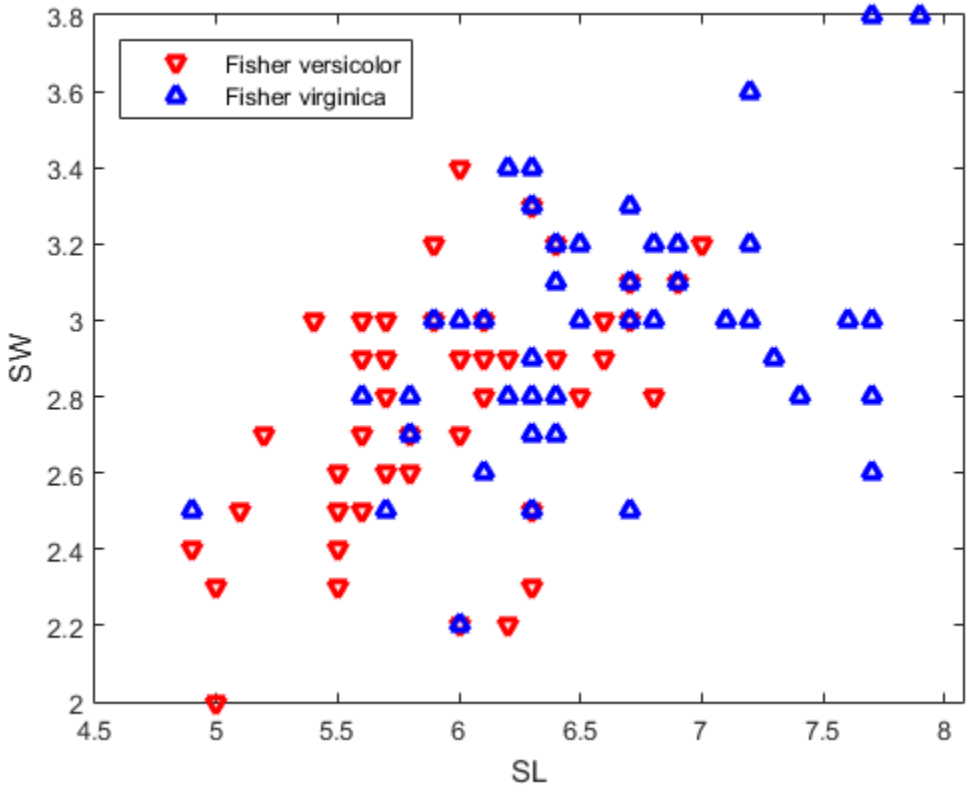
For the `linear` and `diaglinear` types, the `quadratic` field is absent, and a row `x` from the `sample` array is classified into group `I` rather than group `J` if `0 < K+x*L`. For the other types, `x` is classified into group `I` if `0 < K+x*L+x*Q*x'`.

Examples

Classify Using Discriminant Analysis

For training data, use Fisher's sepal measurements for iris versicolor and virginica:

```
load fisheriris
SL = meas(51:end,1);
SW = meas(51:end,2);
group = species(51:end);
h1 = gscatter(SL,SW,group,'rb','v^',[],'off');
set(h1,'LineWidth',2)
legend('Fisher versicolor','Fisher virginica',...
       'Location','NW')
```



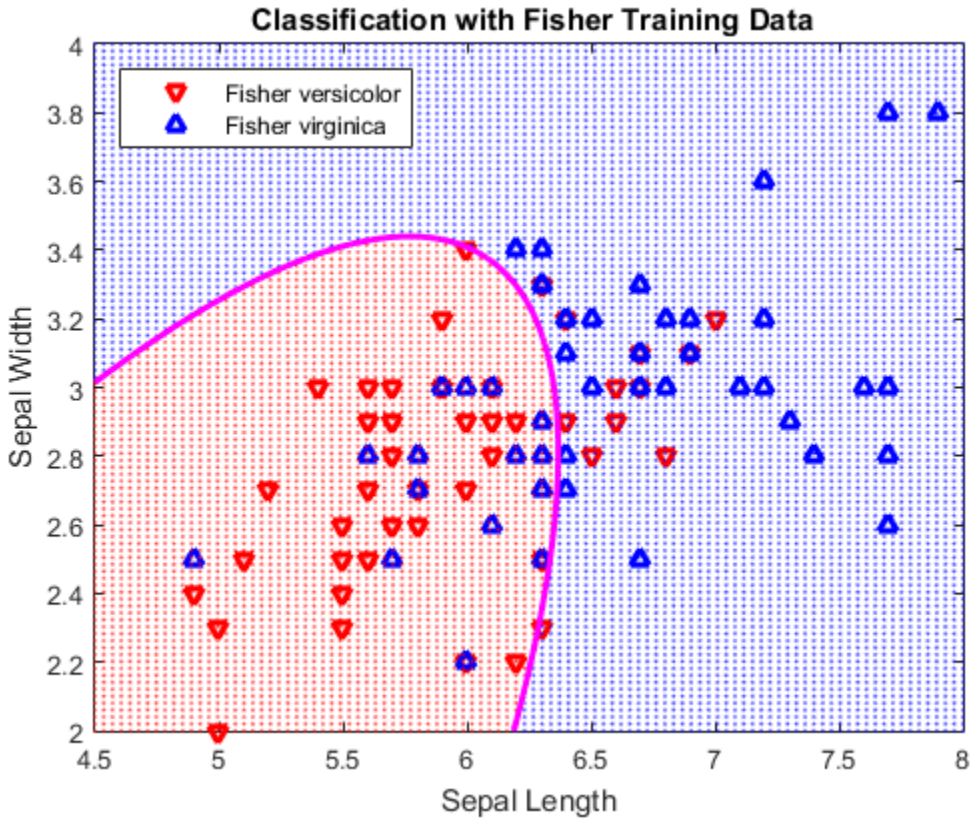
Classify a grid of measurements on the same scale:

```
[X,Y] = meshgrid(linspace(4.5,8),linspace(2,4));
X = X(:); Y = Y(:);
[C,err,P,logp,coeff] = classify([X Y],[SL SW],...
                                 group,'Quadratic');
```

Visualize the classification:

```
hold on;
gscatter(X,Y,C,'rb','.',1,'off');
K = coeff(1,2).const;
L = coeff(1,2).linear;
Q = coeff(1,2).quadratic;
% Function to compute K + L*v + v'*Q*v for multiple vectors
```

```
% v=[x;y]. Accepts x and y as scalars or column vectors.
f = @(x,y) K + [x y]*L + sum(([x y]*Q) .* [x y], 2);

h2 = ezplot(f,[4.5 8 2 4]);
set(h2,'Color','m','LineWidth',2)
axis([4.5 8 2 4])
xlabel('Sepal Length')
ylabel('Sepal Width')
title('{\bf Classification with Fisher Training Data}')
```



More About

- "Grouping Variables" on page 2-52

References

[1] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[2] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`mahal` | `fitctree` | `fitNaiveBayes`

classname

Class: classregtree

Class names for classification decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
CNAMES = classname(T)
CNAMES = classname(T,J)
```

Description

`CNAMES = classname(T)` returns a cell array of strings with class names for this classification decision tree.

`CNAMES = classname(T,J)` takes an array `J` of class numbers and returns the class names for the specified numbers.

See Also

`classregtree`

ClassNames property

Class: TreeBagger

Names of classes

Description

The `ClassNames` property is a cell array containing the class names for the response variable `Y`. This property is empty for regression trees.

classprob

Class: classregtree

Class probabilities

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
P = classprob(t)
P = classprob(t,nodes)
```

Description

`P = classprob(t)` returns an *n*-by-*m* array `P` of class probabilities for the nodes in the classification tree `t`, where *n* is the number of nodes and *m* is the number of classes. For any node number `i`, the class probabilities `P(i,:)` are the estimated probabilities for each class for a point satisfying the conditions for node `i`.

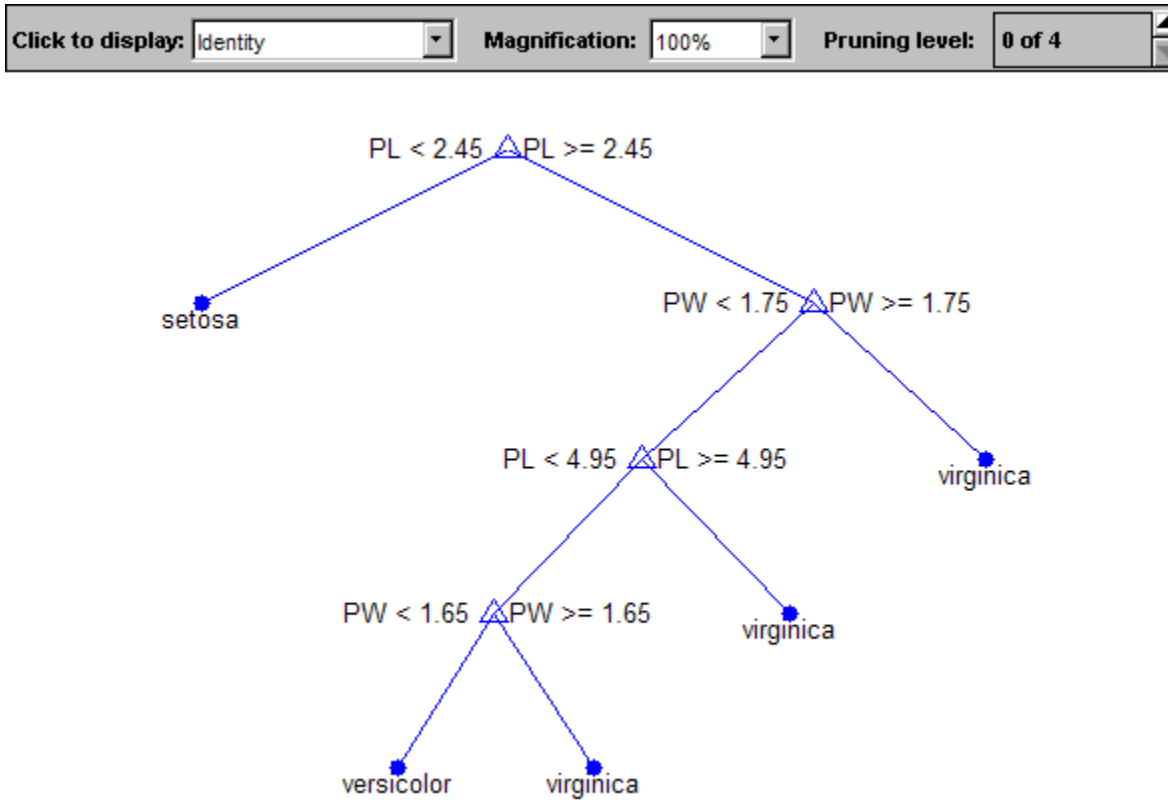
`P = classprob(t,nodes)` takes a vector `nodes` of node numbers and returns the class probabilities for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
```

```
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
P = classprob(t)
P =
    0.3333    0.3333    0.3333
    1.0000         0         0
         0    0.5000    0.5000
```

```
0    0.9074    0.0926
0    0.0217    0.9783
0    0.9792    0.0208
0    0.3333    0.6667
0    1.0000         0
0         0    1.0000
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes`

classregtree class

Classification and regression trees

Compatibility

Use `ClassificationTree` and `RegressionTree` classes instead. This class is superseded by `ClassificationTree` and `RegressionTree` classes and is maintained only for backwards compatibility.

Construction

.classregtree	Construct classification and regression trees

Methods

catsplit	Categorical splits used for branches in decision tree
children	Child nodes
classcount	Class counts
classname	Class names for classification decision tree
classprob	Class probabilities
cutcategories	Cut categories
cutpoint	Decision tree cut point values

cuttype	Cut types
cutvar	Cut variable names
disp	Display `classregtree` object
display	Display `classregtree` object
eval	Predicted responses
isbranch	Test node for branch
meansurrvarassoc	Mean predictive measure of association for surrogate splits in decision tree
nodeclass	Class values of nodes of classification tree
nodeerr	Return vector of node errors
nodemean	Mean values of nodes of regression tree
nodeprob	Node probabilities
nodesize	Return node size
numnodes	Number of nodes
parent	Parent node
prune	Prune tree
prunelist	Pruning levels for decision tree nodes

risk	Node risks
subsasgn	Subscripted reference for `classregtree` object
subsref	Subscripted reference for `classregtree` object
surrcutcategories	Categories used for surrogate splits in decision tree
surrcutflip	Numeric cutpoint assignments used for surrogate splits in decision tree
surrcutpoint	Cutpoints used for surrogate splits in decision tree
surrcuttype	Types of surrogate splits used at branches in decision tree
surrcutvar	Variables used for surrogate splits in decision tree
surrvarassoc	Predictive measure of association for surrogate splits in decision tree
test	Error rate
type	Tree type
varimportance	Compute embedded estimates of input feature importance
view	Plot tree

Properties

Objects of the `classregtree` class have no properties accessible by dot indexing, `get` methods, or `set` methods. To obtain information about a `classregtree` object, use the appropriate method.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

How To

- "Ensemble Methods" on page 16-68
- "Classification Trees and Regression Trees" on page 16-33
- "Grouping Variables" on page 2-52

classregtree

Class: classregtree

Construct classification and regression trees

Compatibility

Use `fitctree` or `fitrtree` instead. This function is superseded by `fitctree` and `fitrtree` of `ClassificationTree` and `RegressionTree` classes. It is maintained only for backwards compatibility.

Syntax

```
t = classregtree(X,y)
t = classregtree(X,y,'Name',value)
```

Description

`t = classregtree(X,y)` creates a decision tree `t` for predicting the response `y` as a function of the predictors in the columns of `X`. `X` is an n-by-m matrix of predictor values. If `y` is a vector of n response values, `classregtree` performs regression. If `y` is a categorical variable, character array, or cell array of strings, `classregtree` performs classification. Either way, `t` is a binary tree where each branching node is split based on the values of a column of `X`. `NaN` values in `X` or `y` are taken to be missing values. Observations with all missing values for `X` or missing values for `y` are not used in the fit. Observations with some missing values for `X` are used to find splits on variables for which these observations have valid values.

`t = classregtree(X,y,'Name',value)` specifies one or more optional parameter name/value pairs. Specify *`Name`* in single quotes. The following options are available:

For all trees:

- `categorical` — Vector of indices of the columns of `X` that are to be treated as unordered categorical variables

- `method` — Either `'classification'` (default if `y` is text or a categorical variable) or `'regression'` (default if `y` is numeric).
- `names` — A cell array of names for the predictor variables, in the order in which they appear in the `X` from which the tree was created.
- `prune` — `'on'` (default) to compute the full tree and the optimal sequence of pruned subtrees, or `'off'` for the full tree without pruning.
- `minparent` — A number *k* such that impure nodes must have *k* or more observations to be split (default is `10`).
- `minleaf` — A minimal number of observations per tree leaf (default is `1`). If you supply both `'minparent'` and `'minleaf'`, `classregtree` uses the setting which results in larger leaves: `minparent = max(minparent,2*minleaf)`
- `mergeleaves` — `'on'` (default) to merge leaves that originate from the same parent node and give the sum of risk values greater or equal to the risk associated with the parent node. If `'off'`, `classregtree` does not merge leaves.
- `nvartosample` — Number of predictor variables randomly selected for each split. By default all variables are considered for each decision split.
- `stream` — Random number stream. Default is the MATLAB default random number stream.
- `surrogate` — `'on'` to find surrogate splits at each branch node. Default is `'off'`. If you set this parameter to `'on'`,`classregtree` can run significantly slower and consume significantly more memory.
- `weights` — Vector of observation weights. By default the weight of every observation is 1. The length of this vector must be equal to the number of rows in `X`.

For regression trees only:

- `qetoler` — Defines tolerance on quadratic error per node for regression trees. Splitting nodes stops when quadratic error per node drops below `qetoler*qed`, where `qed` is the quadratic error for the entire data computed before the decision tree is grown: `qed = norm(y-ybar)` with `ybar` estimated as the average of the input array `Y`. Default value is 1e-6.

For classification trees only:

- `cost` — Square matrix `C`, where `C(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (default has `C(i,j)=1` if `i~=j`, and `C(i,j)=0` if `i=j`). Alternatively, this value can be a structure `S` having two fields: `S.group` containing

the group names as a categorical variable, character array, or cell array of strings; and `S.cost` containing the cost matrix C.

- `splitcriterion` — Criterion for choosing a split. One of `'gdi'` (default) or Gini's diversity index, `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction.
- `priorprob` — Prior probabilities for each class, specified as a string (`'empirical'` or `'equal'`) or as a vector (one value for each distinct group name) or as a structure `S` with two fields:
  - `S.group` containing the group names as a categorical variable, character array, or cell array of strings
  - `S.prob` containing a vector of corresponding probabilities.

  If the input value is `'empirical'` (default), class probabilities are determined from class frequencies in `Y`. If the input value is `'equal'`, all class probabilities are set equal. If both observation weights and class prior probabilities are supplied, the weights are renormalized to add up to the value of the prior probability in the respective class.

Examples

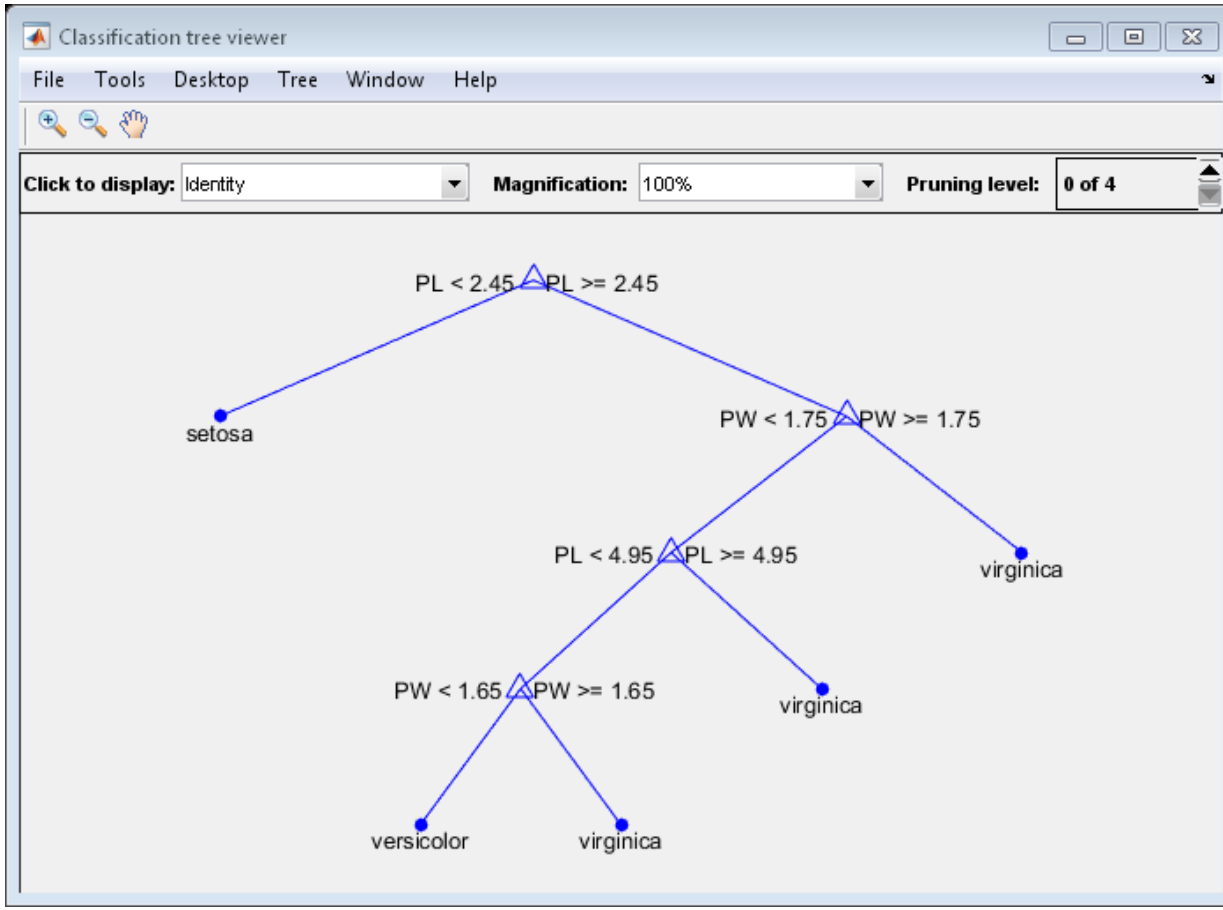
Plot a Classification Tree

Create a classification decision tree for Fisher's iris data:

```
load fisheriris;
t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
view(t)
```

```
t =

Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
```

```
7  class = virginica
8  class = versicolor
9  class = virginica
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`eval` | `test` | `view` | `fitctree` | `fitrtree` | `prune`

How To

- "Grouping Variables" on page 2-52
- "Ensemble Methods" on page 16-68

ClassLevels property

Class: NaiveBayes

Class levels

Description

The `ClassLevels` property is a vector of the same type as the grouping variable, containing the unique levels of the grouping variable.

cluster

Construct agglomerative clusters from linkages

Syntax

```
T = cluster(Z,'cutoff',c)
T = cluster(Z,'cutoff',c,'depth',d)
T = cluster(Z,'cutoff',c,'criterion',criterion)
T = cluster(Z,'maxclust',n)
```

Description

`T = cluster(Z,'cutoff',c)` constructs clusters from the agglomerative hierarchical cluster tree, `Z`, as generated by the `linkage` function. `Z` is a matrix of size (`m` – 1)-by-3, where `m` is the number of observations in the original data. `c` is a threshold for cutting `Z` into clusters. Clusters are formed when a node and all of its subnodes have `inconsistent` value less than `c`. All leaves at or below the node are grouped into a cluster. `t` is a vector of size `m` containing the cluster assignments of each observation.

If `c` is a vector, `T` is a matrix of cluster assignments with one column per cutoff value.

`T = cluster(Z,'cutoff',c,'depth',d)` evaluates inconsistent values by looking to a depth `d` below each node. The default depth is `2`.

`T = cluster(Z,'cutoff',c,'criterion',criterion)` uses the specified criterion for forming clusters, where `criterion` is one of the strings `'inconsistent'` (default) or `'distance'`. The `'distance'` criterion uses the distance between the two subnodes merged at a node to measure node height. All leaves at or below a node with height less than `c` are grouped into a cluster.

`T = cluster(Z,'maxclust',n)` constructs a maximum of `n` clusters using the `'distance'` criterion. `cluster` finds the smallest height at which a horizontal cut through the tree leaves `n` or fewer clusters.

If `n` is a vector, `T` is a matrix of cluster assignments with one column per maximum value.

Examples

Compare clusters from Fisher iris data with species:

```
load fisheriris
d = pdist(meas);
Z = linkage(d);
c = cluster(Z,'maxclust',3:5);

crosstab(c(:,1),species)
ans =
     0     0     2
     0    50    48
    50     0     0

crosstab(c(:,2),species)
ans =
     0     0     1
     0    50    47
     0     0     2
    50     0     0

crosstab(c(:,3),species)
ans =
     0     4     0
     0    46    47
     0     0     1
     0     0     2
    50     0     0
```

See Also

`clusterdata` | `linkage` | `pdist` | `cophenet` | `inconsistent`

cluster

Class: gmdistribution

Construct clusters from Gaussian mixture distribution

Syntax

```
idx = cluster(obj,X)
[idx,nlogl] = cluster(obj,X)
[idx,nlogl,P] = cluster(obj,X)
[idx,nlogl,P,logpdf] = cluster(obj,X)
[idx,nlogl,P,logpdf,M] = cluster(obj,X)
```

Description

`idx = cluster(obj,X)` partitions data in the n-by-d matrix `X`, where n is the number of observations and d is the dimension of the data, into k clusters determined by the k components of the Gaussian mixture distribution defined by `obj`. `obj` is an object created by `gmdistribution` or `fitgmdist`. `idx` is an n-by-1 vector, where `idx(I)` is the cluster index of observation `I`. The cluster index gives the component with the largest posterior probability for the observation, weighted by the component probability.

Note: The data in `X` is typically the same as the data used to create the Gaussian mixture distribution defined by `obj`. Clustering with `cluster` is treated as a separate step, apart from density estimation. For `cluster` to provide meaningful clustering with new data, `X` should come from the same population as the data used to create `obj`.

`cluster` treats `NaN` values as missing data. Rows of `X` with `NaN` values are excluded from the partition.

`[idx,nlogl] = cluster(obj,X)` also returns `nlogl`, the negative log-likelihood of the data.

`[idx,nlogl,P] = cluster(obj,X)` also returns the posterior probabilities of each component for each observation in the n-by-k matrix `P`. `P(I,J)` is the probability of component `J` given observation `I`.

`[idx,nlogl,P,logpdf] = cluster(obj,X)` also returns the n-by-1 vector `logpdf` containing the logarithm of the estimated probability density function for each observation. The density estimate for observation `I` is a sum over all components of the component density at `I` times the component probability.

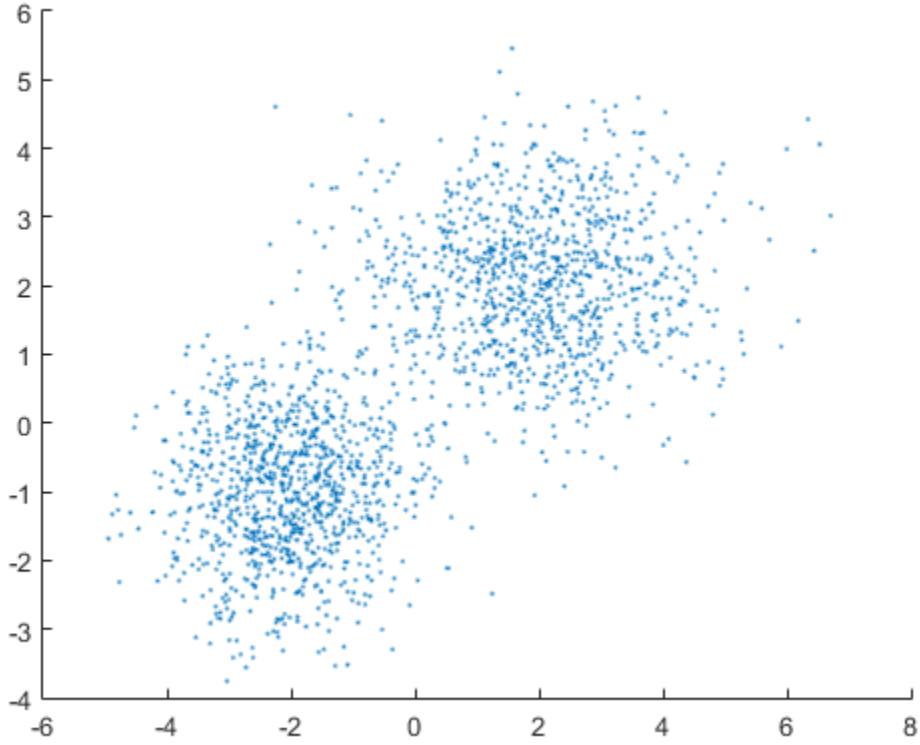
`[idx,nlogl,P,logpdf,M] = cluster(obj,X)` also returns an n-by-k matrix `M` containing Mahalanobis distances in squared units. `M(I,J)` is the Mahalanobis distance of observation `I` from the mean of component `J`.

Examples

Cluster Data from a Gaussian Mixture Distribution

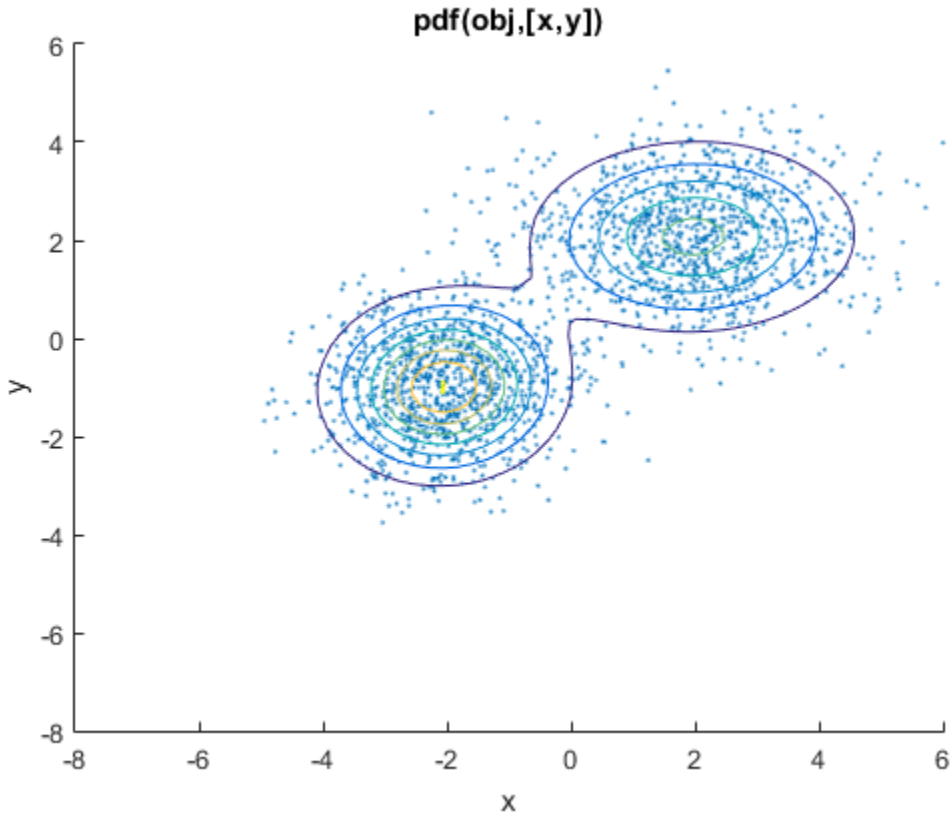
Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function

```
MU1 = [2 2];
SIGMA1 = [2 0; 0 1];
MU2 = [-2 -1];
SIGMA2 = [1 0; 0 1];
rng(1); % For reproducibility
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



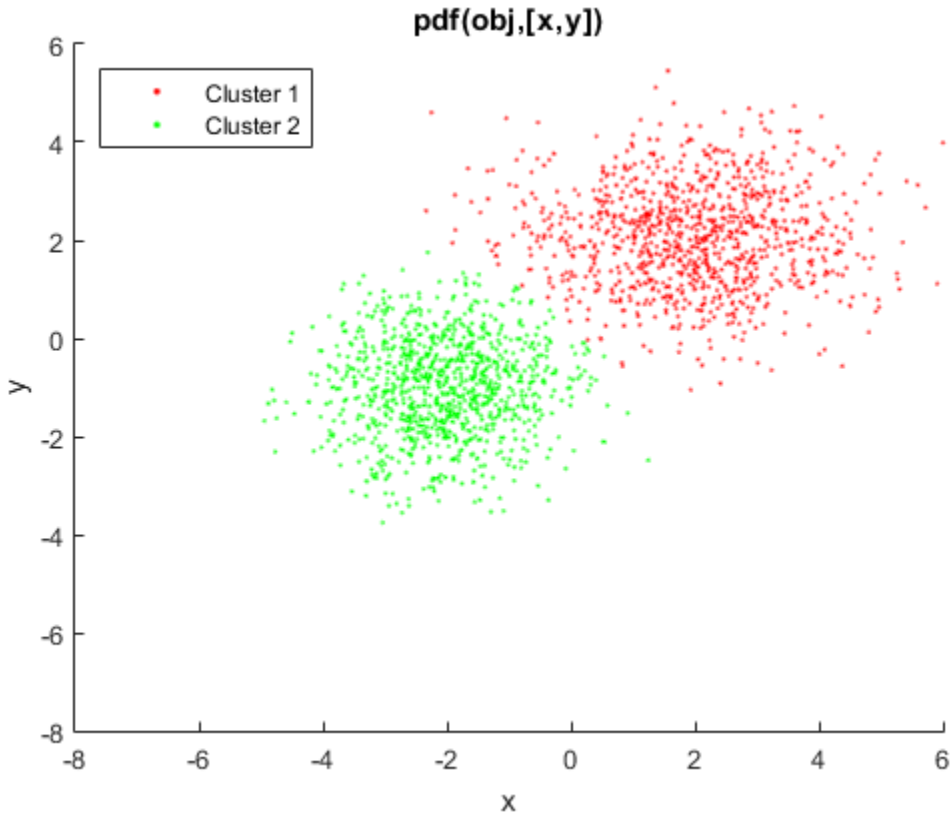
Fit a two-component Gaussian mixture model.

```
obj = fitgmdist(X,2);
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Use the fit to cluster the data.

```
idx = cluster(obj,X);
cluster1 = X(idx == 1,:);
cluster2 = X(idx == 2,:);

delete(h)
h1 = scatter(cluster1(:,1),cluster1(:,2),10,'r.');
h2 = scatter(cluster2(:,1),cluster2(:,2),10,'g.');
legend([h1 h2],'Cluster 1','Cluster 2','Location','NW')
```



See Also

`fitgmdist` | `posterior` | `gmdistribution` | `mahal`

clustering.evaluation.ClusterCriterion class

Package: clustering.evaluation

Clustering evaluation object

Description

Create a clustering evaluation object using `evalclusters`.

Properties

`ClusteringFunction`

Clustering algorithm used to cluster the input data, stored as a valid clustering algorithm name string or function handle. If the clustering solutions are provided in the input, `ClusteringFunction` is empty.

`CriterionName`

Name of the criterion used for clustering evaluation, stored as a valid criterion name string.

`CriterionValues`

Criterion values corresponding to each proposed number of clusters in `InspectedK`, stored as a vector of numerical values.

`InspectedK`

List of the number of proposed clusters for which to compute criterion values, stored as a vector of positive integer values.

`Missing`

Logical flag for excluded data, stored as a column vector of logical values. If `Missing` equals `true`, then the corresponding value in the data matrix `x` is not used in the clustering solution.

`NumObservations`

Number of observations in the data matrix `X`, minus the number of missing (`NaN`) values in `X`, stored as a positive integer value.

`OptimalK`

Optimal number of clusters, stored as a positive integer value.

`OptimalY`

Optimal clustering solution corresponding to `OptimalK`, stored as a column vector of positive integer values. If the clustering solutions are provided in the input, `OptimalY` is empty.

`X`

Data used for clustering, stored as a matrix of numerical values.

Methods

addK	Evaluate additional numbers of clusters
plot	Plot clustering evaluation object criterion values
compact	Compact clustering evaluation object

See Also

`clustering.evaluation.CalinskiHarabaszEvaluation` | `clustering.evaluation.DaviesBouldinEvaluation` | `clustering.evaluation.GapEvaluation` | `clustering.evaluation.SilhouetteEvaluation` | `evalclusters`

More About

- Class Attributes

- Property Attributes

clusterdata

Agglomerative clusters from data

Syntax

```
T = clusterdata(X,cutoff)
T = clusterdata(X,Name,Value)
```

Description

`T = clusterdata(X,cutoff)` returns the cluster indices (`T`) for each observation (row) of the data (`X`) while adhering to a threshold for cutting the hierarchical tree (`cutoff`).

`T = clusterdata(X,Name,Value)` clusters with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`X`

Matrix with two or more rows. The rows represent observations, the columns represent categories or dimensions.

`cutoff`

When `0 < cutoff < 2`, `clusterdata` forms clusters when inconsistent values are greater than `cutoff` (see `inconsistent`). When `cutoff` is an integer ≥ `2`, `clusterdata` interprets `cutoff` as the maximum number of clusters to keep in the hierarchical tree generated by `linkage`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'criterion'`

Either `'inconsistent'` or `'distance'`.

`'cutoff'`

Cutoff for inconsistent or distance measure, a positive scalar. When `0 < cutoff < 2`, `clusterdata` forms clusters when inconsistent values are greater than `cutoff` (see `inconsistent`). When `cutoff` is an integer ≥ `2`, `clusterdata` interprets `cutoff` as the maximum number of clusters to keep in the hierarchical tree generated by `linkage`.

`'depth'`

Depth for computing inconsistent values, a positive integer.

`'distance'`

Any of the distance metric names allowed by `pdist` (follow the `'minkowski'` option by the value of the exponent `p`):

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in X is scaled by dividing by the corresponding element of the standard deviation `S=nanstd(X)`. To specify another value for `S`, use `D=pdist(X,'seuclidean',S)`.
`'cityblock'`	City block metric.
`'minkowski'`	Minkowski distance. The default exponent is 2. To specify a different exponent, use `D = pdist(X,'minkowski',P)`, where `P` is a scalar positive value of the exponent.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist(X,'mahalanobis',C)`, where the matrix `C` is symmetric and positive definite.

Metric	Description
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.

custom distance function	A distance function specified using @:
	`D = pdist(X,@distfun)`
	
	A distance function must be of form
	
	`d2 = distfun(XI,XJ)`
	taking as arguments a 1-by-n vector `XI`, corresponding to a single row of `X`, and an m2-by-n matrix `XJ`, corresponding to multiple rows of `X`. `distfun` must accept a matrix `XJ` with an arbitrary number of rows. `distfun` must return an m2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

`'linkage'`

Any of the linkage methods allowed by the `linkage` function:

- `'average'`
- `'centroid'`
- `'complete'`
- `'median'`
- `'single'`
- `'ward'`
- `'weighted'`

For details, see the definitions in the `linkage` function reference page.

'maxclust'

Maximum number of clusters to form, a positive integer.

'savememory'

A string, either 'on' or 'off'. When applicable, the 'on' setting causes clusterdata to construct clusters without computing the distance matrix. savememory is applicable when:

- linkage is 'centroid', 'median', or 'ward'
- distance is 'euclidean' (default)

When savememory is 'on', linkage run time is proportional to the number of dimensions (number of columns of X). When savememory is 'off', linkage memory requirement is proportional to N^2, where N is the number of observations. So choosing the best (least-time) setting for savememory depends on the problem dimensions, number of observations, and available memory. The default savememory setting is a rough approximation of an optimal setting.

Default: 'on' when X has 20 columns or fewer, or the computer does not have enough memory to store the distance matrix; otherwise 'off'

Output Arguments

T

T is a vector of size m containing a cluster number for each observation.

- When 0 < cutoff < 2, T = clusterdata(X,cutoff) is equivalent to:

```
Y = pdist(X,'euclid');
Z = linkage(Y,'single');
T = cluster(Z,'cutoff',cutoff);
```

- When cutoff is an integer ≥ 2, T = clusterdata(X,cutoff) is equivalent to:

```
Y = pdist(X,'euclid');
Z = linkage(Y,'single');
T = cluster(Z,'maxclust',cutoff);
```

Examples

Create Hierarchical Cluster Tree From Sample Data

This example shows how to create a hierarchical cluster tree from sample data, and visualize the clusters using a 3-dimensional scatter plot.

Generate sample data matrices containing random numbers from the standard uniform distribution.

```
rng default;  % For reproducibility
X = [gallery('uniformdata',[10 3],12);...
    gallery('uniformdata',[10 3],13)+1.2;...
    gallery('uniformdata',[10 3],14)+2.5];
```

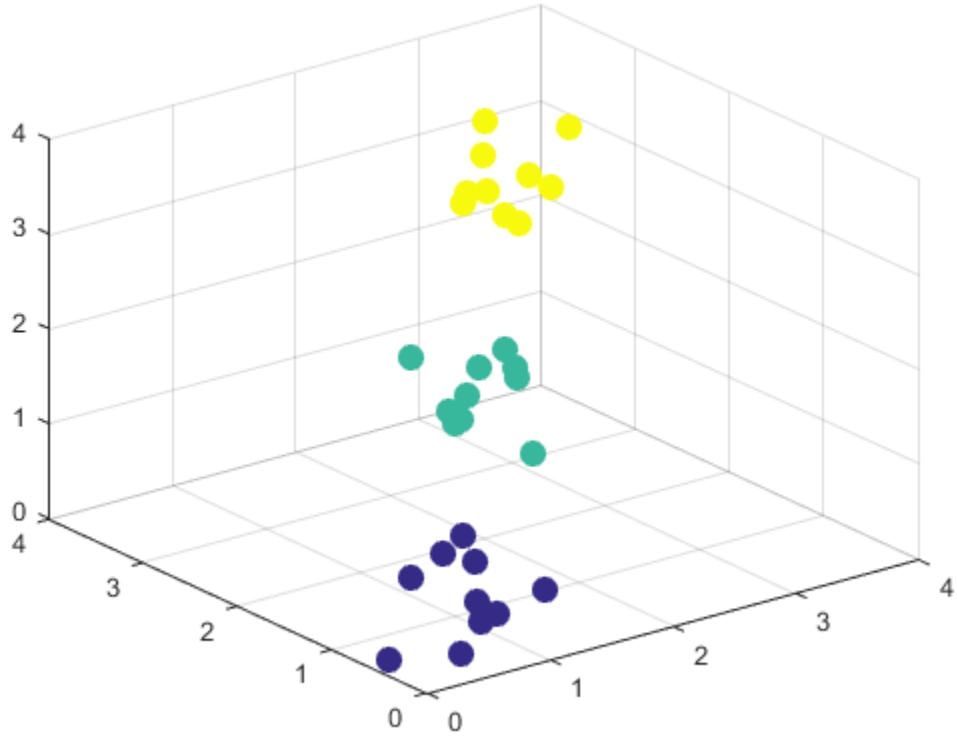
Compute the distances between items and create a hierarchical cluster tree from the sample data. List all of the items in cluster 2.

```
T = clusterdata(X,'maxclust',3);
find(T==2)
```

```
ans =

    11
    12
    13
    14
    15
    16
    17
    18
    19
    20
```

Plot the data with each cluster shown in a different color.

```
scatter3(X(:,1),X(:,2),X(:,3),100,T,'filled')
```



Create Hierarchical Cluster Tree Using Ward's Linkage

This example shows how to create a hierarchical cluster tree using Ward's linkage, and visualize the clusters using a 3-dimensional scatter plot.

Create a 20,000-by-3 matrix of sample data generated from the standard uniform distribution.

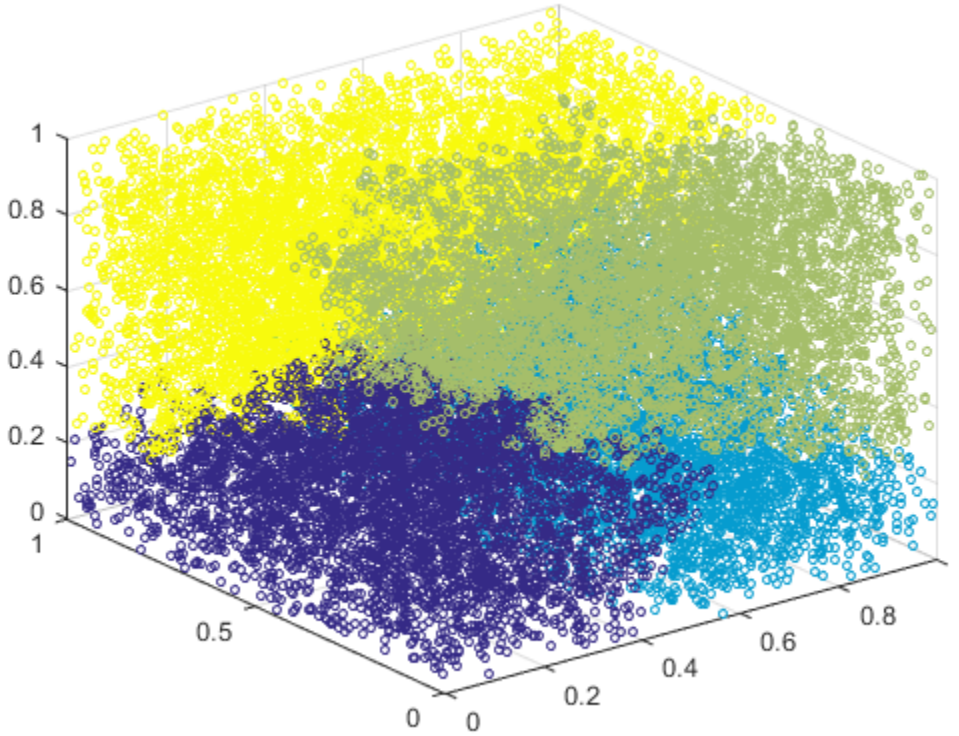
```
rng default;  % For reproducibility
X = rand(20000,3);
```

Create a hierarchical cluster tree from the sample data using Ward's linkage. Set `'savememory'` to `'on'` to construct clusters without computing the distance matrix.

```
c = clusterdata(X,'linkage','ward','savememory','on','maxclust',4);
```

Plot the data with each cluster shown in a different color.

```
scatter3(X(:,1),X(:,2),X(:,3),10,c)
```

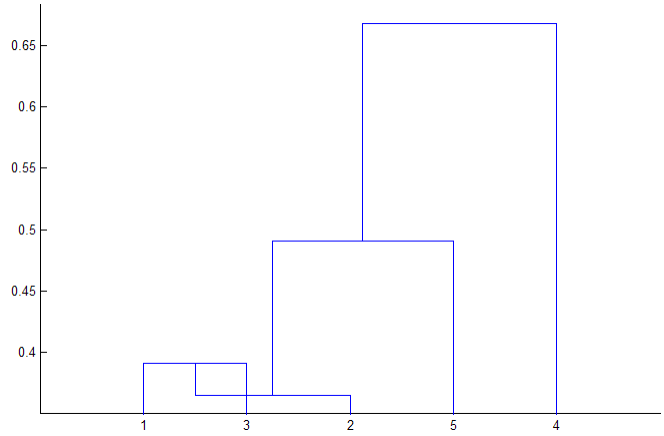


More About

Tips

- The `centroid` and `median` methods can produce a cluster tree that is not monotonic. This occurs when the distance from the union of two clusters, *r* and *s*, to a third

cluster is less than the distance between *r* and *s*. In this case, in a dendrogram drawn with the default orientation, the path from a leaf to the root node takes some downward steps. To avoid this, use another method. The following image shows a nonmonotonic cluster tree.



In this case, cluster 1 and cluster 3 are joined into a new cluster, while the distance between this new cluster and cluster 2 is less than the distance between cluster 1 and cluster 3. This leads to a nonmonotonic tree.

- You can provide the output `T` to other functions including `dendrogram` to display the tree, `cluster` to assign points to clusters, `inconsistent` to compute inconsistent measures, and `cophenet` to compute the cophenetic correlation coefficient.

See Also

`cluster` | `inconsistent` | `kmeans` | `linkage` | `pdist`

cmdscale

Classical multidimensional scaling

Syntax

```
Y = cmdscale(D)
[Y,e] = cmdscale(D)
```

Description

`Y = cmdscale(D)` takes an `n`-by-`n` distance matrix `D`, and returns an `n`-by-`p` configuration matrix `Y`. Rows of `Y` are the coordinates of `n` points in `p`-dimensional space for some `p < n`. When `D` is a Euclidean distance matrix, the distances between those points are given by `D`. `p` is the dimension of the smallest space in which the `n` points whose inter-point distances are given by `D` can be embedded.

`[Y,e] = cmdscale(D)` also returns the eigenvalues of `Y*Y'`. When `D` is Euclidean, the first `p` elements of `e` are positive, the rest zero. If the first `k` elements of `e` are much larger than the remaining `(n-k)`, then you can use the first `k` columns of `Y` as `k`-dimensional points whose inter-point distances approximate `D`. This can provide a useful dimension reduction for visualization, e.g., for `k = 2`.

`D` need not be a Euclidean distance matrix. If it is non-Euclidean or a more general dissimilarity matrix, then some elements of `e` are negative, and `cmdscale` chooses `p` as the number of positive eigenvalues. In this case, the reduction to `p` or fewer dimensions provides a reasonable approximation to `D` only if the negative elements of `e` are small in magnitude.

You can specify `D` as either a full dissimilarity matrix, or in upper triangle vector form such as is output by `pdist`. A full dissimilarity matrix must be real and symmetric, and have zeros along the diagonal and positive elements everywhere else. A dissimilarity matrix in upper triangle form must have real, positive entries. You can also specify `D` as a full similarity matrix, with ones along the diagonal and all other elements less than one. `cmdscale` transforms a similarity matrix to a dissimilarity matrix in such a way that distances between the points returned in `Y` equal or approximate `sqrt(1-D)`. To use a different transformation, you must transform the similarities prior to calling `cmdscale`.

Examples

Generate some points in 4-D space, but close to 3-D space, then reduce them to distances only.

```
X = [normrnd(0,1,10,3) normrnd(0,.1,10,1)];
D = pdist(X,'euclidean');
```

Find a configuration with those inter-point distances.

```
[Y,e] = cmdscale(D);

% Four, but fourth one small
dim = sum(e > eps^(3/4))

% Poor reconstruction
maxerr2 = max(abs(pdist(X)-pdist(Y(:,1:2))))

% Good reconstruction
maxerr3 = max(abs(pdist(X)-pdist(Y(:,1:3))))

% Exact reconstruction
maxerr4 = max(abs(pdist(X)-pdist(Y)))

% D is now non-Euclidean
D = pdist(X,'cityblock');
[Y,e] = cmdscale(D);

% One is large negative
min(e)

% Poor reconstruction
maxerr = max(abs(pdist(X)-pdist(Y)))
```

References

[1] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`mdscale` | `pdist` | `procrustes`

coefCI

Class: GeneralizedLinearModel

Confidence intervals of coefficient estimates of generalized linear model

Syntax

```
ci = coefCI(mdl)
ci = coefCI(mdl,alpha)
```

Description

`ci = coefCI(mdl)` returns confidence intervals for the coefficients in `mdl`.

`ci = coefCI(mdl,alpha)` returns confidence intervals with confidence level `1 - alpha`.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`alpha`

Scalar from `0` to `1`, the probability that the confidence interval does not contain the true value.

Default: `0.05`

Output Arguments

`ci`

`k`-by-`2` matrix of confidence intervals. The `j`th row of `ci` is the confidence interval of coefficient `j` of `mdl`. The name of coefficient `j` of `mdl` is in *`mdl`*`.CoefficientNames`.

Definitions

Confidence Interval

Assume that model assumptions hold (data comes from a generalized linear model represented by the formula *`mdl`*`.Formula` and the specified link function, and with observations that are independent conditional on the predictor values). Then row `j` of the confidence interval matrix `ci` gives a *confidence interval* `[ci(j,1),ci(j,2)]` computed such that, with repeated experimentation, a proportion `1 - alpha` of the intervals will contain the true value of the coefficient.

Examples

Confidence Interval for Coefficients of a Generalized Linear Model

Find confidence intervals for the coefficients of a fitted generalized nonlinear model.

Generate artificial data for the model using Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data.

```
mdl = fitglm(X,y,...
    'y ~ x1 + x2','distr','poisson')

mdl =


Generalized Linear regression model:
    log(y) ~ 1 + x1 + x2
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE           tStat     pValue
    (Intercept)    1.0405       0.022122    47.034    0
```

```
    x1             0.9968       0.003362    296.49    0
    x2              1.987      0.0063433    313.24    0


100 observations, 97 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 2.95e+05, p-value = 0
```

Find 95% (default) confidence intervals on the coefficients of the model.

```
ci = coefCI(mdl)
```

```
ci =

    0.9966    1.0844
    0.9901    1.0035
    1.9744    1.9996
```

Find 99% confidence intervals on the coefficients.

```
alpha = .01;
ci = coefCI(mdl,alpha)
```

```
ci =

    0.9824    1.0986
    0.9880    1.0056
    1.9703    2.0036
```

- “Generalized Linear Model Workflow” on page 10-39

See Also

`GeneralizedLinearModel`

coefCI

Class: GeneralizedLinearMixedModel

Confidence intervals for coefficients of generalized linear mixed-effects model

Syntax

```
feCI = coefCI(glme)
feCI = coefCI(glme,Name,Value)
[feCI,reCI] = coefCI(___)
```

Description

`feCI = coefCI(glme)` returns the 95% confidence intervals for the fixed-effects coefficients in the generalized linear mixed-effects model glme.

`feCI = coefCI(glme,Name,Value)` returns the confidence intervals using additional options specified by one or more Name,Value pair arguments. For example, you can specify a different confidence level or the method used to compute the approximate degrees of freedom.

`[feCI,reCI] = coefCI(___)` also returns the confidence intervals for the random-effects coefficients using any of the previous syntaxes.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range [0,1]

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range [0,1]. For a value α, the confidence level is 100 × (1 – α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single | double`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'residual'` (default) | `'none'`

Method for computing approximate degrees of freedom, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'residual'`	The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'none'`	All degrees of freedom are set to infinity.

Example: `'DFMethod','none'`

Output Arguments

`feCI` — Fixed-effects confidence intervals

p-by-2 matrix

Fixed-effects confidence intervals, returned as a p-by-2 matrix. feCI contains the confidence limits that correspond to the p-by-1 fixed-effects vector returned by the `fixedEffects` method. The first column of feCI contains the lower confidence limits and the second column contains the upper confidence limits.

When fitting a GLME model using `fitglme` and one of the maximum likelihood fit methods (`'Laplace'` or `'ApproximateLaplace'`):

- If you specify the `'CovarianceMethod'` name-value pair argument as `'conditional'`, then the confidence intervals are conditional on the estimated covariance parameters.
- If you specify the `'CovarianceMethod'` name-value pair argument as `'JointHessian'`, then the confidence intervals account for the uncertainty in the estimated covariance parameters.

When fitting a GLME model using `fitglme` and one of the pseudo likelihood fit methods (`'MPL'` or `'REMPL'`), `coefci` uses the fitted linear mixed effects model from the final pseudo likelihood iteration to compute confidence intervals on the fixed effects.

`reCI` — Random-effects confidence intervals

q-by-2 matrix

Random-effects confidence intervals, returned as a *q*-by-2 matrix. `reCI` contains the confidence limits corresponding to the *q*-by-1 random-effects vector `B` returned by the `randomEffects` method. The first column of `reCI` contains the lower confidence limits, and the second column contains the upper confidence limits.

When fitting a GLME model using `fitglme` and one of the maximum likelihood fit methods (`'Laplace'` or `'ApproximateLaplace'`), `coefCI` computes the confidence intervals using the conditional mean squared error of prediction (CMSEP) approach conditional on the estimated covariance parameters and the observed response. Alternatively, you can interpret the confidence intervals from `coefCI` as approximate Bayesian credible intervals conditional on the estimated covariance parameters and the observed response.

When fitting a GLME model using `fitglme` and one of the pseudo likelihood fit methods (`'MPL'` or `'REMPL'`), `coefci` uses the fitted linear mixed effects model from the final pseudo likelihood iteration to compute confidence intervals on the random effects.

Examples

95% Confidence Intervals for Fixed Effects

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

```
load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where $i = 1, 2, ..., 20$) during batch j (where $j = 1, 2, ..., 5$).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Use `fixedEffects` to display the estimates and names of the fixed-effects coefficients in `glme`.

```
[beta,betanames] = fixedEffects(glme)
```

```
beta =

    1.4689
   -0.3677
   -0.0945
   -0.2832
   -0.0719
    0.0711


betanames =

        Name
    _____________

    '(Intercept)'
    'newprocess'
    'time_dev'
    'temp_dev'
    'supplier_C'
    'supplier_B'
```

Each row of `beta` contains the estimated value for the coefficient named in the corresponding row of `betanames`. For example, the value –0.0945 in row 3 of `beta` is the estimated coefficient for the predictor variable `time_dev`.

Compute the 95% confidence intervals for the fixed-effects coefficients.

```
feCI = coefCI(glme)
```

```
feCI =

    1.1515    1.7864
   -0.7202   -0.0151
   -1.7395    1.5505
   -2.1926    1.6263
   -0.2268    0.0831
   -0.0826    0.2247
```

Column 1 of `feCI` contains the lower bound of the 95% confidence interval. Column 2 contains the upper bound. Row 1 corresponds to the intercept term. Rows 2, 3, and 4 correspond to `newprocess`, `time_dev`, and `temp_dev`, respectively. Rows 5 and 6 correspond to the indicator variables `supplier_C` and `supplier_B`, respectively. For example, the 95% confidence interval for the coefficient for `time_dev` is [-1.7395 , 1.5505]. Some of the confidence intervals include 0, which indicates that those predictors are not significant at the 5% significance level. To obtain specific *p*-values for each fixed-effects term, use `fixedEffects`. To test significance for entire terms, use `anova`.

99% Confidence Intervals for Random Effects

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- μ_{ij} is the mean number of defects corresponding to factory i during batch j.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Use `randomEffects` to compute and display the estimates of the empirical Bayes predictors (EBPs) for the random effects associated with `factory`.

```
[B,Bnames] = randomEffects(glme)
```

```
B =

    0.2913
    0.1542
   -0.2633
   -0.4257
    0.5453
   -0.1069
    0.3040
   -0.1653
   -0.1458
   -0.0816
    0.0145
    0.1771
    0.2487
    0.2115
    0.2777
   -0.2518
   -0.1351
   -0.1627
   -0.3208
    0.0584


Bnames =

      Group       Level        Name
    _________    _____    _____________

    'factory'    '1'      '(Intercept)'
    'factory'    '2'      '(Intercept)'
    'factory'    '3'      '(Intercept)'
    'factory'    '4'      '(Intercept)'
    'factory'    '5'      '(Intercept)'
    'factory'    '6'      '(Intercept)'
    'factory'    '7'      '(Intercept)'
    'factory'    '8'      '(Intercept)'
    'factory'    '9'      '(Intercept)'
    'factory'    '10'     '(Intercept)'
    'factory'    '11'     '(Intercept)'
```

```
    'factory'    '12'     '(Intercept)'
    'factory'    '13'     '(Intercept)'
    'factory'    '14'     '(Intercept)'
    'factory'    '15'     '(Intercept)'
    'factory'    '16'     '(Intercept)'
    'factory'    '17'     '(Intercept)'
    'factory'    '18'     '(Intercept)'
    'factory'    '19'     '(Intercept)'
    'factory'    '20'     '(Intercept)'
```

Each row of `B` contains the estimated EBPs for the random-effects coefficient named in the corresponding row of `Bnames`. For example, the value –0.2633 in row 3 of `B` is the estimated coefficient of `'(Intercept)'` for level `'3'` of `factory`.

Compute the 99% confidence intervals of the EBPs for the random effects.

```
[feCI,reCI] = coefCI(glme,'Alpha',0.01);
reCI
```

```
reCI =

   -0.2125    0.7951
   -0.3510    0.6595
   -0.8219    0.2954
   -0.9953    0.1440
    0.0730    1.0176
   -0.6362    0.4224
   -0.1796    0.7877
   -0.7044    0.3738
   -0.6795    0.3880
   -0.6142    0.4509
   -0.5487    0.5777
   -0.3677    0.7219
   -0.2908    0.7883
   -0.3322    0.7551
   -0.2572    0.8126
   -0.8451    0.3416
   -0.7214    0.4513
   -0.7482    0.4228
   -0.9333    0.2916
   -0.5064    0.6232
```

Column 1 of reCI contains the lower bound of the 99% confidence interval. Column 2 contains the upper bound. Each row corresponds to a level of `factory`, in the order

shown in Bnames. For example, row 3 corresponds to the coefficient of `'(Intercept)'` for level `'3'` of `factory`, which has a 99% confidence interval of [-0.8219 , 0.2954]. For additional statistics related to each random-effects term, use `randomEffects`.

References

[1] Booth, J.G., and J.P. Hobert. "Standard Errors of Prediction in Generalized Linear Mixed Models." *Journal of the American Statistical Association*. Vol. 93, 1998, pp. 262–272.

See Also

`GeneralizedLinearMixedModel` | `anova` | `coefTest` | `covarianceParameters` | `fixedEffects` | `randomEffects`

coefCI

Class: LinearModel

Confidence intervals of coefficient estimates of linear model

Syntax

```
ci = coefCI(mdl)
ci = coefCI(mdl,alpha)
```

Description

`ci = coefCI(mdl)` returns confidence intervals for the coefficients in `mdl`.

`ci = coefCI(mdl,alpha)` returns confidence intervals with confidence level `1 - alpha`.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`alpha`

Scalar from `0` to `1`, the probability that the confidence interval does not contain the true value.

Default: `0.05`

Output Arguments

`ci`

`k`-by-`2` matrix of confidence intervals. The `j`th row of `ci` is the confidence interval of coefficient `j` of `mdl`. The name of coefficient `j` of `mdl` is in *`mdl`*`.CoefficientNames`.

Definitions

Confidence Interval

Assume that model assumptions hold (data comes from a generalized linear model represented by the formula *`mdl`*`.Formula`, and with observations that are independent conditional on the predictor values). Then row `j` of the confidence interval matrix `ci` gives a *confidence interval* `[ci(j,1),ci(j,2)]` computed such that, with repeated experimentation, a proportion `1 - alpha` of the intervals will contain the true value of the coefficient.

Examples

Default Confidence Intervals

Create a linear model for auto mileage based on the `carbig` data. Then obtain confidence intervals for the resulting model coefficients.

Load the data and create a model.

```
load carbig
Origin = nominal(Origin);
ds = dataset(Horsepower,Weight,MPG,Origin);
modelspec = 'MPG ~ 1 + Horsepower + Weight + Origin';
mdl = fitlm(ds,modelspec);
```

View the names of the coefficients.

```
mdl.CoefNames
```

```
ans =
  Columns 1 through 4
    '(Intercept)'    'Horsepower'    'Weight'    'Origin_France'

  Columns 5 through 8
    'Origin_Germany'    'Origin_Italy'    'Origin_Japan'    'Origin_Sweden'

  Column 9
    'Origin_USA'
```

Find confidence intervals for the coefficients of the model.

```
ci = coefCI(mdl)
```

```
ci =
       43.361       59.939
```

```
    -0.074778    -0.031499
   -0.0058669   -0.0037122
      -17.362     -0.34772
       -15.75      0.74338
      -17.209       0.0613
      -14.511       1.8738
      -18.582      -1.5036
      -17.311     -0.96419
```

Custom Confidence Intervals

Create a linear model for auto mileage based on the `carbig` data. Then obtain confidence intervals for the resulting model coefficients at the 99% level.

Load the data and create a model.

```
load carbig
Origin = nominal(Origin);
ds = dataset(Horsepower,Weight,MPG,Origin);
modelspec = 'MPG ~ 1 + Horsepower + Weight + Origin';
mdl fitlm(ds,modelspec);
```

Find 99% confidence intervals for the coefficients.

```
ci = coefCI(mdl,.01)
```

```
ci =
       40.737       62.564
    -0.081629    -0.024647
    -0.006208   -0.0033711
      -20.056       2.3459
      -18.361       3.3546
      -19.943       2.7955
      -17.104       4.4676
      -21.286       1.2002
      -19.899       1.6238
```

The confidence intervals are wider than the default 5% confidence intervals of “Default Confidence Intervals” on page 22-501.

Alternatives

You can create the intervals from the model coefficients in *`mdl`*`.Coefficients.Estimate` and an appropriate multiplier of the standard

errors `sqrt(diag(mdl.CoefficientCovariance))`. The multiplier is `tinv(1-alpha/2,dof)`, where `level` is the confidence level, and `dof` is the degrees of freedom (number of data points minus the number of coefficients).

See Also

`LinearModel`

How To

- "Linear Regression" on page 9-11

coefCI

Class: LinearMixedModel

Confidence intervals for coefficients of linear mixed-effects model

Syntax

```
feCI = coefCI(lme)
feCI = coefCI(lme,Name,Value)
[feCI,reCI] = coefCI(___)
```

Description

`feCI = coefCI(lme)` returns the 95% confidence intervals for the fixed-effects coefficients in the linear mixed-effects model `lme`.

`feCI = coefCI(lme,Name,Value)` returns the 95% confidence intervals for the fixed-effects coefficients in the linear mixed-effects model `lme` with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the confidence level or method to compute the degrees of freedom.

`[feCI,reCI] = coefCI(___)` also returns the 95% confidence intervals for the random-effects coefficients in the linear mixed-effects model `lme`.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 to 1

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range 0 to 1. For a value α, the confidence level is 100*(1–α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'Residual'` (default) | `'Satterthwaite'` | `'None'`

Method for computing approximate degrees of freedom for confidence interval computation, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'Residual'`	Default. The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'Satterthwaite'`	Satterthwaite approximation.
`'None'`	All degrees of freedom are set to infinity.

For example, you can specify the Satterthwaite approximation as follows.

Example: `'DFMethod','Satterthwaite'`

Output Arguments

`feCI` — Fixed-effects confidence intervals

p-by-2 matrix

Fixed-effects confidence intervals, returned as a p-by-2 matrix. `feCI` contains the confidence limits that correspond to the p fixed-effects estimates in the vector `beta` returned by the `fixedEffects` method. The first column of `feCI` has the lower confidence limits and the second column has the upper confidence limits.

`reCI` — Random-effects confidence intervals

q-by-2 matrix

Random-effects confidence intervals, returned as a q-by-2 matrix. `reCI` contains the confidence limits corresponding to the q random-effects estimates in the vector `B` returned by the `randomEffects` method. The first column of `reCI` has the lower confidence limits and the second column has the upper confidence limits.

Examples

95% Confidence Intervals for Fixed-Effects Coefficients

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight, Program, Subject,Week, y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)');
```

Compute the fixed-effects coefficient estimates.

```
fe = fixedEffects(lme)

fe =

    0.6610
    0.0032
    0.3608
   -0.0333
    0.1132
    0.1732
    0.0388
    0.0305
    0.0331
```

The first estimate, 0.6610, corresponds to the constant term. The second row, 0.0032, and the third row, 0.3608, are estimates for the coefficient of initial weight and week, respectively. Rows four to six correspond to the indicator variables for programs B-D, and the last three rows correspond to the interaction of programs B-D and week.

Compute the 95% confidence intervals for the fixed-effects coefficients.

```
fecI = coefCI(lme)

fecI =

    0.1480    1.1741
    0.0005    0.0059
    0.1004    0.6211
   -0.2932    0.2267
   -0.1471    0.3734
    0.0395    0.3069
   -0.1503    0.2278
   -0.1585    0.2196
   -0.1559    0.2221
```

Some confidence intervals include 0. To obtain specific *p*-values for each fixed-effects term, use the `fixedEffects` method. To test for entire terms use the `anova` method.

Confidence Intervals with Specified Options

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration and horsepower, and a potentially correlated random effect for intercept and acceleration grouped by model year. First, store the data in a table.

```
tbl = table(Acceleration,Horsepower,Model_Year,MPG);
```

Fit the model.

```
lme = fitlme(tbl, 'MPG ~ Acceleration + Horsepower + (Acceleration|Model_Year)');
```

Compute the fixed-effects coefficient estimates.

```
fe = fixedEffects(lme)
```

```
fe =

   50.1325
   -0.5833
   -0.1695
```

Compute the 99% confidence intervals for fixed-effects coefficients using the residuals method to determine the degrees of freedom. This is the default method.

```
feCI = coefCI(lme,'Alpha',0.01)
```

```
feCI =

   44.2690   55.9961
   -0.9300   -0.2365
   -0.1883   -0.1507
```

Compute the 99% confidence intervals for fixed-effects coefficients using the Satterthwaite approximation to compute the degrees of freedom.

```
feCI = coefCI(lme,'Alpha',0.01,'DFMethod','Satterthwaite')
```

```
feCI =

   44.0949   56.1701
   -0.9640   -0.2025
   -0.1884   -0.1507
```

The Satthertwaite approximation produces similar confidence intervals to the residual method.

Compute Confidence Intervals for Random Effects

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data shows the deviations from the target quality characteristic measured from the products that five operators manufacture during three shifts: morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the deviation of the quality characteristics from the target value. This is simulated data.

`Shift` and `Operator` are nominal variables.

```
shift.Shift = nominal(shift.Shift);
shift.Operator = nominal(shift.Operator);
```

Fit a linear mixed-effects model with a random intercept grouped by operator to assess if there is significant difference in the performance according to the time of the shift.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)');
```

Compute the estimate of the BLUPs for random effects.

```
randomEffects(lme)
```

```
ans =

    0.5775
    1.1757
   -2.1715
    2.3655
   -1.9472
```

Compute the 95% confidence intervals for random effects.

```
[~,reCI] = coefCI(lme)

reCI =

   -1.3916    2.5467
   -0.7934    3.1449
   -4.1407   -0.2024
    0.3964    4.3347
   -3.9164    0.0219
```

Compute the 99% confidence intervals for random effects using the residuals method to determine the degrees of freedom. This is the default method.

```
[~,reCI] = coefCI(lme,'Alpha',0.01)

reCI =

   -2.1831    3.3382
   -1.5849    3.9364
   -4.9322    0.5891
   -0.3951    5.1261
   -4.7079    0.8134
```

Compute the 99% confidence intervals for random effects using the Satterthwaite approximation to determine the degrees of freedom.

```
[~,reCI] = coefCI(lme,'Alpha',0.01,'DFMethod','Satterthwaite')

reCI =

   -2.6840    3.8390
   -2.0858    4.4372
   -5.4330    1.0900
   -0.8960    5.6270
   -5.2087    1.3142
```

The Satterthwaite approximation might produce smaller `DF` values than the residual method. That is why these confidence intervals are larger than the previous ones computed using the residual method.

See Also

`coefTest` | `fixedEffects` | `LinearMixedModel` | `randomEffects`

coefCI

Class: NonLinearModel

Confidence intervals of coefficient estimates of nonlinear regression model

Syntax

```
ci = coefCI(mdl)
ci = coefCI(mdl,alpha)
```

Description

`ci = coefCI(mdl)` returns confidence intervals for the coefficients in `mdl`.

`ci = coefCI(mdl,alpha)` returns confidence intervals with confidence level `1 - alpha`.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

`alpha`

Scalar from `0` to `1`, the probability that the confidence interval does not contain the true value.

Default: `0.05`

Output Arguments

`ci`

`k`-by-`2` matrix of confidence intervals. The `j`th row of `ci` is the confidence interval of coefficient `j` of `mdl`. The name of coefficient `j` of `mdl` is in *`mdl`*`.CoefNames`.

Definitions

Confidence Interval

Assume that model assumptions hold (the data comes from a model represented by the formula *`mdl`*`.Formula`, with independent normally distributed errors). Then row `j` of the confidence interval matrix `ci` gives a *confidence interval* `[ci(j,1),ci(j,2)]` that contains coefficient `j` with probability `1 - alpha`.

Examples

Default Confidence Intervals

Create a nonlinear model for auto mileage based on the `carbig` data. Then obtain confidence intervals for the resulting model coefficients.

Load the data and create a nonlinear model.

```
load carbig
ds = dataset(Horsepower,Weight,MPG);
modelfun = @(b,x)b(1) + b(2)*x(:,1) + ...
    b(3)*x(:,2) + b(4)*x(:,1).*x(:,2);
beta0 = [1 1 1 1];
mdl = fitnlm(ds,modelfun,beta0)

mdl =

Nonlinear regression model:
    MPG ~ b1 + b2*Horsepower + b3*Weight + b4*Horsepower*Weight

Estimated Coefficients:
          Estimate      SE            tStat      pValue
    b1        63.558        2.3429     27.127    1.2343e-91
    b2      -0.25084      0.027279    -9.1952    2.3226e-18
    b3     -0.010772    0.00077381    -13.921    5.1372e-36
    b4    5.3554e-05    6.6491e-06     8.0542    9.9336e-15

Number of observations: 392, Error degrees of freedom: 388
Root Mean Squared Error: 3.93
R-Squared: 0.748,  Adjusted R-Squared 0.746
F-statistic vs. constant model: 385, p-value = 7.26e-116
```

All the coefficients have extremely small *p*-values. This means a confidence interval around the coefficients will not contain the point `0`, unless the confidence level is very high.

Find 95% confidence intervals for the coefficients of the model.

```
ci = coefCI(mdl)
```

```
ci =

   58.9515   68.1644
   -0.3045   -0.1972
   -0.0123   -0.0093
    0.0000    0.0001
```

The confidence interval for `b4` seems to contain `0`. Examine it in more detail.

```
ci(4,:)
```

```
ans =
   1.0e-04 *
    0.4048    0.6663
```

As expected, the confidence interval does not contain the point `0`.

- "Nonlinear Regression Workflow" on page 11-14

Alternatives

You can create the intervals from the model coefficients in `*mdl*.Coefficients.Estimate` and an appropriate multiplier of the standard errors `sqrt(diag(*mdl*.CoefficientCovariance))`. The multiplier is `tinv(1-alpha/2,dof)`, where `level` is the confidence level, and `dof` is the degrees of freedom (number of data points minus the number of coefficients).

See Also

`NonLinearModel`

More About

- "Nonlinear Regression" on page 11-2

coefTest

Class: GeneralizedLinearModel

Linear hypothesis test on generalized linear regression model coefficients

Syntax

```
p = coefTest(mdl)
p = coefTest(mdl,H)
p = coefTest(mdl,H,C)
[p,F] = coefTest(mdl,...)
[p,F,r] = coefTest(mdl,...)
```

Description

`p = coefTest(mdl)` computes the p-value for an F test that all coefficient estimates in `mdl` are zero, except for the intercept term.

`p = coefTest(mdl,H)` performs an F test that `H*B = 0`, where `B` represents the coefficient vector.

`p = coefTest(mdl,H,C)` performs an F test that `H*B = C`.

`[p,F] = coefTest(mdl,...)` returns the F test statistic.

`[p,F,r] = coefTest(mdl,...)` returns the numerator degrees of freedom for the test.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`H`

Numeric matrix having one column for each coefficient in the model. When `H` is an input, the output `p` is the *p*-value for an *F* test that `H*B = 0`, where `B` represents the coefficient vector.

`C`

Numeric vector with the same number of rows as `H`. When `C` is an input, the output `p` is the *p*-value for an *F* test that `H*B = C`, where `B` represents the coefficient vector.

Output Arguments

`p`

p-value of the *F* test (see "Definitions" on page 22-515).

`F`

Value of the test statistic for the *F* test (see "Definitions" on page 22-515).

`r`

Numerator degrees of freedom for the *F* test (see "Definitions" on page 22-515). The *F* statistic has `r` degrees of freedom in the numerator and `mdl.DFE` degrees of freedom in the denominator.

Definitions

Test Statistics

The *p*-value, *F* statistic, and numerator degrees of freedom are valid under these assumptions:

- The data comes from a model represented by the formula *`mdl`*`.Formula`.
- The observations are independent conditional on the predictor values.

Suppose these assumptions hold. Let β represent the (unknown) coefficient vector of the linear regression. Suppose H is a full-rank matrix of size r-by-s, where s is the number

of terms in β. Let v be a vector the same size as β. The following is a test statistic for the hypothesis that $H\beta = v$:

$$F = \left(H\hat{\beta} - v\right)' (HCH')^{-1} \left(H\hat{\beta} - v\right).$$

Here $\hat{\beta}$ is the estimate of the coefficient vector β in `mdl.Coefs`, and C is the estimated covariance of the coefficient estimates in `mdl.CoefCov`. When the hypothesis is true, the test statistic F has an "F Distribution" on page B-45 with r and u degrees of freedom.

Examples

Test Generalized Linear Model Coefficients

Test a generalized linear model to see if its coefficients differ from zero.

Create a generalized linear regression model of Poisson data.

```
X = 2 + randn(100,1);
mu = exp(1 + X/2);
y = poissrnd(mu);
mdl = fitglm(X,y,'y ~ x1','distr','poisson');
```

Test whether the fitted model has coefficients that differ significantly from zero.

```
p = coefTest(mdl)
```

```
p =

   1.2461e-30
```

There is no doubt that the coefficient of `x1` is nonzero.

- "Generalized Linear Model Workflow" on page 10-39

Alternatives

The values of commonly used test statistics are available in the *`mdl`*`.Coefficients` table.

See Also

`GeneralizedLinearModel` | `linhyptest`

More About

- “Generalized Linear Models” on page 10-12

coefTest

Class: GeneralizedLinearMixedModel

Hypothesis test on fixed and random effects of generalized linear mixed-effects model

Syntax

```
pVal = coefTest(glme)
pVal = coefTest(glme,H)
pVal = coefTest(glme,H,C)
pVal = coefTest(glme,H,C,Name,Value)
[pVal,F,DF1,DF2] = coefTest( ___ )
```

Description

`pVal = coefTest(glme)` returns the *p*-value of an *F*-test of the null hypothesis that all fixed-effects coefficients of the generalized linear mixed-effects model glme, except for the intercept, are equal to 0.

`pVal = coefTest(glme,H)` returns the *p*-value of an *F*-test using a specified contrast matrix, H. The null hypothesis is H_0: $H\beta = 0$, where β is the fixed-effects vector.

`pVal = coefTest(glme,H,C)` returns the *p*-value for an *F*-test using the hypothesized value, C. The null hypothesis is H_0: $H\beta = C$, where β is the fixed-effects vector.

`pVal = coefTest(glme,H,C,Name,Value)` returns the *p*-value for an *F*-test on the fixed- and/or random-effects coefficients of the generalized linear mixed-effects model glme, with additional options specified by one or more name-value pair arguments. For example, you can specify the method to compute the approximate denominator degrees of freedom for the *F*-test.

`[pVal,F,DF1,DF2] = coefTest( ___ )` also returns the *F*-statistic, F, and the numerator and denominator degrees of freedom for F, respectively DF1 and DF2, using any of the previous syntaxes.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

`H` — Fixed-effects contrasts

m-by-*p* matrix

Fixed-effects contrasts, specified as an *m*-by-*p* matrix, where *p* is the number of fixed-effects coefficients in glme. Each row of H represents one contrast. The columns of H (left to right) correspond to the rows of the *p*-by-1 fixed-effects vector `beta` (top to bottom) whose estimate is returned by the `fixedEffects` method.

Data Types: `single` | `double`

`C` — Hypothesized value

m-by-1 vector

Hypothesized value for testing the null hypothesis $H\beta = C$, specified as an *m*-by-1 vector. Here, β is the vector of fixed-effects whose estimate is returned by `fixedEffects`.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'DFMethod'` — Method for computing approximate degrees of freedom

`'residual'` (default) | `'none'`

Method for computing approximate degrees of freedom, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'residual'`	The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.

`'none'`	All degrees of freedom are set to infinity.

Example: `'DFMethod','none'`

`'REContrast'` — Random-effects contrasts
m-by-*q* matrix

Random-effects contrasts, specified as the comma-separated pair consisting of `'REContrast'` and an *m*-by-*q* matrix, where *q* is the number of random effects parameters in glme. The columns of the matrix (left to right) correspond to the rows of the *q*-by-1 random-effects vector `B` (top to bottom), whose estimate is returned by the `randomEffects` method.

Data Types: `single | double`

Output Arguments

`pVal` — *p*-value
scalar value

p-value for the *F*-test on the fixed- and/or random-effects coefficients of the generalized linear mixed-effects model glme, returned as a scalar value.

When fitting a GLME model using `fitglme` and one of the maximum likelihood fit methods (`'Laplace'` or `'ApproximateLaplace'`), `coefTest` uses an approximation of the conditional mean squared error of prediction (CMSEP) of the estimated linear combination of fixed- and random-effects to compute *p*-values. This accounts for the uncertainty in the fixed-effects estimates, but not for the uncertainty in the covariance parameter estimates. For tests on fixed effects only, if you specify the `'CovarianceMethod'` name-value pair argument in `fitglme` as `'JointHessian'`, then `coefTest` accounts for the uncertainty in the estimation of covariance parameters.

When fitting a GLME model using fitglme and one of the pseudo likelihood fit methos (`'MPL'` or `'REMPL'`), `coefTest` bases the inference on the fitted linear mixed effects model from the final pseudo likelihood iteration.

`F` — *F*-statistic
scalar value

F-statistic, returned as a scalar value.

`DF1` — Numerator degrees of freedom for `F`

scalar value

Numerator degrees of freedom for the F-statistic F, returned as a scalar value.

- If you test the null hypothesis H_0: $H\beta = 0$ or H_0: $H\beta = C$, then DF1 is equal to the number of linearly independent rows in H.
- If you test the null hypothesis H_0: $H\beta + KB = C$, then DF1 is equal to the number of linearly independent rows in `[H,K]`.

`DF2` — Denominator degrees of freedom for `F`

scalar value

Denominator degrees of freedom for the F-statistic F, returned as a scalar value. The value of DF2 depends on the option specified by the `'DFMethod'` name-value pair argument.

Examples

Test the Significance of Coefficients

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)

- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Test if there is any significant difference between supplier C and supplier B.

```
H = [0,0,0,0,1,-1];

[pVal,F,DF1,DF2] = coefTest(glme,H)
```

```
pVal =

    0.2793


F =

    1.1842


DF1 =

     1


DF2 =

    94
```

The large *p*-value indicates that there is no significant difference between supplier C and supplier B at the 5% significance level. Here, `coefTest` also returns the *F*-statistic, the numerator degrees of freedom, and the approximate denominator degrees of freedom.

Test if there is any significant difference between supplier A and supplier B.

If you specify the `'DummyVarCoding'` name-value pair argument as `'effects'` when fitting the model using `fitglme`, then

$$\beta_A + \beta_B + \beta_C = 0,$$

where β_A, β_B, and β_C correspond to suppliers A, B, and C, respectively. β_A is the effect of A minus the average effect of A, B, and C. To determine the contrast matrix corresponding to a test between supplier A and supplier B,

$$\beta_B - \beta_A = \beta_B - (-\beta_B - \beta_C) = 2\beta_B + \beta_C .$$

From the output of `disp(glme)`, column 5 of the contrast matrix corresponds to β_C, and column 6 corresponds to β_B. Therefore, the contrast matrix for this test is specified as `H = [0,0,0,0,1,2]`.

```
H = [0,0,0,0,1,2];

[pVal,F,DF1,DF2] = coefTest(glme,H)
```

```
[pVal,F,DF1,DF2] = coefTest(glme,H)

pVal =

    0.6177


F =

    0.2508


DF1 =

     1


DF2 =

    94
```

The large p-value indicates that there is no significant difference between supplier A and supplier B at the 5% significance level.

References

[1] Booth, J.G., and J.P. Hobert. "Standard Errors of Prediction in Generalized Linear Mixed Models." *Journal of the American Statistical Association*, Vol. 93, 1998, pp. 262–272.

See Also

`GeneralizedLinearMixedModel` | `anova` | `coefCI` | `covarianceParameters` | `fixedEffects` | `randomEffects`

coefTest

Class: LinearModel

Linear hypothesis test on linear regression model coefficients

Syntax

```
p = coefTest(mdl)
p = coefTest(mdl,H)
p = coefTest(mdl,H,C)
[p,F] = coefTest(mdl,...)
[p,F,r] = coefTest(mdl,...)
```

Description

`p = coefTest(mdl)` computes the p-value for an F test that all coefficient estimates in `mdl` are zero, except for the intercept term.

`p = coefTest(mdl,H)` performs an F test that `H*B = 0`, where `B` represents the coefficient vector.

`p = coefTest(mdl,H,C)` performs an F test that `H*B = C`.

`[p,F] = coefTest(mdl,...)` returns the F test statistic.

`[p,F,r] = coefTest(mdl,...)` returns the numerator degrees of freedom for the test.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

H

Numeric matrix having one column for each coefficient in the model. When `H` is an input, the output `p` is the *p*-value for an *F* test that `H*B = 0`, where `B` represents the coefficient vector.

C

Numeric vector with the same number of rows as `H`. When `C` is an input, the output `p` is the *p*-value for an *F* test that `H*B = C`, where `B` represents the coefficient vector.

Output Arguments

p

p-value of the *F* test (see "Definitions" on page 22-526).

F

Value of the test statistic for the *F* test (see "Definitions" on page 22-526).

r

Numerator degrees of freedom for the *F* test (see "Definitions" on page 22-526). The *F* statistic has `r` degrees of freedom in the numerator and `mdl.DFE` degrees of freedom in the denominator.

Definitions

Test Statistics

The *p*-value, *F* statistic, and numerator degrees of freedom are valid under these assumptions:

- The data comes from a model represented by the formula *`mdl`*`.Formula`.
- The observations are independent conditional on the predictor values.

Suppose these assumptions hold. Let β represent the (unknown) coefficient vector of the linear regression. Suppose H is a full-rank matrix of size r-by-s, where s is the number

of terms in β. Let v be a vector the same size as β. The following is a test statistic for the hypothesis that $H\beta = v$:

$$F = \left(H\hat{\beta} - v\right)' (HCH')^{-1} \left(H\hat{\beta} - v\right).$$

Here $\hat{\beta}$ is the estimate of the coefficient vector β in `mdl.Coefs`, and C is the estimated covariance of the coefficient estimates in `mdl.CoefCov`. When the hypothesis is true, the test statistic F has an "F Distribution" on page B-45 with r and u degrees of freedom.

Examples

Test Linear Regression Model

Make a linear model of mileage as a function of the weight, weight squared, and model year from the `carsmall` data set. Test the coefficients to see if all should be zero.

Load the data and make a table, where the model year is an ordinal variable.

```
load carsmall
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
mdl = fitlm(tbl,'MPG ~ Year + Weight + Weight^2');
```

Test the model for significant differences from a constant model.

```
p = coefTest(mdl)
```

```
p =

   5.5208e-41
```

There is no doubt that the model contains more than the intercept term.

Test a Particular Coefficient

Test the `Weight^2` coefficient in a linear model of mileage as a function of the weight, weight squared, and model year.

Load the data and make a table, where the model year is an ordinal variable.

```
load carsmall
```

```
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
mdl = fitlm(tbl,'MPG ~ Year + Weight + Weight^2');
```

Test the significance of the `Weight^2` coefficient. To do so, find the coefficient corresponding to `Weight^2`.

```
mdl.CoefficientNames
```

```
ans =

    '(Intercept)'    'Weight'    'Year_76'    'Year_82'    'Weight^2'
```

`Weight^2` is the fifth (final) coefficient.

Test the significance of the `Weight^2` coefficient.

```
p = coefTest(mdl,[0 0 0 0 1])
```

```
p =

    0.0022
```

Alternatives

The values of commonly used test statistics are available in the *`mdl`*`.Coefficients` table.

`anova` provides a test for each model term.

See Also

`anova` | `LinearModel` | `linhyptest`

How To

- “Linear Regression” on page 9-11

coefTest

Class: LinearMixedModel

Hypothesis test on fixed and random effects of linear mixed-effects model

Syntax

```
pVal = coefTest(lme)
pVal = coefTest(lme,H)
pVal = coefTest(lme,H,C)
pVal = coefTest(lme,H,C,'REContrast',K)
pVal = coefTest(___,Name,Value)
[pVal,F,DF1,DF2] = coefTest(___)
```

Description

`pVal = coefTest(lme)` returns the p-value for an F-test that all fixed-effects coefficients except for the intercept are 0.

`pVal = coefTest(lme,H)` returns the p-value for an F-test on fixed-effects coefficients of linear mixed-effects model `lme`, using the contrast matrix H. It tests the null hypothesis that H_0: $H\beta = 0$, where β is the fixed-effects vector.

`pVal = coefTest(lme,H,C)` returns the p-value for an F-test on fixed-effects coefficients of the linear mixed-effects model `lme`, using the contrast matrix H. It tests the null hypothesis that H_0: $H\beta = C$, where β is the fixed-effects vector.

`pVal = coefTest(lme,H,C,'REContrast',K)` returns the p-value for an F-test on the fixed- and random-effects coefficients of the linear mixed-effects model `lme`, using the contrast matrices H and K. It tests the null hypothesis that H_0: $H\beta + KB = C$, where β is the fixed-effects vector and B is the random-effects vector.

`pVal = coefTest(___,Name,Value)` returns the p-value for an F-test on the fixed- and/or random-effects coefficients of the linear mixed-effects model `lme`, with additional options specified by one or more Name,Value pair arguments. It can accept any of the input arguments in the previous syntaxes.

For example, you can specify the method to compute the degrees of freedom.

`[pVal,F,DF1,DF2] = coefTest( ___ )` also returns the F-statistic `F`, and the numerator and denominator degrees of freedom for `F`, respectively `DF1` and `DF2`.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

`H` — Fixed-effects contrasts

m-by-p matrix

Fixed-effects contrasts, specified as an m-by-p matrix, where p is the number of fixed-effects coefficients in lme. Each row of H represents one contrast. The columns of H (left to right) correspond to the rows of the p-by-1 fixed-effects vector `beta` (top to bottom), returned by the `fixedEffects` method.

Data Types: `single` | `double`

`C` — Hypothesized value

m-by-1 vector

Hypothesized value for testing the null hypothesis `H*beta = C`, specified as an m-by-1 matrix. Here, `beta` is the vector of fixed-effects estimates returned by the `fixedEffects` method.

Data Types: `single` | `double`

`K` — Random-effects contrasts

m-by-q matrix

Random-effects contrasts, specified as an m-by-q matrix, where q is the number of random effects parameters in lme. The columns of K (left to right) correspond to the rows of the random-effects best linear unbiased predictor vector `B` (top to bottom), returned by the `randomEffects` method.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'DFMethod'` — Method for computing approximate denominator degrees of freedom

`'Residual'` (default) | `'Satterthwaite'` | `'None'`

Method for computing the approximate denominator degrees of freedom for the *F*-test, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'Residual'`	Default. The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'Satterthwaite'`	Satterthwaite approximation.
`'None'`	All degrees of freedom are set to infinity.

For example, you can specify the Satterthwaite approximation as follows.

Example: `'DFMethod','Satterthwaite'`

Output Arguments

`pVal` — *p*-value

scalar value

p-value for the *F*-test on the fixed and/or random-effects coefficients of the linear mixed-effects model lme, returned as a scalar value.

`F` — *F*-statistic

scalar value

F-statistic, returned as a scalar value.

DF1 — Numerator degrees of freedom for F

scalar value

Numerator degrees of freedom for F, returned as a scalar value.

- If you test the null hypothesis H_0: $H\beta = 0$, or H_0: $H\beta = C$, then DF1 is equal to the number of linearly independent rows in H.
- If you test the null hypothesis H_0: $H\beta + KB = C$, then DF1 is equal to the number of linearly independent rows in [H,K].

DF2 — Denominator degrees of freedom for F

scalar value

Denominator degrees of freedom for F, returned as a scalar value. The value of DF2 depends on the option you select for DFMethod.

Examples

Randomized Block Design

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data shows the absolute deviations from the target quality characteristic measured from the products that five operators manufacture during three different shifts: morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the absolute deviation of the quality characteristics from the target value. This is simulated data.

Shift and Operator are nominal variables.

```
shift.Shift = nominal(shift.Shift);
shift.Operator = nominal(shift.Operator);
```

Fit a linear mixed-effects model with a random intercept grouped by operator to assess if there is significant difference in the performance according to the time of the shift.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             15
    Fixed effects coefficients          3
    Random effects coefficients         5
    Covariance parameters               2

Formula:
    QCDev ~ 1 + Shift + (1 | Operator)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    59.012    62.552    -24.506          49.012

Fixed effects coefficients (95% CIs):
    Name                   Estimate    SE         tStat       DF    pValue       Lower
    '(Intercept)'           3.1196     0.88681      3.5178    12    0.0042407     1.187
    'Shift_Morning'        -0.3868     0.48344    -0.80009    12      0.43921    -1.440
    'Shift_Night'           1.9856     0.48344      4.1072    12    0.0014535    0.9322

Random effects covariance parameters (95% CIs):
Group: Operator (5 Levels)
    Name1                Name2                Type         Estimate    Lower      Upper
    '(Intercept)'        '(Intercept)'        'std'        1.8297      0.94915    3.527

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.76439     0.49315    1.1848
```

Test if all fixed-effects coefficients except for the intercept are 0.

```
pVal = coefTest(lme)
```

```
pVal =

   7.5956e-04
```

The small p-value indicates that not all fixed-effects coefficients are 0.

Test the significance of the `Shift` term using a contrast matrix.

```
H = [0 1 0; 0 0 1];
pVal = coefTest(lme,H)
```

```
pVal =

   7.5956e-04
```

Test the significance of the `Shift` term using the `anova` method.

```
anova(lme)
```

```
ans =


    ANOVA marginal tests: DFMethod = 'Residual'

    Term                FStat     DF1    DF2    pValue
    '(Intercept)'       12.375    1      12      0.0042407
    'Shift'             13.864    2      12     0.00075956
```

The p-value for `Shift`, 0.00075956, is the same as the p-value of the previous hypothesis test.

Test if there is any difference between the evening and morning shifts.

```
pVal = coefTest(lme,[0 1 -1])
```

```
pVal =

   3.6147e-04
```

This small p-value indicates that the performance of the operators are not the same in the morning and the evening shifts.

Hypothesis Test for Fixed Effects

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           9
    Random effects coefficients         40
    Covariance parameters                4

Formula:
    y ~ 1 + InitialWeight + Program*Week + (1 + Week | Subject)

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -22.981    13.257    24.49            -48.981

Fixed effects coefficients (95% CIs):
    Name                   Estimate     SE           tStat       DF     pValue       l
    '(Intercept)'            0.66105      0.25892      2.5531    111     0.012034
    'InitialWeight'        0.0031879    0.0013814      2.3078    111     0.022863    (
    'Program_B'              0.36079      0.13139       2.746    111    0.0070394
    'Program_C'             -0.033263     0.13117    -0.25358    111      0.80029
```

```
    'Program_D'               0.11317      0.13132     0.86175    111       0.39068
    'Week'                     0.1732     0.067454      2.5677    111      0.011567
    'Program_B:Week'          0.038771     0.095394     0.40644    111       0.68521
    'Program_C:Week'          0.030543     0.095394     0.32018    111       0.74944
    'Program_D:Week'          0.033114     0.095394     0.34713    111       0.72915

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1                Name2                Type          Estimate    Lower      Upp
    '(Intercept)'        '(Intercept)'        'std'         0.18407     0.12281    0.27
    'Week'               '(Intercept)'        'corr'        0.66841     0.21076    0.88
    'Week'               'Week'               'std'         0.15033     0.11004    0.20

Group: Error
    Name             Estimate    Lower       Upper
    'Res Std'        0.10261     0.087882    0.11981
```

Test for the significance of the interaction between `Program` and `Week`.

```
H = [0 0 0 0 0 0 1 0 0;
     0 0 0 0 0 0 0 1 0;
     0 0 0 0 0 0 0 0 1];
pVal = coefTest(lme,H)

pVal =

    0.9775
```

The high p-value indicates that the interaction between `Program` and `Week` is not statistically significant.

Now, test whether all coefficients involving `Program` are 0.

```
H = [0 0 1 0 0 0 0 0 0;
     0 0 0 1 0 0 0 0 0;
     0 0 0 0 1 0 0 0 0;
     0 0 0 0 0 0 1 0 0;
     0 0 0 0 0 0 0 1 0;
     0 0 0 0 0 0 0 0 1];
C = [0;0;0;0;0;0];
pVal = coefTest(lme,H,C)

pVal =

    0.0274
```

The p-value of 0.0274 indicates that not all coefficients involving `Program` are zero.

Test for Fixed and Random Effects

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables containing estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the CDC).

To fit a linear-mixed effects model, your data must be in a properly formatted dataset array. To fit a linear mixed-effects model with the influenza rates as the responses and region as the predictor variable, combine the nine columns corresponding to the regions into a tall array. The new dataset array, `flu2`, must have the response variable, `FluRate`, the nominal variable, `Region`, that shows which region each estimate is from, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Fit a linear mixed-effects model with fixed effects for the region and a random intercept that varies by `Date`.

```
lme = fitlme(flu2,'FluRate ~ 1 + Region + (1|Date)')
```

```
Linear mixed-effects model fit by ML

Model information:
    Number of observations             468
    Fixed effects coefficients           9
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    FluRate ~ 1 + Region + (1|Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    318.71    364.35    -148.36          296.71

Fixed effects coefficients (95% CIs):
```

```
    Name                      Estimate    SE          tStat      DF     pValue        L
    '(Intercept)'               1.2233    0.096678     12.654    459     1.085e-31
    'Region_MidAtl'           0.010192    0.052221    0.19518    459       0.84534
    'Region_ENCentral'        0.051923    0.052221     0.9943    459        0.3206
    'Region_WNCentral'         0.23687    0.052221     4.5359    459    7.3324e-06
    'Region_SAtl'             0.075481    0.052221     1.4454    459       0.14902
    'Region_ESCentral'         0.33917    0.052221      6.495    459    2.1623e-10
    'Region_WSCentral'           0.069    0.052221     1.3213    459       0.18705
    'Region_Mtn'              0.046673    0.052221    0.89377    459       0.37191
    'Region_Pac'              -0.16013    0.052221    -3.0665    459     0.0022936

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1               Name2               Type         Estimate    Lower     Upper
    '(Intercept)'       '(Intercept)'       'std'        0.6443      0.5297    0.783

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.26627     0.24878    0.285
```

Test the hypothesis that the random effects-term for week 10/9/2005 is zero.

```
[~,~,STATS] = randomEffects(lme); % Compute the random-effects statistics (STATS)
STATS.Level = nominal(STATS.Level);
K = zeros(length(STATS),1);
K(STATS.Level == '10/9/2005') = 1;
pVal = coefTest(lme,[0 0 0 0 0 0 0 0 0],0,'REContrast',K')
```

```
pVal =

    0.1692
```

Refit the model this time with a random intercept and slope.

```
lme = fitlme(flu2,'FluRate ~ 1 + Region + (1 + Region|Date)');
```

Test the hypothesis that the combined coefficient of region `WNCentral` for week 10/9/2005 is zero.

```
[~,~,STATS] = randomEffects(lme); STATS.Level = nominal(STATS.Level);
K = zeros(length(STATS),1);
K(STATS.Level == '10/9/2005' & flu2.Region == 'WNCentral') = 1;
pVal = coefTest(lme,[0 0 0 1 0 0 0 0 0],0,'REContrast',K')
```

```
ans =
```

```
   1.4536e-12
```

Also return the *F*-statistic with the numerator and denominator degrees of freedom.

```
[pVal,F,DF1,DF2] = coefTest(lme,[0 0 0 1 0 0 0 0 0],0,'REContrast',K')
```

```
pVal =

   1.4536e-12


F =

   53.0081


DF1 =

     1


DF2 =

   459
```

Repeat the test using the Satterthwaite approximation for the denominator degrees of freedom.

```
[pVal,F,DF1,DF2] = coefTest(lme,[0 0 0 1 0 0 0 0 0],0,'REContrast',K',...
   'DFMethod','Satterthwaite')
```

```
pVal =

    0.0055


F =

   53.0081


DF1 =

     1
```

```
DF2 =

    2.9795
```

See Also

`anova` | `coefCI` | `LinearMixedModel`

coefTest

Class: NonLinearModel

Linear hypothesis test on nonlinear regression model coefficients

Syntax

```
p = coefTest(mdl)
p = coefTest(mdl,H)
p = coefTest(mdl,H,C)
[p,F] = coefTest(mdl,...)
[p,F,r] = coefTest(mdl,...)
```

Description

`p = coefTest(mdl)` computes the p-value for an F test that all coefficient estimates in `mdl` are zero.

`p = coefTest(mdl,H)` performs an F test that `H*B = 0`, where `B` represents the coefficient vector.

`p = coefTest(mdl,H,C)` performs an F test that `H*B = C`.

`[p,F] = coefTest(mdl,...)` returns the F test statistic.

`[p,F,r] = coefTest(mdl,...)` returns the numerator degrees of freedom for the test.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

H

Numeric matrix having one column for each coefficient in the model. When `H` is an input, the output `p` is the *p*-value for an *F* test that `H*B = 0`, where `B` represents the coefficient vector.

C

Numeric vector with the same number of rows as `H`. When `C` is an input, the output `p` is the *p*-value for an *F* test that `H*B = C`, where `B` represents the coefficient vector.

Output Arguments

p

p-value of the *F* test (see "Definitions" on page 22-542).

F

Value of the test statistic for the *F* test (see "Definitions" on page 22-542).

r

Numerator degrees of freedom for the *F* test (see "Definitions" on page 22-542). The *F* statistic has `r` degrees of freedom in the numerator and `mdl.DFE` degrees of freedom in the denominator.

Definitions

Test Statistics

The *p*-value, *F* statistic, and numerator degrees of freedom are valid under these assumptions:

- The data comes from a normal distribution.
- The entries are independent.

Suppose these assumptions hold. Let β represent the unknown coefficient vector of the linear regression. Suppose H is a full-rank matrix of size r-by-s, where s is the number

of terms in β. Let v be a vector the same size as β. The following is a test statistic for the hypothesis that $H\beta = v$:

$$F = \left(H\hat{\beta} - v\right)' (HCH')^{-1} \left(H\hat{\beta} - v\right).$$

Here $\hat{\beta}$ is the estimate of the coefficient vector β in `mdl.Coefs`, and C is the estimated covariance of the coefficient estimates in `mdl.CoefCov`. When the hypothesis is true, the test statistic F has an "F Distribution" on page B-45 with r and u degrees of freedom.

Examples

Test Nonlinear Regression Model Coefficients

Make a nonlinear model of mileage as a function of the weight from the `carsmall` data set. Test the coefficients to see if all should be zero.

Create an exponential model of car mileage as a function of weight from the `carsmall` data. Scale the weight by a factor of 1000 so all the variables are roughly equal in size.

```
load carsmall
X = Weight;
y = MPG;
modelfun = 'y ~ b1 + b2*exp(-b3*x/1000)';
beta0 = [1 1 1];
mdl = fitnlm(X,y,modelfun,beta0);
```

Test the model for significant differences from a constant model.

```
p = coefTest(mdl)
```

```
p =

   1.3708e-36
```

There is no doubt that the model contains nonzero terms.

Alternatives

The values of commonly used test statistics are available in the *`mdl`*`.Coefficients` table.

See Also

`NonLinearModel`

More About

- “Nonlinear Regression” on page 11-2

coeftest

Class: RepeatedMeasuresModel

Linear hypothesis test on coefficients of repeated measures model

Syntax

```
tbl = coeftest(rm,A,C,D)
```

Description

`tbl = coeftest(rm,A,C,D)` returns a table tbl containing the multivariate analysis of variance (manova) for the repeated measures model rm.

Tips

- This test is defined as `A*B*C = D`, where `B` is the matrix of coefficients in the repeated measures model. `A` and `C` are numeric matrices of the proper size for this multiplication. `D` is a scalar or numeric matrix of the proper size. The default is `D = 0`.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`A` — Specification representing between-subjects model

a-by-*p* matrix

Specification representing the between-subjects model, specified as an a-by-p numeric matrix, with rank $a \le p$.

Data Types: `single` | `double`

`C` — Specification representing within-subjects hypothesis

r-by-c matrix

Specification representing the within-subjects (within time) hypotheses, specified as an r-by-c numeric matrix, with rank $c \le r \le n - p$.

Data Types: `single` | `double`

`D` — Hypothesized value

0 (default) | scalar value | a-by-c matrix

Hypothesized value, specified as a scalar value or an a-by-c matrix.

Data Types: `single` | `double`

Output Arguments

`tbl` — Results of multivariate analysis of variance

table

Results of multivariate analysis of variance for the repeated measures model rm, returned as a table containing the following columns.

`Statistic`	Type of test statistic used
`Value`	Value of the corresponding test statistic
`F`	F-statistic value
`RSquare`	Measure of variance explained
`df1`	Numerator degrees of freedom for the F-statistic
`df2`	Denominator degrees of freedom for the F-statistic
`pValue`	p-value associated with the test statistic value

Examples

Test Coefficients for First and Last Repeated Measures

Load the sample data.

```
load repeatedmeas
```

The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ through $y8$ as responses. The table `within` includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ through $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Test that the coefficients of all terms in the between-subjects model are the same for the first and last repeated measurement variable.

```
coeftest(rm,eye(8),[1 0 0 0 0 0 0 -1]')
```

```
ans =

    Statistic      Value       F       RSquare     df1     df2     pValue
    _________     _______    ______    _______     ___     ___    _______

    Pillai         0.3355    1.3884    0.3355      8       22     0.25567
    Wilks          0.6645    1.3884    0.3355      8       22     0.25567
    Hotelling     0.50488    1.3884    0.3355      8       22     0.25567
    Roy           0.50488    1.3884    0.3355      8       22     0.25567
```

The p-value of 0.25567 indicates that there is not enough statistical evidence to conclude that the coefficients of all terms in the between-subjects model for the first and last repeated measures variable are different.

See Also

`fitrm` | `manova`

combine

Class: CompactTreeBagger

Combine two ensembles

Syntax

```
B1 = combine(B1,B2)
```

Description

`B1 = combine(B1,B2)` appends decision trees from ensemble `B2` to those stored in `B1` and returns ensemble `B1`. This method requires that the class and variable names be identical in both ensembles.

See Also

`TreeBagger.append`

combnk

Enumeration of combinations

Syntax

```
C = combnk(v,k)
```

Description

`C = combnk(v,k)` returns all combinations of the n elements in `v` taken `k` at a time.

`C = combnk(v,k)` produces a matrix `C` with `k` columns and $n!/k!(n-k!$ rows, where each row contains `k` of the elements in the vector `v`.

It is not practical to use this function if `v` has more than about 15 elements.

Examples

Combinations of characters from a string.

```
C = combnk('tendril',4);
last5 = C(31:35,:)
last5 =
tedr
tenl
teni
tenr
tend
```

Combinations of elements from a numeric vector.

```
c = combnk(1:4,2)
c =
   3   4
   2   4
   2   3
   1   4
```

```
     1     3
     1     2
```

See Also

`perms`

compact

Class: ClassificationDiscriminant

Compact discriminant analysis classifier

Syntax

```
cobj = compact(obj)
```

Description

`cobj = compact(obj)` creates a compact version of `obj`.

Input Arguments

`obj`

Discriminant analysis classifier created using `fitcdiscr`.

Output Arguments

`cobj`

Compact classifier. `cobj` has class `CompactClassificationDiscriminant`. You can predict classifications using `cobj` exactly as you can using `obj`. However, since `cobj` does not contain training data, you cannot perform some actions, such as cross validation.

Examples

Compare the size of the discriminant analysis classifier for Fisher's iris data to the compact version of the classifier:

```
load fisheriris
fullobj = fitcdiscr(meas,species);
cobj = compact(fullobj);
b = whos('fullobj'); % b.bytes = size of fullobj
c = whos('cobj'); % c.bytes = size of cobj
[b.bytes c.bytes] % shows cobj uses 60% of the memory

ans =
       18578       11498
```

See Also

`ClassificationDiscriminant` | `fitcdiscr`

How To

- “Discriminant Analysis” on page 15-3

compact

Class: ClassificationECOC

Compact error-correcting output codes multiclass model

Syntax

```
CMdl = compact(Mdl)
```

Description

`CMdl = compact(Mdl)` returns a compact error-correcting output codes (ECOC) model (`CMdl`), which is the compact version of the trained ECOC model `Mdl`.

`CMdl` does not contain the training data, whereas `Mdl` contains the training data in its properties `Mdl.X` and `Mdl.Y`.

Input Arguments

`Mdl` — ECOC multiclass model

`ClassificationECOC` model

ECOC multiclass model, specified as a `ClassificationECOC` model returned by `fitcecoc`.

Output Arguments

`CMdl` — Compact ECOC model

`CompactClassificationECOC` model

Compact ECOC model, returned as a `CompactClassificationECOC` model.

Predict class labels using `CMdl` exactly as you would using `Mdl`. However, since `CMdl` does not contain training data, you cannot implement cross validation.

Examples

Reduce the Size of Full ECOC Models

Full ECOC models (i.e., `ClassificationECOC` models) hold the training data. For efficiency, you might not want to predict new labels using a large classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y);
```

Train an ECOC model using SVM binary classifiers. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
Mdl = fitcecoc(X,Y,'Learners',t,'ClassNames',classOrder);
```

`t` is an SVM template object. The software uses default values for empty options in `t` during training. `Mdl` is a `ClassificationECOC` model.

Reduce the size of the trained ECOC model.

```
CMdl = compact(Mdl)
```

```
CMdl =

  classreg.learning.classif.CompactClassificationECOC
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: [1x3 categorical]
    ScoreTransform: 'none'
    BinaryLearners: {3x1 cell}
      CodingMatrix: [3x3 double]
```

`CMdl` is a `CompactClassificationECOC` model. It does not store the training data nor some of the properties that `Mdl` stores.

Display how much memory each classifier uses.

```
whos('Mdl','CMdl')
```

```
  Name      Size             Bytes  Class

  CMdl      1x1              11738  classreg.learning.classif.CompactClassificationECOC
  Mdl       1x1              24820  ClassificationECOC
```

The full ECOC model (`Mdl`) is approximately double the size of the compact ECOC model (`CMdl`).

You can remove `Mdl` from the MATLAB® Workspace, and pass `CMdl` and new predictor values to `predict` to efficiently label new observations.

See Also

`ClassificationECOC` | `CompactClassificationECOC` | `fitcecoc` | `predict`

compact

Class: ClassificationEnsemble

Compact classification ensemble

Syntax

```
cens = compact(ens)
```

Description

`cens = compact(ens)` creates a compact version of `ens`. You can predict classifications using `cens` exactly as you can using `ens`. However, since `cens` does not contain training data, you cannot perform some actions, such as cross validation.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Output Arguments

`cens`

A compact classification ensemble. `cens` has class `CompactClassificationEnsemble`.

Examples

Compare the size of a classification ensemble for Fisher's iris data to the compact version of the ensemble:

```
load fisheriris
```

```
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cens = compact(ens);
b = whos('ens'); % b.bytes = size of ens
c = whos('cens'); % c.bytes = size of ens
[b.bytes c.bytes] % shows cens uses less memory

ans =
      571727      532476
```

See Also

`ClassificationTree` | `fitensemble`

How To

- "Ensemble Methods" on page 16-68

compact

Class: ClassificationNaiveBayes

Compact naive Bayes classifier

Syntax

```
CMdl = compact(Mdl)
```

Description

`CMdl = compact(Mdl)` returns a compact naive Bayes classifier (`CMdl`), which is the compact version of the trained naive Bayes classifier `Mdl`.

`CMdl` stores less than `Mdl`, e.g., `CMdl` does not store the training data.

Input Arguments

`Mdl` — Fully trained naive Bayes classifier

`ClassificationNaiveBayes` model

A fully trained naive Bayes classifier, specified as a `ClassificationNaiveBayes` model trained by `fitcnb`.

Output Arguments

`CMdl` — Compact naive Bayes classifier

`CompactClassificationNaiveBayes` model

Compact naive Bayes classifier, returned as a `CompactClassificationNaiveBayes` model.

Predict class labels using `CMdl` exactly as you would using `Mdl`. However, since `CMdl` does not contain training data, you cannot perform certain tasks, such as cross validation.

Examples

Reduce the Size of Naive Bayes Classifiers

Full naive Bayes classifiers (i.e., ClassificationNaiveBayes class models) hold the training data. For efficiency, you might not want to predict new labels using a large classifier. This example shows how to reduce the size of a full naive Bayes classifier.

Load the `ionosphere` data set.

```
load ionosphere
X = X(:,3:end); % Remove two predictors for stability
```

Train a naive Bayes classifier. Assume that each predictor is conditionally, normally distributed given its label. It is good practice to specify the order of the labels.

```
Mdl = fitcnb(X,Y,'ClassNames',{'b','g'})
```

```
Mdl =

  ClassificationNaiveBayes
           PredictorNames: {1x32 cell}
             ResponseName: 'Y'
                ClassNames: {'b'  'g'}
           ScoreTransform: 'none'
          NumObservations: 351
        DistributionNames: {1x32 cell}
   DistributionParameters: {2x32 cell}
```

`Mdl` is a `ClassificationNaiveBayes` model.

Reduce the size of the naive Bayes classifier.

```
CMdl = compact(Mdl)
```

```
CMdl =

  classreg.learning.classif.CompactClassificationNaiveBayes
           PredictorNames: {1x32 cell}
             ResponseName: 'Y'
```

```
               ClassNames: {'b'  'g'}
           ScoreTransform: 'none'
        DistributionNames: {1x32 cell}
    DistributionParameters: {2x32 cell}
```

`CMdl` is a `CompactClassificationNaiveBayes` model.

Display how much memory each classifier uses.

```
whos('Mdl','CMdl')
```

```
  Name      Size              Bytes  Class

  CMdl      1x1               14796  classreg.learning.classif.CompactClassificationNai
  Mdl       1x1              111581  ClassificationNaiveBayes
```

The full naive Bayes classifier (`Mdl`) is much larger than the compact naive Bayes classifier (`CMdl`).

You can remove `Mdl` from the MATLAB® Workspace, and pass `CMdl` and new predictor values to predict (CompactClassificationNaiveBayes) to efficiently label new observations.

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `fitcnb` | `predict`

compact

Class: ClassificationSVM

Compact support vector machine classifier

Syntax

```
CompactSVMModel = compact(SVMModel)
```

Description

`CompactSVMModel = compact(SVMModel)` returns a compact support vector machine (SVM) classifier (`CompactSVMModel`), the compact version of the trained SVM classifier `SVMModel`.

`CompactSVMModel` does not contain the training data, whereas `SVMModel` contains the training data in its properties `SVMModel.X` and `SVMModel.Y`.

Input Arguments

`SVMModel` — Full, trained SVM classifier

`ClassificationSVM` classifier

Full, trained SVM classifier, specified as a `ClassificationSVM` model trained using `fitcsvm`.

Output Arguments

`CompactSVMModel` — Compact SVM classifier

`CompactClassificationSVM` classifier

Compact SVM classifier, returned as a `CompactClassificationSVM` classifier.

Predict class labels using `CompactSVMModel` exactly as you would using `SVMModel`. However, since `CompactSVMModel` does not contain training data, you cannot perform certain tasks, such as cross validation.

Examples

Reduce the Size of Support Vector Machine Classifiers

Full SVM classifiers (i.e., `ClassificationSVM` classifiers) hold the training data. For efficiency, you might not want to predict new labels using a large classifier. This example shows how to reduce the size of a full SVM classifier.

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to standardize the predictors and specify the order of the classes.

```
SVMModel = fitcsvm(X,Y,'Standardize',true,...
    'ClassNames',{'b','g'})
```

```
SVMModel =

  ClassificationSVM
      PredictorNames: {1x34 cell}
        ResponseName: 'Y'
          ClassNames: {'b'  'g'}
      ScoreTransform: 'none'
     NumObservations: 351
               Alpha: [90x1 double]
                Bias: -0.1343
    KernelParameters: [1x1 struct]
                  Mu: [1x34 double]
               Sigma: [1x34 double]
      BoxConstraints: [351x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [351x1 logical]
              Solver: 'SMO'
```

`SVMModel` is a `ClassificationSVM` classifier.

Reduce the size of the SVM classifier.

```
CompactSVMModel = compact(SVMModel)
```

```
CompactSVMModel =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
                  Alpha: [90x1 double]
                   Bias: -0.1343
       KernelParameters: [1x1 struct]
                     Mu: [1x34 double]
                  Sigma: [1x34 double]
         SupportVectors: [90x34 double]
    SupportVectorLabels: [90x1 double]
```

`CompactSVMModel` is a `CompactClassificationSVM` classifier.

Display how much memory each classifier uses.

```
whos('SVMModel','CompactSVMModel')
```

```
  Name                 Size              Bytes  Class

  CompactSVMModel      1x1               30152  classreg.learning.classif.CompactClassif
  SVMModel             1x1              141126  ClassificationSVM
```

The full SVM classifier (`SVMModel`) is more than four times the compact SVM classifier (`CompactSVMModel`).

You can remove `SVMModel` from the MATLAB® Workspace, and pass `CompactSVMModel` and new predictor values to `predict` to efficiently label new observations.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm`

compact

Class: ClassificationTree

Compact tree

Syntax

```
ctree = compact(tree)
```

Description

`ctree = compact(tree)` creates a compact version of `tree`.

Input Arguments

`tree`

A classification tree created using `fitctree`.

Output Arguments

`ctree`

A compact decision tree. `ctree` has class `CompactClassificationTree`. You can predict classifications using `ctree` exactly as you can using `tree`. However, since `ctree` does not contain training data, you cannot perform some actions, such as cross validation.

Examples

Create a Compact Classification Tree

Compare the size of the classification tree for Fisher's iris data to the compact version of the tree.

```
load fisheriris
fulltree = fitctree(meas,species);
ctree = compact(fulltree);
b = whos('fulltree'); % b.bytes = size of fulltree
c = whos('ctree'); % c.bytes = size of ctree
[b.bytes c.bytes] % shows ctree uses half the memory

ans =
       13913        6818
```

See Also

ClassificationTree | CompactClassificationTree | fitctree | predict

compact

Class: RegressionEnsemble

Create compact regression ensemble

Syntax

```
cens = compact(ens)
```

Description

`cens = compact(ens)` creates a compact version of `ens`. You can predict regressions using `cens` exactly as you can using `ens`. However, since `cens` does not contain training data, you cannot perform some actions, such as cross validation.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Output Arguments

`cens`

A compact regression ensemble. `cens` is of class `CompactRegressionEnsemble`.

Examples

Compare the size of a regression ensemble for the `carsmall` data to the compact version of the ensemble:

```
load carsmall
```

```
X = [Acceleration Cylinders Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
cens = compact(ens);
b = whos('ens'); % b.bytes = size of ens
c = whos('cens'); % c.bytes = size of cens
[b.bytes c.bytes] % shows ctree uses less memory

ans =
      311789      287368
```

See Also

CompactRegressionEnsemble | RegressionEnsemble

compact

Class: RegressionTree

Compact regression tree

Syntax

```
ctree = compact(tree)
```

Description

`ctree = compact(tree)` creates a compact version of `tree`.

Input Arguments

`tree`

A regression tree created using `fitrtree`.

Output Arguments

`ctree`

A compact regression tree. `ctree` has class `CompactRegressionTree`. You can predict regressions using `ctree` exactly as you can using `tree`. However, since `ctree` does not contain training data, you cannot perform some actions, such as cross validation.

Examples

Compare the size of a regression tree for the `carsmall` data to the compact version of the tree:

```
load carsmall
```

```
X = [Acceleration Cylinders Displacement Horsepower Weight];
fulltree = fitrtree(X,MPG);
ctree = compact(fulltree);
b = whos('fulltree'); % b.bytes = size of fulltree
c = whos('ctree'); % c.bytes = size of ctree
[b.bytes c.bytes] % shows ctree uses 2/3 the memory

ans =
       15715       10258
```

See Also

predict | fitrtree | CompactRegressionTree | RegressionTree

compact

Class: TreeBagger

Compact ensemble of decision trees

Description

Return an object of class `CompactTreeBagger` holding the structure of the trained ensemble. The class is more compact than the full `TreeBagger` class because it does not contain information for growing more trees for the ensemble. In particular, it does not contain `X` and `Y` used for training.

See Also

`CompactTreeBagger`

CompactClassificationDiscriminant class

Compact discriminant analysis class

Description

A `CompactClassificationDiscriminant` object is a compact version of a discriminant analysis classifier. The compact version does not include the data for training the classifier. Therefore, you cannot perform some tasks with a compact classifier, such as cross validation. Use a compact classifier for making predictions (classifications) of new data.

Construction

`cobj = compact(obj)` constructs a compact classifier from a full classifier.

`cobj = makecdiscr(Mu,Sigma)` constructs a compact discriminant analysis classifier from the class means `Mu` and covariance matrix `Sigma`. For syntax details, see `makecdiscr`.

Input Arguments

`obj`

Discriminant analysis classifier, created using `fitcdiscr`.

Properties

`BetweenSigma`

`p`-by-`p` matrix, the between-class covariance, where `p` is the number of predictors.

`CategoricalPredictors`

List of categorical predictors, which is always empty (`[ ]`) for SVM and discriminant analysis classifiers.

ClassNames

List of the elements in the training data Y with duplicates removed. ClassNames can be a categorical array, cell array of strings, character array, logical vector, or a numeric vector. ClassNames has the same data type as the data in the argument Y.

Coeffs

k-by-k structure of coefficient matrices, where k is the number of classes. Coeffs(i,j) contains coefficients of the linear or quadratic boundaries between classes i and j. Fields in Coeffs(i,j):

- DiscrimType
- Class1 — ClassNames(i)
- Class2 — ClassNames(j)
- Const — A scalar
- Linear — A vector with p components, where p is the number of columns in X
- Quadratic — p-by-p matrix, exists for quadratic DiscrimType

The equation of the boundary between class i and class j is
Const + Linear * x + x' * Quadratic * x = 0,

where x is a column vector of length p.

If fitcdiscr had the FillCoeffs name-value pair set to 'off' when constructing the classifier, Coeffs is empty ([]).

Cost

Square matrix, where Cost(i,j) is the cost of classifying a point into class j if its true class is i (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of Cost corresponds to the order of the classes in ClassNames. The number of rows and columns in Cost is the number of unique classes in the response.

Change a Cost matrix using dot notation: obj.Cost = costMatrix.

Delta

Value of the Delta threshold for a linear discriminant model, a nonnegative scalar. If a coefficient of obj has magnitude smaller than Delta, obj sets this coefficient to 0, and

so you can eliminate the corresponding predictor from the model. Set `Delta` to a higher value to eliminate more predictors.

`Delta` must be `0` for quadratic discriminant models.

Change `Delta` using dot notation: `obj.Delta = newDelta`.

`DeltaPredictor`

Row vector of length equal to the number of predictors in `obj`. If `DeltaPredictor(i) < Delta` then coefficient `i` of the model is `0`.

If `obj` is a quadratic discriminant model, all elements of `DeltaPredictor` are `0`.

`DiscrimType`

String specifying the discriminant type. One of:

- `'linear'`
- `'quadratic'`
- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

Change `DiscrimType` using dot notation: `obj.DiscrimType = newDiscrimType`.

You can change between linear types, or between quadratic types, but cannot change between linear and quadratic types.

`Gamma`

Value of the Gamma regularization parameter, a scalar from `0` to `1`. Change `Gamma` using dot notation: `obj.Gamma = newGamma`.

- If you set `1` for linear discriminant, the discriminant sets its type to `'diagLinear'`.
- If you set a value between `MinGamma` and `1` for linear discriminant, the discriminant sets its type to `'linear'`.
- You cannot set values below the value of the `MinGamma` property.
- For quadratic discriminant, you can set either `0` (for `DiscrimType 'quadratic'`) or `1` (for `DiscrimType 'diagQuadratic'`).

LogDetSigma

Logarithm of the determinant of the within-class covariance matrix. The type of `LogDetSigma` depends on the discriminant type:

- Scalar for linear discriminant analysis
- Vector of length `K` for quadratic discriminant analysis, where `K` is the number of classes

MinGamma

Nonnegative scalar, the minimal value of the Gamma parameter so that the correlation matrix is invertible. If the correlation matrix is not singular, `MinGamma` is `0`.

Mu

Class means, specified as a `K`-by-`p` matrix of scalar values class means of size. `K` is the number of classes, and `p` is the number of predictors. Each row of `Mu` represents the mean of the multivariate normal distribution of the corresponding class. The class indices are in the ClassNames attribute.

PredictorNames

Cell array of names for the predictor variables, in the order in which they appear in the training data `X`.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames.

Add or change a `Prior` vector using dot notation: `obj.Prior = priorVector`.

ResponseName

String describing the response variable `Y`.

ScoreTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `fitcdiscr`.

Implement dot notation to add or change a `ScoreTransform` function using one of the following:

- `cobj.ScoreTransform = '`*`function`*`'`
- `cobj.ScoreTransform = @`*`function`*

`Sigma`

Within-class covariance matrix or matrices. The dimensions depend on DiscrimType:

- `'linear'` (default) — Matrix of size `p`-by-`p`, where `p` is the number of predictors
- `'quadratic'` — Array of size `p`-by-`p`-by-`K`, where `K` is the number of classes
- `'diagLinear'` — Row vector of length `p`
- `'diagQuadratic'` — Array of size `1`-by-`p`-by-`K`
- `'pseudoLinear'` — Matrix of size `p`-by-`p`
- `'pseudoQuadratic'` — Array of size `p`-by-`p`-by-`K`

Methods

compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge
logP	Log unconditional probability density for discriminant analysis classifier
loss	Classification error
mahal	Mahalanobis distance to class means
margin	Classification margins
nLinearCoeffs	Number of nonzero linear coefficients

predict

Predict classification

Definitions

Discriminant Classification

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. That is, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class, only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

For details, see “How the predict Method Classifies” on page 15-6.

Regularization

Regularization is the process of finding a small set of predictors that yield an effective predictive model. For linear discriminant analysis, there are two parameters, γ and δ,

that control regularization as follows. `cvshrink` helps you select appropriate values of the parameters.

Let Σ represent the covariance matrix of the data X, and let $\hat{X}$ be the centered data (the data X minus the mean by class). Define

$$D = \mathrm{diag}\left(\hat{X}^T * \hat{X}\right).$$

The regularized covariance matrix $\tilde{\Sigma}$ is

$$\tilde{\Sigma} = (1-\gamma)\Sigma + \gamma D.$$

Whenever $\gamma \geq$ `MinGamma`, $\tilde{\Sigma}$ is nonsingular.

Let μ_k be the mean vector for those elements of X in class k, and let μ_0 be the global mean vector (the mean of the rows of X). Let C be the correlation matrix of the data X, and let $\tilde{C}$ be the regularized correlation matrix:

$$\tilde{C} = (1-\gamma)C + \gamma I,$$

where I is the identity matrix.

The linear term in the regularized discriminant analysis classifier for a data point x is

$$(x-\mu_0)^T \tilde{\Sigma}^{-1}(\mu_k - \mu_0) = \left[(x-\mu_0)^T D^{-1/2}\right]\left[\tilde{C}^{-1}D^{-1/2}(\mu_k - \mu_0)\right].$$

The parameter δ enters into this equation as a threshold on the final term in square brackets. Each component of the vector $\left[\tilde{C}^{-1}D^{-1/2}(\mu_k - \mu_0)\right]$ is set to zero if it is smaller in magnitude than the threshold δ. Therefore, for class k, if component j is thresholded to zero, component j of x does not enter into the evaluation of the posterior probability.

The `DeltaPredictor` property is a vector related to this threshold. When $\delta \geq$ `DeltaPredictor(i)`, all classes k have

$$\left|\tilde{C}^{-1}D^{-1/2}(\mu_k - \mu_0)\right| \leq \delta.$$

Therefore, when $\delta \geq$ `DeltaPredictor(i)`, the regularized classifier does not use predictor `i`.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a Compact Discriminant Analysis Classifier

Load the sample data.

```
load fisheriris
```

Construct a discriminant analysis classifier for the sample data.

```
fullobj = fitcdiscr(meas,species);
```

Construct a compact discriminant analysis classifier, and compare its size to that of the full classifier.

```
cobj = compact(fullobj);
b = whos('fullobj'); % b.bytes = size of fullobj
c = whos('cobj'); % c.bytes = size of cobj
[b.bytes c.bytes] % shows cobj uses 60% of the memory
```

```
ans =
       18578       11498
```

The compact classifier is smaller than the full classifier.

Construct Classifier Using Means and Covariances

Construct a compact discriminant analysis classifier from the means and covariances of the Fisher iris data.

```
load fisheriris
mu(1,:) = mean(meas(1:50,:));
mu(2,:) = mean(meas(51:100,:));
```

```
mu(3,:) = mean(meas(101:150,:));

mm1 = repmat(mu(1,:),50,1);
mm2 = repmat(mu(2,:),50,1);
mm3 = repmat(mu(3,:),50,1);
cc = meas;
cc(1:50,:) = cc(1:50,:) - mm1;
cc(51:100,:) = cc(51:100,:) - mm2;
cc(101:150,:) = cc(101:150,:) - mm3;
sigstar = cc' * cc / 147;
cpct = makecdiscr(mu,sigstar,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

See Also

compact | predict | ClassificationDiscriminant | makecdiscr | fitcdiscr

How To

- “Discriminant Analysis” on page 15-3

CompactClassificationECOC class

Compact multiclass model for support vector machines or other classifiers

Description

`CompactClassificationECOC` is a compact, error-correcting output codes (ECOC) multiclass model.

The compact classifier does not include the data used for training the ECOC multiclass model. Therefore, you cannot perform tasks, such as cross validation, using the compact classifier.

Use a compact ECOC multiclass model for labeling new data (in other words, predicting the labels of new data).

Construction

`CompactMdl = compact(Mdl)` returns a compact ECOC multiclass model (`CompactSVMModel`) from a full, trained ECOC multiclass model (Mdl).

Input Arguments

`Mdl` — Trained, full ECOC multiclass model

`ClassificationECOC` classifier

Trained, full ECOC multiclass model, specified as a `ClassificationECOC` classifier trained by `fitcecoc`.

Properties

`BinaryLearners` — Trained binary learners

cell vector of model objects

Trained binary learners, specified as a cell vector of model objects. `BinaryLearners` has as many elements as classes in Y.

`BinaryLearner{j}` was trained by the software to solve the binary problem specified by CodingMatrix`(:,j)`. For example, for multiclass learning using SVM learners, each element of `BinaryLearners` is a `CompactClassificationSVM` classifier.

Data Types: `cell`

`BinaryLoss` — Binary learner loss function

string

Binary learner loss function, specified as a string.

If you train using binary learners that use different loss functions, then the software sets `BinaryLoss` to `'hamming'`. To potentially increase accuracy, set a different binary loss function than this default during prediction or loss computation using the `BinaryLoss` name-value pair argument of `predict` or `loss`.

Data Types: `char`

`CategoricalPredictors` — Categorical predictor indices

numeric vector

Categorical predictor indices, specified as a numeric vector. `CategoricalPredictors` contains indices `1` through `p`, where `p` is the number of columns of `X` (`size(X,2)`).

Data Types: `single` | `double`

`ClassNames` — Unique class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Unique class labels in the response data (Y), specified as a categorical or character array, logical or numeric vector, or cell array of strings. `ClassNames` has the same data type as `Y`.

`CodingMatrix` — Codes specifying class assignments

numeric matrix

Codes specifying class assignments for the binary learners, specified as a numeric matrix. `CodingMatrix` is a K-by-L matrix, where K is the number of classes and L is the number of binary learners.

Elements of `CodingMatrix` are `-1`, `0`, or `1`, and the value corresponds to a dichotomous class assignment. This table describes the meaning of `CodingMatrix(i,j)`, that is, the class that learner `j` assigns to observations in class `i`.

Value	Dichotomous Class Assignment
-1	Negative class
0	Before training, learner j removes observations in class i from the data set.
1	Positive class

Data Types: double | single | int8 | int16 | int32 | int64

Cost — Misclassification costs

square numeric matrix

Misclassification costs, specified as a square numeric matrix. Cost has K rows and columns, where K is the number of classes.

Cost(i,j) is the cost of misclassifying a point into class j if its true class is i. The order of the rows and columns of Cost corresponds to the order of the classes in ClassNames.

fitcecoc incorporates misclassification costs differently among different types of binary learners.

This property is read-only.

Data Types: double

LearnerWeights — Binary learner weights

numeric row vector

Binary learner weights, specified as a numeric row vector. LeanerWeights has length equal to the number of binary learners (size(CodingMatrix,2)).

LearnerWeights(j) is the sum of the observation weights that binary learner j used to train its classifier.

The software uses LearnerWeights to fit posterior probabilities by minimizing the Kullback-Leibler divergence.

Data Types: double | single

PredictorNames — Predictors names

cell array of strings

Predictors names in the order that they appear in X, specified as a cell array of strings containing the predictor names. `PredictorNames` has length equal to the number of columns in `X`.

Data Types: `cell`

`Prior` — Prior class probabilities

numeric vector

Prior class probabilities, specified as a numeric vector. `Prior` has as many elements as classes in Y, and the order of the elements corresponds to the elements of `ClassNames`.

`fitcecoc` incorporates misclassification costs differently among different types of binary learners.

This property is read only.

Data Types: `double`

`ResponseName` — Response variable name

string

Response variable name, specified as a string.

Data Types: `char`

`ScoreTransform` — Score transformation function

string | function handle

Score transformation function, specified as a string or function handle. `ScoreTransform` describes how the software transforms raw, predicted classification scores.

To change the score transformation function to, e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

  ```
  SVMModel.ScoreTransform = 'function';
  ```

  This table lists the supported, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$

String	Formula
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  SVMModel.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Data Types: `char` | `function_handle`

Methods

compareHoldout	Compare accuracies of two classification models using new data
discardSupportVectors	Discard support vectors of linear support vector machine binary learners
edge	Classification edge for error-correcting output code mutliclass classifiers

loss	Classification loss for error-correcting output code multiclass classifiers
margin	Classification margins for error-correcting output code multiclass classifiers
predict	Predict labels for error-correcting output code multiclass classifiers

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Reduce the Size of Full ECOC Models

Full ECOC models (i.e., `ClassificationECOC` classifiers) hold the training data. For efficiency, you might not want to predict new labels using a large classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

Train an ECOC model using default SVMs as binary learners.

```
Mdl = fitcecoc(X,Y)
```

```
Mdl =

  ClassificationECOC
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
```

```
    BinaryLearners: {3x1 cell}
        CodingName: 'onevsone'
```

`Mdl` is a `ClassificationECOC` model.

Reduce the size of the ECOC model.

```
CMdl = compact(Mdl)
```

```
CMdl =

  classreg.learning.classif.CompactClassificationECOC
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
    BinaryLearners: {3x1 cell}
      CodingMatrix: [3x3 double]
```

`CMdl` is a `CompactClassificationECOC` model.

Display how much memory each classifier consumes.

```
whos('Mdl','CMdl')
```

```
  Name      Size             Bytes  Class

  CMdl      1x1              11546  classreg.learning.classif.CompactClassificationECOC
  Mdl       1x1              24373  ClassificationECOC
```

The full ECOC model (`Mdl`) is almost twice the size of the compact ECOC model (`CMdl`).

You can remove `Mdl` from the MATLAB® Workspace, and pass `CMdl` and new predictor values to `predict` to efficiently label new observations.

Train and Cross Validate ECOC Classifiers

Train an ECOC classifier using different binary learners and the one-versus-all coding design. Then, cross validate the classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
classNames = unique(species(~strcmp(species,''))) % Remove empty classes
K = numel(classNames) % Number of classes
rng(1);  % For reproducibility
```

```
classNames =

    'setosa'
    'versicolor'
    'virginica'


K =

     3
```

`classNames` are the unique classes in the data set, and `K` is the number of classes. You can use `classNames` to specify the order of the classes during training.

For a one-versus-all coding design, there are `K` = 3 binary learners. Specify templates for the binary learners such that: * Binary learner 1 and 2 are naive Bayes classifiers. By default, each predictor is conditionally, normally distributed given its label. * Binary learner 3 is an SVM classifier. Specify to use the Gaussian kernel.

```
tNB = templateNaiveBayes();
tSVM = templateSVM('KernelFunction','gaussian');
tLearners = {tNB tNB tSVM};
```

`tNB` and `tSVM` are template objects for naive Bayes and SVM learning, respectively. They indicate what options to use during training. Most of their properties are empty, except for those specified using name-value pair arguments. The software fills in the empty properties with their default values during training.

Train and cross validate an ECOC classifier using the binary learner templates and the one-versus-all coding design. Specify the order of the classes. By default, naive Bayes classifiers use posterior probabilities as scores, whereas SVM classifiers use distance from the decision boundary. Therefore, to aggregate the binary learners, you must specify to fit posterior probabilities.

```
CVMdl = fitcecoc(X,Y,'ClassNames',classNames,'CrossVal','on',...
    'Learners',tLearners,'FitPosterior',1);
```

`CVMdl` is not a `ClassificationECOC` model, but a `ClassificationPartitionedECOC` cross-validated, ECOC model. By default, the software implements 10-fold cross validation. The the scores across the binary learners are the same form (i.e., they are posterior probabilities), and so the software can aggregate the results of the binary classifications properly.

Inspect one of the trained folds using dot notation.

```
CVMdl.Trained{1}
```

```
ans =

  classreg.learning.classif.CompactClassificationECOC
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
    BinaryLearners: {3x1 cell}
      CodingMatrix: [3x3 double]
```

Each fold is a `CompactClassificationECOC` model trained on 90% of the data.

You can access the results of the binary learners using dot notation and cell indexing. Display the trained SVM classifier (the third binary learner) in the first fold.

```
CVMdl.Trained{1}.BinaryLearners{3}
```

```
ans =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {'x1'  'x2'  'x3'  'x4'}
           ResponseName: 'Y'
             ClassNames: [-1 1]
         ScoreTransform: '@(S)sigmoid(S,-4.016735e+00,-3.243073e-01)'
                  Alpha: [33x1 double]
                   Bias: -0.1345
       KernelParameters: [1x1 struct]
         SupportVectors: [33x4 double]
```

```
    SupportVectorLabels: [33x1 double]
```

Estimate the generalization error.

```
genError = kfoldLoss(CVMdl)
```

```
genError =

    0.0333
```

On average, the generalization error is approximately 3%.

Algorithms

Random Coding Design Matrices

For a given number of classes, e.g., K, the software generates random coding design matrices as follows.

1. The software generates one of the following:
   a. Dense random — The software sets each element of the K-by-L_d coding design matrix with a 1 or a -1 with equal probability, where $L_d \approx \lceil 10 \log_2 K \rceil$.
   b. Sparse random — The software sets each element of the K-by-L_s coding design matrix with a 1, with probability 0.25, a -1 with probability 0.25, and a 0 with probability 0.5, where $L_s \approx \lceil 15 \log_2 K \rceil$.
2. If a column does not contain at least one 1 and at least one -1, then the software removes that column.
3. For distinct columns u and v, if $u = v$ or $u \neq -v$, then the software removes v from the coding design matrix.

The software randomly generates 10,000 matrices by default, and retains the matrix with the largest, minimal pair-wise row distance based on the Hamming measure ([4]) given by

$$\Delta(k_1,k_2)=0.5\sum_{l=1}^{L}\left|m_{k_1l}\right|\left|m_{k_2l}\right|\left|m_{k_1l}-m_{k_2l}\right|,$$

where m_{k_jl} is an element of coding design matrix j.

Support Vector Storage

For linear, SVM binary learners, and for efficiency, `fitcecoc` empties the properties `Alpha`, `SupportVectorLabels`, and `SupportVectors`. `fitcecoc` lists `Beta`, rather than `Alpha`, in the model display.

To store `Alpha`, `SupportVectorLabels`, and `SupportVectors`, pass a linear, SVM template that specifies storing support vectors to `fitcecoc`. For example, enter:

```
t = templateSVM('SaveSupportVectors','on')
Mdl = fitcecoc(X,Y,'Learners',t);
```

You can subsequently remove the support vectors and related values by passing the resulting `ClassificationECOC` model to `discardSupportVectors`.

References

[1] Fürnkranz, Johannes. “Round Robin Classification.” *J. Mach. Learn. Res.*, Vol. 2, 2002, pp. 721–747.

[2] Escalera, S., O. Pujol, and P. Radeva. “Separability of ternary codes for sparse designs of error-correcting output codes.” *Pattern Recog. Lett.*, Vol. 30, Issue 3, 2009, pp. 285–297.

See Also

`ClassificationECOC` | `compact` | `fitcecoc`

CompactClassificationEnsemble class

Compact classification ensemble class

Description

Compact version of a classification ensemble (of class `ClassificationEnsemble`). The compact version does not include the data for training the classification ensemble. Therefore, you cannot perform some tasks with a compact classification ensemble, such as cross validation. Use a compact classification ensemble for making predictions (classifications) of new data.

Construction

`cens = compact(ens)` constructs a compact decision ensemble from a full decision ensemble.

Input Arguments

`ens`

A classification ensemble created by `fitensemble`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`ClassNames`

List of the elements in Y with duplicates removed. `ClassNames` can be a numeric vector, vector of categorical variables, logical vector, character array, or cell array of strings. `ClassNames` has the same data type as the data in the argument Y.

CombineWeights

String describing how ens combines weak learner weights, either 'WeightedSum' or 'WeightedAverage'.

Cost

Square matrix, where Cost(i,j) is the cost of classifying a point into class j if its true class is i (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of Cost corresponds to the order of the classes in ClassNames. The number of rows and columns in Cost is the number of unique classes in the response. This property is read-only.

NumTrained

Number of trained weak learners in cens, a scalar.

PredictorNames

A cell array of names for the predictor variables, in the order in which they appear in X.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of Prior corresponds to the order of the classes in ClassNames. The number of elements of Prior is the number of unique classes in the response. This property is read-only.

ResponseName

String with the name of the response variable Y.

ScoreTransform

Function handle for transforming scores, or string representing a built-in transformation function. 'none' means no transformation; equivalently, 'none' means @(x)x. For a list of built-in transformation functions and the syntax of custom transformation functions, see fitctree.

Add or change a ScoreTransform function using dot notation:

```
cens.ScoreTransform = 'function'
```

or

```
cens.ScoreTransform = @function
```

`Trained`

Trained learners, a cell array of compact classification models.

`TrainedWeights`

Numeric vector of trained weights for the weak learners in ens. `TrainedWeights` has `T` elements, where `T` is the number of weak learners in learners.

`UsePredForLearner`

Logical matrix of size `P`-by-`NumTrained`, where `P` is the number of predictors (columns) in the training data `X`. `UsePredForLearner(i,j)` is `true` when learner `j` uses predictor `i`, and is `false` otherwise. For each learner, the predictors have the same order as the columns in the training data `X`.

If the ensemble is not of type `Subspace`, all entries in `UsePredForLearner` are `true`.

Methods

compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge
loss	Classification error
margin	Classification margins
predict	Predict classification
predictorImportance	Estimates of predictor importance
removeLearners	Remove members of compact classification ensemble

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Create a compact classification ensemble for the `ionosphere` data:

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
cens = compact(ens)
```

```
cens =

  classreg.learning.classif.CompactClassificationEnsemble
    PredictorNames: {1x34 cell}
      ResponseName: 'Y'
        ClassNames: {'b'  'g'}
    ScoreTransform: 'none'
        NumTrained: 100


  Properties, Methods
```

See Also

`ClassificationEnsemble` | `predict` | `compact` | `fitctree` | `fitensemble`

CompactClassificationNaiveBayes class

Compact naive Bayes classifier

Description

`CompactClassificationNaiveBayes` is a compact naive Bayes classifier.

The compact classifier does not include the data used for training the naive Bayes classifier. Therefore, you cannot perform tasks, such as cross validation, using the compact classifier.

Use a compact naive Bayes classifier to label new data (i.e., predicting the labels of new data) more efficiently.

Construction

`CMdl = compact(Mdl)` returns a compact naive Bayes classifier (`CMdl`) from a full, trained naive Bayes classifier (Mdl).

Input Arguments

`Mdl` — Fully trained naive Bayes classifier

`ClassificationNaiveBayes` model

A fully trained naive Bayes classifier, specified as a `ClassificationNaiveBayes` model trained by `fitcnb`.

Properties

`CategoricalPredictors` — Categorical predictor indices

numeric vector

Categorical predictor indices, specified as a numeric vector.

Data Types: `double`

`CategoricalLevels` — Multivariate multinomial levels

cell vector of numeric vectors

Multivariate multinomial levels, specified as a cell vector of numeric vectors. `CategoricalLevels` has length equal to the number of predictors (`size(X,2)`).

The cells of `CategoricalLevels` correspond to predictors that you specified as `'mvmn'` (i.e., having a multivariate multinomial distribution) during training. Cells that do not correspond to a multivariate multinomial distribution are empty (`[]`).

If predictor *j* is multivariate multinomial, then `CategoricalLevels{`*j*`}` is a list of all distinct values of predictor *j* in the sample (`NaN`s removed from `unique(X(:,j))`).

Data Types: `cell`

`ClassNames` — Distinct class names

categorical array | character array | logical vector | numeric vector | cell array of strings

Distinct class names, specified as a categorical or character array, logical or numeric vector, or cell vector of strings.

`ClassNames` is the same data type as Y, and has as *K* elements or rows for character arrays.

`Cost` — Misclassification cost

square matrix

Misclassification cost, specified as a *K*-by-*K* square matrix.

The value of `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. The order of the rows and columns of `Cost` correspond to the order of the classes in `ClassNames`.

The value of `Cost` does not influence training. You can reset `Cost` after training `Mdl` using dot notation, e.g., `Mdl.Cost = [0 0.5; 1 0];`.

Data Types: `double` | `single`

`DistributionNames` — Predictor distributions

`'normal'` (default) | `'kernel'` | `'mn'` | `'mvmn'` | cell array of strings

Predictor distributions `fitcnb` uses to model the predictors, specified as a string or cell array of strings.

This table summarizes the available distributions.

Value	Description
`'kernel'`	Kernel smoothing density estimate.
`'mn'`	Multinomial bag-of-tokens model. Indicates that all predictors have this distribution.
`'mvmn'`	Multivariate multinomial distribution.
`'normal'`	Normal (Gaussian) distribution.

If `Distribution` is a 1-by-*P* cell array of strings, then the software models feature *j* using the distribution in element *j* of the cell array.

Data Types: `cell` | `char`

`DistributionParameters` — Distribution parameter estimates

cell array

Distribution parameter estimates, specified as a cell array. `DistributionParameters` is a *K*-by-*P* cell array, where cell (*k*,*d*) contains the distribution parameter estimates for instances of predictor *d* in class *k*. The order of the rows follows the order of the classes in the property ClassNames, and the order of the predictors follows the order of the columns of X.

If class *k* has no observations for predictor *j*, then `Distribution{`*k*`,`*j*`}` is empty (`[]`).

The elements of `DistributionParameters` depends on the distributions of the predictors. This table describes the values in `DistributionParameters{`*k*`,`*j*`}`.

Value	\Distribution of Predictor *j*
`kernel`	A `prob.KernelDistribution` model. Display properties using cell indexing and dot notation. For example, to display the estimated bandwidth of the kernel density for predictor 2 in the third class, use `Mdl.DistributionParameters{3,2}.BandWidth`.
`mn`	A scalar representing the probability that token *j* appears in class *k*. For details, see "Algorithms".
`mvmn`	A numeric vector containing the probabilities for each possible level of

Value	\Distribution of Predictor *j*
	predictor *j* in class *k*. The software orders the probabilities by the sorted order of all unique levels of predictor *j* (stored in the property CategoricalLevels). For more details, see "Algorithms".
`normal`	A 2-by-1 numeric vector. The first element is the sample mean and the second element is the sample standard deviation.

`Kernel` — Kernel smoother types

`'normal'` (default) | `'box'` | `'epanechnikov'` | `'triangle'` | cell array of strings

Kernel smoother types, specified as a string or cell array of strings. `Kernel` has length equal to the number of predictors (`size(X,2)`). `Kernel{j}` corresponds to predictor *j*, and contains a string describing the type of kernel smoother. This table describes the supported kernel smoother types. Let $I\{u\}$ denote the indictor function.

Value	Kernel	Formula
`'box'`	Box (uniform)	$f(x) = 0.5I\{\lvert x\rvert \le 1\}$
`'epanechni`	Epanechnikov	$f(x) = 0.75\left(1 - x^2\right)I\{\lvert x\rvert \le 1\}$
`'normal'`	Gaussian	$f(x) = \frac{1}{\sqrt{2\pi}}\exp\left(-0.5x^2\right)$
`'triangle'`	Triangular	$f(x) = \left(1 - \lvert x\rvert\right)I\{\lvert x\rvert \le 1\}$

If a cell is empty ([ ]), then the software did not fit a kernel distribution to the corresponding predictor.

`PredictorNames` — Predictor names

string

Predictor names, specified as a cell vector of strings. The order of the elements in `PredictorNames` corresponds to the order in X.

Data Types: `cell`

`Prior` — Class prior probabilities

numeric vector

Class prior probabilities, specified as a numeric row vector. `Prior` is a 1-by-K vector, and the order of its elements correspond to the elements of `ClassNames`.

`fitcnb` normalizes the prior probabilities you set using the name-value pair parameter `'Prior'` so that `sum(Prior) = 1`.

The value of `Prior` does not change the best-fitting model. Therefore, you can reset `Prior` after training `Mdl` using dot notation, e.g., `Mdl.Prior = [0.2 0.8];`.

Data Types: `double | single`

`ResponseName` — Response name

string

Response name, specified as a string.

Data Types: `char`

`ScoreTransform` — Classification score transformation function

function handle | string

Classification score transformation function, specified as a function handle or a string.

To change the score transformation function to e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

  ```
  Mdl.ScoreTransform = 'function';
  ```

  This table lists available, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)

String	Formula
`'sign'`	–1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  Mdl.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Data Types: `char` | `function_handle`

`Support` — Kernel smoother density support

cell vector

Kernel smoother density support, specified as a cell vector. `Support` has length equal to the number of predictors (`size(X,2)`). The cells represent the regions to apply the kernel density.

This table describes the supported options.

Value	Description
1-by-2 numeric row vector	For example, `[L,U]`, where `L` and `U` are the finite lower and upper bounds, respectively, for the density support.
`'positive'`	The density support is all positive real values.
`'unbounded'`	The density support is all real values.

If a cell is empty (`[ ]`), then the software did not fit a kernel distribution to the corresponding predictor.

`Width` — Kernel smoother window width

numeric matrix

Kernel smoother window width, specified as a numeric matrix. `Width` is a K-by-P matrix, where K is the number of classes in the data, and P is the number of predictors (`size(X,2)`).

`Width(`k`,`j`)` is the kernel smoother window width for the kernel smoothing density of predictor j within class k. `NaN`s in column j indicate that the software did not fit predictor j using a kernel density.

Methods

compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge for naive Bayes classifiers
logP	Log unconditional probability density for naive Bayes classifier
loss	Classification error for naive Bayes classifier
margin	Classification margins for naive Bayes classifiers
predict	Predict classification for naive Bayes models

Definitions

Bag-of-Tokens Model

In the bag-of-tokens model, the value of predictor j is the nonnegative number of occurrences of token j in this observation. The number of categories (bins) in this multinomial model is the number of distinct tokens, that is, the number of predictors.

Naive Bayes

Naive Bayes is a classification algorithm that applies density estimation to the data.

The algorithm leverages Bayes theorem, and (naively) assumes that the predictors are conditionally independent, given the class. Though the assumption is usually violated in practice, naive Bayes classifiers tend to yield posterior distributions that are robust to biased class density estimates, particularly where the posterior is 0.5 (the decision boundary) [1].

Naive Bayes classifiers assign observations to the most probable class (in other words, the *maximum a posteriori* decision rule). Explicitly, the algorithm:

1. Estimates the densities of the predictors within each class.
2. Models posterior probabilities according to Bayes rule. That is, for all $k = 1,...,K$,

$$\hat{P}(Y = k \mid X_1,..,X_P) = \frac{\pi(Y = k)\prod_{j=1}^{P} P(X_j \mid Y = k)}{\sum_{k=1}^{K}\pi(Y = k)\prod_{j=1}^{P} P(X_j \mid Y = k)},$$

   where:

   - Y is the random variable corresponding to the class index of an observation.
   - $X_1,...,X_P$ are the random predictors of an observation.
   - $\pi(Y = k)$ is the prior probability that a class index is k.

3. Classifies an observation by estimating the posterior probability for each class, and then assigns the observation to the class yielding the maximum posterior probability.

If the predictors compose a multinomial distribution, then the posterior probability $\hat{P}(Y = k \mid X_1,..,X_P) \propto \pi(Y = k)P_{mn}(X_1,...,X_P \mid Y = k)$, where $P_{mn}(X_1,...,X_P \mid Y = k)$ is the probability mass function of a multinomial distribution.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Reduce the Size of Naive Bayes Classifiers

Full naive Bayes classifiers (i.e., ClassificationNaiveBayes class models) hold the training data. For efficiency, you might not want to predict new labels using a large classifier. This example shows how to reduce the size of a full naive Bayes classifier.

Load the `ionosphere` data set.

```
load ionosphere
X = X(:,3:end); % Remove two predictors for stability
```

Train a naive Bayes classifier. Assume that each predictor is conditionally, normally distributed given its label. It is good practice to specify the order of the labels.

```
Mdl = fitcnb(X,Y,'ClassNames',{'b','g'})
```

```
Mdl =

  ClassificationNaiveBayes
             PredictorNames: {1x32 cell}
               ResponseName: 'Y'
                 ClassNames: {'b'  'g'}
             ScoreTransform: 'none'
            NumObservations: 351
         DistributionNames: {1x32 cell}
    DistributionParameters: {2x32 cell}
```

`Mdl` is a `ClassificationNaiveBayes` model.

Reduce the size of the naive Bayes classifier.

```
CMdl = compact(Mdl)
```

```
CMdl =

  classreg.learning.classif.CompactClassificationNaiveBayes
           PredictorNames: {1x32 cell}
             ResponseName: 'Y'
                ClassNames: {'b'  'g'}
           ScoreTransform: 'none'
       DistributionNames: {1x32 cell}
  DistributionParameters: {2x32 cell}
```

`CMdl` is a `CompactClassificationNaiveBayes` model.

Display how much memory each classifier uses.

```
whos('Mdl','CMdl')
```

```
  Name      Size              Bytes  Class

  CMdl      1x1               14796  classreg.learning.classif.CompactClassificationNaiv
  Mdl       1x1              111581  ClassificationNaiveBayes
```

The full naive Bayes classifier (`Mdl`) is much larger than the compact naive Bayes classifier (`CMdl`).

You can remove `Mdl` from the MATLAB® Workspace, and pass `CMdl` and new predictor values to predict (CompactClassificationNaiveBayes) to efficiently label new observations.

Train and Cross Validate Naive Bayes Classifiers

Load the `ionosphere` data set.

```
load ionosphere
X = X(:,3:end); % Remove two predictors for stability
```

Train and cross validate a naive Bayes classifier. Assume that each predictor is conditionally, normally distributed given its label. It is good practice to specify the order of the classes.

```
rng(1);  % For reproducibility
CVMdl = fitcnb(X,Y,'ClassNames',{'b','g'},'CrossVal','on')
```

```
CVMdl =

  classreg.learning.partition.ClassificationPartitionedModel
    CrossValidatedModel: 'NaiveBayes'
         PredictorNames: {1x32 cell}
           ResponseName: 'Y'
        NumObservations: 351
                  KFold: 10
              Partition: [1x1 cvpartition]
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
```

`CVMdl` is not a `ClassificationNaiveBayes` model, but a `ClassificationPartitionedModel` cross-validated, naive Bayes model. By default, the software implements 10-fold cross validation.

Alternatively, you can cross validate a trained `ClassificationNaiveBayes` model by passing it to crossval (ClassificationNaiveBayes).

Inspect one of the trained folds using dot notation.

```
CVMdl.Trained{1}
```

```
ans =

  classreg.learning.classif.CompactClassificationNaiveBayes
            PredictorNames: {1x32 cell}
              ResponseName: 'Y'
                ClassNames: {'b'  'g'}
            ScoreTransform: 'none'
         DistributionNames: {1x32 cell}
    DistributionParameters: {2x32 cell}
```

Each fold is a `CompactClassificationNaiveBayes` model trained on 90% of the data.

Estimate the generalization error.

```
genError = kfoldLoss(CVMdl)
```

```
genError =
```

```
    0.1795
```

On average, the generalization error is approximately 17%.

One way to attempt reducing an unsatisfactory generalization error is to specify different conditional distributions for the predictors, or tune the parameters of the conditional distributions.

Algorithms

- If you specify `'Distribution','mn'` when training Mdl using `fitcnb`, then the software fits a multinomial distribution using the bag-of-tokens model. The software stores the probability that token j appears in class k in the property `DistributionParameters{`k`,`j`}`. Using additive smoothing [2], the estimated probability is

  $$P(\text{token } j \mid \text{class } k) = \frac{1 + c_{j|k}}{P + c_k},$$

  where:

  - $c_{j|k} = n_k \frac{\sum_{i:y_i \in \text{class } k} x_{ij} w_i}{\sum_{i:y_i \in \text{class } k} w_i}$; which is the weighted number of occurrences of token j in class k.
  - n_k is the number of observations in class k.
  - w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.
  - $c_k = \sum_{j=1}^{P} c_{j|k}$; which is the total weighted number of occurrences of all tokens in class k.

- If you specify `'Distribution','mvmn'` when training Mdl using `fitcnb`, then:

  1. For each predictor, the software collects a list of the unique levels, stores the sorted list in `CategoricalLevels`, and considers each level a bin. Each predictor/class combination is a separate, independent multinomial random variable.
  2. For predictor j in class k, the software counts instances of each categorical level using the list stored in `CategoricalLevels{`j`}`.
  3. The software stores the probability that predictor j, in class k, has level L in the property `DistributionParameters{`k`,`j`}`, for all levels in `CategoricalLevels{`j`}`. Using additive smoothing [2], the estimated probability is

$$P(\text{predictor } j = L \mid \text{class } k) = \frac{1 + m_{j|k}(L)}{m_j + m_k},$$

     where:

     - $m_{j|k}(L) = n_k \dfrac{\sum_{i:y_i \in \text{ class } k} I\{x_{ij} = L\} w_i}{\sum_{i:y_i \in \text{ class } k} w_i}$; which is the weighted number of observations for which predictor j equals L in class k.
     - n_k is the number of observations in class k.
     - $I\{x_{ij} = L\} = 1$ if $x_{ij} = L$, 0 otherwise.
     - w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.
     - m_j is the number of distinct levels in predictor j.
     - m_k is the weighted number of observations in class k.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[2] Manning, C. D., P. Raghavan, and M. Schütze. *Introduction to Information Retrieval*, NY: Cambridge University Press, 2008.

See Also

`ClassificationNaiveBayes` | `fitcnb` | `loss` | `predict`

More About

- "Naive Bayes Classification" on page 15-31
- "Grouping Variables" on page 2-52

CompactClassificationSVM class

Compact support vector machine for binary classification

Description

`CompactClassificationSVM` is a compact support vector machine (SVM) classifier.

The compact classifier does not include the data used for training the SVM classifier. Therefore, you cannot perform tasks, such as cross validation, using the compact classifier.

Use a compact SVM classifier for labeling new data (i.e., predicting the labels of new data).

Construction

`CompactSVMModel = compact(SVMModel)` returns a compact SVM classifier (`CompactSVMModel`) from a full, trained support vector machine classifier (SVMModel).

Input Arguments

`SVMModel`

A full, trained `ClassificationSVM` classifier trained by `fitcsvm`.

Properties

`Alpha`

Numeric vector of trained classifier coefficients from the dual problem (i.e., the estimated Lagrange multipliers). `Alpha` has length equal to the number of support vectors in the trained classifier (i.e., `sum(SVMModel.IsSupportVector)`).

Beta

Numeric vector of linear predictor coefficients. `Beta` has length equal to the number of predictors (i.e., `size(SVMModel.X,2)`).

If KernelParameters`.Function` is `'linear'`, then the software estimates the classification score for the observation x using

$$f(x) = (x / s)'\beta + b.$$

SVMModel stores β, b, and s in the properties Beta, Bias, and KernelParameters`.Scale`, respectively.

If KernelParameters`.Function` is not `'linear'`, then `Beta` is empty (`[]`).

Bias

Scalar corresponding to the trained classifier bias term.

CategoricalPredictors

List of categorical predictors, which is always empty (`[]`) for SVM and discriminant analysis classifiers.

ClassNames

List of elements in Y with duplicates removed. `ClassNames` has the same data type as the data in the argument Y, and therefore can be a categorical or character array, logical or numeric vector, or cell array of strings.

Cost

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.

During training, the software updates the prior probabilities by incorporating the penalties described in the cost matrix. Therefore,

- For two-class learning, `Cost` always has this form: `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j` (i.e., the rows correspond to the true class and the

columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames.

- For one-class learning, `Cost = 0`.

This property is read-only. For more details, see Algorithms.

`KernelParameters`

Structure array containing the kernel name and parameter values.

To display the values of `KernelParameters`, use dot notation, e.g., `SVMModel.KernelParameters.Scale` displays the scale parameter value.

The software accepts `KernelParameters` as inputs, and does not modify them. Alter `KernelParameters` by setting the appropriate name-value pair arguments when you train the SVM classifier using `fitcsvm`.

`Mu`

Numeric vector of predictor means.

If you specify `'Standardize',1` or `'Standardize',true` when you train an SVM classifier using `fitcsvm`, then `Mu` has length equal to the number of predictors (i.e., `size(SVMModel.X,2)`). Otherwise, `Mu` is an empty vector (`[]`).

`PredictorNames`

Cell array of strings containing the predictor names, in the order that they appear in `X`.

`Prior`

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the elements of `SVMModel.ClassNames`.

For two-class learning, if you specify a cost matrix, then the software updates the prior probabilities by incorporating the penalties described in the cost matrix.

This property is read-only. For more details, see Algorithms.

`ScoreTransform`

String representing a built-in transformation function, or a function handle for transforming predicted classification scores.

To change the score transformation function to, e.g., *`function`*, use dot notation.

- For a built-in function, enter a string.

  ```
  SVMModel.ScoreTransform = 'function';
  ```

  This table contains the available, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  SVMModel.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

`Sigma`

Numeric vector of predictor standard deviations.

If you specify `'Standardize',1` or `'Standardize',true` when you train the SVM classifier, then `Sigma` has length equal to the number of predictors (i.e., `size(SVMModel.X,2)`). Otherwise, `Sigma` is an empty vector (`[]`).

`SupportVectors`

Matrix containing rows of `X` that the software considers the support vectors.

If you specify `'Standardize',1` or `'Standardize',true`, then `SupportVectors` are the standardized rows of `X`.

`SupportVectorLabels`

Numeric vector of support vector class labels. `SupportVectorLabels` has length equal to the number of support vectors (i.e., `sum(SVMModel.IsSupportVector)`).

`+1` indicates that the corresponding support vector is in the positive class (`SVMModel.ClassNames{2}`). `-1` indicates that the corresponding support vector is in the negative class (`SVMModel.ClassNames{1}`).

Methods

compareHoldout	Compare accuracies of two classification models using new data
discardSupportVectors	Discard support vectors for linear support vector machine models
edge	Classification edge for support vector machine classifiers
fitPosterior	Fit posterior probabilities
loss	Classification error for support vector machine classifiers
margin	Classification margins for support vector machine classifiers
predict	Predict labels for support vector machine classifiers

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Reduce the Size of Support Vector Machine Classifiers

Full SVM classifiers (i.e., `ClassificationSVM` classifiers) hold the training data. For efficiency, you might not want to predict new labels using a large classifier. This example shows how to reduce the size of a full SVM classifier.

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to standardize the predictors and specify the order of the classes.

```
SVMModel = fitcsvm(X,Y,'Standardize',true,...
    'ClassNames',{'b','g'})
```

```
SVMModel =

  ClassificationSVM
      PredictorNames: {1x34 cell}
        ResponseName: 'Y'
          ClassNames: {'b'  'g'}
      ScoreTransform: 'none'
     NumObservations: 351
               Alpha: [90x1 double]
                Bias: -0.1343
    KernelParameters: [1x1 struct]
                  Mu: [1x34 double]
               Sigma: [1x34 double]
      BoxConstraints: [351x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [351x1 logical]
              Solver: 'SMO'
```

`SVMModel` is a `ClassificationSVM` classifier.

Reduce the size of the SVM classifier.

```
CompactSVMModel = compact(SVMModel)
```

```
CompactSVMModel =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
                  Alpha: [90x1 double]
                   Bias: -0.1343
       KernelParameters: [1x1 struct]
                     Mu: [1x34 double]
                  Sigma: [1x34 double]
         SupportVectors: [90x34 double]
    SupportVectorLabels: [90x1 double]
```

`CompactSVMModel` is a `CompactClassificationSVM` classifier.

Display how much memory each classifier uses.

```
whos('SVMModel','CompactSVMModel')
```

```
  Name                 Size              Bytes  Class

  CompactSVMModel      1x1               30152  classreg.learning.classif.CompactClassif
  SVMModel             1x1              141126  ClassificationSVM
```

The full SVM classifier (`SVMModel`) is more than four times the compact SVM classifier (`CompactSVMModel`).

You can remove `SVMModel` from the MATLAB® Workspace, and pass `CompactSVMModel` and new predictor values to `predict` to efficiently label new observations.

Train and Cross Validate Support Vector Machine Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train and cross validate an SVM classifier. It is good practice to standardize the predictors and specify the order of the classes.

```
rng(1);  % For reproducibility
CVSVMModel = fitcsvm(X,Y,'Standardize',true,...
    'ClassNames',{'b','g'},'CrossVal','on')
```

```
CVSVMModel =

  classreg.learning.partition.ClassificationPartitionedModel
    CrossValidatedModel: 'SVM'
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
        NumObservations: 351
                  KFold: 10
              Partition: [1x1 cvpartition]
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
```

`CVSVMModel` is not a `ClassificationSVM` classifier, but a `ClassificationPartitionedModel` cross-validated, SVM classifier. By default, the software implements 10-fold cross validation.

Alternatively, you can cross validate a trained `ClassificationSVM` classifier by passing it to `crossval`.

Inspect one of the trained folds using dot notation.

```
CVSVMModel.Trained{1}
```

```
ans =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
                  Alpha: [78x1 double]
                   Bias: -0.2209
```

```
       KernelParameters: [1x1 struct]
                     Mu: [1x34 double]
                  Sigma: [1x34 double]
          SupportVectors: [78x34 double]
    SupportVectorLabels: [78x1 double]
```

Each fold is a `CompactClassificationSVM` classifier trained on 90% of the data.

Estimate the generalization error.

```
genError = kfoldLoss(CVSVMModel)
```

```
genError =

    0.1168
```

On average, the generalization error is approximately 12%.

- Using Support Vector Machines

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[2] Scholkopf, B., J. C. Platt, J. C. Shawe-Taylor, A. J. Smola, and R. C. Williamson. "Estimating the Support of a High-Dimensional Distribution." *Neural Comput.*, Vol. 13, Number 7, 2001, pp. 1443–1471.

[3] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[4] Scholkopf, B. and A. Smola. *Learning with Kernels: Support Vector Machines, Regularization, Optimization and Beyond, Adaptive Computation and Machine Learning* Cambridge, MA: The MIT Press, 2002.

See Also

`ClassificationSVM` | `compact` | `fitcsvm`

More About

- Understanding Support Vector Machines

CompactClassificationTree class

Compact classification tree

Description

Compact version of a classification tree (of class `ClassificationTree`). The compact version does not include the data for training the classification tree. Therefore, you cannot perform some tasks with a compact classification tree, such as cross validation. Use a compact classification tree for making predictions (classifications) of new data.

Construction

`ctree = compact(tree)` constructs a compact decision tree from a full decision tree.

Input Arguments

`tree`

A decision tree constructed using `fitctree`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CategoricalSplits`

An n-by-2 cell array, where n is the number of categorical splits in tree. Each row in `CategoricalSplits` gives left and right values for a categorical split. For each branch node with categorical split `j` based on a categorical predictor variable `z`, the left child

is chosen if z is in CategoricalSplits(j,1) and the right child is chosen if z is in CategoricalSplits(j,2). The splits are in the same order as nodes of the tree. Find the nodes for these splits by selecting 'categorical' cuts from top to bottom in the CutType property.

Children

An *n*-by-2 array containing the numbers of the child nodes for each node in tree, where *n* is the number of nodes. Leaf nodes have child node 0.

ClassCount

An *n*-by-*k* array of class counts for the nodes in tree, where *n* is the number of nodes and *k* is the number of classes. For any node number i, the class counts ClassCount(i,:) are counts of observations (from the data used in fitting the tree) from each class satisfying the conditions for node i.

ClassNames

List of the elements in Y with duplicates removed. ClassNames can be a numeric vector, vector of categorical variables, logical vector, character array, or cell array of strings. ClassNames has the same data type as the data in the argument Y.

If the value of a property has at least one dimension of length *k*, then ClassNames indicates the order of the elements along that dimension (e.g., Cost and Prior).

ClassProbability

An *n*-by-*k* array of class probabilities for the nodes in tree, where *n* is the number of nodes and *k* is the number of classes. For any node number i, the class probabilities ClassProbability(i,:) are the estimated probabilities for each class for a point satisfying the conditions for node i.

Cost

Square matrix, where Cost(i,j) is the cost of classifying a point into class j if its true class is i (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of Cost corresponds to the order of the classes in ClassNames. The number of rows and columns in Cost is the number of unique classes in the response. This property is read-only.

CutCategories

An *n*-by-2 cell array of the categories used at branches in tree, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `x` is among those listed in `CutCategories{i,2}`. Both columns of `CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

CutPoint

An *n*-element vector of the values used as cut points in tree, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `x<CutPoint(i)` and the right child is chosen if `x>=CutPoint(i)`. `CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

CutType

An *n*-element cell array indicating the type of cut at each node in tree, where *n* is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

CutPredictor

An *n*-element cell array of the names of the variables used for branching in each node in tree, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `CutPredictor` contains an empty string.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`IsBranchNode`

An *n*-element logical vector that is `true` for each branch node and `false` for each leaf node of tree.

`NodeClass`

An *n*-element cell array with the names of the most probable classes in each node of tree, where *n* is the number of nodes in the tree. Every element of this array is a string equal to one of the class names in ClassNames.

`NodeError`

An *n*-element vector of the errors of the nodes in tree, where *n* is the number of nodes. `NodeError(i)` is the misclassification probability for node `i`.

`NodeProbability`

An *n*-element vector of the probabilities of the nodes in tree, where *n* is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

`NodeRisk`

An *n*-element vector of the risk of the nodes in the tree, where *n* is the number of nodes. The risk for each node is the measure of impurity (Gini index or deviance) for this node weighted by the node probability. If the tree is grown by twoing, the risk for each node is zero.

`NodeSize`

An *n*-element vector of the sizes of the nodes in tree, where *n* is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

`NumNodes`

The number of nodes in tree.

Parent

An n-element vector containing the number of the parent node for each node in tree, where n is the number of nodes. The parent of the root node is `0`.

PredictorNames

A cell array of names for the predictor variables, in the order in which they appear in `X`.

Prior

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames. The number of elements of `Prior` is the number of unique classes in the response. This property is read-only.

PruneAlpha

Numeric vector with one element per pruning level. If the pruning level ranges from 0 to M, then `PruneAlpha` has $M + 1$ elements sorted in ascending order. `PruneAlpha(1)` is for pruning level 0 (no pruning), `PruneAlpha(2)` is for pruning level 1, and so on.

PruneList

An n-element numeric vector with the pruning levels in each node of tree, where n is the number of nodes. The pruning levels range from 0 (no pruning) to M, where M is the distance between the deepest leaf and the root node.

ResponseName

String describing the response variable Y.

ScoreTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`. For a list of built-in transformation functions and the syntax of custom transformation functions, see `fitctree`.

Add or change a `ScoreTransform` function using dot notation:

```
ctree.ScoreTransform = 'function'
or
ctree.ScoreTransform = @function
```

SurrogateCutCategories

An n-element cell array of the categories used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutCategories{k}` is a cell array. The length of `SurrogateCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutCategories{k}` is either an empty string for a continuous surrogate predictor, or is a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutCategories` contains an empty cell.

SurrogateCutFlip

An n-element cell array of the numeric cut assignments used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrSurrogateCutFlip{k}` is a numeric vector. The length of `SurrogateCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and the cut assignment for this surrogate split is +1, or if $Z\geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and the cut assignment for this surrogate split is +1, or if $Z<C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutFlip` contains an empty array.

SurrogateCutPoint

An n-element cell array of the numeric values used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutPoint{k}` is a numeric vector. The length of `SurrogateCutPoint{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutPoint{k}` is either `NaN` for a categorical surrogate predictor, or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `SurrogateCutFlip` for this surrogate split is +1, or if $Z\geq C$ and `SurrogateCutFlip` for this surrogate split is –1. Similarly,

the right child is chosen if $Z \geq C$ and `SurrogateCutFlip` for this surrogate split is +1, or if $Z < C$ and `SurrogateCutFlip` for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutPoint` contains an empty cell.

`SurrogateCutType`

An n-element cell array indicating types of surrogate splits at each node in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutType{k}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutType` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cut point `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

`SurrogateCutPredictor`

An n-element cell array of the names of the variables used for surrogate splits in each node in tree, where n is the number of nodes in tree. Every element of `SurrogateCutPredictor` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutPredictor` contains an empty cell.

`SurrogatePredictorAssociation`

An n-element cell array of the predictive measures of association for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogatePredictorAssociation{k}` is a numeric vector. The length of `SurrogatePredictorAssociation{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogatePredictorAssociation{k}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogatePredictorAssociation` contains an empty cell.

Methods

compareHoldout	Compare accuracies of two classification models using new data
edge	Classification edge
loss	Classification error
margin	Classification margins
surrogateAssociation	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict classification
predictorImportance	Estimates of predictor importance
view	View tree

Definitions

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*.

Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair argument:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

$$1 - \sum_i p^2(i),$$

where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined the same as for the Gini index, the deviance of a node is

$$-\sum_i p(i)\log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

$$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

  where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with the largest number of training samples at a node, the node error is $1 - p(j)$.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a Compact Classification Tree

Construct a compact classification tree for the Fisher iris data.

```
load fisheriris
tree = fitctree(meas,species);
ctree = compact(tree);
```

Compare the size of the resulting tree to that of the original tree.

```
t = whos('tree'); % t.bytes = size of tree in bytes
c = whos('ctree'); % c.bytes = size of ctree in bytes
[c.bytes t.bytes]
```

```
ans =
        6818       13913
```

The compact tree is smaller than the original tree.

See Also

`compact` | `ClassificationTree` | `fitctree`

CompactRegressionEnsemble class

Compact regression ensemble class

Description

Compact version of a regression ensemble (of class `RegressionEnsemble`). The compact version does not include the data for training the regression ensemble. Therefore, you cannot perform some tasks with a compact regression ensemble, such as cross validation. Use a compact regression ensemble for making predictions (regressions) of new data.

Construction

`cens = compact(ens)` constructs a compact decision ensemble from a full decision ensemble.

Input Arguments

`ens`

A regression ensemble created by `fitensemble`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

A string describing how the ensemble combines learner predictions.

`NumTrained`

Number of trained learners in the ensemble, a positive scalar.

PredictorNames

A cell array of names for the predictor variables, in the order in which they appear in `X`.

ResponseName

A string with the name of the response variable `Y`.

ResponseTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function using dot notation:

```
cens.ResponseTransform = @function
```

Trained

The trained learners, a cell array of compact regression models.

TrainedWeights

A numeric vector of weights the ensemble assigns to its learners. The ensemble computes predicted response by aggregating weighted predictions from its learners.

Methods

loss	Regression error
predict	Predict response of ensemble
predictorImportance	Estimates of predictor importance
removeLearners	Remove members of compact regression ensemble

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a regression ensemble for the `carsmall` data. Make a compact version of the ensemble, and compare its size to that of the full ensemble:

```
load carsmall
learner = templateTree('MinParent',20);
ens = fitensemble([Weight, Cylinders],MPG,...
    'LSBoost',100,learner,'PredictorNames',{'W','C'},...
    'categoricalpredictors',2);
cens = compact(ens);
ee = whos('ens'); % ee.bytes = size of ensemble in bytes
cee = whos('cens');
[ee.bytes cee.bytes]

ans =
      606903      587096
```

See Also

`RegressionEnsemble` | `fitensemble` | `predict` | `compact` | `templateTree`

CompactRegressionTree class

Compact regression tree

Description

Compact version of a regression tree (of class `RegressionTree`). The compact version does not include the data for training the regression tree. Therefore, you cannot perform some tasks with a compact regression tree, such as cross validation. Use a compact regression tree for making predictions (regressions) of new data.

Construction

`ctree = compact(tree)` constructs a compact decision tree from a full decision tree.

Input Arguments

`tree`

A decision tree constructed by `fitrtree`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CategoricalSplits`

An n-by-2 cell array, where n is the number of categorical splits in tree. Each row in `CategoricalSplits` gives left and right values for a categorical split. For each branch node with categorical split `j` based on a categorical predictor variable `z`, the left child is chosen if `z` is in `CategoricalSplits(j,1)` and the right child is chosen if `z` is in `CategoricalSplits(j,2)`. The splits are in the same order as nodes of the tree. Nodes

for these splits can be found by running `cuttype` and selecting `'categorical'` cuts from top to bottom.

`Children`

An *n*-by-2 array containing the numbers of the child nodes for each node in tree, where *n* is the number of nodes. Leaf nodes have child node `0`.

`CutCategories`

An *n*-by-2 cell array of the categories used at branches in tree, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `x` is among those listed in `CutCategories{i,2}`. Both columns of `CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

`CutPoint`

An *n*-element vector of the values used as cut points in tree, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `CutPoint<v(i)` and the right child is chosen if `x>=CutPoint(i)`. `CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

`CutType`

An *n*-element cell array indicating the type of cut at each node in tree, where *n* is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

CutPredictor

An *n*-element cell array of the names of the variables used for branching in each node in tree, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `CutPredictor` contains an empty string.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

IsBranchNode

An *n*-element logical vector `ib` that is `true` for each branch node and `false` for each leaf node of tree.

NodeError

An *n*-element vector `e` of the errors of the nodes in tree, where *n* is the number of nodes. `e(i)` is the misclassification probability for node `i`.

NodeMean

An *n*-element numeric array with mean values in each node of tree, where *n* is the number of nodes in the tree. Every element in `NodeMean` is the average of the true `Y` values over all observations in the node.

NodeProbability

An *n*-element vector `p` of the probabilities of the nodes in tree, where *n* is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

NodeRisk

An *n*-element vector of the risk of the nodes in the tree, where *n* is the number of nodes. The risk for each node is the node error weighted by the node probability.

NodeSize

An *n*-element vector `sizes` of the sizes of the nodes in tree, where *n* is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

NumNodes

The number of nodes `n` in tree.

Parent

An *n*-element vector `p` containing the number of the parent node for each node in tree, where *n* is the number of nodes. The parent of the root node is `0`.

PredictorNames

A cell array of names for the predictor variables, in the order in which they appear in `X`.

PruneAlpha

Numeric vector with one element per pruning level. If the pruning level ranges from 0 to *M*, then `PruneAlpha` has *M* + 1 elements sorted in ascending order. `PruneAlpha(1)` is for pruning level 0 (no pruning), `PruneAlpha(2)` is for pruning level 1, and so on.

PruneList

An *n*-element numeric vector with the pruning levels in each node of tree, where *n* is the number of nodes. The pruning levels range from 0 (no pruning) to *M*, where *M* is the distance between the deepest leaf and the root node.

ResponseName

Name of the response variable Y, a string.

ResponseTransform

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function using dot notation:

```
ctree.ResponseTransform = @function
```

SurrogateCutCategories

An *n*-element cell array of the categories used for surrogate splits in tree, where *n* is the number of nodes in tree. For each node `k`, `SurrogateCutCategories{k}` is a cell array. The length of `SurrogateCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutCategories{k}` is either

an empty string for a continuous surrogate predictor, or is a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split, and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutCategories` contains an empty cell.

`SurrogateCutFlip`

An n-element cell array of the numeric cut assignments used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutFlip{k}` is a numeric vector. The length of `SurrogateCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and the cut assignment for this surrogate split is +1, or if $Z\geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and the cut assignment for this surrogate split is +1, or if $Z<C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutFlip` contains an empty array.

`SurrogateCutPoint`

An n-element cell array of the numeric values used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutPoint{k}` is a numeric vector. The length of `SurrogateCutPoint{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutPoint{k}` is either `NaN` for a categorical surrogate predictor, or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `SurrogateCutFlip` for this surrogate split is +1, or if $Z\geq C$ and `SurrogateCutFlip` for this surrogate split is –1. Similarly, the right child is chosen if $Z\geq C$ and `SurrogateCutFlip` for this surrogate split is +1, or if $Z<C$ and `SurrogateCutFlip` for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by `SurrogateCutVar`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutPoint` contains an empty cell.

SurrogateCutType

An n-element cell array indicating types of surrogate splits at each node in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutType{k}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutType` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cut point `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

SurrogateCutPredictor

An n-element cell array of the names of the variables used for surrogate splits in each node in tree, where n is the number of nodes in tree. Every element of `SurrogateCutPredictor` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutPredictor` contains an empty cell.

SurrogatePredictorAssociation

An n-element cell array of the predictive measures of association for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogatePredictorAssociation{k}` is a numeric vector. The length of `SurrogatePredictorAssociation{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogatePredictorAssociation{k}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogatePredictorAssociation` contains an empty cell.

Methods

loss	Regression error

surrogateAssociation	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict response of regression tree
predictorImportance	Estimates of predictor importance
view	View tree

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct and Compact a Regression Tree

Load the sample data.

```
load carsmall
```

Construct a regression tree for the sample data.

```
tree = fitrtree([Weight, Cylinders],MPG,...
    'MinParentSize',20,...
    'PredictorNames',{'W','C'});
```

Make a compact version of the tree.

```
ctree = compact(tree);
```

Compare the size of the compact tree to that of the full tree.

```
t = whos('tree'); % t.bytes = size of tree in bytes
c = whos('ctree'); % c.bytes = size of ctree in bytes
[c.bytes t.bytes]
```

```
ans =
        4972        8173
```

The compact tree is smaller than the full tree.

See Also

`fitrtree` | `compact` | `RegressionTree`

CompactTreeBagger class

Compact ensemble of decision trees grown by bootstrap aggregation

Description

`CompactTreeBagger` class is a lightweight class that contains the trees grown using `TreeBagger`. `CompactTreeBagger` does not preserve any information about how `TreeBagger` grew the decision trees. It does not contain the input data used for growing trees, nor does it contain training parameters such as minimal leaf size or number of variables sampled for each decision split at random. You can only use `CompactTreeBagger` for predicting the response of the trained ensemble given new data `X`, and other related functions.

`CompactTreeBagger` lets you save the trained ensemble to disk, or use it in any other way, while discarding training data and various parameters of the training configuration irrelevant for predicting response of the fully grown ensemble. This reduces storage and memory requirements, especially for ensembles trained on large data sets.

Construction

.CompactTreeBagger	Create CompactTreeBagger object

Methods

combine	Combine two ensembles
error	Error (misclassification probability or MSE)
margin	Classification margin

mdsProx	Multidimensional scaling of proximity matrix
meanMargin	Mean classification margin
outlierMeasure	Outlier measure for data
predict	Predict response
proximity	Proximity matrix for data
setDefaultYfit	Set default value for `predict`

Properties

`ClassNames`

The `ClassNames` property is a cell array containing the class names for the response variable `Y` supplied to `TreeBagger`. This property is empty for regression trees.

`DeltaCritDecisionSplit`

The `DeltaCritDecisionSplit` property is a numeric array of size 1-by-`Nvars` of changes in the split criterion summed over splits on each variable, averaged across the entire ensemble of grown trees.

See also `TreeBagger.DeltaCritDecisionSplit`, `ClassificationTree.predictorImportance`, and `RegressionTree.predictorImportance`

`DefaultYfit`

The `DefaultYfit` property controls what predicted value `CompactTreeBagger` returns when no prediction is possible, for example when the `predict` method needs to predict for an observation which has only false values in the matrix supplied through `'useifort'` argument.

For classification, you can set this property to either `''` or `'MostPopular'`. If you choose `'MostPopular'` (default), the property value becomes the name of the most probable class in the training data.

For regression, you can set this property to any numeric scalar. The default is the mean of the response for the training data.

See also `predict`, `setDefaultYfit`, `TreeBagger.DefaultYfit`.

`Method`

The `Method` property is `'classification'` for classification ensembles and `'regression'` for regression ensembles.

`NTrees`

The `NTrees` property is a scalar equal to the number of decision trees in the ensemble.

`NVarSplit`

The `NVarSplit` property is a numeric array of size 1-by-*Nvars*, where every element gives a number of splits on this predictor summed over all trees.

`Trees`

The `Trees` property is a cell array of size `NTrees`-by-1 containing the trees in the ensemble.

`VarAssoc`

The `VarAssoc` property is a matrix of size *Nvars*-by-*Nvars* with predictive measures of variable association, averaged across the entire ensemble of grown trees. If you grew the ensemble setting `'surrogate'` to `'on'`, this matrix for each tree is filled with predictive measures of association averaged over the surrogate splits. If you grew the ensemble setting `'surrogate'` to `'off'` (default), `VarAssoc` is diagonal.

See also `ClassificationTree.surrogateAssociation`, `RegressionTree.surrogateAssociation`.

`VarNames`

The `VarNames` property is a cell array containing the names of the predictor variables (features). These names are taken from the optional `'names'` parameter that supplied to `TreeBagger`. The default names are `'x1'`, `'x2'`, etc.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

See Also

`TreeBagger` | `ClassificationTree` | `TreeBagger.compact` | `RegressionTree`

How To

- “Ensemble Methods” on page 16-68
- “Classification Trees and Regression Trees” on page 16-33
- “Grouping Variables” on page 2-52

CompactTreeBagger

Class: CompactTreeBagger

Create CompactTreeBagger object

Description

When you use the `TreeBagger` constructor to grow trees, it creates a `CompactTreeBagger` object. You can obtain the compact object from the full `TreeBagger` object using the `TreeBagger/compact` method. You do not create an instance of `CompactTreeBagger` directly.

See Also

`TreeBagger`

How To

- “Grouping Variables” on page 2-52
- “Ensemble Methods” on page 16-68

compare

Class: GeneralizedLinearMixedModel

Compare generalized linear mixed-effects models

Syntax

```
results = compare(glme,altglme)
results = compare(glme,altglme,Name,Value)
```

Description

`results = compare(glme,altglme)` returns the results of a likelihood ratio test that compares the generalized linear mixed-effects models glme and altglme. To conduct a valid likelihood ratio test, both models must use the same response vector in the fit, and glme must be nested in altglme. Always input the smaller model first, and the larger model second.

`compare` tests the following null and alternate hypotheses:

- H_0: Observed response vector is generated by glme.
- H_1: Observed response vector is generated by model altglme.

`results = compare(glme,altglme,Name,Value)` returns the results of a likelihood ratio test using additional options specified by one or more `Name,Value` pair arguments. For example, you can check if the first input model, glme, is nested in the second input model, altglme.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

You can create a GeneralizedLinearMixedModel object by fitting a generalized linear mixed-effects model to your sample data using fitglme. To conduct a valid likelihood ratio test on two models that have response distributions other than normal, you must fit both models using the 'ApproximateLaplace' or 'Laplace' fit method. Models with response distributions other than normal that are fitted using 'MPL' or 'REMPL' cannot be compared using a likelihood ratio test.

altglme — Alternative generalized linear mixed-effects model
GeneralizedLinearMixedModel object

Alternative generalized linear mixed-effects model, specified as a GeneralizedLinearMixedModel object. altglme be must fit to the same response vector as glme, but with different model specifications. glme must be nested in altglme, such that you can obtain glme from altglme by setting some of the model parameters of altglme to fixed values such as 0.

You can create a GeneralizedLinearMixedModel object by fitting a generalized linear mixed-effects model to your sample data using fitglme. To conduct a valid likelihood ratio test on two models that have response distributions other than normal, you must fit both models using the 'ApproximateLaplace' or 'Laplace' fit method. Models with response distributions other than normal that are fitted using 'MPL' or 'REMPL' cannot be compared using a likelihood ratio test.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. Name is the argument name and Value is the corresponding value. Name must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as Name1,Value1,...,NameN,ValueN.

'CheckNesting' — Indicator to check nesting between two models
true (default) | false

Indicator to check nesting between two models, specified as the comma-separated pair consisting of 'CheckNesting' and either true or false. If 'CheckNesting' is true, then compare checks if the smaller model glme is nested in the larger model altglme. If the nesting requirements are not satisfied, then compare returns an error. If 'CheckNesting' is false, then compare does not perform this check.

Example: 'CheckNesting',true

Output Arguments

`results` — Results of likelihood ratio test

table

Results of the likelihood ratio test, returned as a table with two rows. The first row is for glme, and the second row is for altglme. The columns of results contain the following.

`Model`	Name of the model
`DF`	Degrees of freedom
`AIC`	Akaike information criterion for the model
`BIC`	Bayesian information criterion for the model
`LogLik`	Maximized log likelihood for the model
`LRStat`	Likelihood ratio test statistic for comparing altglme and glme
`deltaDF`	`DF` for altglme minus `DF` for glme
`pValue`	*p*-value for the likelihood ratio test

Definitions

Likelihood Ratio Test

A *likelihood ratio test* compares the specifications of two nested models by assessing the significance of restrictions to an extended model with unrestricted parameters. Under the null hypothesis H_0, the likelihood ratio test statistic has an approximate chi-squared reference distribution with degrees of freedom `deltaDF`.

When comparing two models, `compare` computes the *p*-value for the likelihood ratio test by comparing the observed likelihood ratio test statistic with this chi-squared reference distribution. A small *p*-value leads to a rejection of H_0 in favor of H_1, and acceptance of the alternate model altglme. On the other hand, a large *p*-value indicates that we cannot reject H_0, and reflects insufficient evidence to accept the model altglme.

The *p*-values obtained using the likelihood ratio test can be conservative when testing for the presence or absence of random-effects terms, and anti-conservative when testing

for the presence or absence of fixed-effects terms. Instead, use the `fixedEffects` or `coefTest` methods to test for fixed effects.

To conduct a valid likelihood ratio test on GLME models, both models must be fitted using a Laplace or approximate Laplace fit method. Models fitted using a maximum pseudo likelihood (MPL) or restricted maximum pseudo likelihood (REMPL) method cannot be compared using a likelihood ratio test. When comparing models fitted using MPL, the maximized log likelihood of the pseudodata from the final pseudo likelihood iteration is used in the likelihood ratio test. If you compare models with non-normal distributions fitted using MPL, then `compare` gives a warning that the likelihood ratio test is using maximized log likelihood of pseudodata from the final pseudo likelihood iteration. To use the true maximized log likelihood in the likelihood ratio test, fit both glme and altglme using approximate Laplace or Laplace prior to model comparison.

Nesting Requirements

To conduct a valid likelihood ratio test, glme must be nested in altglme. The `'CheckNesting',true` name-value pair argument checks the following requirements, and returns an error if any are not satisfied:

- You must fit both models (glme and altglme) using the `'ApproximateLaplace'` or `'Laplace'` fit method. You cannot compare GLME models fitted using `'MPL'` or `'REMPL'` using a likelihood ratio test.
- You must fit both models using the same response vector, response distribution, and link function.
- The smaller model (glme) must be nested within the larger model (altglme), such that you can obtain glme from altglme by setting some of the model parameters of altglme to fixed values such as 0.
- The maximized log likelihood of the larger model (altglme) must be greater than or equal to the maximized log likelihood of the smaller model (glme).
- The weight vectors used to fit glme and altglme must be identical.
- The random-effects design matrix of the larger model (altglme) must contain the random-effects design matrix of the smaller model (glme).
- The fixed-effects design matrix of the larger model (altglme) must contain the fixed-effects design matrix of the smaller model (glme).

Akaike and Bayesian Information Criteria

The *Akaike information criterion* (AIC) is $AIC = -2\log L_M + 2(param)$.

$\log L_M$ depends on the method used to fit the model.

- If you use `'Laplace'` or `'ApproximateLaplace'`, then $\log L_M$ is the maximized log likelihood.
- If you use `'MPL'`, then $\log L_M$ is the maximized log likelihood of the pseudo data from the final pseudo likelihood iteration.
- If you use `'REMPL'`, then $\log L_M$ is the maximized restricted log likelihood of the pseudo data from the final pseudo likelihood iteration.

param is the total number of parameters estimated in the model. For most GLME models, *param* is equal to $nc + p + 1$, where nc is the total number of parameters in the random-effects covariance, excluding the residual variance, and p is the number of fixed-effects coefficients. However, if the dispersion parameter is fixed at 1.0 for binomial or Poisson distributions, then *param* is equal to $(nc + p)$.

The *Bayesian information criterion* (BIC) is $BIC = -2*\log L_M + \ln(n_{eff})(param)$.

$\log L_M$ depends on the method used to fit the model.

- If you use `'Laplace'` or `'ApproximateLaplace'`, then $\log L_M$ is the maximized log likelihood.
- If you use `'MPL'`, then $\log L_M$ is the maximized log likelihood of the pseudo data from the final pseudo likelihood iteration.
- If you use `'REMPL'`, then $\log L_M$ is the maximized restricted log likelihood of the pseudo data from the final pseudo likelihood iteration.

n_{eff} is the effective number of observations.

- If you use `'MPL'`, `'Laplace'`, or `'ApproximateLaplace'`, then $n_{eff} = n$, where n is the number of observations.
- If you use `'REMPL'`, then $n_{eff} = n - p$.

param is the total number of parameters estimated in the model. For most GLME models, *param* is equal to $nc + p + 1$, where nc is the total number of parameters in the random-effects covariance, excluding the residual variance, and p is the number of fixed-effects coefficients. However, if the dispersion parameter is fixed at 1.0 for binomial or Poisson distributions, then *param* is equal to $(nc + p)$.

A lower value of deviance indicates a better fit. As the value of deviance decreases, both AIC and BIC tend to decrease. Both AIC and BIC also include penalty terms based on

the number of parameters estimated, p. So, when the number of parameters increase, the values of AIC and BIC tend to increase as well. When comparing different models, the model with the lowest AIC or BIC value is considered as the best fitting model.

For models fitted using `'MPL'` and `'REMPL'`, AIC and BIC are based on the log likelihood (or restricted log likelihood) of pseudo data from the final pseudo likelihood iteration. Therefore, a direct comparison of AIC and BIC values between models fitted using `'MPL'` and `'REMPL'` is not appropriate.

Examples

Compare Mixed-Effects Models

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a fixed-effects-only model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Specify the response distribution as Poisson, the link function as log, and the fit method as Laplace. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

```
FEglme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier','Distr
```

Fit a second model that uses the same fixed-effects predictors, response distribution, link function, and fit method. This time, include a random-effects intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Compare the two models using a theoretical likelihood ratio test. Specify `'CheckNesting'` as `true`, so `compare` returns a warning if the nesting requirements are not satisfied.

```
results = compare(FEglme,glme,'CheckNesting',true)
```

```
results =


    Theoretical Likelihood Ratio Test

    Model     DF    AIC       BIC       LogLik     LRStat    deltaDF
    FEglme    6     431.02    446.65    -209.51
    glme      7     416.35    434.58    -201.17    16.672    1


    pValue

    4.4435e-05
```

Since `compare` did not return an error, the nesting requirements are satisfied. The small *p*-value indicates that `compare` rejects the null hypothesis that the observed response vector is generated by the model `FEglme`, and instead accepts the alternate model `glme`. The smaller `AIC` and `BIC` values for `glme` also support the conclusion that `glme` provides a better fitting model for the response.

See Also

`GeneralizedLinearMixedModel` | `covarianceParameters` | `fixedEffects` | `randomEffects`

compare

Class: LinearMixedModel

Compare linear mixed-effects models

Syntax

```
results = compare(lme,altlme)
results = compare( ___ ,Name,Value)

[results,siminfo] = compare(lme,altlme,'NSim',nsim)
[results,siminfo] = compare( ___ ,Name,Value)
```

Description

`results = compare(lme,altlme)` returns the results of a likelihood ratio test that compares the linear mixed-effects models `lme` and `altlme`. Both models must use the same response vector in the fit and `lme` must be nested in `altlme` for a valid theoretical likelihood ratio test. Always input the smaller model first, and the larger model second.

`compare` tests the following null and alternate hypotheses:

H_0: Observed response vector is generated by `lme`.

H_1: Observed response vector is generated by model `altlme`.

It is recommended that you fit `lme` and `altlme` using the maximum likelihood (ML) method prior to model comparison. If you use the restricted maximum likelihood (REML) method, then both models must have the same fixed-effects design matrix.

To test for fixed effects, use `compare` with the simulated likelihood ratio test when `lme` and `altlme` are fit using ML or use the `fixedEffects`, `anova`, or `coefTest` methods.

`results = compare( ___ ,Name,Value)` also returns the results of a likelihood ratio test that compares linear mixed-effects models `lme` and `altlme` with additional options specified by one or more `Name,Value` pair arguments.

For example, you can check if the first input model is nested in the second input model.

`[results,siminfo] = compare(lme,altlme,'NSim',nsim)` returns the results of a simulated likelihood ratio test that compares linear mixed-effects models `lme` and `altlme`.

You can fit `lme` and `altlme` using ML or REML. Also, `lme` does not have to be nested in `altlme`. If you use the restricted maximum likelihood (REML) method to fit the models, then both models must have the same fixed-effects design matrix.

`[results,siminfo] = compare( ___ ,Name,Value)` also returns the results of a simulated likelihood ratio test that compares linear mixed-effects models `lme` and `altlme` with additional options specified by one or more `Name,Value` pair arguments.

For example, you can change the options for performing the simulated likelihood ratio test, or change the confidence level of the confidence interval for the *p*-value.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

`altlme` — Alternative linear mixed-effects model

`LinearMixedModel` object

Alternative linear mixed-effects model fit to the same response vector but with different model specifications, specified as a `LinearMixedModel` object. lme must be nested in `altlme`, that is, `lme` should be obtained from `altlme` by setting some parameters to fixed values, such as 0. You can create a linear mixed-effects object using `fitlme` or `fitlmematrix`.

`nsim` — Number of replications for simulations

positive integer number

Number of replications for simulations in the simulated likelihood ratio test, specified as a positive integer number. You must specify `nsim` to do a simulated likelihood ratio test.

Example: `'NSim',1000`

Data Types: `double` | `single`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 to 1

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range 0 to 1. For a value α, the confidence level is 100*(1–α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Options'` — Options for performing simulated likelihood ratio test

structure

Options for performing the simulated likelihood ratio test, specified as the comma-separated pair consisting of `'Options'`, and a structure created by `statset('LinearMixedModel')`.

`compare` uses the following fields.

`'UseParallel'`	• `False` for serial computation. Default. • `True` for parallel computation.
`'UseSubstreams'`	• `False` for not using a separate substream of the random number generator for each iteration. Default. • `True` for using a separate substream of the random number generator for each iteration. You can only use this option with random stream types that support substreams.

`'Streams'`	• If `'UseSubstreams'` is `True`, then `'Streams'` must be a single random number stream, or a scalar cell array containing a single stream.
	• If `'UseSubstreams'` is `False` and
	  • `'UseParallel'` is `False`, then `'Streams'` must be a single random number stream, or a scalar cell array containing a single stream.
	  • `'UseParallel'` is `True`, then `'Streams'` must be equal to the number of processors used. If a parallel pool is open, then the `'Streams'` is the same length as the size of the parallel pool. If `'UseParallel'` is `True`, a parallel pool might open up for you. But since `'Streams'` must be equal to the number of processors used, it is best to open a pool explicitly using the `parpool` command, before calling `compare` with the `'UseParallel','True'` option.

For information on parallel statistical computing at the command line, enter

```
help parallelstats
```

Data Types: `struct`

`'CheckNesting'` — Indicator to check nesting between two models

`false` (default) | `true`

Indicator to check nesting between two models, specified as the comma-separated pair consisting of `'CheckNesting'` and one of the following.

`false`	Default. No checks.
`true`	`compare` checks if the smaller model `lme` is nested in the bigger model `altlme`.

`lme` must be nested in the alternate model `altlme` for a valid theoretical likelihood ratio test. `compare` returns an error message if the nesting requirements are not satisfied.

Although valid for both tests, the nesting requirements are weaker for the simulated likelihood ratio test.

Example: `'CheckNesting',true`

Data Types: `single | double`

Output Arguments

`results` — Results of likelihood ratio test or simulated likelihood ratio test

dataset array

Results of the likelihood ratio test or simulated likelihood ratio test, returned as a dataset array with two rows. The first row is for lme, and the second row is for altlme. The columns of `results` depend on whether the test is a likelihood ratio or a simulated likelihood ratio test.

- If you use the likelihood ratio test, then `results` contains the following columns.

`Model`	Name of the model
`DF`	Degrees of freedom, that is, the number of free parameters in the model
`AIC`	Akaike information criterion for the model
`BIC`	Bayesian information criterion for the model
`LogLik`	Maximized log likelihood for the model
`LRStat`	Likelihood ratio test statistic for comparing `altlme` versus `lme`
`deltaDF`	`DF` for `altlme` minus `DF` for `lme`
`pValue`	*p*-value for the likelihood ratio test

- If you use the simulated likelihood ratio test, then `results` contains the following columns.

`Model`	Name of the model

`DF`	Degrees of freedom, that is, the number of free parameters in the model
`LogLik`	Maximized log likelihood for the model
`LRStat`	Likelihood ratio test statistic for comparing `altlme` versus `lme`
`pValue`	*p*-value for the likelihood ratio test
`Lower`	Lower limit of the confidence interval for `pValue`
`Upper`	Upper limit of the confidence interval for `pValue`

`siminfo` — Simulation output

structure

Simulation output, returned as a structure with the following fields.

`nsim`	Value set for `nsim`.
`alpha`	Value set for `'Alpha'`.
`pValueSim`	Simulation-based *p*-value.
`pValueSimCI`	Confidence interval for `pValueSim`. The first element of the vector is the lower limit and the second element of the vector contains the upper limit.
`deltaDF`	The number of free parameters in `altlme` minus the number of free parameters in `lme`. `DF` for `altlme` minus `DF` for `lme`.
`THO`	A vector of simulated likelihood ratio test statistics under the null hypothesis that the model `lme` generated the observed response vector `y`.

Examples

Test for Random Effects

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables containing estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the CDC).

To fit a linear-mixed effects model, your data must be in a properly formatted dataset array. To fit a linear mixed-effects model with the influenza rates as the responses and region as the predictor variable, combine the nine columns corresponding to the regions into a tall array. The new dataset array, `flu2`, must have the response variable, `FluRate`, the nominal variable, `Region`, that shows which region each estimate is from, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Fit a linear mixed-effects model, with a varying intercept and varying slope for each region, grouped by `Date`.

```
altlme = fitlme(flu2,'FluRate ~ 1 + Region + (1 + Region|Date)');
```

Fit a linear mixed-effects model with fixed effects for the region and a random intercept that varies by `Date`.

```
lme = fitlme(flu2,'FluRate ~ 1 + Region + (1|Date)');
```

Compare the two models. Also check if `lme2` is nested in `lme`.

```
compare(lme,altlme,'CheckNesting',true)
```

```
ans =


    Theoretical Likelihood Ratio Test

    Model     DF    AIC        BIC        LogLik     LRStat    deltaDF    pValue
    lme       11     318.71     364.35    -148.36
    altlme    55    -305.51    -77.346     207.76    712.22    44         0
```

The small p-value of 0 indicates that model `altlme` is significantly better than the simpler model `lme`.

Test for Fixed and Random Effects

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type) and the plots within blocks (tomato types within soil types) independently.

```
lmeBig = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Refit the model after removing the interaction term `Tomato:Fertilizer` and the random-effects term `(1 | Soil)`.

```
lmeSmall = fitlme(ds,'Yield ~ Fertilizer + Tomato + (1|Soil:Tomato)');
```

Compare the two models using the simulated likelihood ratio test with 1000 replications. You must use this test to test for both fixed- and random-effect terms. Note that both models are fit using the default fitting method, ML. That's why, there is no restriction on the fixed-effects design matrices. If you use restricted maximum likelihood (REML) method, both models must have identical fixed-effects design matrices.

```
[table,siminfo] = compare(lmeSmall,lmeBig,'nsim',1000)

table =
```

```
    Simulated Likelihood Ratio Test: Nsim = 1000, Alpha = 0.05

    Model    DF    AIC       BIC       LogLik     LRStat    pValue     Lower      Upper
    lme2     10    511.06       532    -245.53
    lme      23    522.57    570.74    -238.29    14.491    0.54845    0.51702    0.579


siminfo =

           nsim: 1000
          alpha: 0.0500
      pvalueSim: 0.5485
    pvalueSimCI: [0.5170 0.5796]
        deltaDF: 13
            TH0: [1000x1 double]
```

The high p-value 0.5485 suggests that the larger model, `lme` is not significantly better than the smaller model, `lme2`. The smaller values of AIC and BIC for `lme2` also support this.

Models with Correlated and Uncorrelated Random Effects

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower, and the cylinders, and potentially correlated random effects for intercept and acceleration grouped by model year.

First, prepare the design matrices.

```
X = [ones(406,1) Acceleration Horsepower];
Z = [ones(406,1) Acceleration];
Model_Year = nominal(Model_Year);
G = Model_Year;
```

Now, fit the model using `fitlmematrix` with the defined design matrices and grouping variables.

```
lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept','Acceleration'}},'RandomEffectGroups',{'Model_Year'});
```

Refit the model with uncorrelated random effects for intercept and acceleration. First prepare the random effects design and the random effects grouping variables.

```
Z = {ones(406,1),Acceleration};
G = {Model_Year,Model_Year};

lme2 = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept'},{'Acceleration'}},'RandomEffectGroups',...
{'Model_Year','Model_Year'});
```

Compare `lme` and `lme2` using the simulated likelihood ratio test.

```
compare(lme2,lme,'CheckNesting',true,'NSim',1000)
```

```
ans =


    Simulated Likelihood Ratio Test: Nsim = 1000, Alpha = 0.05

    Model    DF    AIC       BIC       LogLik     LRStat    pValue      Lower       Upp
    lme2     6     2194.5    2218.3    -1091.3
    lme      7     2193.5    2221.3    -1089.7    3.0323    0.095904    0.078373    0.1
```

The high p-value of 0.095904 indicates that `lme2` is not a significantly better fit than `lme`.

Simulated Likelihood Ratio Test Using Parallel Computing

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Refit the model after removing the interaction term `Tomato:Fertilizer` and the random-effects term `(1|Soil)`.

```
lme2 = fitlme(ds,'Yield ~ Fertilizer + Tomato + (1|Soil:Tomato)');
```

Create the options structure for `LinearMixedModel`.

```
opt = statset('LinearMixedModel')
```

```
opt =

          Display: 'off'
      MaxFunEvals: []
          MaxIter: 10000
           TolBnd: []
           TolFun: 1.0000e-06
       TolTypeFun: []
             TolX: 1.0000e-12
         TolTypeX: []
          GradObj: []
         Jacobian: []
        DerivStep: []
      FunValCheck: []
           Robust: []
     RobustWgtFun: []
           WgtFun: []
             Tune: []
      UseParallel: []
    UseSubstreams: []
          Streams: {}
        OutputFcn: []
```

Change the options for parallel testing.

```
opt.UseParallel = true;
```

Start a parallel environment.

```
mypool = parpool();
```

```
Starting parpool using the 'local' profile ... connected to 2 workers.

mypool =

  Pool with properties:

    AttachedFiles: {0x1 cell}
       NumWorkers: 2
          Cluster: [1x1 parallel.cluster.Local]
      SpmdEnabled: 1
```

Compare `lme2` and `lme` using the simulated likelihood ratio test with 1000 replications and parallel computing.

```
compare(lme2,lme,'nsim',1000,'Options',opt)
```

```
ans =


    Simulated Likelihood Ratio Test: Nsim = 1000, Alpha = 0.05

    Model    DF    AIC       BIC       LogLik     LRStat    pValue     Lower      Upper
    lme2     10    511.06       532    -245.53
    lme      23    522.57    570.74    -238.29    14.491    0.54845    0.51702    0.579
```

The high p-value, 0.5485 suggests that the larger model, `lme` is not significantly better than the smaller model, `lme2`. The smaller values of `AIC` and `BIC` for `lme2` also support this.

Definitions

Likelihood Ratio Test

Under the null hypothesis H_0, the observed likelihood ratio test statistic has an approximate chi-squared reference distribution with degrees of freedom `deltaDF`. When

comparing two models, `compare` computes the *p*-value for the likelihood ratio test by comparing the observed likelihood ratio test statistic with this chi-squared reference distribution.

The *p*-values obtained using the likelihood ratio test can be conservative when testing for the presence or absence of random-effects terms and anticonservative when testing for the presence or absence of fixed-effects terms. Hence, use the `fixedEffects`, `anova`, or `coefTest` method or the simulated likelihood ratio test while testing for fixed effects.

Simulated Likelihood Ratio Test

To perform the simulated likelihood ratio test, `compare` first generates the reference distribution of the likelihood ratio test statistic under the null hypothesis. Then, it assesses the statistical significance of the alternate model by comparing the observed likelihood ratio test statistic to this reference distribution.

`compare` produces the simulated reference distribution of the likelihood ratio test statistic under the null hypothesis as follows:

- Generate random data `ysim` from the fitted model `lme`.
- Fit the model specified in `lme` and alternate model `altlme` to the simulated data `ysim`.
- Calculate the likelihood ratio test statistic using results from step 2 and store the value.
- Repeat step 1 to 3 `nsim` times.

Then, `compare` computes the *p*-value for the simulated likelihood ratio test by comparing the observed likelihood ratio test statistic with the simulated reference distribution. The *p*-value estimate is the ratio of the number of times the simulated likelihood ratio test statistic is equal to or exceeds the observed value plus one, to the number of replications plus one.

Suppose the observed likelihood ratio statistic is T, and the simulated reference distribution is stored in vector T_{H_0}. Then,

$$p-value=\frac{\left[\sum_{j=1}^{nsim} I\left(T_{H_0}(j)\geq T\right)\right]+1}{nsim+1}.$$

To account for the uncertainty in the simulated reference distribution, `compare` computes a 100*(1 – α)% confidence interval for the true *p*-value.

You can use the simulated likelihood ratio test to compare arbitrary linear mixed-effects models. That is, when you are using the simulated likelihood ratio test, `lme` does not have to be nested within `altlme`, and you can fit `lme` and `altlme` using either maximum likelihood (ML) or restricted maximum likelihood (REML) methods. If you use the restricted maximum likelihood (REML) method to fit the models, then both models must have the same fixed-effects design matrix.

Nesting Requirements

The 'CheckNesting','True' name-value pair argument checks the following requirements.

For a simulated likelihood ratio test:

- You must use the same method to fit both models (`lme` and `altlme`). `compare` cannot compare a model fit using ML to a model fit using REML.
- You must fit both models to the same response vector.
- If you use REML to fit `lme` and `altlme`, then both models must have the same fixed-effects design matrix.
- The maximized log likelihood or restricted log likelihood of the bigger model (`altlme`) must be greater than or equal to that of the smaller model (`lme`).

For a theoretical test, `'CheckNesting','True'` checks all the requirements listed for a simulated likelihood ratio test and the following:

- Weight vectors you use to fit `lme` and `altlme` must be identical.
- If you use ML to fit `lme` and `altlme`, the fixed-effects design matrix of the bigger model (`altlme`) must contain that of the smaller model (`lme`).
- The random-effects design matrix of the bigger model (`altlme`) must contain that of the smaller model (`lme`).

Akaike and Bayesian Information Criteria

Akaike information criterion (AIC) is $AIC = -2*\log L_M + 2*(nc + p + 1)$, where $\log L_M$ is the maximized log likelihood (or maximized restricted log likelihood) of the model, and $nc + p + 1$ is the number of parameters estimated in the model. p is the number of fixed-effects

coefficients, and nc is the total number of parameters in the random-effects covariance excluding the residual variance.

Bayesian information criterion (BIC) is $BIC = -2*\log L_M + \ln(n_{eff})*(nc + p + 1)$, where $\log L_M$ is the maximized log likelihood (or maximized restricted log likelihood) of the model, n_{eff} is the effective number of observations, and $(nc + p + 1)$ is the number of parameters estimated in the model.

- If the fitting method is maximum likelihood (ML), then $n_{eff} = n$, where n is the number of observations.
- If the fitting method is restricted maximum likelihood (REML), then $n_{eff} = n - p$.

A lower value of deviance indicates a better fit. As the value of deviance decreases, both AIC and BIC tend to decrease. Both AIC and BIC also include penalty terms based on the number of parameters estimated, p. So, when the number of parameters increase, the values of AIC and BIC tend to increase as well. When comparing different models, the model with the lowest AIC or BIC value is considered as the best fitting model.

Deviance

`LinearMixedModel` computes the deviance of model M as minus two times the loglikelihood of that model. Let L_M denote the maximum value of the likelihood function for model M. Then, the deviance of model M is

$$-2 * \log L_M .$$

A lower value of deviance indicates a better fit. Suppose M_1 and M_2 are two different models, where M_1 is nested in M_2. Then, the fit of the models can be assessed by comparing the deviances Dev_1 and Dev_2 of these models. The difference of the deviances is

$$Dev = Dev_1 - Dev_2 = 2\left(\log LM_2 - \log LM_1\right).$$

Usually, the asymptotic distribution of this difference has a chi-square distribution with degrees of freedom v equal to the number of parameters that are estimated in one model but fixed (typically at 0) in the other. That is, it is equal to the difference in the number of parameters estimated in M_1 and M_2. You can get the p-value for this test using `1 - chi2cdf(Dev,V)`, where $Dev = Dev_2 - Dev_1$.

However, in mixed-effects models, when some variance components fall on the boundary of the parameter space, the asymptotic distribution of this difference is more complicated. For example, consider the hypotheses

H_0: $D = \begin{pmatrix} D_{11} & 0 \\ 0 & 0 \end{pmatrix}$, D is a q-by-q symmetric positive semidefinite matrix.

H_1: D is a (q+1)-by-(q+1) symmetric positive semidefinite matrix.

That is, H_1 states that the last row and column of D are different from zero. Here, the bigger model M_2 has q + 1 parameters and the smaller model M_1 has q parameters. And Dev has a 50:50 mixture of χ^2_q and $\chi^2_{(q+1)}$ distributions (Stram and Lee, 1994).

References

[1] Hox, J. *Multilevel Analysis, Techniques and Applications*. Lawrence Erlbaum Associates, Inc., 2002.

[2] Stram D. O. and J. W. Lee. "Variance components testing in the longitudinal mixed-effects model". *Biometrics*, Vol. 50, 4, 1994, pp. 1171–1177.

See Also

`anova` | `covarianceParameters` | `fitlme` | `fitlmematrix` | `fixedEffects` | `LinearMixedModel` | `randomEffects`

compareHoldout

Class: ClassificationKNN

Compare accuracies of two models using new data

`compareHoldout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `compareHoldout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = compareHoldout(C1,C2,X1,X2,Y)
h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = compareHoldout(___)
```

Description

`h = compareHoldout(C1,C2,X1,X2,Y)` returns the test decision from testing the null hypothesis that the trained classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model `C1` uses predictor data `X1` and `C2` uses `X2`. The software conducts the mid-*p*-value McNemar test to compare the accuracies.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a model that is more complex by passing the same set of predictor data (i.e., `X1 = X2`).

- Compare the accuracies of two perhaps different models using two perhaps different sets of predictors.
- Perform various types of feature selection. For example, you can compare the accuracy of a model trained using a set of predictors to the accuracy of one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, and the type of test, or you can supply a cost matrix.

`[h,p,e1,e2] = compareHoldout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification losses of each set of predicted class labels (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Tips

- One way to perform cost-insensitive feature selection is:

  1. Train the first classification model (C1) using the full predictor set.
  2. Train the second classification model (C2) using the reduced predictor set.
  3. Specify `X1` as the full, test-set predictor data and `X2` as the reduced test-set predictor data.
  4. Enter `compareHoldout(C1,C2,X1,X2,'Alternative','less')`. If `compareHoldout` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','greater'` specification in step 4. `compareHoldout` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data

sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-803.

Input Arguments

C1 — Trained *k*NN classification model

`ClassificationKNN` model object

Trained *k*NN classification model, specified as a `ClassificationKNN` model object. That is, `C1` is a trained classification model returned by `fitcknn`.

C2 — Trained classification model

Trained classification model object | Trained, compact classification model object

Trained classification model, specified as any trained or compact classification model object described in this table.

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
Error-correcting output codes (ECOC), multiclass classification model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
Support vector machine (SVM)	`ClassificationSVM`	`fitcsvm`
Compact discriminant analysis	`CompactClassificationDiscriminant`	`compact`

Trained Model Type	Model Object	Returned By
Compact ECOC	`CompactClassificationECOC`	`compact`
Compact ensemble of classification models	`CompactClassificationEnsemble`	`compact`
Compact naive Bayes	`CompactClassificationNaiveBayes`	`compact`
Compact SVM	`CompactClassificationSVM`	`compact`
Compact classification tree	`ClassificationTree`	`compact`

`X1` — Test-set predictor data for first classification model

numeric matrix

Test-set predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double` | `single`

`X2` — Test-set predictor data for second classification model

numeric matrix

Test-set predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double` | `single`

`Y` — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` twice as much as for misclassifying observations with the true label `ClassNames{2}`.

`'Alpha'` — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

`'Alternative'` — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of these values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.

Value	Alternative hypothesis
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class

and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `ClassificationKNN.compareHoldout` cannot conduct one-sided, exact, or mid-p tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `ClassificationKNN.compareHoldout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: `'CostTest','chisquare'`

Data Types: char

'Test' — Test to conduct

'asymptotic' | 'exact' | 'midp'

Test to conduct, specified as the comma-separated pair consisting of 'Test' and 'asymptotic', 'exact', and 'midp'. This table summarizes the available options for cost-insensitive testing.

Value	Description
'asymptotic'	Asymptotic McNemar test
'exact'	Exact-conditional McNemar test
'midp' (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, Test must be 'asymptotic'. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, 'asymptotic' is the default.

Example: 'Test','asymptotic'

Data Types: char

Note: NaNs, <undefined> values, and empty strings ('') indicate missing values. ClassificationKNN.compareHoldout:

- Removes missing values in Y and the corresponding rows of X1 and X2
- Predicts classes whether X1 and X2 have missing observations.

Output Arguments

h — Hypothesis test result

1 | 0

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

`p` — *p*-value

scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`ClassificationKNN.compareHoldout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

`e1` — Classification loss

scalar

Classification loss, returned as a scalar. `e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y).

`ClassificationKNN.compareHoldout` applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels. Then, the function compares the estimated labels to `Y` to obtain the classification loss.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

`e2` — Classification loss

scalar

Classification loss, returned as a scalar. `e2` summarizes the accuracy of the second set of class labels predicting the true class labels (Y). `ClassificationKNN.compareHoldout` applies the second test-set predictor data (X2) to the second classification model (C2) to estimate the second set of class labels. Then the function compares the estimated labels to Y to obtain the classification loss.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

Definitions

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is Π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}.\ \sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1..$
- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.

- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K}\sum_{j=1}^{K}\sum_{k=1}^{K}\left(c_{ki} - c_{kj}\right)\pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

  The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any n_{ijk} = 0. The test statistic is

$$t^*_{\chi^2} = \sum_{i\neq j}\sum_{k}\frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3\right)\hat{\pi}^{(1)}_{ijk}\right)^2}{n_{ijk} + 1}.$$

  If $1 - F_{\chi^2}\left(t^*_{\chi^2};1\right) < \alpha$, then reject H_0.

  - $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.
  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification model assigns label i. The second classification model assigns label j. Jointly, their distribution is multinomial.

  The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

If $1 - F_{\chi^2}\left(t^*_{LRT}; 1\right) < \alpha,$, then reject H_0.

- $\hat{\pi}^{(2)}_{ijk} = \frac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of π_{ijk}.
- $\hat{\pi}^{(3)}_{ijk} = \frac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

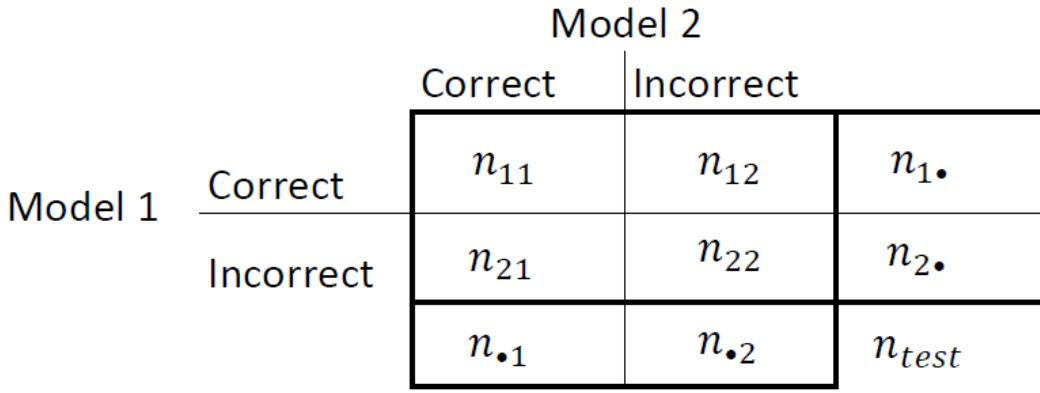
- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.



n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

    $$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^*\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

    $$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^*; m\right) < \alpha$, where $F_{\chi^2}(x;m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

$t_1^* = n_{12}$

If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

- For two-sided tests, the test statistic

$t_2^* = \min(n_{12}, n_{21})$

If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

$t_1^* = n_{12}$

If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

$t_2^* = \min(n_{12}, n_{21})$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`ClassificationKNN.compareHoldout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
```

```
    'Type','classification');
```

`C1` is a trained `ClassificationSVM` model. `C2` is a trained `ClassificationBaggedEnsemble` model.

Test whether the two models have equal predictive accuracies. Use the same test-set predictor data for each model.

```
h = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
```

```
C2 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`C1` and `C2` are trained `ClassificationSVM` models.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- *p*-value test (the cost-insensitive testing default). Request to return *p*-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater',...
    'Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          __________    __________

    h             1             1
    p     7.2801e-09    2.7649e-10
    e1       0.13714       0.13714
    e2       0.33143       0.33143
```

The *p*-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `compareHoldout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or for data sets with imbalanced false-positive and false-negative costs, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate the predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
C1 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',cost);
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',cost);
```

`C1` and `C2` are trained `ClassificationEnsemble` models.

Test whether the AdaBoostM1 ensemble (`C1`) and the LogitBoost ensemble (`C2`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest),...
    'Cost',cost)
```

```
h =

     0


p =

    0.0743


e1 =

    1.3581


e2 =

    1.6186
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Select Features Using Statistical Accuracy Comparison

Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the out-of-sample accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

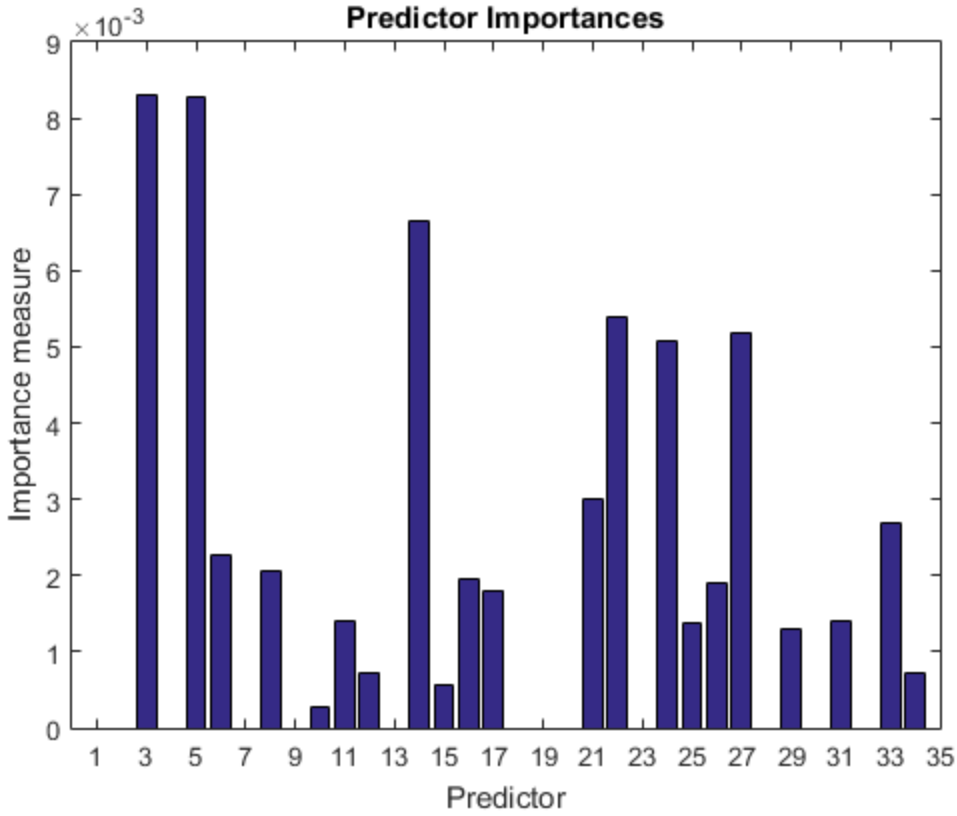
`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C2);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2)
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```

```
h =

  Axes with properties:

            XLim: [0 35]
            YLim: [0 0.0090]
          XScale: 'linear'
          YScale: 'linear'
```

```
    GridLineStyle: '-'
         Position: [0.1300 0.1100 0.7750 0.8150]
            Units: 'normalized'

  Use GET to show all properties
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Train another ensemble of 100 boosted classification trees using AdaBoostM1 and the five predictors with the best importance.

```
C1 = fitensemble(X(idxTrain,idx5),Y(idxTrain),'AdaBoostM1',nTrees,...
    'Tree');
```

Test whether the two models have equal predictive accuracies. Specify the reduced test-set predictor data for `C1` and the full test-set predictor data for `C2`.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,idx5),X(idxTest,:),Y(idxTest))
```

```
h =

     0


p =

    0.7744


e1 =

    0.0914


e2 =

    0.0857
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble, `C1`.

Alternatives

To directly compare the accuracy of two sets of class labels in predicting a set of true class labels, use `testcholdout`.

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

[2] Fagerlan, M.W., S Lydersen, P. Laake. “The McNemar Test for Binary Matched-Pairs Data: Mid-p and Asymptotic Are Better Than Exact Conditional.” *BMC Medical Research Methodology*. Vol. 13, 2013, pp. 1–8.

[3] Lancaster, H.O. “Significance Tests in Discrete Distributions.” *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. “Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages.” *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. “Some Statistical Problems in Measuring the Subjective Response to Drugs.” *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`fitcknn` | `predict` | `testcholdout` | `testckfold`

More About

- “Hypothesis Tests”

Introduced in R2015a

compareHoldout

Class: CompactClassificationDiscriminant

Compare accuracies of two classification models using new data

`compareHoldout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `compareHoldout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = compareHoldout(C1,C2,X1,X2,Y)
h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = compareHoldout(___)
```

Description

`h = compareHoldout(C1,C2,X1,X2,Y)` returns the test decision from testing the null hypothesis that the trained classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model `C1` uses predictor data `X1` and `C2` uses `X2`. The software conducts the mid-*p*-value McNemar test to compare the accuracies.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a model that is more complex by passing the same set of predictor data (i.e., `X1 = X2`).

- Compare the accuracies of two perhaps different models using two perhaps different sets of predictors.
- Perform various types of feature selection. For example, you can compare the accuracy of a model trained using a set of predictors and one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, and the type of test, or you can supply a cost matrix.

`[h,p,e1,e2] = compareHoldout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification losses of each set of predicted class labels (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Tips

- One way to perform cost-insensitive feature selection is:

  1. Train the first classification model (C1) using the full predictor set.
  2. Train the second classification model (C2) using the reduced predictor set.
  3. Specify `X1` as the full, test-set predictor data and `X2` as the reduced test-set predictor data.
  4. Enter `compareHoldout(C1,C2,X1,X2,'Alternative','less')`. If `compareHoldout` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','greater'` specification in step 4. `compareHoldout` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data

sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-803.

Input Arguments

C1 — Trained discriminant analysis classification model

`ClassificationDiscriminant` model object | `CompactClassificationDiscriminant` model object

Trained discriminant analysis classification model, specified as a `ClassificationDiscriminant` or `CompactClassificationDiscriminant` model object. That is, `C1` is a trained classification model returned by `fitcdiscr` or `compact`.

C2 — Trained classification model

Trained classification model object | Trained, compact classification model object

Trained classification model, specified as any trained or compact classification model object described in this table.

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
Error-correcting output codes (ECOC), multiclass classification model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
Support vector machine (SVM)	`ClassificationSVM`	`fitcsvm`

Trained Model Type	Model Object	Returned By
Compact discriminant analysis	`CompactClassificationDiscriminant`	`compact`
Compact ECOC	`CompactClassificationECOC`	`compact`
Compact ensemble of classification models	`CompactClassificationEnsemble`	`compact`
Compact naive Bayes	`CompactClassificationNaiveBayes`	`compact`
Compact SVM	`CompactClassificationSVM`	`compact`
Compact classification tree	`ClassificationTree`	`compact`

`X1` — Test-set predictor data for first classification model

numeric matrix

Test-set predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double | single`

`X2` — Test-set predictor data for second classification model

numeric matrix

Test-set predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double | single`

Y — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If Y is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` twice as much as for misclassifying observations with the true label `ClassNames{2}`.

'Alpha' — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

'Alternative' — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of these values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class

and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `CompactClassificationDiscriminant.compareHoldout` cannot conduct one-sided, exact, or mid-p tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `CompactClassificationDiscriminant.compareHoldout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: `'CostTest','chisquare'`

Data Types: `char`

`'Test'` — Test to conduct

`'asymptotic' | 'exact' | 'midp'`

Test to conduct, specified as the comma-separated pair consisting of `'Test'` and `'asymptotic'`, `'exact'`, and `'midp'`. This table summarizes the available options for cost-insensitive testing.

Value	Description
`'asymptotic'`	Asymptotic McNemar test
`'exact'`	Exact-conditional McNemar test
`'midp'` (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, `Test` must be `'asymptotic'`. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, `'asymptotic'` is the default.

Example: `'Test','asymptotic'`

Data Types: `char`

Note: `NaN`s, `<undefined>` values, and empty strings (`''`) indicate missing values. `CompactClassificationDiscriminant.compareHoldout`:

- Removes missing values in Y and the corresponding rows of X1 and X2
- Predicts classes whether `X1` and `X2` have missing observations.

Output Arguments

`h` — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

p — *p*-value

scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`CompactClassificationDiscriminant.compareHoldout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

e1 — Classification loss

scalar

Classification loss, returned as a scalar. `e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y).

`CompactClassificationDiscriminant.compareHoldout` applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels. Then, the function compares the estimated labels to `Y` to obtain the classification loss.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

e2 — Classification loss

scalar

Classification loss, returned as a scalar. `e2` summarizes the accuracy of the second set of class labels predicting the true class labels (Y). `CompactClassificationDiscriminant.compareHoldout` applies the second test-

set predictor data (X2) to the second classification model (C2) to estimate the second set of class labels. Then the function compares the estimated labels to Y to obtain the classification loss.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

Definitions

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. $\sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1$. .

- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.
- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K}\sum_{j=1}^{K}\sum_{k=1}^{K}\left(c_{ki} - c_{kj}\right)\pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

  The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any $n_{ijk} = 0$. The test statistic is

$$t^*_{\chi^2} = \sum_{i \neq j}\sum_{k}\frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3\right)\hat{\pi}^{(1)}_{ijk}\right)^2}{n_{ijk} + 1}.$$

  If $1 - F_{\chi^2}\left(t^*_{\chi^2}; 1\right) < \alpha$, then reject H_0.

  - $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.
  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.
- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification

model assigns label *i*. The second classification model assigns label *j*. Jointly, their distribution is multinomial.

The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

If $1 - F_{\chi^2}\left(t^*_{LRT}; 1\right) < \alpha,$, then reject H_0.

- $\hat{\pi}^{(2)}_{ijk} = \frac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of Π_{ijk}.
- $\hat{\pi}^{(3)}_{ijk} = \frac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.

		Model 2: Correct	Model 2: Incorrect	
Model 1	Correct	n_{11}	n_{12}	$n_{1\bullet}$
	Incorrect	n_{21}	n_{22}	$n_{2\bullet}$
		$n_{\bullet 1}$	$n_{\bullet 2}$	n_{test}

n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

    $$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^{*}\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

    $$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^{*}; m\right) < \alpha$, where $F_{\chi^2}(x; m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

- For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`CompactClassificationDiscriminant.compareHoldout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
```

```
    'Type','classification');
```

`C1` is a trained `ClassificationSVM` model. `C2` is a trained `ClassificationBaggedEnsemble` model.

Test whether the two models have equal predictive accuracies. Use the same test-set predictor data for each model.

```
h = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
```

```
C2 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`C1` and `C2` are trained `ClassificationSVM` models.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- p-value test (the cost-insensitive testing default). Request to return p-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater',...
    'Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          __________    __________

    h             1             1
    p     7.2801e-09    2.7649e-10
    e1       0.13714       0.13714
    e2       0.33143       0.33143
```

The p-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `compareHoldout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or for data sets with imbalanced false-positive and false-negative costs, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate the predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
C1 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',cost);
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',cost);
```

`C1` and `C2` are trained `ClassificationEnsemble` models.

Test whether the AdaBoostM1 ensemble (`C1`) and the LogitBoost ensemble (`C2`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest),...
    'Cost',cost)
```

```
h =

     0


p =

    0.0743


e1 =

    1.3581


e2 =

    1.6186
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Select Features Using Statistical Accuracy Comparison

Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the out-of-sample accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

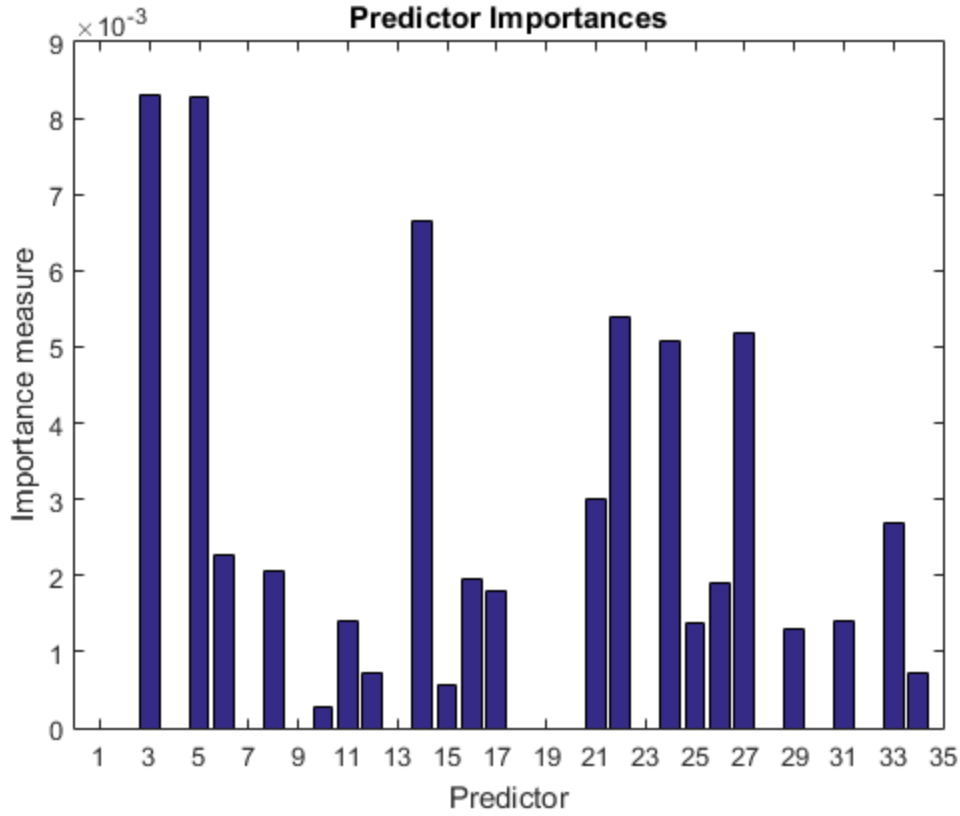
`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C2);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2)
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```

```
h =

  Axes with properties:

            XLim: [0 35]
            YLim: [0 0.0090]
          XScale: 'linear'
          YScale: 'linear'
```

```
    GridLineStyle: '-'
         Position: [0.1300 0.1100 0.7750 0.8150]
            Units: 'normalized'

  Use GET to show all properties
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Train another ensemble of 100 boosted classification trees using AdaBoostM1 and the five predictors with the best importance.

```
C1 = fitensemble(X(idxTrain,idx5),Y(idxTrain),'AdaBoostM1',nTrees,...
    'Tree');
```

Test whether the two models have equal predictive accuracies. Specify the reduced test-set predictor data for `C1` and the full test-set predictor data for `C2`.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,idx5),X(idxTest,:),Y(idxTest))
```

```
h =

     0


p =

    0.7744


e1 =

    0.0914


e2 =

    0.0857
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble, `C1`.

Alternatives

To directly compare the accuracy of two sets of class labels in predicting a set of true class labels, use `testcholdout`.

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

[2] Fagerlan, M.W., S Lydersen, P. Laake. “The McNemar Test for Binary Matched-Pairs Data: Mid-p and Asymptotic Are Better Than Exact Conditional.” *BMC Medical Research Methodology*. Vol. 13, 2013, pp. 1–8.

[3] Lancaster, H.O. “Significance Tests in Discrete Distributions.” *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. “Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages.” *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. “Some Statistical Problems in Measuring the Subjective Response to Drugs.” *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`fitcdiscr` | `predict` | `testcholdout` | `testckfold`

More About

- “Hypothesis Tests”

Introduced in R2015a

compareHoldout

Class: CompactClassificationECOC

Compare accuracies of two classification models using new data

`compareHoldout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `compareHoldout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = compareHoldout(C1,C2,X1,X2,Y)
h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = compareHoldout(___)
```

Description

`h = compareHoldout(C1,C2,X1,X2,Y)` returns the test decision from testing the null hypothesis that the trained classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model `C1` uses predictor data `X1` and `C2` uses `X2`. The software conducts the mid-*p*-value McNemar test to compare the accuracies.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a model that is more complex by passing the same set of predictor data (i.e., `X1 = X2`).

- Compare the accuracies of two perhaps different models using two perhaps different sets of predictors.
- Perform various types of feature selection. For example, you can compare the accuracy of a model trained using a set of predictors to the accuracy of one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, and the type of test, or you can supply a cost matrix.

`[h,p,e1,e2] = compareHoldout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification losses of each set of predicted class labels (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Tips

- One way to perform cost-insensitive feature selection is:

  1. Train the first classification model (C1) using the full predictor set.
  2. Train the second classification model (C2) using the reduced predictor set.
  3. Specify `X1` as the full, test-set predictor data and `X2` as the reduced test-set predictor data.
  4. Enter `compareHoldout(C1,C2,X1,X2,'Alternative','less')`. If `compareHoldout` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','greater'` specification in step 4. `compareHoldout` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data

sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-803.

Input Arguments

`C1` — Trained error-correcting output codes classification model

`ClassificationECOC` model object | `CompactClassificationECOC` model object

Trained error-correcting output codes (ECOC) classification model, specified as a `ClassificationECOC` or `CompactClassificationECOC` model object. That is, `C1` is a trained classification model returned by `fitcecoc` or `compact`.

`C2` — Trained classification model

Trained classification model object | Trained, compact classification model object

Trained classification model, specified as any trained or compact classification model object described in this table.

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
Error-correcting output codes (ECOC), multiclass classification model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
Support vector machine (SVM)	`ClassificationSVM`	`fitcsvm`
Compact discriminant analysis	`CompactClassificationDiscriminant`	`compact`

Trained Model Type	Model Object	Returned By
Compact ECOC	`CompactClassificationECOC`	`compact`
Compact ensemble of classification models	`CompactClassificationEnsemble`	`compact`
Compact naive Bayes	`CompactClassificationNaiveBayes`	`compact`
Compact SVM	`CompactClassificationSVM`	`compact`
Compact classification tree	`ClassificationTree`	`compact`

`X1` — Test-set predictor data for first classification model

numeric matrix

Test-set predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double` | `single`

`X2` — Test-set predictor data for second classification model

numeric matrix

Test-set predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double` | `single`

`Y` — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` twice as much as for misclassifying observations with the true label `ClassNames{2}`.

`'Alpha'` — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

`'Alternative'` — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of these values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.

Value	Alternative hypothesis
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class

and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `CompactClassificationECOC.compareHoldout` cannot conduct one-sided, exact, or mid-p tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `CompactClassificationECOC.compareHoldout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: `'CostTest','chisquare'`

Data Types: `char`

`'Test'` — Test to conduct

`'asymptotic' | 'exact' | 'midp'`

Test to conduct, specified as the comma-separated pair consisting of `'Test'` and `'asymptotic'`, `'exact'`, and `'midp'`. This table summarizes the available options for cost-insensitive testing.

Value	Description
`'asymptotic'`	Asymptotic McNemar test
`'exact'`	Exact-conditional McNemar test
`'midp'` (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, `Test` must be `'asymptotic'`. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, `'asymptotic'` is the default.

Example: `'Test','asymptotic'`

Data Types: `char`

Note: `NaN`s, `<undefined>` values, and empty strings (`''`) indicate missing values. `CompactClassificationECOC.compareHoldout`:

- Removes missing values in Y and the corresponding rows of X1 and X2
- Predicts classes whether `X1` and `X2` have missing observations.

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

p — *p*-value
scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`CompactClassificationECOC.compareHoldout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

e1 — Classification loss
scalar

Classification loss, returned as a scalar. `e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y).

`CompactClassificationECOC.compareHoldout` applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels. Then, the function compares the estimated labels to `Y` to obtain the classification loss.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

e2 — Classification loss
scalar

Classification loss, returned as a scalar. `e2` summarizes the accuracy of the second set of class labels predicting the true class labels (Y).

`CompactClassificationECOC.compareHoldout` applies the second test-set predictor data (X2) to the second classification model (C2) to estimate the second set of class labels. Then the function compares the estimated labels to Y to obtain the classification loss.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

Definitions

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. $\sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1$. .

- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.
- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K}\sum_{j=1}^{K}\sum_{k=1}^{K}\left(c_{ki} - c_{kj}\right)\pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

  The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any $n_{ijk} = 0$. The test statistic is

$$t^*_{\chi^2} = \sum_{i \neq j}\sum_{k}\frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3\right)\hat{\pi}^{(1)}_{ijk}\right)^2}{n_{ijk} + 1}.$$

  If $1 - F_{\chi^2}\left(t^*_{\chi^2};1\right) < \alpha$, then reject H_0.

  - $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.
  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.
- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification

model assigns label *i*. The second classification model assigns label *j*. Jointly, their distribution is multinomial.

The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

If $1 - F_{\chi^2}\left(t^*_{LRT}; 1\right) < \alpha,$, then reject H_0.

- $\hat{\pi}^{(2)}_{ijk} = \frac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of Π_{ijk}.
- $\hat{\pi}^{(3)}_{ijk} = \frac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.

		Model 2: Correct	Model 2: Incorrect	
Model 1	Correct	n_{11}	n_{12}	$n_{1\bullet}$
	Incorrect	n_{21}	n_{22}	$n_{2\bullet}$
		$n_{\bullet 1}$	$n_{\bullet 2}$	n_{test}

n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

    $$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^{*}\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

    $$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^{*}; m\right) < \alpha$, where $F_{\chi^2}(x; m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

$t_1^* = n_{12}$

If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

- For two-sided tests, the test statistic

$t_2^* = \min(n_{12}, n_{21})$

If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

$t_1^* = n_{12}$

If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

$t_2^* = \min(n_{12}, n_{21})$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`CompactClassificationECOC.compareHoldout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
```

```
    'Type','classification');
```

`C1` is a trained `ClassificationSVM` model. `C2` is a trained `ClassificationBaggedEnsemble` model.

Test whether the two models have equal predictive accuracies. Use the same test-set predictor data for each model.

```
h = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
```

```
C2 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`C1` and `C2` are trained `ClassificationSVM` models.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- *p*-value test (the cost-insensitive testing default). Request to return *p*-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater',...
    'Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          __________    __________

    h             1             1
    p     7.2801e-09    2.7649e-10
    e1       0.13714       0.13714
    e2       0.33143       0.33143
```

The *p*-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `compareHoldout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or for data sets with imbalanced false-positive and false-negative costs, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate the predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
C1 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',cost);
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',cost);
```

`C1` and `C2` are trained `ClassificationEnsemble` models.

Test whether the AdaBoostM1 ensemble (`C1`) and the LogitBoost ensemble (`C2`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest),...
    'Cost',cost)
```

```
h =

     0


p =

    0.0743


e1 =

    1.3581


e2 =

    1.6186
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Select Features Using Statistical Accuracy Comparison

Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the out-of-sample accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

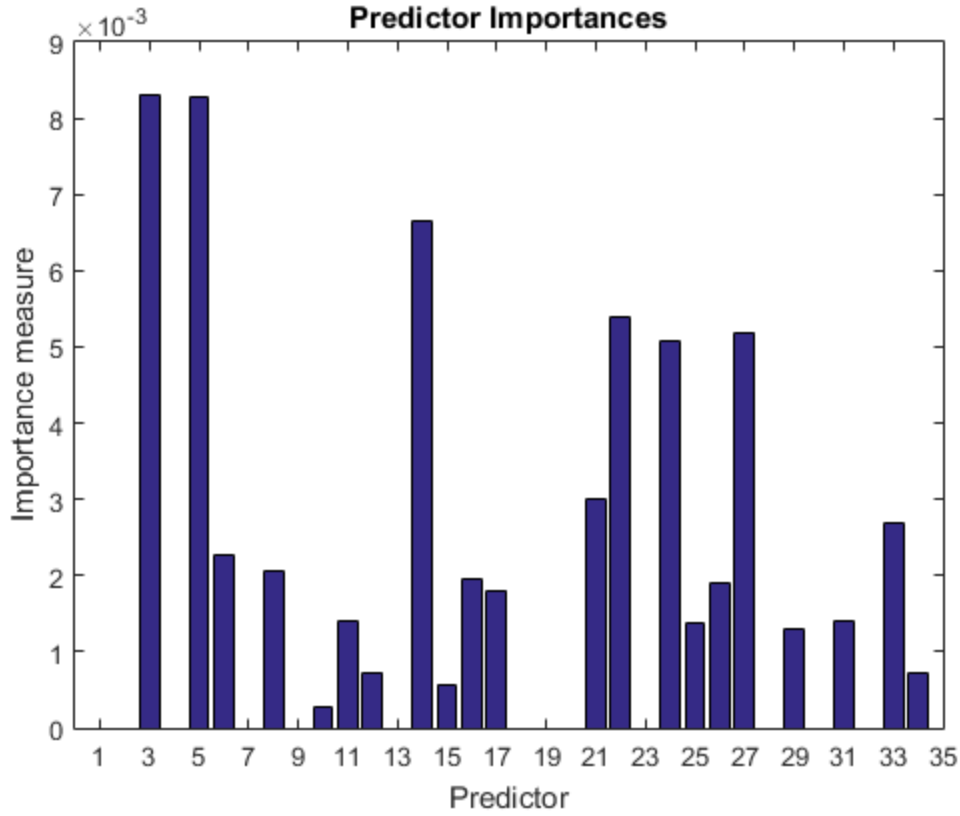
`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C2);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2)
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```

```
h =

  Axes with properties:

            XLim: [0 35]
            YLim: [0 0.0090]
          XScale: 'linear'
          YScale: 'linear'
```

```
    GridLineStyle: '-'
         Position: [0.1300 0.1100 0.7750 0.8150]
            Units: 'normalized'

  Use GET to show all properties
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Train another ensemble of 100 boosted classification trees using AdaBoostM1 and the five predictors with the best importance.

```
C1 = fitensemble(X(idxTrain,idx5),Y(idxTrain),'AdaBoostM1',nTrees,...
    'Tree');
```

Test whether the two models have equal predictive accuracies. Specify the reduced test-set predictor data for `C1` and the full test-set predictor data for `C2`.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,idx5),X(idxTest,:),Y(idxTest))
```

```
h =

     0


p =

    0.7744


e1 =

    0.0914


e2 =

    0.0857
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble, `C1`.

Alternatives

To directly compare the accuracy of two sets of class labels in predicting a set of true class labels, use `testcholdout`.

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

[2] Fagerlan, M.W., S Lydersen, P. Laake. “The McNemar Test for Binary Matched-Pairs Data: Mid-p and Asymptotic Are Better Than Exact Conditional.” *BMC Medical Research Methodology*. Vol. 13, 2013, pp. 1–8.

[3] Lancaster, H.O. “Significance Tests in Discrete Distributions.” *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. “Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages.” *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. “Some Statistical Problems in Measuring the Subjective Response to Drugs.” *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`fitcecoc` | `predict` | `testcholdout` | `testckfold`

More About

- “Hypothesis Tests”

Introduced in R2015a

compareHoldout

Class: CompactClassificationEnsemble

Compare accuracies of two classification models using new data

`compareHoldout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `compareHoldout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = compareHoldout(C1,C2,X1,X2,Y)
h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = compareHoldout(___)
```

Description

`h = compareHoldout(C1,C2,X1,X2,Y)` returns the test decision from testing the null hypothesis that the trained classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model `C1` uses predictor data `X1` and `C2` uses `X2`. The software conducts the mid-*p*-value McNemar test to compare the accuracies.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a model that is more complex by passing the same set of predictor data (i.e., `X1 = X2`).

- Compare the accuracies of two perhaps different models using two perhaps different sets of predictors.
- Perform various types of feature selection. For example, compare the accuracies of a model trained using a set of predictors and one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, specify the type of alternative hypothesis, specify the type of test, or supply a cost matrix.

`[h,p,e1,e2] = compareHoldout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification losses of each set of predicted class labels (`e1` and `e2`).

Tips

- One way to perform cost-insensitive feature selection is:

  1. Train the first classification model (C1) using the full predictor set.
  2. Train the second classification model (C2) using the reduced predictor set.
  3. Specify `X1` as the full, test-set predictor data and `X2` as the reduced test-set predictor data.
  4. Enter `compareHoldout(C1,C2,X1,X2,'Alternative','less')`. If `compareHoldout` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','greater'` specification in step 4. `compareHoldout` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data

sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-803.

Input Arguments

`C1` — Trained ensemble of classification models

`ClassificationBaggedEnsemble` model object | `ClassificationEnsemble` model object | `CompactClassificationEnsemble` model object

Trained ensemble of classification models, specified as a `ClassificationBaggedEnsemble`, `ClassificationEnsemble`, or `CompactClassificationEnsemble` model object. That is, `C1` is a trained classification model returned by `fitensemble` or `compact`.

`C2` — Trained classification model

Trained classification model object | Trained, compact classification model object

Trained classification model, specified as any trained or compact classification model object described in this table.

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
Error-correcting output codes (ECOC), multiclass classification model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`

Trained Model Type	Model Object	Returned By
Support vector machine (SVM)	`ClassificationSVM`	`fitcsvm`
Compact discriminant analysis	`CompactClassificationDiscriminant`	`compact`
Compact ECOC	`CompactClassificationECOC`	`compact`
Compact ensemble of classification models	`CompactClassificationEnsemble`	`compact`
Compact naive Bayes	`CompactClassificationNaiveBayes`	`compact`
Compact SVM	`CompactClassificationSVM`	`compact`
Compact classification tree	`ClassificationTree`	`compact`

`X1` — Test-set predictor data for first classification model

numeric matrix

Test-set predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double | single`

`X2` — Test-set predictor data for second classification model

numeric matrix

Test-set predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double` | `single`

Y — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` two times the penalty of misclassifying observations with the true label `ClassNames{2}`.

'Alpha' — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

'Alternative' — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of these values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class

and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `CompactClassificationEnsemble.compareHoldout` cannot conduct one-sided, exact, or mid-p tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `CompactClassificationEnsemble.compareHoldout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: `'CostTest','chisquare'`

Data Types: `char`

`'Test'` — Test to conduct

`'asymptotic' | 'exact' | 'midp'`

Test to conduct, specified as the comma-separated pair consisting of `'Test'` and `'asymptotic'`, `'exact'`, and `'midp'`. This table summarizes the available options for cost-insensitive testing.

Value	Description
`'asymptotic'`	Asymptotic McNemar test
`'exact'`	Exact-conditional McNemar test
`'midp'` (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, `Test` must be `'asymptotic'`. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, `'asymptotic'` is the default.

Example: `'Test','asymptotic'`

Data Types: `char`

Note: `NaN`s, `<undefined>` values, and empty strings (`''`) indicate missing values. `CompactClassificationEnsemble.compareHoldout`:

- Removes missing values in Y and the corresponding rows of X1 and X2
- Predicts classes whether `X1` and `X2` have missing observations.

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

p — *p*-value
scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`CompactClassificationEnsemble.compareHoldout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

e1 — Classification loss
scalar

Classification loss, returned as a scalar. `e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y).

`CompactClassificationEnsemble.compareHoldout` applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels. Then, the function compares the estimated labels to `Y` to obtain the classification loss.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

e2 — Classification loss
scalar

Classification loss, returned as a scalar. `e2` summarizes the accuracy of the second set of class labels predicting the true class labels (Y). `CompactClassificationEnsemble.compareHoldout` applies the second test-set

predictor data (X2) to the second classification model (C2) to estimate the second set of class labels. Then the function compares the estimated labels to Y to obtain the classification loss.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

Definitions

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. $\sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1$. .

- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.
- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K}\sum_{j=1}^{K}\sum_{k=1}^{K}\left(c_{ki} - c_{kj}\right)\pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

  The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any $n_{ijk} = 0$. The test statistic is

$$t^*_{\chi^2} = \sum_{i \neq j}\sum_{k}\frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3\right)\hat{\pi}^{(1)}_{ijk}\right)^2}{n_{ijk} + 1}.$$

  If $1 - F_{\chi^2}\left(t^*_{\chi^2}; 1\right) < \alpha$, then reject H_0.

  - $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.
  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.
- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification

model assigns label *i*. The second classification model assigns label *j*. Jointly, their distribution is multinomial.

The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

If $1 - F_{\chi^2}\left(t^*_{LRT}; 1\right) < \alpha,$, then reject H_0.

- $\hat{\pi}^{(2)}_{ijk} = \frac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of Π_{ijk}.
- $\hat{\pi}^{(3)}_{ijk} = \frac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.

		Model 2: Correct	Model 2: Incorrect	
Model 1	Correct	n_{11}	n_{12}	$n_{1\bullet}$
	Incorrect	n_{21}	n_{22}	$n_{2\bullet}$
		$n_{\bullet 1}$	$n_{\bullet 2}$	n_{test}

n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

    $$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^*\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

    $$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^*; m\right) < \alpha$, where $F_{\chi^2}(x;m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

- For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`CompactClassificationEnsemble.compareHoldout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
```

```
    'Type','classification');
```

`C1` is a trained `ClassificationSVM` model. `C2` is a trained `ClassificationBaggedEnsemble` model.

Test whether the two models have equal predictive accuracies. Use the same test-set predictor data for each model.

```
h = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
```

```
C2 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`C1` and `C2` are trained `ClassificationSVM` models.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- p-value test (the cost-insensitive testing default). Request to return p-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater',...
    'Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          __________    __________

    h             1             1
    p     7.2801e-09    2.7649e-10
    e1       0.13714       0.13714
    e2       0.33143       0.33143
```

The p-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `compareHoldout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or for data sets with imbalanced false-positive and false-negative costs, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate the predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
C1 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',cost);
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',cost);
```

`C1` and `C2` are trained `ClassificationEnsemble` models.

Test whether the AdaBoostM1 ensemble (`C1`) and the LogitBoost ensemble (`C2`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest),...
    'Cost',cost)
```

```
h =

     0


p =

    0.0743


e1 =

    1.3581


e2 =

    1.6186
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Select Features Using Statistical Accuracy Comparison

Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the out-of-sample accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

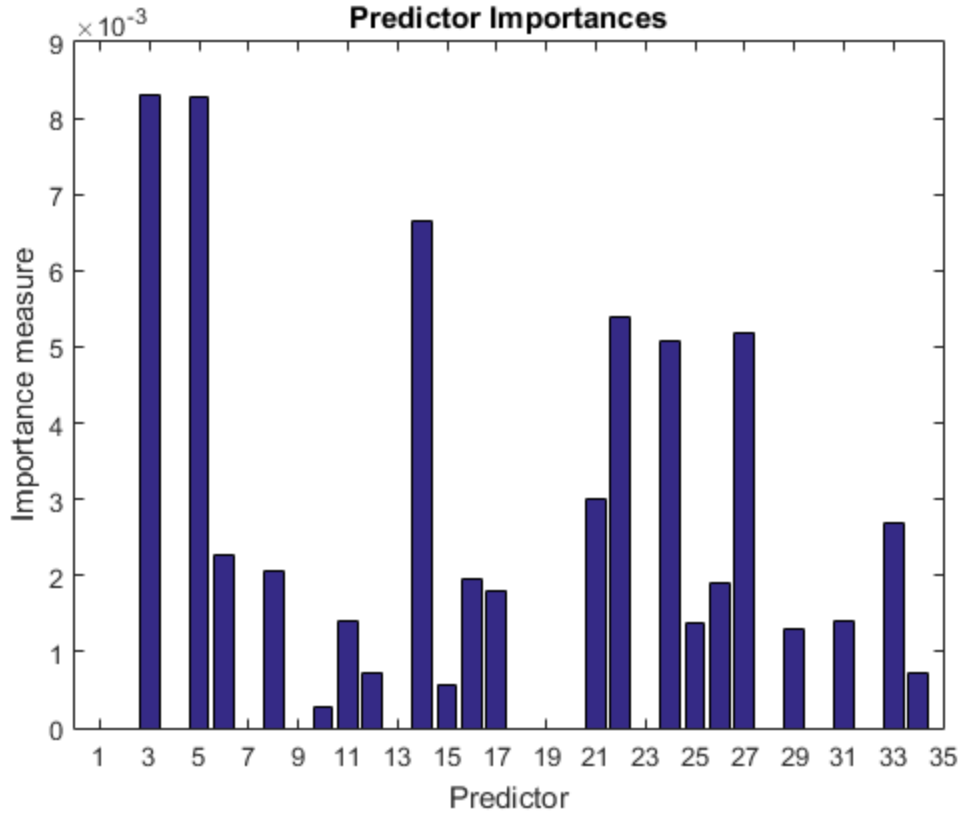
`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C2);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2)
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```

```
h =

  Axes with properties:

            XLim: [0 35]
            YLim: [0 0.0090]
          XScale: 'linear'
          YScale: 'linear'
```

```
    GridLineStyle: '-'
         Position: [0.1300 0.1100 0.7750 0.8150]
            Units: 'normalized'

  Use GET to show all properties
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Train another ensemble of 100 boosted classification trees using AdaBoostM1 and the five predictors with the best importance.

```
C1 = fitensemble(X(idxTrain,idx5),Y(idxTrain),'AdaBoostM1',nTrees,...
    'Tree');
```

Test whether the two models have equal predictive accuracies. Specify the reduced test-set predictor data for `C1` and the full test-set predictor data for `C2`.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,idx5),X(idxTest,:),Y(idxTest))
```

```
h =

     0


p =

    0.7744


e1 =

    0.0914


e2 =

    0.0857
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble, `C1`.

Alternatives

To directly compare the accuracy of two sets of class labels in predicting a set of true class labels, use `testcholdout`.

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

[2] Fagerlan, M.W., S Lydersen, P. Laake. "The McNemar Test for Binary Matched-Pairs Data: Mid-p and Asymptotic Are Better Than Exact Conditional." *BMC Medical Research Methodology*. Vol. 13, 2013, pp. 1–8.

[3] Lancaster, H.O. "Significance Tests in Discrete Distributions." *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. "Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages." *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. "Some Statistical Problems in Measuring the Subjective Response to Drugs." *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`fitensemble` | `predict` | `testcholdout` | `testckfold`

More About

- "Hypothesis Tests"

Introduced in R2015a

compareHoldout

Class: CompactClassificationNaiveBayes

Compare accuracies of two classification models using new data

`compareHoldout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `compareHoldout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = compareHoldout(C1,C2,X1,X2,Y)
h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = compareHoldout(___)
```

Description

`h = compareHoldout(C1,C2,X1,X2,Y)` returns the test decision from testing the null hypothesis that the trained classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model `C1` uses predictor data `X1` and `C2` uses `X2`. The software conducts the mid-*p*-value McNemar test to compare the accuracies.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a model that is more complex by passing the same set of predictor data (i.e., `X1 = X2`).

- Compare the accuracies of two perhaps different models using two perhaps different sets of predictors.
- Perform various types of feature selection. For example, you can compare the accuracy of a model trained using a set of predictors to the accuracy of one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, and the type of test, or you can supply a cost matrix.

`[h,p,e1,e2] = compareHoldout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification losses of each set of predicted class labels (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Tips

- One way to perform cost-insensitive feature selection is:

  1. Train the first classification model (C1) using the full predictor set.
  2. Train the second classification model (C2) using the reduced predictor set.
  3. Specify `X1` as the full, test-set predictor data and `X2` as the reduced test-set predictor data.
  4. Enter `compareHoldout(C1,C2,X1,X2,'Alternative','less')`. If `compareHoldout` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','greater'` specification in step 4. `compareHoldout` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data

sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-803.

Input Arguments

C1 — Trained naive Bayes classification model

`ClassificationNaiveBayes` model object | `CompactClassificationNaiveBayes` model object

Trained naive Bayes classification model, specified as a `ClassificationNaiveBayes` or `CompactClassificationNaiveBayes` model object. That is, `C1` is a trained classification model returned by `fitcnb` or `compact`.

C2 — Trained classification model

Trained classification model object | Trained, compact classification model object

Trained classification model, specified as any trained or compact classification model object described in this table.

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
Error-correcting output codes (ECOC), multiclass classification model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
Support vector machine (SVM)	`ClassificationSVM`	`fitcsvm`

Trained Model Type	Model Object	Returned By
Compact discriminant analysis	`CompactClassificationDiscriminant`	`compact`
Compact ECOC	`CompactClassificationECOC`	`compact`
Compact ensemble of classification models	`CompactClassificationEnsemble`	`compact`
Compact naive Bayes	`CompactClassificationNaiveBayes`	`compact`
Compact SVM	`CompactClassificationSVM`	`compact`
Compact classification tree	`ClassificationTree`	`compact`

`X1` — Test-set predictor data for first classification model

numeric matrix

Test-set predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double | single`

`X2` — Test-set predictor data for second classification model

numeric matrix

Test-set predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double | single`

Y — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If Y is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` twice as much as for misclassifying observations with the true label `ClassNames{2}`.

'Alpha' — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

'Alternative' — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of these values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class

and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `CompactClassificationNaiveBayes.compareHoldout` cannot conduct one-sided, exact, or mid-p tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `CompactClassificationNaiveBayes.compareHoldout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: `'CostTest','chisquare'`

Data Types: `char`

`'Test'` — Test to conduct

`'asymptotic' | 'exact' | 'midp'`

Test to conduct, specified as the comma-separated pair consisting of `'Test'` and `'asymptotic'`, `'exact'`, and `'midp'`. This table summarizes the available options for cost-insensitive testing.

Value	Description
`'asymptotic'`	Asymptotic McNemar test
`'exact'`	Exact-conditional McNemar test
`'midp'` (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, `Test` must be `'asymptotic'`. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, `'asymptotic'` is the default.

Example: `'Test','asymptotic'`

Data Types: `char`

Note: `NaN`s, `<undefined>` values, and empty strings (`''`) indicate missing values. `CompactClassificationNaiveBayes.compareHoldout`:

- Removes missing values in Y and the corresponding rows of X1 and X2
- Predicts classes whether `X1` and `X2` have missing observations.

Output Arguments

`h` — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

p — *p*-value

scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`CompactClassificationNaiveBayes.compareHoldout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

e1 — Classification loss

scalar

Classification loss, returned as a scalar. `e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y).

`CompactClassificationNaiveBayes.compareHoldout` applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels. Then, the function compares the estimated labels to `Y` to obtain the classification loss.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

e2 — Classification loss

scalar

Classification loss, returned as a scalar. `e2` summarizes the accuracy of the second set of class labels predicting the true class labels (Y). `CompactClassificationNaiveBayes.compareHoldout` applies the second test-

set predictor data (X2) to the second classification model (C2) to estimate the second set of class labels. Then the function compares the estimated labels to Y to obtain the classification loss.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

Definitions

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. $\sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1$. .

- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.
- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K}\sum_{j=1}^{K}\sum_{k=1}^{K}\left(c_{ki} - c_{kj}\right)\pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

  The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any $n_{ijk} = 0$. The test statistic is

$$t^*_{\chi^2} = \sum_{i \neq j}\sum_{k}\frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3\right)\hat{\pi}^{(1)}_{ijk}\right)^2}{n_{ijk} + 1}.$$

  If $1 - F_{\chi^2}\left(t^*_{\chi^2};1\right) < \alpha$, then reject H_0.

  - $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.
  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.
- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification

model assigns label *i*. The second classification model assigns label *j*. Jointly, their distribution is multinomial.

The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

If $1 - F_{\chi^2}\left(t^*_{LRT}; 1\right) < \alpha,$, then reject H_0.

- $\hat{\pi}^{(2)}_{ijk} = \frac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of Π_{ijk}.
- $\hat{\pi}^{(3)}_{ijk} = \frac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.

		Model 2: Correct	Model 2: Incorrect	
Model 1	Correct	n_{11}	n_{12}	$n_{1\bullet}$
	Incorrect	n_{21}	n_{22}	$n_{2\bullet}$
		$n_{\bullet 1}$	$n_{\bullet 2}$	n_{test}

n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

$$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^{*}\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

$$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^{*}; m\right) < \alpha$, where $F_{\chi^2}(x; m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

$t_1^* = n_{12}$

If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

- For two-sided tests, the test statistic

$t_2^* = \min(n_{12}, n_{21})$

If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

$t_1^* = n_{12}$

If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

$t_2^* = \min(n_{12}, n_{21})$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`CompactClassificationNaiveBayes.compareHoldout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
```

```
    'Type','classification');
```

`C1` is a trained `ClassificationSVM` model. `C2` is a trained `ClassificationBaggedEnsemble` model.

Test whether the two models have equal predictive accuracies. Use the same test-set predictor data for each model.

```
h = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
```

```
C2 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`C1` and `C2` are trained `ClassificationSVM` models.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- p-value test (the cost-insensitive testing default). Request to return p-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater',...
    'Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          __________    __________

    h             1             1
    p     7.2801e-09    2.7649e-10
    e1       0.13714       0.13714
    e2       0.33143       0.33143
```

The p-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `compareHoldout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or for data sets with imbalanced false-positive and false-negative costs, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate the predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
C1 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',cost);
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',cost);
```

`C1` and `C2` are trained `ClassificationEnsemble` models.

Test whether the AdaBoostM1 ensemble (`C1`) and the LogitBoost ensemble (`C2`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest),...
    'Cost',cost)
```

```
h =

     0


p =

    0.0743


e1 =

    1.3581


e2 =

    1.6186
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Select Features Using Statistical Accuracy Comparison

Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the out-of-sample accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

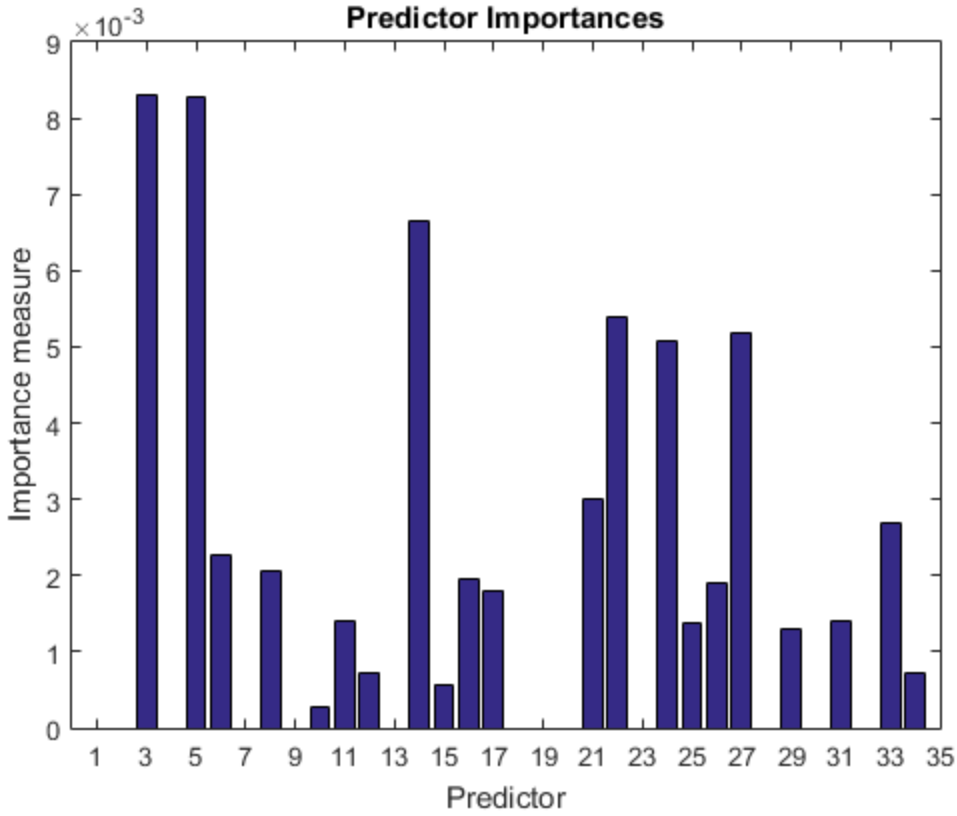
`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C2);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2)
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```

```
h =

  Axes with properties:

            XLim: [0 35]
            YLim: [0 0.0090]
          XScale: 'linear'
          YScale: 'linear'
```

```
    GridLineStyle: '-'
         Position: [0.1300 0.1100 0.7750 0.8150]
            Units: 'normalized'

  Use GET to show all properties
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Train another ensemble of 100 boosted classification trees using AdaBoostM1 and the five predictors with the best importance.

```
C1 = fitensemble(X(idxTrain,idx5),Y(idxTrain),'AdaBoostM1',nTrees,...
    'Tree');
```

Test whether the two models have equal predictive accuracies. Specify the reduced test-set predictor data for `C1` and the full test-set predictor data for `C2`.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,idx5),X(idxTest,:),Y(idxTest))
```

```
h =

     0


p =

    0.7744


e1 =

    0.0914


e2 =

    0.0857
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble, `C1`.

Alternatives

To directly compare the accuracy of two sets of class labels in predicting a set of true class labels, use `testcholdout`.

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

[2] Fagerlan, M.W., S Lydersen, P. Laake. “The McNemar Test for Binary Matched-Pairs Data: Mid-p and Asymptotic Are Better Than Exact Conditional.” *BMC Medical Research Methodology*. Vol. 13, 2013, pp. 1–8.

[3] Lancaster, H.O. “Significance Tests in Discrete Distributions.” *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. “Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages.” *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. “Some Statistical Problems in Measuring the Subjective Response to Drugs.” *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`fitcnb` | `predict` | `testcholdout` | `testckfold`

More About

- “Hypothesis Tests”

Introduced in R2015a

compareHoldout

Class: CompactClassificationSVM

Compare accuracies of two classification models using new data

`compareHoldout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `compareHoldout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = compareHoldout(C1,C2,X1,X2,Y)
h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = compareHoldout(___)
```

Description

`h = compareHoldout(C1,C2,X1,X2,Y)` returns the test decision from testing the null hypothesis that the trained classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model `C1` uses predictor data `X1` and `C2` uses `X2`. The software conducts the mid-*p*-value McNemar test to compare the accuracies.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a model that is more complex by passing the same set of predictor data (i.e., `X1 = X2`).

- Compare the accuracies of two perhaps different models using two perhaps different sets of predictors.
- Perform various types of feature selection. For example, you can compare the accuracy of a model trained using a set of predictors to the accuracy of one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, and the type of test, or you can supply a cost matrix.

`[h,p,e1,e2] = compareHoldout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification losses of each set of predicted class labels (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Tips

- One way to perform cost-insensitive feature selection is:

  1. Train the first classification model (C1) using the full predictor set.
  2. Train the second classification model (C2) using the reduced predictor set.
  3. Specify `X1` as the full, test-set predictor data and `X2` as the reduced test-set predictor data.
  4. Enter `compareHoldout(C1,C2,X1,X2,'Alternative','less')`. If `compareHoldout` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','greater'` specification in step 4. `compareHoldout` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data

sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-803.

Input Arguments

C1 — Trained support vector machine classification model

`ClassificationSVM` model object | `CompactClassificationSVM` model object

Trained support vector machine (SVM) classification model, specified as a `ClassificationSVM` or `CompactClassificationSVM` model object. That is, `C1` is a trained classification model returned by `fitcsvm` or `compact`.

C2 — Trained classification model

Trained classification model object | Trained, compact classification model object

Trained classification model, specified as any trained or compact classification model object described in this table.

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
Error-correcting output codes (ECOC), multiclass classification model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
Support vector machine (SVM)	`ClassificationSVM`	`fitcsvm`
Compact discriminant analysis	`CompactClassificationDiscriminant`	`compact`

Trained Model Type	Model Object	Returned By
Compact ECOC	`CompactClassificationECOC`	`compact`
Compact ensemble of classification models	`CompactClassificationEnsemble`	`compact`
Compact naive Bayes	`CompactClassificationNaiveBayes`	`compact`
Compact SVM	`CompactClassificationSVM`	`compact`
Compact classification tree	`ClassificationTree`	`compact`

`X1` — Test-set predictor data for first classification model

numeric matrix

Test-set predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double` | `single`

`X2` — Test-set predictor data for second classification model

numeric matrix

Test-set predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double` | `single`

`Y` — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` twice as much as for misclassifying observations with the true label `ClassNames{2}`.

`'Alpha'` — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

`'Alternative'` — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of these values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.

Value	Alternative hypothesis
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class

and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `CompactClassificationSVM.compareHoldout` cannot conduct one-sided, exact, or mid-*p* tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `CompactClassificationSVM.compareHoldout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: `'CostTest','chisquare'`

Data Types: `char`

`'Test'` — Test to conduct

`'asymptotic' | 'exact' | 'midp'`

Test to conduct, specified as the comma-separated pair consisting of `'Test'` and `'asymptotic'`, `'exact'`, and `'midp'`. This table summarizes the available options for cost-insensitive testing.

Value	Description
`'asymptotic'`	Asymptotic McNemar test
`'exact'`	Exact-conditional McNemar test
`'midp'` (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, `Test` must be `'asymptotic'`. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, `'asymptotic'` is the default.

Example: `'Test','asymptotic'`

Data Types: `char`

Note: `NaN`s, `<undefined>` values, and empty strings (`''`) indicate missing values. `CompactClassificationSVM.compareHoldout`:

- Removes missing values in Y and the corresponding rows of X1 and X2
- Predicts classes whether `X1` and `X2` have missing observations.

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

p — *p*-value
scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`CompactClassificationSVM.compareHoldout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

e1 — Classification loss
scalar

Classification loss, returned as a scalar. `e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y).

`CompactClassificationSVM.compareHoldout` applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels. Then, the function compares the estimated labels to `Y` to obtain the classification loss.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

e2 — Classification loss
scalar

Classification loss, returned as a scalar. `e2` summarizes the accuracy of the second set of class labels predicting the true class labels (Y).

`CompactClassificationSVM.compareHoldout` applies the second test-set predictor data (X2) to the second classification model (C2) to estimate the second set of class labels. Then the function compares the estimated labels to Y to obtain the classification loss.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

Definitions

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. $\sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1$. .

- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.
- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K}\sum_{j=1}^{K}\sum_{k=1}^{K}\left(c_{ki} - c_{kj}\right)\pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

  The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any $n_{ijk} = 0$. The test statistic is

$$t^*_{\chi^2} = \sum_{i \neq j}\sum_{k}\frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3\right)\hat{\pi}^{(1)}_{ijk}\right)^2}{n_{ijk} + 1}.$$

  If $1 - F_{\chi^2}\left(t^*_{\chi^2}; 1\right) < \alpha$, then reject H_0.

  - $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.
  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.
- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification

model assigns label *i*. The second classification model assigns label *j*. Jointly, their distribution is multinomial.

The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

If $1 - F_{\chi^2}\left(t^*_{LRT}; 1\right) < \alpha,$, then reject H_0.

- $\hat{\pi}^{(2)}_{ijk} = \frac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of Π_{ijk}.
- $\hat{\pi}^{(3)}_{ijk} = \frac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.

		Model 2: Correct	Model 2: Incorrect	
Model 1	Correct	n_{11}	n_{12}	$n_{1\bullet}$
	Incorrect	n_{21}	n_{22}	$n_{2\bullet}$
		$n_{\bullet 1}$	$n_{\bullet 2}$	n_{test}

n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

    $$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^*\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

    $$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^*; m\right) < \alpha$, where $F_{\chi^2}(x;m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

- For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`CompactClassificationSVM.compareHoldout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
```

```
    'Type','classification');
```

`C1` is a trained `ClassificationSVM` model. `C2` is a trained `ClassificationBaggedEnsemble` model.

Test whether the two models have equal predictive accuracies. Use the same test-set predictor data for each model.

```
h = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
```

```
C2 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`C1` and `C2` are trained `ClassificationSVM` models.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- *p*-value test (the cost-insensitive testing default). Request to return *p*-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater',...
    'Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          __________    __________

    h             1             1
    p     7.2801e-09    2.7649e-10
    e1       0.13714       0.13714
    e2       0.33143       0.33143
```

The *p*-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `compareHoldout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or for data sets with imbalanced false-positive and false-negative costs, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate the predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
C1 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',cost);
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',cost);
```

`C1` and `C2` are trained `ClassificationEnsemble` models.

Test whether the AdaBoostM1 ensemble (`C1`) and the LogitBoost ensemble (`C2`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest),...
    'Cost',cost)
```

```
h =

     0


p =

    0.0743


e1 =

    1.3581


e2 =

    1.6186
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Select Features Using Statistical Accuracy Comparison

Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the out-of-sample accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

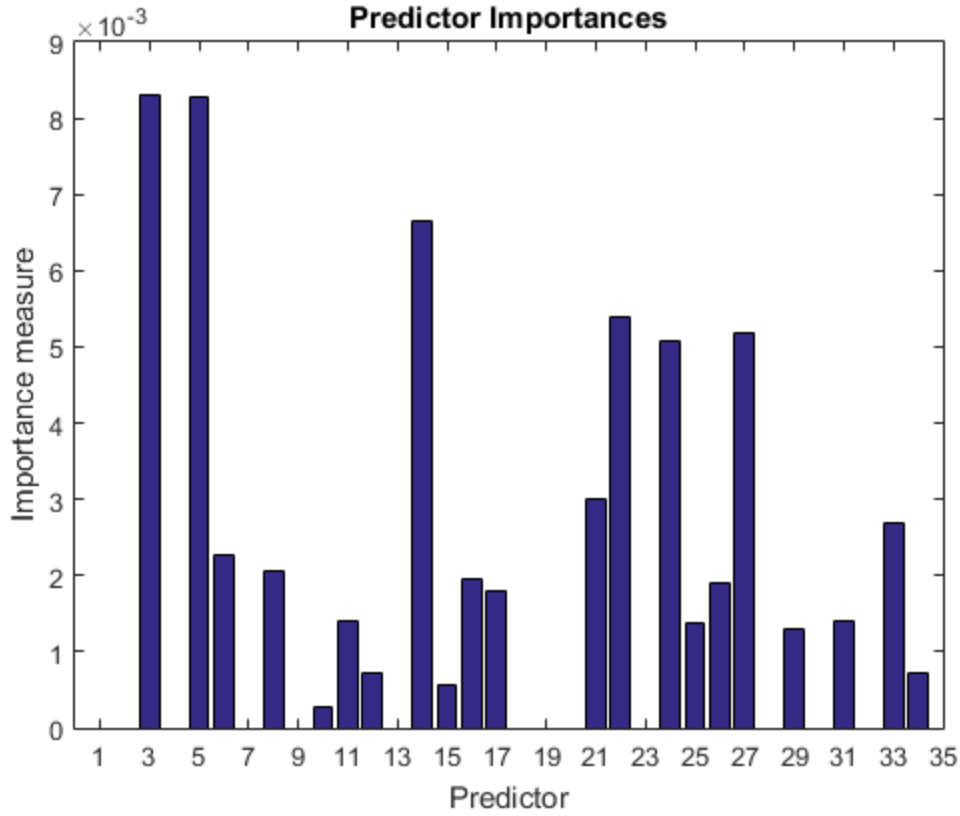
`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C2);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2)
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```

```
h =

  Axes with properties:

            XLim: [0 35]
            YLim: [0 0.0090]
          XScale: 'linear'
          YScale: 'linear'
```

```
    GridLineStyle: '-'
         Position: [0.1300 0.1100 0.7750 0.8150]
            Units: 'normalized'

  Use GET to show all properties
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Train another ensemble of 100 boosted classification trees using AdaBoostM1 and the five predictors with the best importance.

```
C1 = fitensemble(X(idxTrain,idx5),Y(idxTrain),'AdaBoostM1',nTrees,...
    'Tree');
```

Test whether the two models have equal predictive accuracies. Specify the reduced test-set predictor data for `C1` and the full test-set predictor data for `C2`.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,idx5),X(idxTest,:),Y(idxTest))
```

```
h =

     0


p =

    0.7744


e1 =

    0.0914


e2 =

    0.0857
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble, `C1`.

Alternatives

To directly compare the accuracy of two sets of class labels in predicting a set of true class labels, use `testcholdout`.

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

[2] Fagerlan, M.W., S Lydersen, P. Laake. “The McNemar Test for Binary Matched-Pairs Data: Mid-p and Asymptotic Are Better Than Exact Conditional.” *BMC Medical Research Methodology*. Vol. 13, 2013, pp. 1–8.

[3] Lancaster, H.O. “Significance Tests in Discrete Distributions.” *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. “Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages.” *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. “Some Statistical Problems in Measuring the Subjective Response to Drugs.” *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`fitcsvm` | `predict` | `testcholdout` | `testckfold`

More About

- “Hypothesis Tests”

Introduced in R2015a

compareHoldout

Class: CompactClassificationTree

Compare accuracies of two classification models using new data

`compareHoldout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `compareHoldout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = compareHoldout(C1,C2,X1,X2,Y)
h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = compareHoldout(___)
```

Description

`h = compareHoldout(C1,C2,X1,X2,Y)` returns the test decision from testing the null hypothesis that the trained classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model `C1` uses predictor data `X1` and `C2` uses `X2`. The software conducts the mid-*p*-value McNemar test to compare the accuracies.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a model that is more complex by passing the same set of predictor data (i.e., `X1 = X2`).

- Compare the accuracies of two perhaps different models using two perhaps different sets of predictors.
- Perform various types of feature selection. For example, you can compare the accuracy of a model trained using a set of predictors to the accuracy of one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = compareHoldout(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, and the type of test, or you can supply a cost matrix.

`[h,p,e1,e2] = compareHoldout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification losses of each set of predicted class labels (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Tips

- One way to perform cost-insensitive feature selection is:

  1. Train the first classification model (C1) using the full predictor set.
  2. Train the second classification model (C2) using the reduced predictor set.
  3. Specify `X1` as the full, test-set predictor data and `X2` as the reduced test-set predictor data.
  4. Enter `compareHoldout(C1,C2,X1,X2,'Alternative','less')`. If `compareHoldout` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','greater'` specification in step 4. `compareHoldout` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data

sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-803.

Input Arguments

`C1` — Trained classification tree

`ClassificationTree` model object | `CompactClassificationTree` model object

Trained classification tree, specified as a `ClassificationTree` or `CompactClassificationTree` model object. That is, `C1` is a trained classification model returned by `fitctree` or `compact`.

`C2` — Trained classification model

Trained classification model object | Trained, compact classification model object

Trained classification model, specified as any trained or compact classification model object described in this table.

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
Error-correcting output codes (ECOC), multiclass classification model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
Support vector machine (SVM)	`ClassificationSVM`	`fitcsvm`
Compact discriminant analysis	`CompactClassificationDiscriminant`	`compact`

Trained Model Type	Model Object	Returned By
Compact ECOC	`CompactClassificationECOC`	`compact`
Compact ensemble of classification models	`CompactClassificationEnsemble`	`compact`
Compact naive Bayes	`CompactClassificationNaiveBayes`	`compact`
Compact SVM	`CompactClassificationSVM`	`compact`
Compact classification tree	`ClassificationTree`	`compact`

`X1` — Test-set predictor data for first classification model

numeric matrix

Test-set predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double` | `single`

`X2` — Test-set predictor data for second classification model

numeric matrix

Test-set predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double` | `single`

`Y` — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` twice as much as for misclassifying observations with the true label `ClassNames{2}`.

`'Alpha'` — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

`'Alternative'` — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of these values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.

Value	Alternative hypothesis
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class

and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `CompactClassificationTree.compareHoldout` cannot conduct one-sided, exact, or mid-p tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `CompactClassificationTree.compareHoldout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: 'CostTest','chisquare'

Data Types: char

'Test' — Test to conduct

'asymptotic' | 'exact' | 'midp'

Test to conduct, specified as the comma-separated pair consisting of 'Test' and 'asymptotic', 'exact', and 'midp'. This table summarizes the available options for cost-insensitive testing.

Value	Description
'asymptotic'	Asymptotic McNemar test
'exact'	Exact-conditional McNemar test
'midp' (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, Test must be 'asymptotic'. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, 'asymptotic' is the default.

Example: 'Test','asymptotic'

Data Types: char

Note: NaNs, <undefined> values, and empty strings ('') indicate missing values. CompactClassificationTree.compareHoldout:

- Removes missing values in Y and the corresponding rows of X1 and X2
- Predicts classes whether X1 and X2 have missing observations.

Output Arguments

h — Hypothesis test result

1 | 0

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

`p` — *p*-value
scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`CompactClassificationTree.compareHoldout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

`e1` — Classification loss
scalar

Classification loss, returned as a scalar. `e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y).

`CompactClassificationTree.compareHoldout` applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels. Then, the function compares the estimated labels to `Y` to obtain the classification loss.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

`e2` — Classification loss
scalar

Classification loss, returned as a scalar. `e2` summarizes the accuracy of the second set of class labels predicting the true class labels (Y).

`CompactClassificationTree.compareHoldout` applies the second test-set predictor data (X2) to the second classification model (C2) to estimate the second set of class labels. Then the function compares the estimated labels to Y to obtain the classification loss.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

Definitions

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. $\sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1$. .

- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.
- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K}\sum_{j=1}^{K}\sum_{k=1}^{K}\left(c_{ki} - c_{kj}\right)\pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

  The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any $n_{ijk} = 0$. The test statistic is

$$t^*_{\chi^2} = \sum_{i \neq j}\sum_{k}\frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3\right)\hat{\pi}^{(1)}_{ijk}\right)^2}{n_{ijk} + 1}.$$

  If $1 - F_{\chi^2}\left(t^*_{\chi^2};1\right) < \alpha$, then reject H_0.

  - $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.
  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.
- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification

model assigns label *i*. The second classification model assigns label *j*. Jointly, their distribution is multinomial.

The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

If $1 - F_{\chi^2}\left(t^*_{LRT}; 1\right) < \alpha,$, then reject H_0.

- $\hat{\pi}^{(2)}_{ijk} = \frac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of Π_{ijk}.
- $\hat{\pi}^{(3)}_{ijk} = \frac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.

		Model 2: Correct	Model 2: Incorrect	
Model 1	Correct	n_{11}	n_{12}	$n_{1\bullet}$
	Incorrect	n_{21}	n_{22}	$n_{2\bullet}$
		$n_{\bullet 1}$	$n_{\bullet 2}$	n_{test}

n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

    $$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^*\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

    $$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^*; m\right) < \alpha$, where $F_{\chi^2}(x;m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

- For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

$$t_1^* = n_{12}$$

If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

$$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`CompactClassificationTree.compareHoldout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
```

```
    'Type','classification');
```

`C1` is a trained `ClassificationSVM` model. `C2` is a trained `ClassificationBaggedEnsemble` model.

Test whether the two models have equal predictive accuracies. Use the same test-set predictor data for each model.

```
h = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
C1 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
```

```
C2 = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`C1` and `C2` are trained `ClassificationSVM` models.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- *p*-value test (the cost-insensitive testing default). Request to return *p*-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater',...
    'Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = compareHoldout(C1,C2,...
    X(idxTest,:),X(idxTest,:),Y(idxTest),'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          __________    __________

    h             1             1
    p     7.2801e-09    2.7649e-10
    e1       0.13714       0.13714
    e2       0.33143       0.33143
```

The *p*-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `compareHoldout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or for data sets with imbalanced false-positive and false-negative costs, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate the predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
C1 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',cost);
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',cost);
```

`C1` and `C2` are trained `ClassificationEnsemble` models.

Test whether the AdaBoostM1 ensemble (`C1`) and the LogitBoost ensemble (`C2`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,:),X(idxTest,:),Y(idxTest),...
    'Cost',cost)
```

```
h =

     0


p =

    0.0743


e1 =

    1.3581


e2 =

    1.6186
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Select Features Using Statistical Accuracy Comparison

Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the out-of-sample accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

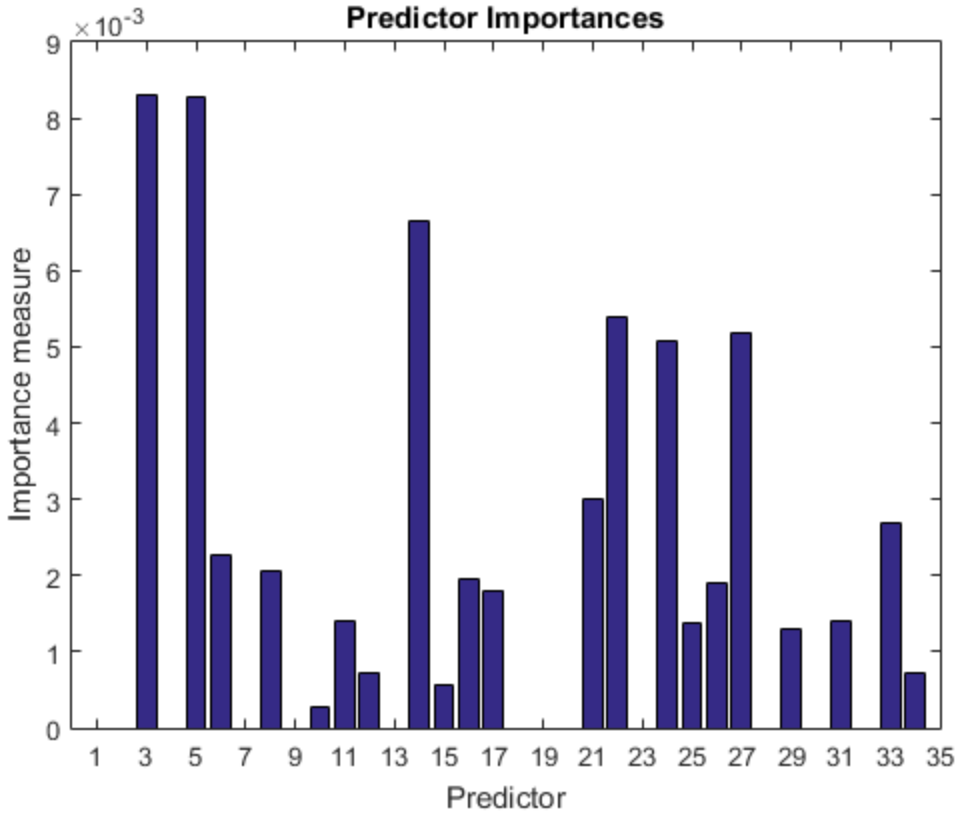
`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C2 = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C2);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2)
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```

```
h =

  Axes with properties:

            XLim: [0 35]
            YLim: [0 0.0090]
          XScale: 'linear'
          YScale: 'linear'
```

```
    GridLineStyle: '-'
         Position: [0.1300 0.1100 0.7750 0.8150]
            Units: 'normalized'

  Use GET to show all properties
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Train another ensemble of 100 boosted classification trees using AdaBoostM1 and the five predictors with the best importance.

```
C1 = fitensemble(X(idxTrain,idx5),Y(idxTrain),'AdaBoostM1',nTrees,...
    'Tree');
```

Test whether the two models have equal predictive accuracies. Specify the reduced test-set predictor data for `C1` and the full test-set predictor data for `C2`.

```
[h,p,e1,e2] = compareHoldout(C1,C2,X(idxTest,idx5),X(idxTest,:),Y(idxTest))
```

```
h =

     0


p =

    0.7744


e1 =

    0.0914


e2 =

    0.0857
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble, `C1`.

Alternatives

To directly compare the accuracy of two sets of class labels in predicting a set of true class labels, use `testcholdout`.

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

[2] Fagerlan, M.W., S Lydersen, P. Laake. “The McNemar Test for Binary Matched-Pairs Data: Mid-p and Asymptotic Are Better Than Exact Conditional.” *BMC Medical Research Methodology*. Vol. 13, 2013, pp. 1–8.

[3] Lancaster, H.O. “Significance Tests in Discrete Distributions.” *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. “Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages.” *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. “Some Statistical Problems in Measuring the Subjective Response to Drugs.” *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`fitctree` | `predict` | `testcholdout` | `testckfold`

More About

- “Hypothesis Tests”

Introduced in R2015a

ComputeOOBPrediction property

Class: TreeBagger

Flag to compute out-of-bag predictions

Description

The `ComputeOOBPrediction` property is a logical flag specifying whether out-of-bag predictions for training observations should be computed. The default is `false`.

If this flag is true, the following properties are available:

- `OOBIndices`
- `OOBInstanceWeight`

If this flag is true, the following methods can be called:

- `oobError`
- `oobMargin`
- `oobMeanMargin`

See Also

`OOBIndices` | `oobMargin` | `oobError` | `OOBInstanceWeight` | `oobMeanMargin`

ComputeOOBVarImp property

Class: TreeBagger

Flag to compute out-of-bag variable importance

Description

The `ComputeOOBVarImp` property is a logical flag specifying whether `TreeBagger` should compute out-of-bag estimates of variable importance. The default is false.

If this flag is true, the following properties are available:

- `OOBPermutedVarDeltaError`
- `OOBPermutedVarDeltaMeanMargin`
- `OOBPermutedVarCountRaiseMargin`

See Also

`oobMeanMargin` | `ComputeOOBPrediction` | `OOBPermutedVarDeltaError` | `OOBPermutedVarDeltaMeanMargin` | `OOBPermutedVarCountRaiseMargin` | `TreeBagger`

confusionmat

Confusion matrix

Syntax

```
C = confusionmat(group,grouphat)
C = confusionmat(group,grouphat,'order',grouporder)
[C,order] = confusionmat(...)
```

Description

`C = confusionmat(group,grouphat)` returns the confusion matrix `C` determined by the known and predicted groups in `group` and `grouphat`, respectively. `group` and `grouphat` are grouping variables with the same number of observations, as described in "Grouping Variables" on page 2-52. Input vectors must be of the same type. `C` is a square matrix with size equal to the total number of distinct elements in `group` and `grouphat`. `C(i,j)` is a count of observations known to be in group `i` but predicted to be in group `j`. Group indices and their order are the same for the rows and columns of `C`, computed by `grp2idx` using `grp2idx(group;grouphat)`. `NaN`, empty, or `'undefined'` groups are not counted.

`C = confusionmat(group,grouphat,'order',grouporder)` uses `grouporder` to order the rows and columns of `C`. `grouporder` is a grouping variable containing all of the distinct elements in `group` and `grouphat`. If `grouporder` contains elements that are not in `group` or `grouphat`, the corresponding entries in `C` will be `0`.

`[C,order] = confusionmat(...)` also returns the order of the rows and columns of `C` in a variable `order` the same type as `group` and `grouphat`.

Examples

Example 1

Display the confusion matrix for data with two misclassifications and one missing classification:

```
g1 = [1 1 2 2 3 3]';  % Known groups
g2 = [1 1 2 3 4 NaN]'; % Predicted groups

[C,order] = confusionmat(g1,g2)
C =
     2     0     0     0
     0     1     1     0
     0     0     0     1
     0     0     0     0
order =
     1
     2
     3
     4
```

Example 2

Randomize the measurements and groups in Fisher's iris data:

```
load fisheriris
numObs = length(species);
p = randperm(numObs);
meas = meas(p,:);
species = species(p);
```

Use `classify` to classify measurements in the second half of the data, using the first half of the data for training:

```
half = floor(numObs/2);
training = meas(1:half,:);
trainingSpecies = species(1:half);
sample = meas(half+1:end,:);
grouphat = classify(sample,training,trainingSpecies);
```

Display the confusion matrix for the resulting classification:

```
group = species(half+1:end);
[C,order] = confusionmat(group,grouphat)
C =
    22     0     0
     2    22     0
     0     0    29
order =
    'virginica'
```

```
    'versicolor'
    'setosa'
```

More About

- "Grouping Variables" on page 2-52

See Also

`crosstab` | `grp2idx`

controlchart

Shewhart control charts

Syntax

```
controlchart(X)
controlchart(x,group)
controlchart(X,group)
[stats,plotdata] = controlchart(x,[group])
controlchart(x,group,'name',value)
```

Description

`controlchart(X)` produces an xbar chart of the measurements in matrix `X`. Each row of `X` is considered to be a subgroup of measurements containing replicate observations taken at the same time. The rows should be in time order. If `X` is a time series object, the time samples should contain replicate observations.

The chart plots the means of the subgroups in time order, a center line (`CL`) at the average of the means, and upper and lower control limits (`UCL`, `LCL`) at three standard errors from the center line. The standard error is the estimated process standard deviation divided by the square root of the subgroup size. Process standard deviation is estimated from the average of the subgroup standard deviations. Out of control measurements are marked as violations and drawn with a red circle. Data cursor mode is enabled, so clicking any data point displays information about that point.

`controlchart(x,group)` accepts a grouping variable `group` for a vector of measurements `x`. `group` is a categorical variable, vector, string array, or cell array of strings the same length as `x`. Consecutive measurements `x(n)` sharing the same value of `group(n)` for $1 \le n \le$ `length(x)` are defined to be a subgroup. Subgroups can have different numbers of observations.

`controlchart(X,group)` accepts a grouping variable `group` for a matrix of measurements in `X`. In this case, `group` is only used to label the time axis; it does not change the default grouping by rows.

`[stats,plotdata] = controlchart(x,[group])` returns a structure `stats` of subgroup statistics and parameter estimates, and a structure `plotdata` of plotted values. `plotdata` contains one record for each chart.

The fields in `stats` and `plotdata` depend on the chart type.

The fields in `stats` are selected from the following:

- `mean` — Subgroup means
- `std` — Subgroup standard deviations
- `range` — Subgroup ranges
- `n` — Subgroup size, or total inspection size or area
- `i` — Individual data values
- `ma` — Moving averages
- `mr` — Moving ranges
- `count` — Count of defects or defective items
- `mu` — Estimated process mean
- `sigma` — Estimated process standard deviation
- `p` — Estimated proportion defective
- `m` — Estimated mean defects per unit

The fields in `plotdata` are the following:

- `pts` — Plotted point values
- `cl` — Center line
- `lcl` — Lower control limit
- `ucl` — Upper control limit
- `se` — Standard error of plotted point
- `n` — Subgroup size
- `ooc` — Logical that is true for points that are out of control

`controlchart(x,group,'name',value)` specifies one or more of the following optional parameter name/value pairs, with *`name`* in single quotes:

- `charttype` — The name of a chart type chosen from among the following:
  - `'xbar'` — Xbar or mean

- `'s'` — Standard deviation
- `'r'` — Range
- `'ewma'` — Exponentially weighted moving average
- `'i'` — Individual observation
- `'mr'` — Moving range of individual observations
- `'ma'` — Moving average of individual observations
- `'p'` — Proportion defective
- `'np'` — Number of defectives
- `'u'` — Defects per unit
- `'c'` — Count of defects

Alternatively, a parameter can be a cell array listing multiple compatible chart types. There are four sets of compatible types:

- `'xbar'`, `'s'`, `'r'`, and `'ewma'`
- `'i'`, `'mr'`, and `'ma'`
- `'p'` and `'np'`
- `'u'` and `'c'`

- `display` — Either `'on'` (default) to display the control chart, or `'off'` to omit the display
- `label` — A string array or cell array of strings, one per subgroup. This label is displayed as part of the data cursor for a point on the plot.
- `lambda` — A parameter between 0 and 1 controlling how much the current prediction is influenced by past observations in an EWMA plot. Higher values of `'lambda'` give less weight to past observations and more weight to the current observation. The default is 0.4.
- `limits'` — A three-element vector specifying the values of the lower control limit, center line, and upper control limits. Default is to estimate the center line and to compute control limits based on the estimated value of sigma. Not permitted if there are multiple chart types.
- `mean` — Value for the process mean, or an empty value (default) to estimate the mean from `X`. This is the `p` parameter for `p` and `np` charts, the mean defects per unit for `u` and `c` charts, and the normal `mu` parameter for other charts.

- `nsigma` — The number of sigma multiples from the center line to a control limit. Default is 3.
- `parent` — The handle of the axes to receive the control chart plot. Default is to create axes in a new figure. Not permitted if there are multiple chart types.
- `rules` — The name of a control rule, or a cell array containing multiple control rule names. These rules, together with the control limits, determine if a point is marked as out of control. The default is to apply no control rules, and to use only the control limits to decide if a point is out of control. See `controlrules` for more information. Control rules are applied to charts that measure the process level (`xbar`, `i`, `c`, `u`, `p`, and `np`) rather than the variability (`r`, `s`), and they are not applied to charts based on moving statistics (`ma`, `mr`, `ewma`).
- `sigma` — Either a value for sigma, or a method of estimating sigma chosen from among `'std'` (the default) to use the average within-subgroup standard deviation, `'range'` to use the average subgroup range, and `'variance'` to use the square root of the pooled variance. When creating `i`, `mr`, or `ma` charts for data not in subgroups, the estimate is always based on a moving range.
- `specs` — A vector specifying specification limits. Typically this is a two-element vector of lower and upper specification limits. Since specification limits typically apply to individual measurements, this parameter is primarily suitable for `i` charts. These limits are not plotted on `r`, `s`, or `mr` charts.
- `unit` — The total number of inspected items for `p` and `np` charts, and the size of the inspected unit for `u` and `c` charts. In both cases `X` must be the count of the number of defects or defectives found. Default is 1 for `u` and `c` charts. This argument is required (no default) for `p` and `np` charts.
- `width` — The width of the window used for computing the moving ranges and averages in `mr` and `ma` charts, and for computing the sigma estimate in `i`, `mr`, and `ma` charts. Default is 5.

Examples

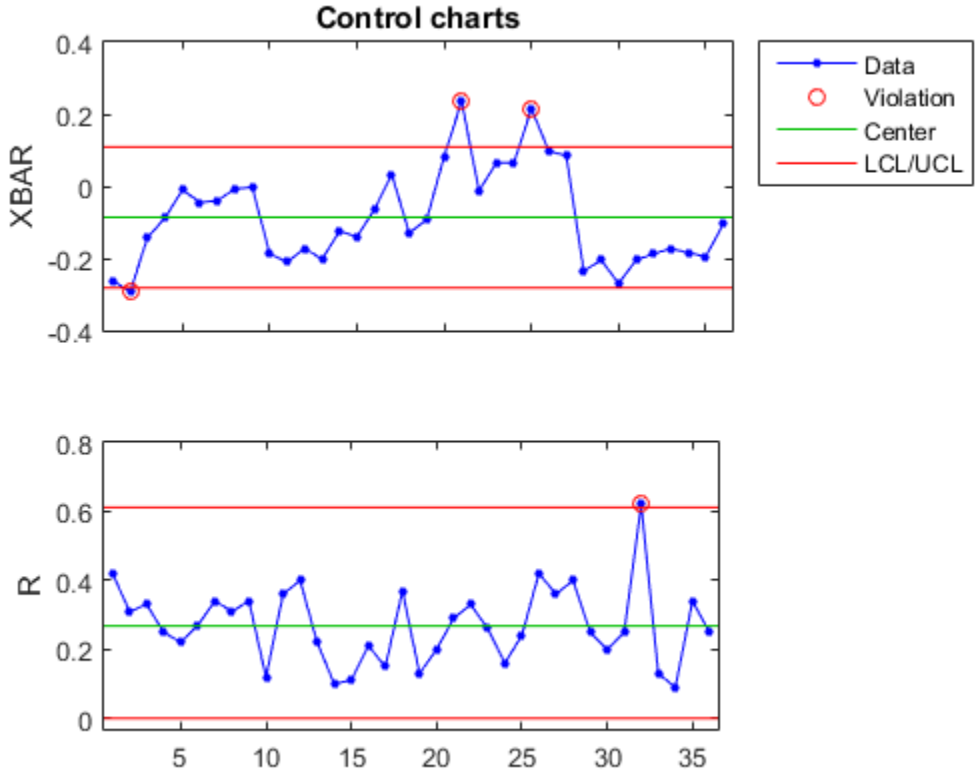
XBar and R Charts

Load the sample data.

```
load parts
```

Create xbar and r control charts for the data.

```
st = controlchart(runout,'chart',{'xbar' 'r'});
```



Display the process mean and standard deviation.

```
fprintf('Parameter estimates:  mu = %g, sigma = %g\n',st.mu,st.sigma);
```

```
Parameter estimates:  mu = -0.0863889, sigma = 0.130215
```

More About

- "Grouping Variables" on page 2-52

See Also

`controlrules`

controlrules

Western Electric and Nelson control rules

Syntax

```
R = controlrules('rules',x,cl,se)
[R,RULES] = controlrules('rules',x,cl,se)
```

Description

`R = controlrules('rules',x,cl,se)` determines which points in the vector `x` violate the control rules in *`rules`*. `cl` is a vector of center-line values. `se` is a vector of standard errors. (Typically, control limits on a control chart are at the values `cl – 3*se` and `cl + 3*se`.) `rules` is the name of a control rule, or a cell array containing multiple control rule names, from the list below. If `x` has n values and *`rules`* contains m rules, then `R` is an n-by-m logical array, with `R(i,j)` assigned the value `1` if point `i` violates rule `j`, `0` if it does not.

The following are accepted values for *`rules`* (specified inside single quotes):

- `we1` — 1 point above `cl + 3*se`
- `we2` — 2 of 3 above `cl + 2*se`
- `we3` — 4 of 5 above `cl + se`
- `we4` — 8 of 8 above `cl`
- `we5` — 1 below `cl – 3*se`
- `we6` — 2 of 3 below `cl – 2*se`
- `we7` — 4 of 5 below `cl – se`
- `we8` — 8 of 8 below `cl`
- `we9` — 15 of 15 between `cl – se` and `cl + se`
- `we10` — 8 of 8 below `cl – se` or above `cl + se`
- `n1` — 1 point below `cl – 3*se` or above `cl + 3*se`
- `n2` — 9 of 9 on the same side of `cl`

- `n3` — 6 of 6 increasing or decreasing
- `n4` — 14 alternating up/down
- `n5` — 2 of 3 below `cl – 2*se` or above `cl + 2*se`, same side
- `n6` — 4 of 5 below `cl – se` or above `cl + se`, same side
- `n7` — 15 of 15 between `cl – se` and `cl + se`
- `n8` — 8 of 8 below `cl – se` or above `cl + se`, either side
- `we` — All Western Electric rules
- `n` — All Nelson rules

For multi-point rules, a rule violation at point `i` indicates that the set of points ending at point `i` triggered the rule. Point `i` is considered to have violated the rule only if it is one of the points violating the rule's condition.

Any points with `NaN` as their `x`, `cl`, or `se` values are not considered to have violated rules, and are not counted in the rules for other points.

Control rules can be specified in the `controlchart` function as values for the `'rules'` parameter.

`[R,RULES] = controlrules('rules',x,cl,se)` returns a cell array of text strings `RULES` listing the rules applied.

Examples

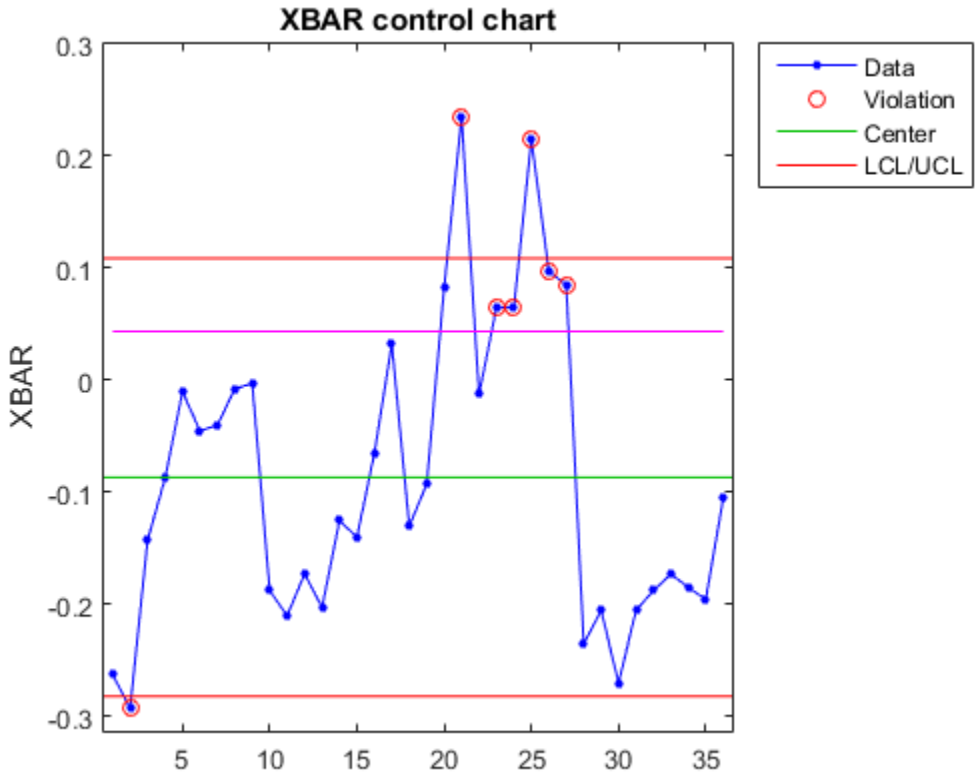
Use Western Electric Control Rule

Load the sample data.

```
load parts;
```

Create an Xbar chart using the `we2` rule to mark out of control measurements.

```
st = controlchart(runout,'rules','we2');
x = st.mean;
cl = st.mu;
se = st.sigma./sqrt(st.n);
hold on
plot(cl+2*se,'m')
```



You can see the out of control points marked with a red circle.

Use `controlrules` to identify the measurements that violate the control rule.

```
R = controlrules('we2',x,cl,se);
I = find(R)
```

```
I =

    21
    23
    24
    25
```

```
26
27
```

See Also

controlchart

Converged property

Class: gmdistribution

Determine if algorithm converged

Description

Logical `true` if the algorithm has converged; logical `false` if the algorithm has not converged.

Note: This property applies only to `gmdistribution` objects constructed with `fitgmdist`.

---

cophenet

Cophenetic correlation coefficient

Syntax

```
c = cophenet(Z,Y)
[c,d] = cophenet(Z,Y)
```

Description

`c = cophenet(Z,Y)` computes the cophenetic correlation coefficient for the hierarchical cluster tree represented by `Z`. `Z` is the output of the `linkage` function. `Y` contains the distances or dissimilarities used to construct `Z`, as output by the `pdist` function. `Z` is a matrix of size (m–1)-by-3, with distance information in the third column. `Y` is a vector of size m*(m–1)/2.

`[c,d] = cophenet(Z,Y)` returns the cophenetic distances `d` in the same lower triangular distance vector format as `Y`.

The cophenetic correlation for a cluster tree is defined as the linear correlation coefficient between the cophenetic distances obtained from the tree, and the original distances (or dissimilarities) used to construct the tree. Thus, it is a measure of how faithfully the tree represents the dissimilarities among observations.

The cophenetic distance between two observations is represented in a dendrogram by the height of the link at which those two observations are first joined. That height is the distance between the two subclusters that are merged by that link.

The output value, `c`, is the cophenetic correlation coefficient. The magnitude of this value should be very close to 1 for a high-quality solution. This measure can be used to compare alternative cluster solutions obtained using different algorithms.

The cophenetic correlation between `Z(:,3)` and `Y` is defined as

$$c = \frac{\sum_{i<j}(Y_{ij} - y)(Z_{ij} - z)}{\sqrt{\sum_{i<j}(Y_{ij} - y)^2 \sum_{i<j}(Z_{ij} - z)^2}}$$

where:

- Y_{ij} is the distance between objects i and j in `Y`.
- Z_{ij} is the cophenetic distance between objects i and j, from `Z(:,3)`.
- y and z are the average of `Y` and `Z(:,3)`, respectively.

Examples

```
X = [rand(10,3); rand(10,3)+1; rand(10,3)+2];
Y = pdist(X);
Z = linkage(Y,'average');

% Compute Spearman's rank correlation between the
% dissimilarities and the cophenetic distances
[c,D] = cophenet(Z,Y);
r = corr(Y',D','type','spearman')
r =
   0.8279
```

See Also

`cluster` | `dendrogram` | `linkage` | `pdist` | `inconsistent` | `squareform`

copulacdf

Copula cumulative distribution function

Syntax

```
y = copulacdf('Gaussian',u,rho)

y = copulacdf('t',u,rho,nu)

y = copulacdf(family,u,alpha)
```

Description

`y = copulacdf('Gaussian',u,rho)` returns the cumulative probability of the Gaussian copula, with linear correlation parameters rho evaluated at the points in u.

`y = copulacdf('t',u,rho,nu)` returns the cumulative probability of the *t* copula, with linear correlation parameters, rho, and degrees of freedom parameter nu evaluated at the points in u.

`y = copulacdf(family,u,alpha)` returns the cumulative probability of the bivariate Archimedean copula of the type specified by family, with scalar parameter `alpha` evaluated at the points in u.

Examples

Compute the Clayton Copula cdf

Define two 10-by-10 matrices containing the values at which to compute the cdf.

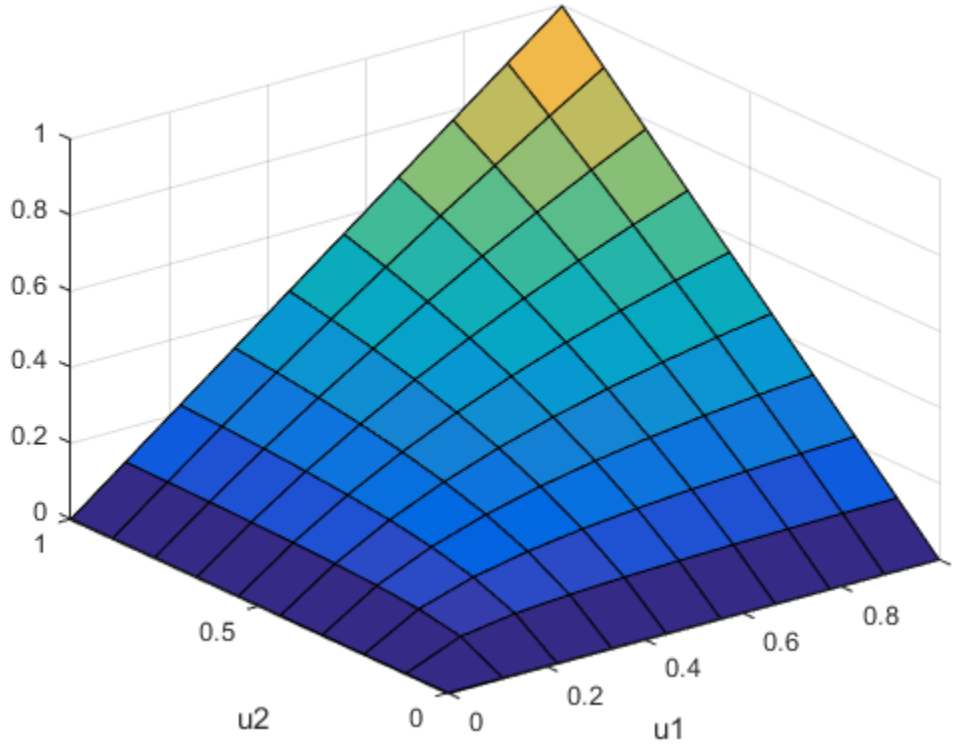
```
u = linspace(0,1,10);
[u1,u2] = meshgrid(u,u);
```

Compute the cdf of a Clayton copula that has an alpha parameter equal to 1, at the values in `u`.

```
y = copulacdf('Clayton',[u1(:),u2(:)],1);
```

Plot the cdf as a surface, and label the axes.

```
surf(u1,u2,reshape(y,10,10))
xlabel('u1')
ylabel('u2')
```



- "Generate Correlated Data Using Rank Correlation" on page 5-144

Input Arguments

u — Values at which to evaluate cdf

matrix of scalar values in the range [0,1]

Values at which to evaluate the cdf, specified as a matrix of scalar values in the range [0,1]. If u is an n-by-p matrix, then its values represent n points in the p-dimensional unit hypercube. If u is an n-by-2 matrix, then its values represent n points in the unit square.

If you specify a bivariate Archimedean copula type (`'Clayton'`, `'Frank'`, or `'Gumbel'`), then u must be an n-by-2 matrix.

Data Types: `single` | `double`

`rho` — Linear correlation parameters

scalar values | matrix of scalar values

Linear correlation parameters for the copula, specified as a scalar value or matrix of scalar values.

- If u is an n-by-p matrix, then rho is a p-by-p correlation matrix.
- If u is an n-by-2 matrix, then rho can be a scalar correlation coefficient.

Data Types: `single` | `double`

`nu` — Degrees of freedom

positive integer value

Degrees of freedom for the t copula, specified as a positive integer value.

Data Types: `single` | `double`

`family` — Bivariate Archimedean copula family

`'Clayton'` | `'Frank'` | `'Gumbel'`

Bivariate Archimedean copula family, specified as one of the following.

`'Clayton'`	Clayton copula
`'Frank'`	Frank copula
`'Gumbel'`	Gumbel copula

Data Types: `single` | `double`

`alpha` — Bivariate Archimedian copula parameter

scalar value

Bivariate Archimedian copula parameter, specified as a scalar value. Permitted values for alpha depend on the specified copula family.

Copula Family	Permitted Alpha Values
`'Clayton'`	$[0,\infty)$
`'Frank'`	$(-\infty,\infty)$
`'Gumbel'`	$[1,\infty)$

Data Types: `single` | `double`

Output Arguments

y — Cumulative distribution function

vector of scalar values

Cumulative distribution function of the copula, evaluated at the points in u, returned as a vector of scalar values.

More About

- “Copulas: Generate Correlated Samples” on page 5-160

See Also

`copulaparam` | `copulapdf` | `copularnd` | `copulastat`

copulafit

Fit copula to data

Syntax

```
rhohat = copulafit('Gaussian',u)

[rhohat,nuhat] = copulafit('t',u)
[rhohat,nuhat,nuci] = copulafit('t',u)

paramhat = copulafit(family,u)
[paramhat,paramci] = copulafit(family,u)

___ = copulafit(___,Name,Value)
```

Description

`rhohat = copulafit('Gaussian',u)` returns an estimate, rhohat, of the matrix of linear correlation parameters for a Gaussian copula, given the data in u.

`[rhohat,nuhat] = copulafit('t',u)` returns an estimate, rhohat, of the matrix of linear correlation parameters for a *t* copula, and an estimate of the degrees of freedom parameter, nuhat, given the data in u.

`[rhohat,nuhat,nuci] = copulafit('t',u)` also returns an approximate 95% confidence interval, nuci, for the degrees of freedom estimated in nuhat.

`paramhat = copulafit(family,u)` returns an estimate, paramhat, of the copula parameter for a bivariate Archimedean copula of the type specified by family, given the data in u.

`[paramhat,paramci] = copulafit(family,u)` also returns an approximate 95% confidence interval, paramci, for the copula parameter estimated in paramhat.

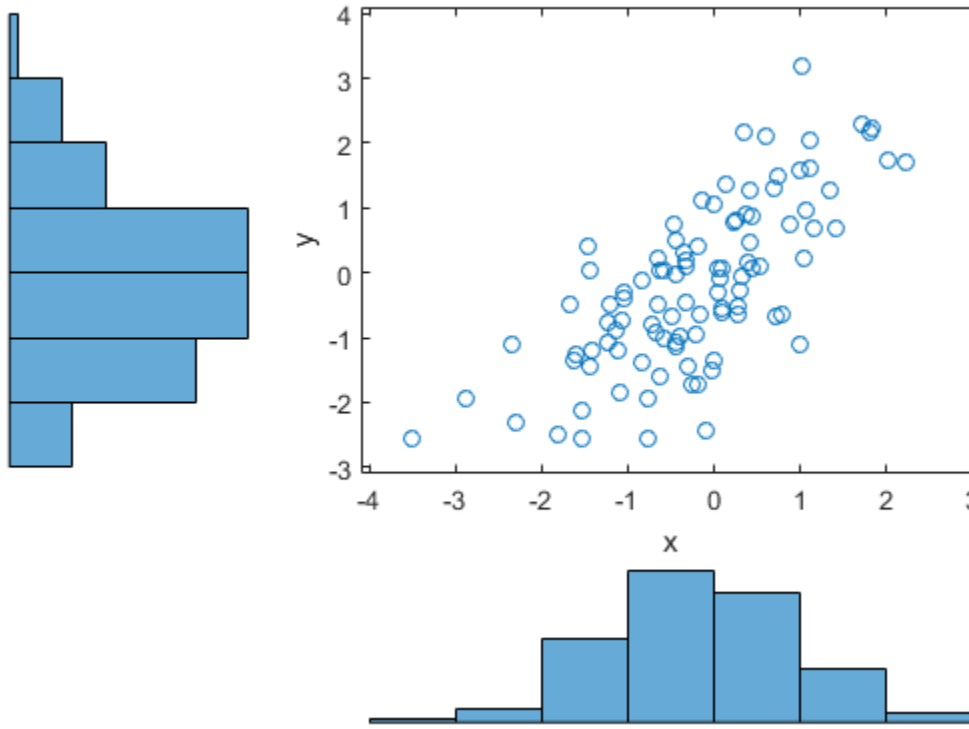
`___ = copulafit(___,Name,Value)` returns any of the previous syntaxes, with additional options specified by one or more Name,Value pair arguments. For example, you can specify the confidence interval to compute, or specify control parameters for the iterative parameter estimation algorithm using a options structure.

Examples

Fit a *t* Copula to Data

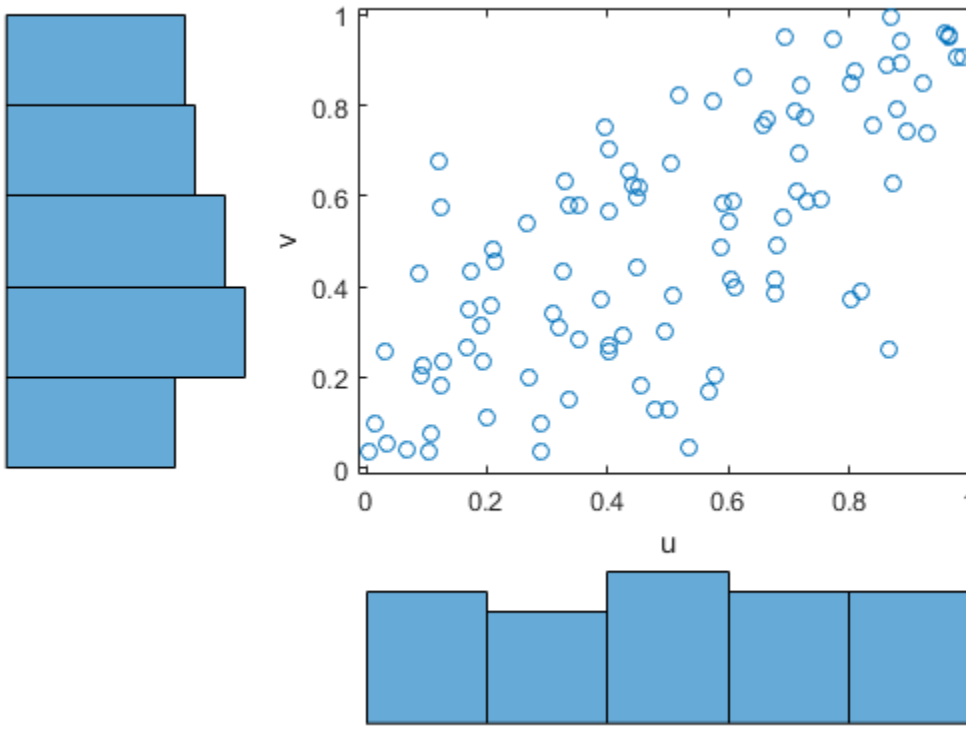
Load and plot simulated stock return data.

```
load stockreturns
x = stocks(:,1);
y = stocks(:,2);

figure;
scatterhist(x,y)
```



Transform the data to the copula scale (unit square) using a kernel estimator of the cumulative distribution function.

```
u = ksdensity(x,x,'function','cdf');
v = ksdensity(y,y,'function','cdf');

figure;
scatterhist(u,v)
xlabel('u')
ylabel('v')
```



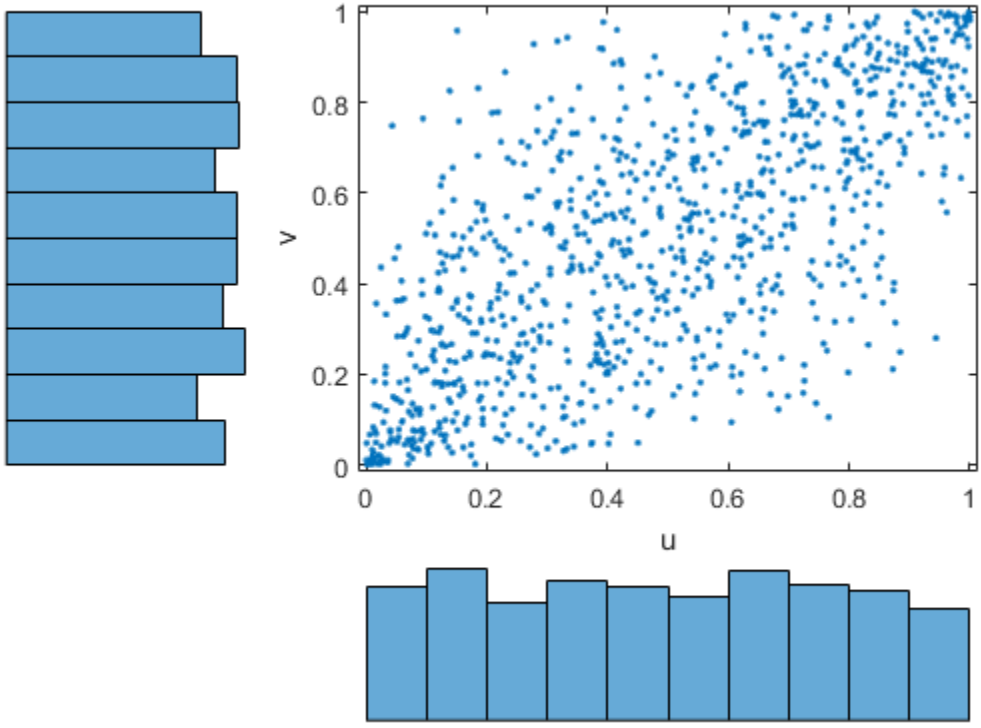
Fit a *t* copula to the data.

```
rng default  % For reproducibility
```

```
[Rho,nu] = copulafit('t',[u v],'Method','ApproximateML')


Rho =

    1.0000    0.7220
    0.7220    1.0000


nu =

   2.6133e+06
```

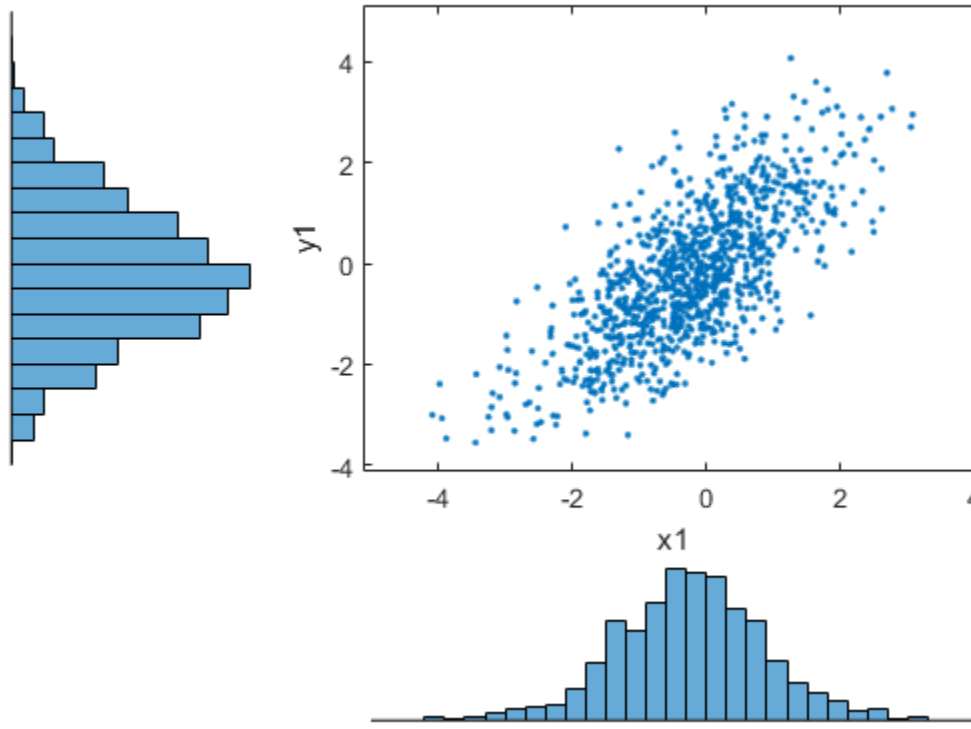
Generate a random sample from the *t* copula.

```
r = copularnd('t',Rho,nu,1000);
u1 = r(:,1);
v1 = r(:,2);

figure;
scatterhist(u1,v1)
xlabel('u')
ylabel('v')
set(get(gca,'children'),'marker','.')
```



Transform the random sample back to the original scale of the data.

```
x1 = ksdensity(x,u1,'function','icdf');
y1 = ksdensity(y,v1,'function','icdf');

figure;
scatterhist(x1,y1)
set(get(gca,'children'),'marker','.')
```



- “Generate Correlated Data Using Rank Correlation” on page 5-144

Input Arguments

u — Copula values

matrix of scalar values in the range (0,1)

Copula values, specified as a matrix of scalar values in the range (0,1). If u is an n-by-p matrix, then its values represent n points in the p-dimensional unit hypercube. If u is an n-by-2 matrix, then its values represent n points in the unit square.

If you specify a bivariate Archimedean copula type (`'Clayton'`, `'Frank'`, or `'Gumbel'`), then u must be an n-by-2 matrix.

Data Types: `single` | `double`

`family` — Bivariate Archimedean copula family

`'Clayton'` | `'Frank'` | `'Gumbel'`

Bivariate Archimedean copula family, specified as one of the following.

`'Clayton'`	Clayton copula
`'Frank'`	Frank copula
`'Gumbel'`	Gumbel copula

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alpha',0.01,'Method','ApproximateML'` computes 99% confidence intervals for the estimated copula parameter and uses an approximation method to fit the copula.

`'Alpha'` — Significance level for confidence intervals

0.05 (default) | scalar value in the range (0,1)

Significance level for confidence intervals, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1). `copulafit` returns approximate 100 × (1–Alpha)% confidence intervals.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Method'` — Method for fitting *t* copula

`'ML'` (default) | `'ApproximateML'`

Method for fitting t copula, specified as the comma-separated pair consisting of `'Method'` and either `'ML'` or `'ApproximateML'`.

If you specify `'ApproximateML'`, then `copulafit` fits a *t* copula for large samples by maximizing an objective function that approximates the profile log likelihood for the degrees of freedom parameter [1]. This method can be significantly faster than maximum likelihood (`'ML'`), but the estimates and confidence limits may not be accurate for small to moderate sample sizes.

Example: `'Method','ApproximateML'`

`'Options'` — Control parameter specifications

structure

Control parameter specifications, specified as the comma-separated pair consisting of `'Options'` and an options structure created by `statset`. To see the fields and default values used by `copulafit`, type `statset('copulafit')` at the command prompt.

This name-value pair is not applicable when you specify the copula type as `'Gaussian'`.

Data Types: `struct`

Output Arguments

`rhohat` — Estimated correlation parameters for the fitted Gaussian copula

matrix of scalar values

Estimated correlation parameters for the fitted Gaussian copula, given the data in u, returned as a matrix of scalar values.

`nuhat` — Estimated degrees of freedom parameter for the fitted *t* copula

scalar value

Estimated degrees of freedom parameter for the fitted *t* copula, returned as a scalar value.

`nuci` — Approximate confidence interval for the degrees of freedom parameter

1-by-2 matrix of scalar values

Approximate confidence interval for the degrees of freedom parameter, returned as a 1-by-2 matrix of scalar values. The first column contains the lower boundary, and the second column contains the upper boundary. By default, `copulafit` returns the approximate 95% confidence interval. You can specify a different confidence interval using the `'Alpha'` name-value pair.

`paramhat` — Estimated copula parameter for the fitted Archimedean copula

scalar value

Estimated copula parameter for the fitted Archimedean copula, returned as a scalar value.

`paramci` — Approximate confidence interval for the copula parameter

1-by-2 matrix of scalar values

Approximate confidence interval for the copula parameter, returned as a 1-by-2 matrix of scalar values. The first column contains the lower boundary, and the second column contains the upper boundary. By default, `copulafit` returns the approximate 95% confidence interval. You can specify a different confidence interval using the `'Alpha'` name-value pair.

More About

Algorithms

By default, `copulafit` uses maximum likelihood to fit a copula to `u`. When `u` contains data transformed to the unit hypercube by parametric estimates of their marginal cumulative distribution functions, this is known as the *Inference Functions for Margins (IFM)* method. When `u` contains data transformed by the empirical cdf (see `ecdf`), this is known as *Canonical Maximum Likelihood (CML)*.

- "Copulas: Generate Correlated Samples" on page 5-160

References

[1] Bouyé, E., V. Durrleman, A. Nikeghbali, G. Riboulet, and T. Roncalli. "Copulas for Finance: A Reading Guide and Some Applications." Working Paper. Groupe de Recherche Opérationnelle, Crédit Lyonnais, Paris, 2000.

See Also

`copulacdf` | `copulaparam` | `copulapdf` | `copularnd` | `copulastat`

copulaparam

Copula parameters as function of rank correlation

Syntax

```
rho = copulaparam('Gaussian',r)

rho = copulaparam('t',r,nu)

alpha = copulaparam(family,r)

___ = copulaparam(___,Name,Value)
```

Description

`rho = copulaparam('Gaussian',r)` returns the linear correlation parameters, rho, that correspond to a Gaussian copula with Kendall's rank correlation, r.

`rho = copulaparam('t',r,nu)` returns the linear correlation parameters, rho, that correspond to a *t* copula with Kendall's rank correlation, r, and degrees of freedom, nu.

`alpha = copulaparam(family,r)` returns the copula parameter, alpha, that corresponds to a bivariate Archimedean copula of the type specified by family, with Kendall's rank correlation, r.

`___ = copulaparam(___,Name,Value)` returns the correlation parameter using any of the previous syntaxes, with additional options specified by one or more Name,Value pair arguments. For example, you can specify whether the input rank correlation value is Spearman's *rho* or Kendell's *tau*.

Examples

Generate Correlated Data Using the Inverse cdf

Generate correlated random data from a beta distribution using a bivariate Gaussian copula with Kendall's *tau* rank correlation equal to -0.5.

Compute the linear correlation parameter from the rank correlation value.

```
rng default  % For reproducibility
tau = -0.5;
rho = copulaparam('Gaussian',tau)
```

```
rho =

   -0.7071
```

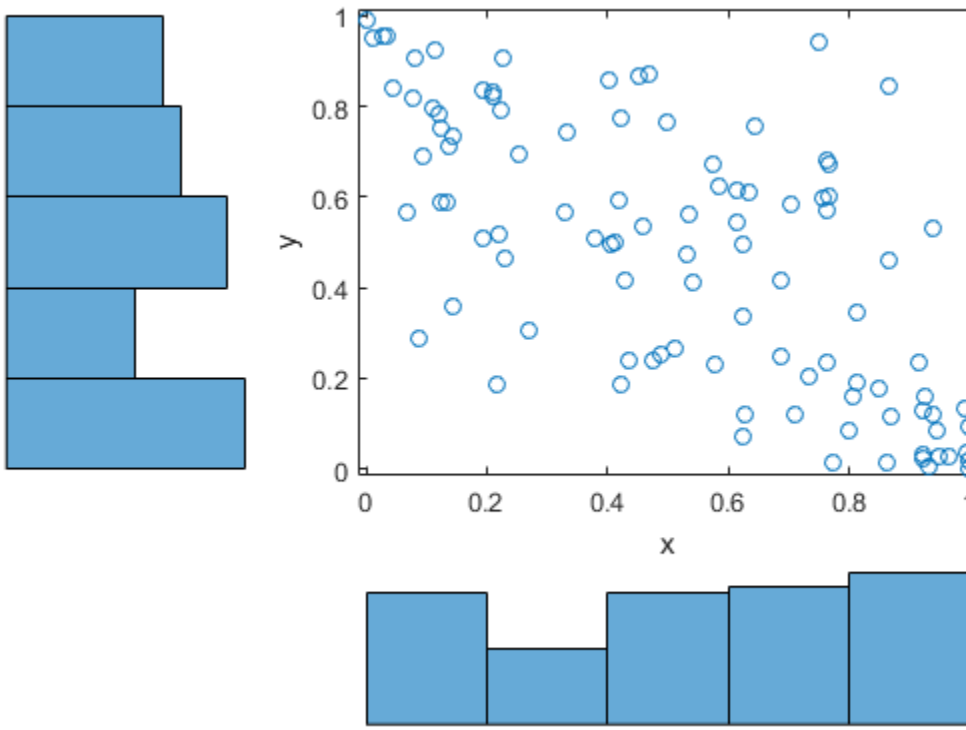
Use a Gaussian copula to generate a two-column matrix of dependent random values.

```
u = copularnd('gaussian',rho,100);
```

Each column contains 100 random values between 0 and 1, inclusive, sampled from a continuous uniform distribution.

Create a `scatterhist` plot to visualize the random numbers generated using the copula.

```
figure
scatterhist(u(:,1),u(:,2))
```



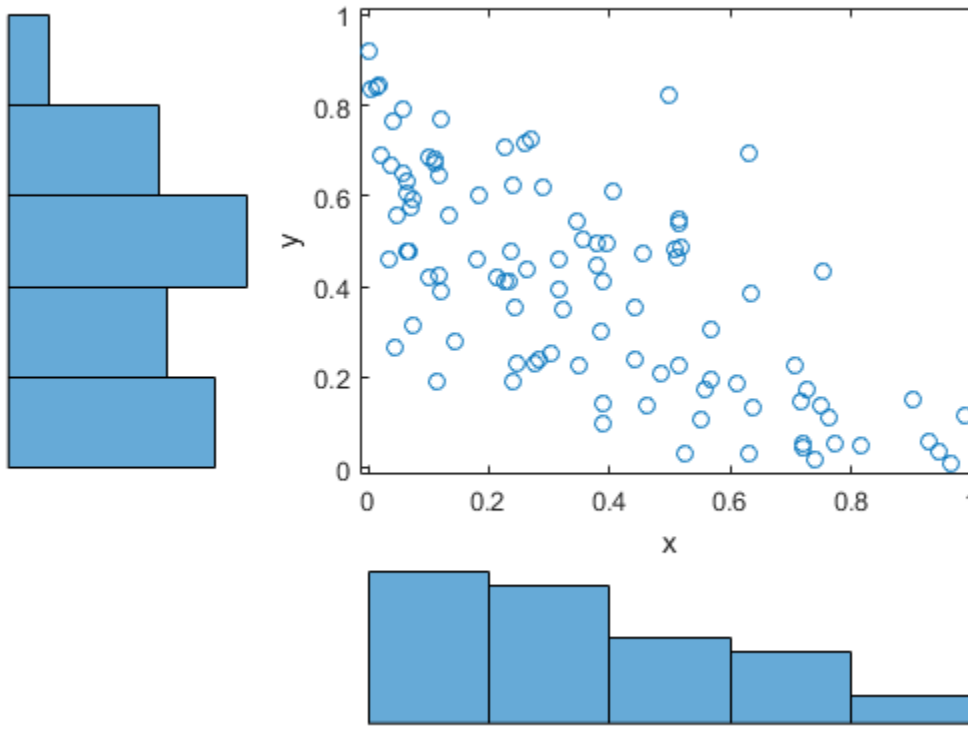
The histograms show that the data in each column of the copula has a marginal uniform distribution. The scatterplot shows that the data in the two columns is negatively correlated.

Use the inverse cdf function `betainv` to transform each column of the uniform marginal distributions into random numbers from a beta distribution. In the first column, the first shape parameter A is equal to 1, and a second shape parameter B is equal to 2. In the second column, the first shape parameter A is equal to 1.5, and a second shape parameter B is equal to 2.

```
b = [betainv(u(:,1),1,2), betainv(u(:,2),1.5,2)];
```

Create a `scatterhist` plot to visualize the correlated beta distribution data.

```
figure
scatterhist(b(:,1),b(:,2))
```



The histograms show the marginal beta distributions for each variable. The scatterplot shows the negative correlation.

Verify that the sample has a rank correlation approximately equal to the initial value for Kendall's *tau*.

```
tau_sample = corr(b,'type','kendall')
```

```
tau_sample =
```

```
    1.0000   -0.5135
   -0.5135    1.0000
```

The sample rank correlation of -0.5135 is approximately equal to the -0.5 initial value for *tau*.

- "Generate Correlated Data Using Rank Correlation" on page 5-144

Input Arguments

r — Copula rank correlation

scalar value | matrix of scalar values

Copula rank correlation, returned as a scalar value or matrix of scalar values.

- If r is a scalar correlation coefficient, then rho is a scalar correlation coefficient corresponding to a bivariate copula.
- If r is a *p*-by-*p* correlation matrix, then rho is a *p*-by-*p* correlation matrix.

If the copula is specified as one of the bivariate Archimedean copula types (`'Clayton'`, `'Frank'`, or `'Gumbel'`), then r is a scalar value.

nu — Degrees of freedom

positive integer value

Degrees of freedom for the *t* copula, specified as a positive integer value.

Data Types: `single` | `double`

family — Bivariate Archimedean copula family

`'Clayton'` | `'Frank'` | `'Gumbel'`

Bivariate Archimedean copula family, specified as one of the following.

`'Clayton'`	Clayton copula
`'Frank'`	Frank copula
`'Gumbel'`	Gumbel copula

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Type','Spearman'` computes Spearman's rank correlation.

`'Type'` — Type of rank correlation

`'Kendall'` (default) | `'Spearman'`

Type of rank correlation, specified as the comma-separated pair consisting of `'Type'` and one of the following.

- `'Kendall'` — Indicates that the input value for r is a Kendall's *tau* correlation value
- `'Spearman'` — Indicates that the input value for r is a Spearman's *rho* rank correlation value

`copulaparam` uses an approximation to Spearman's rank correlation for copula families that do not have an existing analytic formula. The approximation is based on a smooth fit to values computed at discrete values of the copula parameters. For a *t* copula, the approximation is accurate for degrees of freedom larger than 0.05.

Example: `'Type','Spearman'`

Output Arguments

`rho` — Linear correlation parameter

scalar value | matrix of scalar values

Linear correlation parameter, returned as a scalar value or matrix of scalar values.

- If r is a scalar correlation coefficient, then rho is a scalar correlation coefficient corresponding to a bivariate copula.
- If r is a *p*-by-*p* correlation matrix, then rho is a *p*-by-*p* correlation matrix.

`alpha` — Bivariate Archimedian copula parameter

scalar value

Bivariate Archimedian copula parameter, returned as a scalar value. Permitted values for alpha depend on the specified copula family.

Copula Family	Permitted Alpha Values
`'Clayton'`	$[0,\infty)$
`'Frank'`	$(-\infty,\infty)$
`'Gumbel'`	$[1,\infty)$

Data Types: `single` | `double`

More About

- "Copulas: Generate Correlated Samples" on page 5-160

See Also

`copulacdf` | `copulafit` | `copulapdf` | `copularnd` | `copulastat` | `ecdf`

copulapdf

Copula probability density function

Syntax

```
y = copulapdf('Gaussian',u,rho)

y = copulapdf('t',u,rho,nu)

y = copulapdf(family,u,alpha)
```

Description

`y = copulapdf('Gaussian',u,rho)` returns the probability density of the Gaussian copula with linear correlation parameters, rho, evaluated at the points in u.

`y = copulapdf('t',u,rho,nu)` returns the probability density of the *t* copula with linear correlation parameters, rho, and degrees of freedom parameter, nu, evaluated at the points in u.

`y = copulapdf(family,u,alpha)` returns the probability density of the bivariate Archimedean copula of the type specified by family, with scalar parameter, `alpha`, evaluated at the points in u.

Examples

Compute the Clayton Copula pdf

Define two 10-by-10 matrices containing the values at which to compute the pdf.

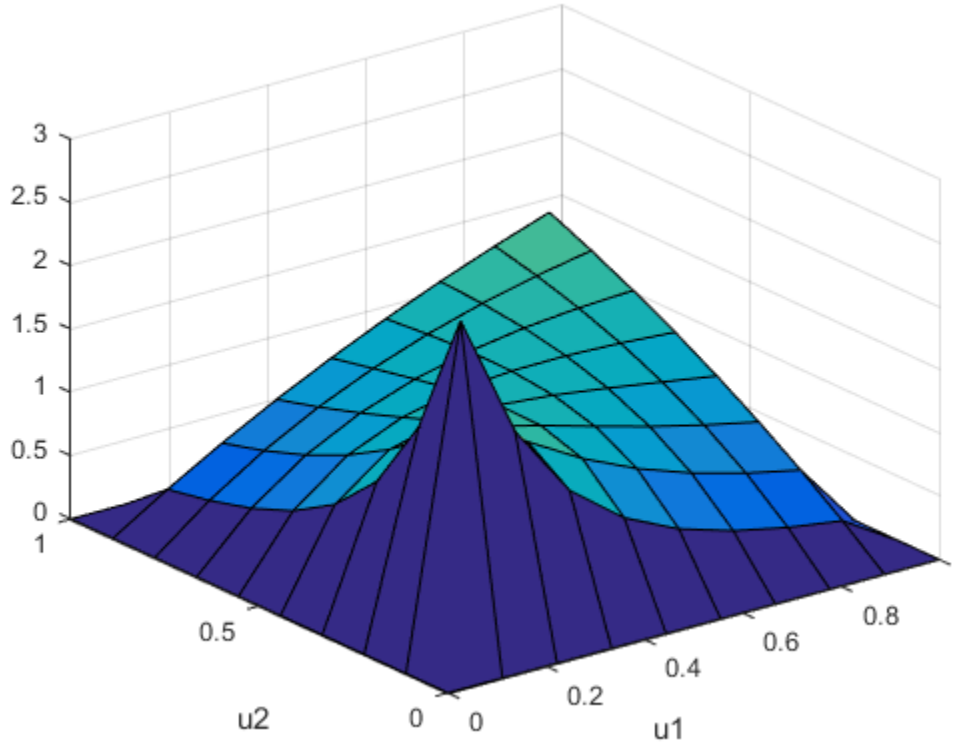
```
u = linspace(0,1,10);
[u1,u2] = meshgrid(u,u);
```

Compute the pdf of a Clayton copula that has an alpha parameter equal to 1, at the values in `u`.

```
y = copulapdf('Clayton',[u1(:),u2(:)],1);
```

Plot the pdf as a surface, and label the axes.

```
surf(u1,u2,reshape(y,10,10))
xlabel('u1')
ylabel('u2')
```



- “Generate Correlated Data Using Rank Correlation” on page 5-144

Input Arguments

u — Values at which to evaluate pdf

matrix of scalar values in the range [0,1]

Values at which to evaluate the pdf, specified as a matrix of scalar values in the range [0,1]. If u is an n-by-p matrix, then its values represent n points in the p-dimensional unit hypercube. If u is an n-by-2 matrix, then its values represent n points in the unit square.

If you specify a bivariate Archimedean copula type (`'Clayton'`, `'Frank'`, or `'Gumbel'`), then u must be an n-by-2 matrix.

Data Types: `single` | `double`

`rho` — Linear correlation parameters

scalar values | matrix of scalar values

Linear correlation parameters for the copula, specified as a scalar value or matrix of scalar values.

- If u is an n-by-p matrix, then rho is a p-by-p correlation matrix.
- If u is an n-by-2 matrix, then rho can be a scalar correlation coefficient.

Data Types: `single` | `double`

`nu` — Degrees of freedom

positive integer value

Degrees of freedom for the t copula, specified as a positive integer value.

Data Types: `single` | `double`

`family` — Bivariate Archimedean copula family

`'Clayton'` | `'Frank'` | `'Gumbel'`

Bivariate Archimedean copula family, specified as one of the following.

`'Clayton'`	Clayton copula
`'Frank'`	Frank copula
`'Gumbel'`	Gumbel copula

Data Types: `single` | `double`

`alpha` — Bivariate Archimedian copula parameter

scalar value

Bivariate Archimedian copula parameter, specified as a scalar value. Permitted values for alpha depend on the specified copula family.

Copula Family	Permitted Alpha Values
`'Clayton'`	$[0,\infty)$
`'Frank'`	$(-\infty,\infty)$
`'Gumbel'`	$[1,\infty)$

Data Types: `single` | `double`

Output Arguments

y — Probability density function

vector of scalar values

Probability density function, evaluated at the values in u, returned as a vector of scalar values.

More About

- “Copulas: Generate Correlated Samples” on page 5-160

See Also

`copulacdf` | `copulaparam` | `copularnd` | `copulastat`

copulastat

Copula rank correlation

Syntax

```
r = copulastat('Gaussian',rho)

r = copulastat('t',rho,nu)

r = copulastat(family,alpha)

r = copulstat( ___ ,Name,Value)
```

Description

`r = copulastat('Gaussian',rho)` returns the Kendall's rank correlation, r, that corresponds to a Gaussian copula with linear correlation parameters rho.

`r = copulastat('t',rho,nu)` returns the Kendall's rank correlation, r, that corresponds to a *t* copula with linear correlation parameters, rho, and degrees of freedom parameter, nu.

`r = copulastat(family,alpha)` returns the Kendall's rank correlation, r, that corresponds to a bivariate Archimedean copula that has the type specified by family and scalar parameter `alpha`.

`r = copulstat( ___ ,Name,Value)` returns the copula rank correlation with additional options specified by one or more Name,Value pair arguments, using any of the previous syntaxes. For example, you can return Spearman's *rho* rank correlation.

Examples

Compute the Gaussian Copula Rank Correlation

Compute the rank correlation for a Gaussian copula with the specified linear correlation parameter `rho`.

```
rho = -.7071;
tau = copulastat('gaussian',rho)


tau =

   -0.5000
```

Use the copula to generate dependent random values from a beta distribution that has parameters a and b equal to 2.

```
rng default  % For reproducibility
u = copularnd('gaussian',rho,100);
b = betainv(u,2,2);
```

Verify that the sample has a rank correlation approximately equal to `tau`.

```
tau_sample = corr(b,'type','k')


tau_sample =

    1.0000   -0.5135
   -0.5135    1.0000
```

- “Generate Correlated Data Using Rank Correlation” on page 5-144

Input Arguments

`rho` — Linear correlation parameters

scalar values | matrix of scalar values

Linear correlation parameters for the copula, specified as a scalar value or matrix of scalar values.

- If rho is a scalar correlation coefficient, then r is a scalar correlation coefficient corresponding to a bivariate copula.
- If rho is a *p*-by-*p* correlation matrix, then r is a *p*-by-*p* correlation matrix.

Data Types: `single` | `double`

`nu` — Degrees of freedom

positive integer value

Degrees of freedom for the *t* copula, specified as a positive integer value.

Data Types: `single` | `double`

`family` — Bivariate Archimedean copula family

`'Clayton'` | `'Frank'` | `'Gumbel'`

Bivariate Archimedean copula family, specified as one of the following.

`'Clayton'`	Clayton copula
`'Frank'`	Frank copula
`'Gumbel'`	Gumbel copula

Data Types: `single` | `double`

`alpha` — Bivariate Archimedian copula parameter

scalar value

Bivariate Archimedian copula parameter, specified as a scalar value. Permitted values for alpha depend on the specified copula family.

Copula Family	Permitted Alpha Values
`'Clayton'`	$[0,\infty)$
`'Frank'`	$(-\infty,\infty)$
`'Gumbel'`	$[1,\infty)$

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Type','Spearman'` computes Spearman's rank correlation.

'Type' — Type of rank correlation

'Kendall' (default) | 'Spearman'

Type of rank correlation, specified as the comma-separated pair consisting of 'Type' and one of the following.

- 'Kendall' — Compute Kendall's *tau*.
- 'Spearman' — Compute Spearman's *rho* (rank correlation).

copulastat uses an approximation to Spearman's rank correlation for copula families that do not have an existing analytic formula. The approximation is based on a smooth fit to values computed at discrete values of the copula parameters. For a *t* copula, the approximation is accurate for degrees of freedom larger than 0.05.

Example: 'Type','Spearman'

Output Arguments

r — Copula rank correlation

scalar value | matrix of scalar values

Copula rank correlation, returned as a scalar value or matrix of scalar values.

- If rho is a scalar correlation coefficient, then r is a scalar correlation coefficient corresponding to a bivariate copula.
- If rho is a *p*-by-*p* correlation matrix, then r is a *p*-by-*p* correlation matrix.

More About

- "Copulas: Generate Correlated Samples" on page 5-160

See Also

copulacdf | copulaparam | copulapdf | copularnd

copularnd

Copula random numbers

Syntax

```
u = copularnd('Gaussian',rho,n)
```

```
u = copularnd('t',rho,nu,n)
```

```
u = copularnd(family,alpha,n)
```

Description

`u = copularnd('Gaussian',rho,n)` returns n random vectors generated from a Gaussian copula with linear correlation parameters `rho`.

`u = copularnd('t',rho,nu,n)` returns n random vectors generated from a *t* copula with linear correlation parameters `rho` and degrees of freedom `nu`.

`u = copularnd(family,alpha,n)` returns n random vectors generated from a bivariate Archimedean copula that has the type specified by family and the scalar parameter `alpha`.

Examples

Generate Correlated Data Using the Inverse cdf

Generate correlated random data from a beta distribution using a bivariate Gaussian copula with Kendall's *tau* rank correlation equal to -0.5.

Compute the linear correlation parameter from the rank correlation value.

```
rng default  % For reproducibility
tau = -0.5;
rho = copulaparam('Gaussian',tau)
```

```
rho =
```

```
    -0.7071
```

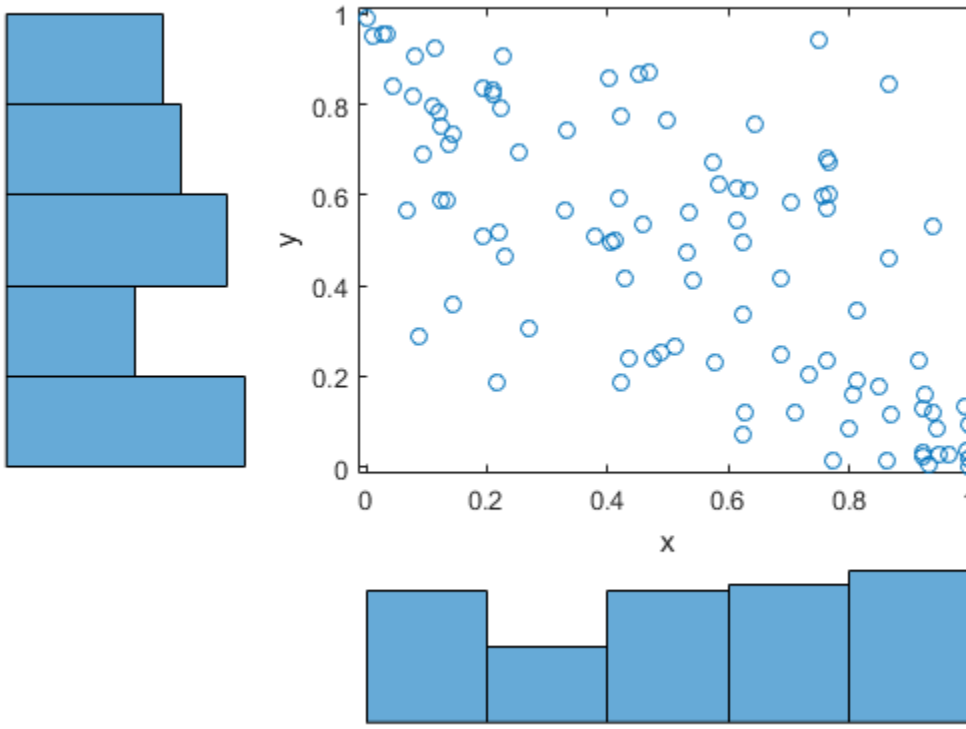
Use a Gaussian copula to generate a two-column matrix of dependent random values.

```
u = copularnd('gaussian',rho,100);
```

Each column contains 100 random values between 0 and 1, inclusive, sampled from a continuous uniform distribution.

Create a `scatterhist` plot to visualize the random numbers generated using the copula.

```
figure
scatterhist(u(:,1),u(:,2))
```



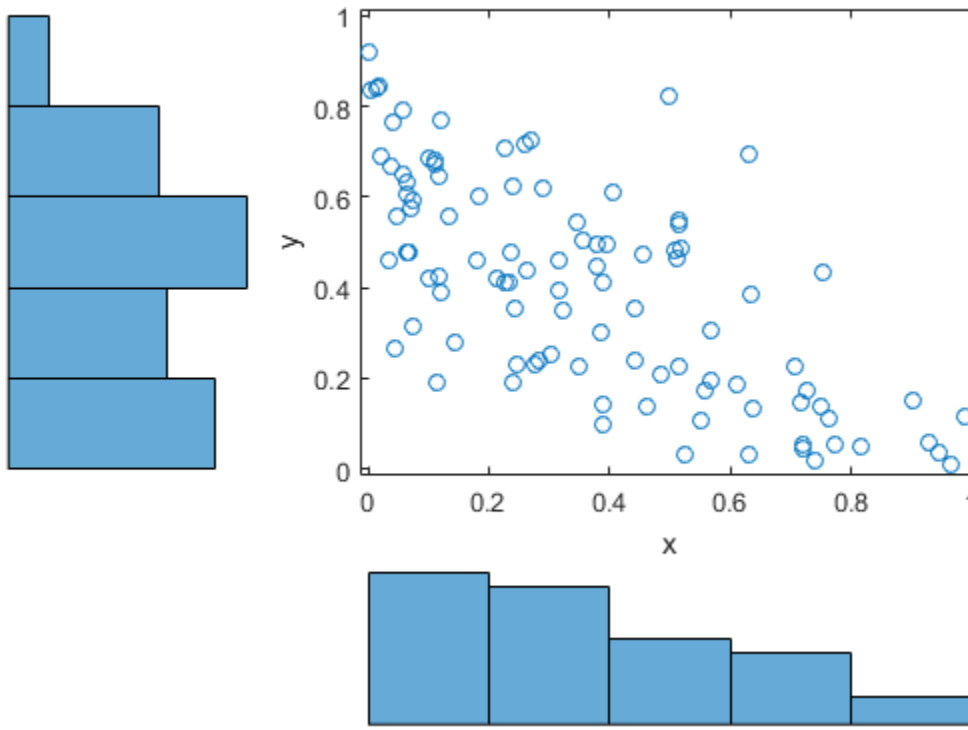
The histograms show that the data in each column of the copula has a marginal uniform distribution. The scatterplot shows that the data in the two columns is negatively correlated.

Use the inverse cdf function `betainv` to transform each column of the uniform marginal distributions into random numbers from a beta distribution. In the first column, the first shape parameter A is equal to 1, and a second shape parameter B is equal to 2. In the second column, the first shape parameter A is equal to 1.5, and a second shape parameter B is equal to 2.

```
b = [betainv(u(:,1),1,2), betainv(u(:,2),1.5,2)];
```

Create a `scatterhist` plot to visualize the correlated beta distribution data.

```
figure
scatterhist(b(:,1),b(:,2))
```



The histograms show the marginal beta distributions for each variable. The scatterplot shows the negative correlation.

Verify that the sample has a rank correlation approximately equal to the initial value for Kendall's *tau*.

```
tau_sample = corr(b,'type','kendall')
```

```
tau_sample =

    1.0000   -0.5135
   -0.5135    1.0000
```

The sample rank correlation of -0.5135 is approximately equal to the -0.5 initial value for *tau*.

• "Generate Correlated Data Using Rank Correlation" on page 5-144

Input Arguments

`rho` — Linear correlation parameters

scalar values | matrix of scalar values

Linear correlation parameters for the copula, specified as a scalar value or matrix of scalar values.

- If rho is a *p*-by-*p* correlation matrix, then the output argument u is an *n*-by-*p* matrix.
- If rho is a scalar correlation coefficient, then the output argument u is an *n*-by-2 matrix.

Data Types: `single` | `double`

`n` — Number of random vectors to return

positive scalar value

Number of random vectors to return, specified as a positive scalar value.

- If you specify the copula type as `'Gaussian'` or `'t'`, and rho is a *p*-by-*p* correlation matrix, then u is an *n*-by-*p* matrix.
- If you specify the copula type as `'Gaussian'` or `'t'`, and rho is a scalar correlation coefficient, then u is an *n*-by-2 matrix.
- If you specify the copula type as `'Clayton'`, `'Frank'`, or `'Gumbel'`, then u is an *n*-by-2 matrix.

Data Types: `single` | `double`

`nu` — Degrees of freedom

positive integer value

Degrees of freedom for the *t* copula, specified as a positive integer value.

Data Types: `single` | `double`

`family` — Bivariate Archimedean copula family

`'Clayton'` | `'Frank'` | `'Gumbel'`

Bivariate Archimedean copula family, specified as one of the following.

`'Clayton'`	Clayton copula
`'Frank'`	Frank copula
`'Gumbel'`	Gumbel copula

Data Types: `single` | `double`

`alpha` — Bivariate Archimedian copula parameter

scalar value

Bivariate Archimedian copula parameter, specified as a scalar value. Permitted values for alpha depend on the specified copula family.

Copula Family	Permitted Alpha Values
`'Clayton'`	$[0,\infty)$
`'Frank'`	$(-\infty,\infty)$
`'Gumbel'`	$[1,\infty)$

Data Types: `single` | `double`

Output Arguments

u — Copula random numbers

matrix of scalar values

Copula random numbers, returned as a matrix of scalar values. Each column of u is a sample from a `Uniform(0,1)` marginal distribution.

- If you specify the copula type as `'Gaussian'` or `'t'`, and rho is a p-by-p correlation matrix, then u is an n-by-p matrix.
- If you specify the copula type as `'Gaussian'` or `'t'`, and rho is a scalar correlation coefficient, then u is an n-by-2 matrix.
- If you specify the copula type as `'Clayton'`, `'Frank'`, or `'Gumbel'`, then u is an n-by-2 matrix.

More About

- "Copulas: Generate Correlated Samples" on page 5-160

See Also

`copulacdf` | `copulaparam` | `copulapdf` | `copulastat`

cordexch

Coordinate exchange

Syntax

```
dCE = cordexch(nfactors,nruns)
[dCE,X] = cordexch(nfactors,nruns)
[dCE,X] = cordexch(nfactors,nruns,'model')
[dCE,X] = cordexch(...,'name',value)
```

Description

`dCE = cordexch(nfactors,nruns)` uses a coordinate-exchange algorithm to generate a *D*-optimal design `dCE` with `nruns` runs (the rows of `dCE`) for a linear additive model with `nfactors` factors (the columns of `dCE`). The model includes a constant term.

`[dCE,X] = cordexch(nfactors,nruns)` also returns the associated design matrix `X`, whose columns are the model terms evaluated at each treatment (row) of `dCE`.

`[dCE,X] = cordexch(nfactors,nruns,'model')` uses the linear regression model specified in `model`. `model` is one of the following strings, specified inside single quotes:

- `linear` — Constant and linear terms. This is the default.
- `interaction` — Constant, linear, and interaction terms
- `quadratic` — Constant, linear, interaction, and squared terms
- `purequadratic` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n – 1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Alternatively, *model* can be a matrix specifying polynomial terms of arbitrary order. In this case, *model* should have one column for each factor and one row for each term in the model. The entries in any row of *model* are powers for the factors in the columns. For example, if a model has factors X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

[dCE,X] = cordexch(...,'*name*',*value*) specifies one or more optional name/value pairs for the design. Valid parameters and their values are listed in the following table. Specify *name* inside single quotes.

name	Value
bounds	Lower and upper bounds for each factor, specified as a 2-by-nfactors matrix. Alternatively, this value can be a cell array containing nfactors elements, each element specifying the vector of allowable values for the corresponding factor.
categorical	Indices of categorical predictors.
display	Either 'on' or 'off' to control display of the iteration counter. The default is 'on'.
excludefun	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with nfactors columns and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the method should exclude ith row S.
init	Initial design as a nruns-by-nfactors matrix. The default is a randomly selected set of points.
levels	Vector of number of levels for each factor. Not used when bounds is specified as a cell array.
maxiter	Maximum number of iterations. The default is 10.
tries	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is 1.
options	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the options structure with statset. Option fields:

name	Value

	• `UseParallel` — Set to `true` to compute in parallel. Default is `false`.
	• `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
	• `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `cordexch` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
	  • You have an open Parallel pool
	  • `UseParallel` is `true`
	  • `UseSubstreams` is `false`
	  In that case, use a cell array the same size as the Parallel pool.

Examples

Suppose you want a design to estimate the parameters in the following three-factor, seven-term interaction model:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{12} x_1 x_2 + \beta_{13} x_1 x_3 + \beta_{23} x_2 x_3 + \varepsilon$$

Use `cordexch` to generate a *D*-optimal design with seven runs:

```
nfactors = 3;
nruns = 7;
[dCE,X] = cordexch(nfactors,nruns,'interaction','tries',10)
dCE =
    -1     1     1
    -1    -1    -1
     1     1     1
    -1     1    -1
     1    -1     1
     1    -1    -1
    -1    -1     1
```

```
X =
     1    -1     1     1    -1    -1     1
     1    -1    -1    -1     1     1     1
     1     1     1     1     1     1     1
     1    -1     1    -1    -1     1    -1
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1    -1
```

Columns of the design matrix `X` are the model terms evaluated at each row of the design `dCE`. The terms appear in order from left to right: constant term, linear terms (1, 2, 3), interaction terms (12, 13, 23). Use `X` to fit the model, as described in "Linear Regression" on page 9-11, to response data measured at the design points in `dCE`.

More About

Algorithms

Both `cordexch` and `rowexch` use iterative search algorithms. They operate by incrementally changing an initial design matrix X to increase $D = |X^TX|$ at each step. In both algorithms, there is randomness built into the selection of the initial design and into the choice of the incremental changes. As a result, both algorithms may return locally, but not globally, D-optimal designs. Run each algorithm multiple times and select the best result for your final design. Both functions have a `'tries'` parameter that automates this repetition and comparison.

Unlike the row-exchange algorithm used by `rowexch`, `cordexch` does not use a candidate set. (Or rather, the candidate set is the entire design space.) At each step, the coordinate-exchange algorithm exchanges a single element of X with a new element evaluated at a neighboring point in design space. The absence of a candidate set reduces demands on memory, but the smaller scale of the search means that the coordinate-exchange algorithm is more likely to become trapped in a local minimum.

See Also

`rowexch` | `daugment` | `dcovary`

corr

Linear or rank correlation

Syntax

```
RHO = corr(X)
RHO = corr(X,Y)
[RHO,PVAL] = corr(X,Y)
[RHO,PVAL] = corr(X,Y,'name',value)
```

Description

`RHO = corr(X)` returns a p-by-p matrix containing the pairwise linear correlation coefficient between each pair of columns in the n-by-p matrix `X`.

`RHO = corr(X,Y)` returns a $p1$-by-$p2$ matrix containing the pairwise correlation coefficient between each pair of columns in the n-by-$p1$ and n-by-$p2$ matrices `X` and `Y`.

The difference between `corr(X,Y)` and the MATLAB function `corrcoef(X,Y)` is that `corrcoef(X,Y)` returns a matrix of correlation coefficients for the two column vectors `X` and `Y`. If `X` and `Y` are not column vectors, `corrcoef(X,Y)` converts them to column vectors.

`[RHO,PVAL] = corr(X,Y)` also returns `PVAL`, a matrix of p-values for testing the hypothesis of no correlation against the alternative that there is a nonzero correlation. Each element of `PVAL` is the p value for the corresponding element of `RHO`. If `PVAL(i,j)` is small, say less than `0.05`, then the correlation `RHO(i,j)` is significantly different from zero.

`[RHO,PVAL] = corr(X,Y,'name',value)` specifies one or more optional name/value pairs. Specify *`name`* inside single quotes. The following table lists valid parameters and their values.

Parameter	Values
`type`	• `'Pearson'` (the default) computes Pearson's linear correlation coefficient

Parameter	Values
	• `'Kendall'` computes Kendall's tau • `'Spearman'` computes Spearman's rho
`rows`	• `'all'` (the default) uses all rows regardless of missing values (`NaN`s) • `'complete'` uses only rows with no missing values • `'pairwise'`computes `RHO(i,j)` using rows with no missing values in column `i` or `j`
`tail` — The alternative hypothesis against which to compute *p*-values for testing the hypothesis of no correlation	• `'both'` — Correlation is not zero (the default) • `'right'` — Correlation is greater than zero • `'left'` — Correlation is less than zero

Using the `'pairwise'` option for the `rows` parameter may return a matrix that is not positive definite. The `'complete'` option always returns a positive definite matrix, but in general the estimates are based on fewer observations.

`corr` computes *p*-values for Pearson's correlation using a Student's t distribution for a transformation of the correlation. This correlation is exact when `X` and `Y` are normal. `corr` computes *p*-values for Kendall's tau and Spearman's rho using either the exact permutation distributions (for small sample sizes), or large-sample approximations.

`corr` computes *p*-values for the two-tailed test by doubling the more significant of the two one-tailed *p*-values.

Examples

Find Correlation Between Two Matrices

Find the correlation between two matrices and compare to the correlation between two column vectors.

Generate sample data.

```
rng('default')
x = randn(30,4);
y = randn(30,4);
y(:,4) = sum(x,2); % introduce correlation
```

Calculate the correlation between columns of `X` and `Y`.

```
[r,p] = corr(x,y)
```

```
r =

   -0.1686   -0.0363    0.2278    0.6901
    0.3022    0.0332   -0.0866    0.2617
   -0.3632   -0.0987   -0.0200    0.3504
   -0.1365   -0.1804    0.0853    0.4908

p =

    0.3731    0.8489    0.2260    0.0000
    0.1045    0.8619    0.6491    0.1624
    0.0485    0.6039    0.9166    0.0577
    0.4721    0.3400    0.6539    0.0059
```

Calculate the correlation between `X` and `Y` using `corrcoef`.

```
[r,p] = corrcoef(x,y)
```

```
r =

    1.0000    0.1252
    0.1252    1.0000

p =

    1.0000    0.1729
    0.1729    1.0000
```

MATLAB function `corrcoef` converts `X` and `Y` into column vectors before computing the correlation between them.

References

[1] Gibbons, J.D. (1985) Nonparametric Statistical Inference, 2nd ed., M. Dekker.

[2] Hollander, M. and D.A. Wolfe (1973) Nonparametric Statistical Methods, Wiley.

[3] Kendall, M.G. (1970) Rank Correlation Methods, Griffin.

[4] Best, D.J. and D.E. Roberts (1975) "Algorithm AS 89: The Upper Tail Probabilities of Spearman's rho", Applied Statistics, 24:377-379.

See Also

`corrcoef` | `corrcov` | `tiedrank` | `partialcorr`

corrcov

Convert covariance matrix to correlation matrix

Syntax

```
R = corrcov(C)
[R,sigma] = corrcov(C)
```

Description

`R = corrcov(C)` computes the correlation matrix `R` corresponding to the covariance matrix `C`. `C` must be square, symmetric, and positive semi-definite.

`[R,sigma] = corrcov(C)` also computes the vector of standard deviations `sigma`.

Examples

Use `cov` and `corrcoef` to compute covariances and correlations, respectively, for sample data on weight and blood pressure (systolic, diastolic) in `hospital.mat`:

```
load hospital
X = [hospital.Weight hospital.BloodPressure];
C = cov(X)
C =
  706.0404   27.7879   41.0202
   27.7879   45.0622   23.8194
   41.0202   23.8194   48.0590
R = corrcoef(X)
R =
    1.0000    0.1558    0.2227
    0.1558    1.0000    0.5118
    0.2227    0.5118    1.0000
```

Compare `R` with the correlation matrix computed from `C` by `corrcov`:

```
corrcov(C)
ans =
```

```
    1.0000    0.1558    0.2227
    0.1558    1.0000    0.5118
    0.2227    0.5118    1.0000
```

See Also

cov | corrcoef | corr | cholcov

Cost property

Class: TreeBagger

Misclassification costs

Description

The `Cost` property is a matrix with misclassification costs. This property is empty for ensembles of regression trees.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

covarianceParameters

Class: GeneralizedLinearMixedModel

Extract covariance parameters of generalized linear mixed-effects model

Syntax

```
psi = covarianceParameters(glme)
[psi,dispersion] = covarianceParameters(glme)
[psi,dispersion,stats] = covarianceParameters(glme)
[___] = covarianceParameters(glme,Name,Value)
```

Description

`psi = covarianceParameters(glme)` returns the estimated prior covariance parameters of random-effects predictors in the generalized linear mixed-effects model glme.

`[psi,dispersion] = covarianceParameters(glme)` also returns an estimate of the dispersion parameter.

`[psi,dispersion,stats] = covarianceParameters(glme)` also returns a cell array stats containing the covariance parameter estimates and related statistics.

`[___] = covarianceParameters(glme,Name,Value)` returns any of the above output arguments using additional options specified by one or more Name,Value pair arguments. For example, you can specify the confidence level for the confidence limits of covariance parameters.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range [0,1]

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range [0,1]. For a value α, the confidence level is 100 × (1 – α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single | double`

Output Arguments

`psi` — Estimated prior covariance parameters

cell array

Estimated prior covariance parameters for the random-effects predictors, returned as a cell array of length R, where R is the number of grouping variables used in the model. `psi{r}` contains the covariance matrix of random effects associated with grouping variable g_r, where $r = 1, 2, ..., R$, The order of grouping variables in psi is the same as the order entered when fitting the model. For more information on grouping variables, see "Grouping Variables" on page 2-52.

`dispersion` — Dispersion parameter

scalar value

Dispersion parameter, returned as a scalar value.

`stats` — Covariance parameter estimates and related statistics

cell array

Covariance parameter estimates and related statistics, returned as a cell array of length (R + 1), where R is the number of grouping variables used in the model. The first R cells of stats each contain a dataset array with the following columns.

`Group`	Grouping variable name
`Name1`	Name of the first predictor variable
`Name2`	Name of the second predictor variable
`Type`	If `Name1` and `Name2` are the same, then `Type` is `std` (standard deviation). If `Name1` and `Name2` are different, then `Type` is `corr` (correlation).
`Estimate`	If `Name1` and `Name2` are the same, then `Estimate` is the standard deviation of the random effect associated with predictor `Name1` or `Name2`. If `Name1` and `Name2` are different, then `Estimate` is the correlation between the random effects associated with predictors `Name1` and `Name2`.
`Lower`	Lower limit of the confidence interval for the covariance parameter
`Upper`	Upper limit of the confidence interval for the covariance parameter

Cell $R + 1$ contains related statistics for the dispersion parameter.

It is recommended that the presence or absence of covariance parameters in glme be tested using the `compare` method, which uses a likelihood ratio test.

When fitting a GLME model using `fitglme` and one of the maximum likelihood fit methods (`'Laplace'` or `'ApproximateLaplace'`), `covarianceParameters` derives the confidence intervals in stats based on a Laplace approximation to the log likelihood of the generalized linear mixed-effects model.

When fitting a GLME model using `fitglme` and one of the pseudo likelihood fit methods (`'MPL'` or `'REMPL'`), `covarianceParameters` derives the confidence intervals in `stats` based on the fitted linear mixed-effects model from the final pseudo likelihood iteration.

Examples

Obtain Estimated Covariance Parameters

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Compute and display the estimate of the prior covariance parameter for the random-effects predictor.

```
[psi,dispersion,stats] = covarianceParameters(glme);
psi{1}
```

```
ans =

    0.0985
```

`psi{1}` is an estimate of the prior covariance matrix of the first grouping variable. In this example, there is only one grouping variable (`factory`), so `psi{1}` is an estimate of σ_b^2.

Display the dispersion parameter.

```
dispersion
```

```
dispersion =

     1
```

Display the estimated standard deviation of the random effect associated with the predictor. The first cell of `stats` contains statistics for `factory`, while the second cell contains statistics for the dispersion parameter.

```
stats{1}
```

```
ans =


    Covariance Type: Isotropic

    Group      Name1               Name2               Type         Estimate
    factory    '(Intercept)'       '(Intercept)'       'std'        0.31381


    Lower      Upper
    0.19253    0.51148
```

The estimated standard deviation of the random effect associated with the predictor is 0.31381. The 95% confidence interval is [0.19253 , 0.51148]. Because the confidence interval does not contain 0, the random intercept is significant at the 5% significance level.

See Also

`GeneralizedLinearMixedModel` | `compare` | `fitglme` | `fixedEffects` | `randomEffects`

covarianceParameters

Class: LinearMixedModel

Extract covariance parameters of linear mixed-effects model

Syntax

```
psi = covarianceParameters(lme)
[psi,mse] = covarianceParameters(lme)
[psi,mse,stats] = covarianceParameters(lme)
[psi,mse,stats] = covarianceParameters(lme,Name,Value)
```

Description

`psi = covarianceParameters(lme)` returns the estimated covariance parameters that parameterize the prior covariance of random effects.

`[psi,mse] = covarianceParameters(lme)` also returns an estimate of the residual variance.

`[psi,mse,stats] = covarianceParameters(lme)` also returns a cell array, `stats`, containing the covariance parameters and related statistics.

`[psi,mse,stats] = covarianceParameters(lme,Name,Value)` returns the covariance parameters and related statistics in `stats` with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the confidence level for the confidence limits of covariance parameters.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 to 1

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range 0 to 1. For a value α, the confidence level is 100*(1–α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single | double`

Output Arguments

`psi` — Estimate of covariance parameters

cell array

Estimate of covariance parameters that parameterize the prior covariance of the random effects, returned as a cell array of length R, such that `psi{r}` contains the covariance matrix of random effects associated with grouping variable g_r, $r = 1, 2, ..., R$. The order of grouping variables is the same order you enter when you fit the model.

`mse` — Residual variance estimate

scalar value

Residual variance estimate, returned as a scalar value.

`stats` — Covariance parameter estimates and related statistics

cell array

Covariance parameter estimates and related statistics, returned as a cell array of length (R + 1) containing dataset arrays with the following columns.

`Group`	Grouping variable name
`Name1`	Name of the first predictor variable
`Name2`	Name of the second predictor variable
`Type`	`std` (standard deviation), if `Name1` and `Name2` are the same `corr` (correlation), if `Name1` and `Name2` are different
`Estimate`	Standard deviation of the random effect associated with predictor `Name1` or `Name2`, if `Name1` and `Name2` are the same Correlation between the random effects associated with predictors `Name1` and `Name2`, if `Name1` and `Name2` are different
`Lower`	Lower limit of a 95% confidence interval for the covariance parameter
`Upper`	Upper limit of a 95% confidence interval for the covariance parameter

`stats{r}` is a dataset array containing statistics on covariance parameters for the rth grouping variable, r = 1, 2, ..., R. `stats{R+1}` contains statistics on the residual standard deviation. The dataset array for the residual error has the fields `Group`, `Name`, `Estimate`, `Lower`, and `Upper`.

Examples

Two Random-Effects Terms for Intercept

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` is the fixed-effects variable, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently. This model corresponds to

$$y_{ijk} = \beta_0 + \sum_{j=2}^{5} \beta_{2j} I[T]_{ij} + b_{0k} S_k + b_{0jk} (S * T)_{jk} + \varepsilon_{ijk},$$

where $i = 1, 2, ..., 60$ corresponds to the observations, $j = 2, ..., 5$ corresponds to the tomato types, and $k = 1, 2, 3$ corresponds to the blocks (soil). S_k represents the k th soil type, and $(S*T)_{jk}$ represents the j th tomato type nested in the k th soil type. $I[T]_{ij}$ is the dummy variable representing the level j of the tomato type.

The random effects and observation error have the following prior distributions: $b_{0k} \sim N(0,\sigma^2_S)$, $b_{0jk} \sim N(0,\sigma^2_{S*T})$, and $\varepsilon_{ijk} \sim N(0,\sigma^2)$.

```
lme = fitlme(ds,'Yield ~ Fertilizer + (1|Soil) + (1|Soil:Tomato)');
```

Compute the covariance parameter estimates (estimates of σ^2_S and σ^2_{S*T}) of the random-effects terms.

```
psi = covarianceParameters(lme)
```

```
psi =
```

```
    [4.4026e-17]
    [  352.8481]
```

Compute the residual variance (σ^2).

```
[~,mse] = covarianceParameters(lme)
```

```
mse =

  151.9007
```

Potentially Correlated Random-Effects Terms

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a dataset array. Define `Subject` and `Program` as categorical variables.

```
ds = dataset(InitialWeight,Program,Subject,Week,y);
ds.Subject = nominal(ds.Subject);
ds.Program = nominal(ds.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

For `'reference'` dummy variable coding, `fitlme` uses Program A as reference and creates the necessary dummy variables $I[.]$. This model corresponds to

$$y_{im} = \beta_0 + \beta_1 IW_i + \beta_2 Week_i + \beta_3 I[PB]_i + \beta_4 I[PC]_i + \beta_5 I[PD]_i + b_{0m} + b_{1m} Week_{im} + \varepsilon_{im},$$

where i corresponds to the observation number, $i = 1, 2, ...,120$, and m corresponds to the subject number, $m = 1, 2, ..., 20$. β_j are the fixed-effects coefficients, $j = 0, 1, ..., 8$, and b_{0m} and b_{1m} are random effects. IW stands for initial weight and I[.] is a dummy variable representing a type of program. For example, $I[PB]_i$ is the dummy variable representing Program B.

The random effects and observation error have the following prior distributions: $\begin{pmatrix} b_{0m} \\ b_1 m \end{pmatrix} \sim N\left(0, \begin{pmatrix} \sigma_0^2 & \sigma_{0,1} \\ \sigma_{0,1} & \sigma_1^2 \end{pmatrix}\right)$ and $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
lme = fitlme(ds,'y ~ InitialWeight + Program + (Week|Subject)');
```

Compute the estimates of covariance parameters for the random effects.

```
[psi,mse,stats] = covarianceParameters(lme)
```

```
psi =

    [2x2 double]


mse =

    0.0105


stats =

    [3x7 classreg.regr.lmeutils.titleddataset]
    [1x5 dataset
```

`mse` is the estimated residual variance. It is the estimate for σ^2.

To see the covariance parameters estimates for the random-effects terms (σ^2_0, σ^2_1, and $\sigma^2_{0,1}$), index into `psi`.

```
psi{1}
```

```
ans =

    0.0572    0.0490
    0.0490    0.0624
```

The estimate of the variance of the random effects term for the intercept, σ^2_0, is 0.0572. The estimate of the variance of the random effects term for week, σ^2_1, is 0.0624. The estimate for the covariance of the random effects terms for the intercept and week, $\sigma_{0,1}$, is 0.0490.

`stats` is a 2-by-1 cell array. The first cell of `stats` contains the confidence intervals for the standard deviation of the random effects and the correlation between the random effects for intercept and week. To display them, index into `stats`.

```
stats{1}
```

```
ans =


    Covariance Type: FullCholesky

    Group      Name1                Name2                Type          Estimate    Lowe
    Subject    '(Intercept)'        '(Intercept)'        'std'         0.23927     0.14
    Subject    'Week'               '(Intercept)'        'corr'        0.81971     0.38
    Subject    'Week'               'Week'               'std'          0.2497     0.18
```

The display shows the name of the grouping parameter (`Group`), the random-effects variables (`Name1`, `Name2`), the type of the covariance parameters (`Type`), the estimate (`Estimate`) for each parameter, and the 95% confidence intervals for the parameters (`Lower`, `Upper`). The estimates in this table are related to the estimates in `psi` as follows.

The standard deviation of the random-effects term for intercept is 0.23927 = sqrt(0.0527). Likewise, the standard deviation of the random effects term for week is 0.2497 = sqrt(0.0624). Finally, the correlation between the random-effects terms of intercept and week is 0.81971 = 0.0490/(0.23927*0.2497).

Note that this display also shows which covariance pattern you use when fitting the model. In this case, the covariance pattern is `FullCholesky`. To change the covariance pattern for the random-effects terms, you must use the `'CovariancePattern'` name-value pair argument when fitting the model.

The second cell of `stats` includes similar statistics for the residual standard deviation. Display the contents of the second cell.

```
stats{2}
```

```
ans =
```

```
Group    Name             Estimate    Lower       Upper
Error    'Res Std'        0.10261     0.087882    0.11981
```

The estimate for residual standard deviation is the square root of `mse`, 0.10261 = sqrt(0.0105).

Two Grouping Variables

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration and weight, a potentially correlated random effect for intercept and acceleration grouped by model year, and an independent random effect for weight, grouped by the origin of the car. This model corresponds to

$$MPG_{imk} = \beta_0 + \beta_1 Acc_i + \beta_2 Weight_i + b_{10m} + b_{11m} Acc_i + b_{21k} Weight_i + \varepsilon_{imk},$$
$$m = 1,2,\ldots,13, \quad k = 1,2,\ldots,8,$$

where m represents the levels for the variable `Model_Year`, and k represents the levels for the variable `Origin`. MPG_{imk} is the miles per gallon for the i th observation, m th model year, and k th origin that correspond to the i th observation. The random-effects terms and the observation error have the following prior distributions:

$$b_{1m} = \begin{pmatrix} b_{10m} \\ b_{11m} \end{pmatrix} \sim N\left(0, \begin{pmatrix} \sigma_{10}^2 & \sigma_{10,11} \\ \sigma_{10,11} & \sigma_{11}^2 \end{pmatrix}\right),$$
$$b_{2k} \sim N\left(0, \sigma_2^2\right),$$
$$\varepsilon_{imk} \sim N\left(0, \sigma^2\right).$$

Here, the random-effects term b_{1m} represents the first random effect at level m of the first grouping variable. The random-effects term b_{10m} corresponds to the first random effects term (1), for the intercept (0), at the m th level (m) of the first grouping variable. Likewise b_{11m} is the level m for the first predictor (1) in the first random-effects term (1).

Similarly, b_{2k} stands for the second random effects-term at level k of the second grouping variable.

σ^2_{10} is the variance of the random-effects term for the intercept, σ^2_{11} is the variance of the random effects term for the predictor acceleration, and $\sigma_{10,11}$ is the covariance of the random-effects terms for the intercept and the predictor acceleration. σ^2_2 is the variance of the second random-effects term, and σ^2 is the residual variance.

First, prepare the design matrices for fitting the linear mixed-effects model.

```
X = [ones(406,1) Acceleration Weight];
Z = {[ones(406,1) Acceleration],[Weight]};
Model_Year = nominal(Model_Year);
Origin = nominal(Origin);
G = {Model_Year,Origin};
```

Fit the model using the design matrices.

```
lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Weight'},'RandomEffectPredictors',...
{{'Intercept','Acceleration'},{'Weight'}},'RandomEffectGroups',{'Model_Year','Origin'})
```

Compute the estimates of covariance parameters for the random effects.

```
[psi,mse,stats] = covarianceParameters(lme)
```

```
psi =

    [2x2 double]
    [6.7989e-08]


mse =

    9.0755


stats =

    [3x7 classreg.regr.lmeutils.titleddataset]
    [1x7 classreg.regr.lmeutils.titleddataset]
    [1x5 dataset                              ]
```

The residual variance `mse` is 9.0755. `psi` is a 2-by-1 cell array, and `stats` is a 3-by-1 cell array. To see the contents, you must index into these cell arrays.

First, index into the first cell of `psi`.

```
psi{1}

ans =

    8.5160   -0.8387
   -0.8387    0.1087
```

The first cell of `psi` contains the covariance parameters for the correlated random effects for intercept σ^2_{10} as 8.5160, and for acceleration σ^2_{11} as 0.1087. The estimate for the covariance of the random-effects terms for the intercept and acceleration $\sigma_{10,11}$ is –0.8387.

Now, index into the second cell of `psi`.

```
psi{2}

ans =

   6.7989e-08
```

The second cell of `psi` contains the estimate for the variance of the random-effects term for weight σ^2_2.

Index into the first cell of `stats`.

```
stats{1}

ans =


    Covariance Type: FullCholesky

    Group         Name1                Name2                Type          Estimate
    Model_Year    'Intercept'          'Intercept'          'std'          2.9182
    Model_Year    'Acceleration'       'Intercept'          'corr'        -0.87172
    Model_Year    'Acceleration'       'Acceleration'       'std'          0.32968
```

This table shows the standard deviation estimates for the random-effects terms for intercept and acceleration. Note that the standard deviations estimates are the square roots of the diagonal elements in the first cell of `psi`. Specifically, 2.9182 = sqrt(8.5160) and 0.32968 = sqrt(0.1087). The correlation is a function of the covariance of intercept and acceleration, and the standard deviations of intercept and acceleration. The covariance of intercept and acceleration is the off-diagonal value in the first cell of psi, –0.8387. So, the correlation is –.8387/(0.32968*2.92182) = –0.87.

The grouping variable for intercept and acceleration is `Model_Year`.

Index into the second cell of `stats`.

```
stats{2}
```

```
ans =


    Covariance Type: FullCholesky

    Group     Name1           Name2           Type         Estimate      Lower
    Origin    'Weight'        'Weight'        'std'        0.00026075    9.2158e-05
```

The second cell of `stats` has the standard deviation estimate and the 95% confidence limits for the standard deviation of the random-effects term for `Weight`. The grouping variable is `Origin`.

Index into the third cell of `stats`.

```
stats{3}
```

```
ans =

    Group    Name            Estimate    Lower     Upper
    Error    'Res Std'       3.0126      2.8028    3.238
```

The third cell of `stats` contains the estimate for residual standard deviation and the 95% confidence limits. The estimate for residual standard deviation is the square root of `mse`, sqrt(9.0755) = 3.0126.

Construct 99% confidence intervals for the covariance parameters.

```
[~,~,stats] = covarianceParameters(lme,'Alpha',0.01);
stats{1}
```

```
ans =


    Covariance Type: FullCholesky

    Group         Name1                Name2                Type          Estimate
    Model_Year    'Intercept'          'Intercept'          'std'           2.9182
    Model_Year    'Acceleration'       'Intercept'          'corr'        -0.87172
    Model_Year    'Acceleration'       'Acceleration'       'std'          0.32968
```

```
stats{2}

ans =


    Covariance Type: FullCholesky

    Group     Name1           Name2           Type         Estimate      Lower
    Origin    'Weight'        'Weight'        'std'        0.00026075    6.6466e-05

stats{3}

ans =

    Group    Name             Estimate    Lower    Upper
    Error    'Res Std'        3.0126      2.74     3.3123
```

See Also

`compare` | `fixedEffects` | `LinearMixedModel` | `randomEffects`

CovarianceType property

Class: gmdistribution

Type of covariance matrices

Description

The string `'diagonal'` if the covariance matrices are restricted to be diagonal; the string `'full'` otherwise.

coxphfit

Cox proportional hazards regression

Syntax

```
b = coxphfit(X,T)
b = coxphfit(X,T,Name,Value)
[b,logl,H,stats] = coxphfit(___)
```

Description

`b = coxphfit(X,T)` returns a p-by-1 vector, `b`, of coefficient estimates for a Cox proportional hazards regression of the observed responses in an n-by-1 vector, `T`, on the predictors in an n-by-p matrix `X`.

The model does not include a constant term, and `X` cannot contain a column of 1s.

`b = coxphfit(X,T,Name,Value)` returns a vector of coefficient estimates, with additional options specified by one or more `Name,Value` pair arguments.

`[b,logl,H,stats] = coxphfit(___)` also returns the loglikelihood, `logl`, a structure, `stats`, that contains additional statistics, and a two-column matrix, `H`, that contains the `T` values in the first column and the estimated baseline cumulative hazard, in the second column. You can use any of the input arguments in the previous syntaxes.

Examples

Lifetime of Light Bulbs

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load lightbulb
```

The first column of the light bulb data has the lifetime (in hours) of two different types of bulbs. The second column has the binary variable indicating whether the bulb is fluorescent or incandescent. 0 indicates that the bulb is incandescent, and 1 indicates that it is fluorescent. The third column contains the censorship information, where 0 indicates the bulb was observed until failure, and 1 indicates the bulb was censored.

Fit a Cox proportional hazards model for the lifetime of the light bulbs, also accounting for censoring. The predictor variable is the type of bulb.

```
b = coxphfit(lightbulb(:,2),lightbulb(:,1),...
'censoring',lightbulb(:,3))
```

```
b =

    4.7262
```

The estimate of the hazard ratio is $exp(b) = 112.8646$. This means that the hazard for the incandescent bulbs is 112.86 times the hazard for the fluorescent bulbs.

Change the Algorithm Parameters

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load lightbulb
```

The first column of the data has the lifetime (in hours) of two types of bulbs. The second column has the binary variable indicating whether the bulb is fluorescent or incandescent. 1 indicates that the bulb is fluorescent and 0 indicates that it is incandescent. The third column contains the censorship information, where 0 indicates the bulb is observed until failure, and 1 indicates the item (bulb) is censored.

Fit a Cox proportional hazards model, also accounting for censoring. The predictor variable is the type of bulb.

```
b = coxphfit(lightbulb(:,2),lightbulb(:,1),...
'censoring',lightbulb(:,3))
```

```
b =
```

```
    4.7262
```

Display the default control parameters for the algorithm `coxphfit` uses to estimate the coefficients.

```
statset('coxphfit')
```

```
ans =

          Display: 'off'
      MaxFunEvals: 200
          MaxIter: 100
           TolBnd: 1.0000e-06
           TolFun: 1.0000e-08
       TolTypeFun: []
             TolX: 1.0000e-08
         TolTypeX: []
          GradObj: []
         Jacobian: []
        DerivStep: []
      FunValCheck: []
           Robust: []
     RobustWgtFun: []
           WgtFun: []
             Tune: []
      UseParallel: []
    UseSubstreams: []
          Streams: {}
        OutputFcn: []
```

Save the options under a different name and change how the results will be displayed and the maximum number of iterations, `Display` and `MaxIter`.

```
coxphopt = statset('coxphfit');
coxphopt.Display = 'final';
coxphopt.MaxIter = 50;
```

Run `coxphfit` with the new algorithm parameters.

```
b = coxphfit(lightbulb(:,2),lightbulb(:,1),...
'censoring',lightbulb(:,3),'options',coxphopt)
```

```
Successful convergence: Norm of gradient less than OPTIONS.TolFun

b =
```

```
    4.7262
```

`coxphfit` displays a report on the final iteration. Changing the maximum number of iterations did not affect the coefficient estimate.

Fit and Compare Cox and Weibull Survivor Functions

Generate Weibull data depending on predictor `X`.

```
rng('default') % for reproducibility
X = 4*rand(100,1);
A = 50*exp(-0.5*X);
B = 2;
y = wblrnd(A,B);
```

The response values are generated from a Weibull distribution with a shape parameter depending on the predictor variable `X` and a scale parameter of 2.

Fit a Cox proportional hazards model.

```
[b,logL,H,stats] = coxphfit(X,y);
[b logL]
```

```
ans =

    0.9409 -331.1479
```

The coefficient estimate is 0.9409 and the log likelihood value is –331.1479.

Request the model statistics.

```
stats
```

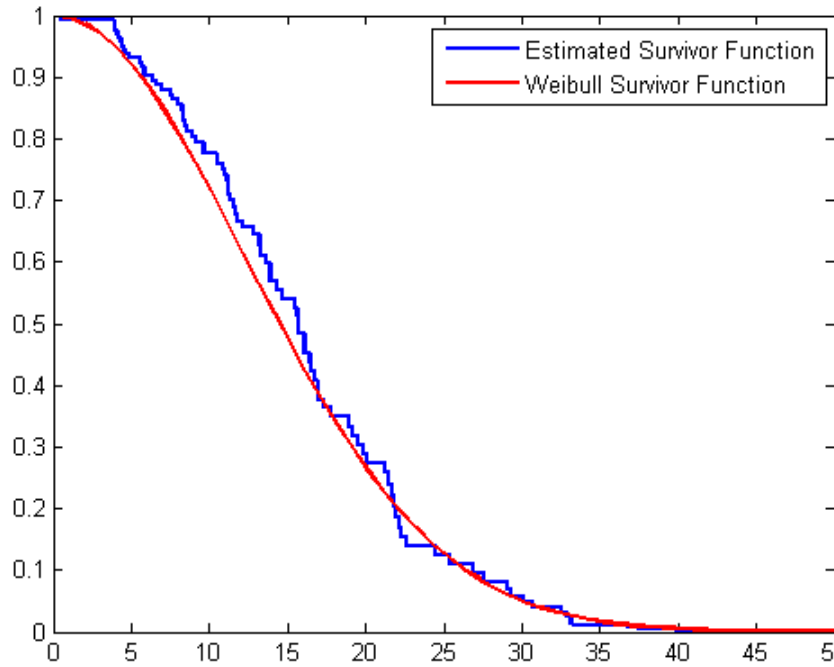
```
stats =

    covb: 0.0158
    beta: 0.9409
      se: 0.1256
       z: 7.4889
       p: 6.9462e-14
```

The covariance matrix of the coefficient estimates, `covb`, contains only one value, which is equal to the variance of the coefficient estimate in this example. The coefficient estimate, `beta`, is the same as `b` and is equal to 0.9409. The standard error of the coefficient estimate, `se`, is 0.1256, which is the square root of the variance 0.0158. The *z*-

statistic, `z`, is `beta/se` = 0.9409/0.1256 = 7.4880. The p-value, `p`, indicates that the effect of `X` is significant.

Plot the Cox estimate of the baseline survivor function together with the known Weibull function.

```
stairs(H(:,1),exp(-H(:,2)),'LineWidth',2)
xx = linspace(0,100);
line(xx,1-wblcdf(xx,50*exp(-0.5*mean(X)),B),'color','r','LineWidth',2)
xlim([0,50])
legend('Estimated Survivor Function','Weibull Survivor Function')
```



The fitted model gives a close estimate to the survivor function of the actual distribution.

- “Hazard and Survivor Functions for Different Groups” on page 12-18
- “Survivor Functions for Two Groups” on page 12-25

- "Cox Proportional Hazards Model for Censored Data" on page 12-33

Input Arguments

X — Observations on predictor variables

matrix

Observations on predictor variables, specified as an n-by-p matrix of p predictors for each of n observations.

The model does not include a constant term, thus `X` cannot contain a column of 1s.

Data Types: `single` | `double`

T — Time-to-event data

vector

Time-to-event data, specified as an n-by-1 vector.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'baseline',0,'censoring',censoreddata,'frequency',freq` specifies that `coxphfit` calculates the baseline hazard rate relative to 0, considering the censoring information in the vector `censoreddata`, and the frequency of observations on `T` and `X` given in the vector `freq`.

'baseline' — X values at which to compute the baseline hazard

`mean(X)` (default) | scalar value

X values at which to compute the baseline hazard, specified as the comma-separated pair consisting of `'baseline'` and a scalar value.

The default is `mean(X)`, so the hazard rate at X is `h(t)*exp((X-mean(X))*b)`. Enter `0` to compute the baseline relative to 0, so the hazard rate at X is `h(t)*exp(X*b)`.

Changing the baseline does not affect the coefficient estimates, but the hazard ratio changes.

Example: `'baseline',0`

Data Types: `single | double`

`'censoring'` — Indicator for censoring

array of 0s (default) | array of 0s and 1s

Indicator for censoring, specified as the comma-separated pair consisting of `'censoring'` and a Boolean array of the same size as T. Use 1 for observations that are right censored and 0 for observations that are fully observed. The default is all observations are fully observed.

Example: `'censoring',cens`

Data Types: `logical`

`'frequency'` — Frequency of observations

array of 1s (default) | vector of nonnegative integer counts

Frequency of observations, specified as the comma-separated pair consisting of `'frequency'` and an array that is the same size as T containing nonnegative integer counts.

The j^{th} element of this vector gives the number of times the method observes the j^{th} element of T and the j^{th} row of X. The default is one observation per row of X and T.

Example: `'frequency',freq`

Data Types: `single | double`

`'init'` — Initial values for estimated coefficients

vector

Initial values for estimated coefficients, specified as the comma-separated pair consisting of `'init'` and a vector containing the coefficient initial values.

Example: `'init',initcoef`

Data Types: `single | double`

`'options'` — Algorithm control parameters

structure

Algorithm control parameters for the iterative algorithm used to estimate b, specified as the comma-separated pair consisting of `'options'` and a structure. A call to `statset` creates this argument. For parameter names and default values, type `statset('coxphfit')`. You can set the options under a new name and use that in the name-value pair argument.

Example: `'options',statset('coxphfit')`

Data Types: `char`

Output Arguments

`b` — Coefficient estimates

vector

Coefficient estimates for a Cox proportional hazards regression, returned as a *p*-by-1 vector.

`logl` — Loglikelihood

scalar

Loglikelihood of the fitted model, returned as a scalar.

You can use log likelihood values to compare different models and assess the significance of effects of terms in the model.

`H` — Estimated baseline cumulative hazard

two-column matrix

Estimated baseline cumulative hazard rate evaluated at T values, returned as a two-column matrix. The first column of the matrix contains T values, and the second column contains cumulative hazard rate estimates.

`stats` — Coefficient statistics

structure

Coefficient statistics, returned as a structure that contains the following fields.

`beta`	Coefficient estimates (same as b)
`se`	Standard errors of coefficient estimates, b

z	z-statistics for b (that is, b divided by standard error)
p	p-values for b
covb	Estimated covariance matrix for b

More About

Cox Proportional Hazards Regression

Cox proportional hazards regression is a semiparametric method for adjusting survival rate estimates to remove the effect of confounding variables and to quantify the effect of predictor variables. The method represents the effects of explanatory and confounding variables as a multiplier of a common baseline hazard function, $h_0(t)$.

For a baseline relative to 0, this model corresponds to

$$h_X(t) = h_0(t)e^{\sum_i X_i b_i},$$

where $h_X(t)$ is the hazard rate at X and $h_0(t)$ is the baseline hazard rate function. The baseline hazard function is the nonparametric part of the Cox proportional hazards regression function, whereas the impact of the predictor variables is a loglinear regression. The assumption is that the baseline hazard function depends on time, t, but the predictor variables do not depend on time.

References

[1] Cox, D.R., and D. Oakes. *Analysis of Survival Data*. London: Chapman & Hall, 1984.

[2] Lawless, J. F. *Statistical Models and Methods for Lifetime Data*. Hoboken, NJ: Wiley-Interscience, 2002.

[3] Kleinbaum, D. G., and M. Klein. *Survival Analysis*. Statistics for Biology and Health. 2nd edition. Springer, 2005.

- "What Is Survival Analysis?" on page 12-2
- "Kaplan-Meier Method" on page 12-11
- "Cox Proportional Hazards Regression" on page 12-30

See Also

ecdf | statset | wblfit

Prior property

Class: NaiveBayes

Class priors

Description

The `Prior` property is a vector of length `NClasses` containing the class priors. The priors for empty classes are zero.

createns

Create object to use in *k*-nearest neighbors search

Syntax

```
NS = createns(X)
NS = createns(X,'Name',Value)
```

Description

`NS = createns(X)` uses the data observations in an *mx*-by-*n* matrix `X` to create an object `NS`. Rows of `X` correspond to observations and columns correspond to variables. `NS` is either an `ExhaustiveSearcher` or a `KDTreeSearcher` model object which you can use to find nearest neighbors in `X` for desired query points. If `NS` is an `ExhaustiveSearcher` model, `knnsearch` and `rangesearch` use the exhaustive search algorithm to find nearest neighbors. If `NS` is a `KDTreeSearcher` model, `createns` grows and saves a *K*d-tree based on `X` in `NS`. `knnsearch` and `rangesearch` use the *K*d-tree to find nearest neighbors. For information on these search methods, see "*k*-Nearest Neighbor Search and Radius Search" on page 16-11.

`NS = createns(X,'Name',Value)` accepts one or more optional name/value pairs. Specify *`Name`* inside single quotes. Specify `NSMethod` to determine which type of object to create. The object's properties save the information when you specify other arguments. For more information on the objects' properties, see Using ExhaustiveSearcher Objects or a Using KDTreeSearcher Objects.

Input Arguments

Name-Value Pair Arguments

`'NSMethod'`

Nearest neighbors search method, used to define the type of object created. Value is either:

- `'kdtree'` — Create a `KDTreeSearcher` model. If you do not specify `NSMethod`, this is the default value when the number of columns of `X` is less than 10, `X` is not sparse, and the distance measure is one of the following measures:
  - `'euclidean'` (default)
  - `'cityblock'`
  - `'minkowski'`
  - `'chebychev'`
- `'exhaustive'` — Create an `ExhaustiveSearcher` model. If you do not specify `NSMethod`, this is the default value when the default criteria for `'kdtree'` do not apply.

`'Distance'`

A string or a function handle specifying the default distance metric used when you call `knnsearch` or `rangesearch` to find nearest neighbors for future query points. If you specify a distance metric but not an `NSMethod`, this input determines the type of object `createns` creates, according to the default values described in `NSMethod`.

For both `KDTreeSearcher` and `ExhaustiveSearcher` models, the following options apply:

- `'euclidean'` (default) — Euclidean distance.
- `'cityblock'` — City block distance.
- `'chebychev'` — Chebychev distance (maximum coordinate difference).
- `'minkowski'` — Minkowski distance.

The following options apply to `ExhaustiveSearcher` models:

- `'seuclidean'` — Standardized Euclidean distance. Each coordinate difference between rows in `X` and the query matrix is scaled by dividing by the corresponding element of the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use the `Scale` argument.
- `'mahalanobis'` — Mahalanobis distance, which is computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of `X`, as computed by `nancov(X)`. To change the value of `C`, use the `Cov` parameter.
- `'cosine'` — One minus the cosine of the included angle between observations (treated as vectors).

- `'correlation'` — One minus the sample linear correlation between observations (treated as sequences of values).
- `'spearman'` — One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
- `'hamming'` — Hamming distance, which is percentage of coordinates that differ.
- `'jaccard'` — One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.
- custom distance function — A distance function specified using `@` (for example, `@distfun`). A distance function must be of the form `function D2 = distfun(ZI, ZJ)`, taking as arguments a 1-by-n vector `ZI` containing a single row from `X` or from the query points `Y`, and an m2-by-n matrix `ZJ` containing multiple rows of `X` or `Y`, and returning an m2-by-1 vector of distances d2, whose jth element is the distance between the observations `ZI` and `ZJ(`j`,:)`.

`'P'`

A positive scalar, p, indicating the exponent of the Minkowski distance. This parameter is only valid when `Distance` is `'minkowski'`. Default is 2.

`'Cov'`

A positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This parameter is only valid when `Distance` is `'mahalanobis'`. Default is `nancov(X)`.

`'Scale'`

A vector `S` with the length equal to the number of columns in `X`. Each coordinate of `X` and each query point is scaled by the corresponding element of `S` when computing the standardized Euclidean distance. This parameter is only valid when `Distance` is `'seuclidean'`. Default is `nanstd(X)`.

`'BucketSize'`

A positive integer, indicating the maximum number of data points in each leaf node of the Kd-tree. This argument is only meaningful when using the Kd-tree search method. Default is 50.

Examples

Grow a *K* d-tree Using the Minkowski Distance Metric

Grow a *K* d-tree that uses the Minkowski distance with an exponent of five.

Load Fisher's iris data set. Create a variable for the petal dimensions.

```
load fisheriris
x = meas(:,3:4);
```

Grow a *K* d-tree. Specify the Minkowski distance with an exponent of five.

```
Mdl = createns(x,'Distance','minkowski','P',5)
```

```
Mdl =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'minkowski'
    DistParameter: 5
                X: [150x2 double]
```

Since `x` has two columns and the distance metric is Minkowski, `createns` creates a `KDTreeSearcher` model by default.

More About

- Using ExhaustiveSearcher Objects
- Using KDTreeSearcher Objects
- “*k*-Nearest Neighbor Search and Radius Search” on page 16-11

See Also

`ExhaustiveSearcher` | `KDTreeSearcher` | `knnsearch` | `rangesearch`

crosstab

Cross-tabulation

Syntax

```
tbl = crosstab(x1,x2)
tbl = crosstab(x1,...,xn)
[tbl,chi2,p] = crosstab( ___ )
[tbl,chi2,p,labels] = crosstab( ___ )
```

Description

`tbl = crosstab(x1,x2)` returns a cross-tabulation, tbl, of two vectors of the same length, x1 and x2.

`tbl = crosstab(x1,...,xn)` returns a multi-dimensional cross-tabulation, tbl, of data for multiple input vectors, `x1`, `x2`, ..., `xn`.

`[tbl,chi2,p] = crosstab( ___ )` also returns the chi-square statistic, chi2, and its *p*-value, p, for a test that tbl is independent in each dimension. You can use any of the previous syntaxes.

`[tbl,chi2,p,labels] = crosstab( ___ )` also returns a cell array, `labels`, which contains one column of labels for each input argument, `x1` ... `xn`.

Examples

Cross-Tabulate Two Data Vectors

Create two sample data vectors, containing three and four distinct values, respectively.

```
x = [1 1 2 3 1];
y = [1 2 5 3 1];
```

Cross-tabulate `x` and `y`.

```
table = crosstab(x,y)


table =

     2     1     0     0
     0     0     0     1
     0     0     1     0
```

The rows in `table` correspond to the three distinct values in `x`, and the columns correspond to the four distinct values in `y`.

Cross-Tabulate Independent Data Vectors

Generate two independent vectors, `x1` and `x2`, each containing 50 discrete uniform random numbers in the range `1:3`.

```
rng default;  % for reproducibility
x1 = unidrnd(3,50,1);
x2 = unidrnd(3,50,1);
```

Cross-tabulate `x1` and `x2`.

```
[table,chi2,p] = crosstab(x1,x2)


table =

     1     6     7
     5     5     2
    11     7     6


chi2 =

    7.5449


p =

    0.1097
```

The returned `p` value of `0.1097` indicates that, at the 5% significance level, `crosstab` fails to reject the null hypothesis that `table` is independent in each dimension.

Cross-Tabulate Grouped Data

Load the sample data, which contains measurements of large model cars during the years 1970-1982.

```
load carbig
```

Cross-tabulate the data of four-cylinder cars (`cyl4`) based on model year (`when`) and country of origin (`org`).

```
[table,chi2,p,labels] = crosstab(cyl4,when,org);
```

Use `labels` to determine the index location in `table` for the number of four-cylinder cars made in the USA during the late period of the data.

```
labels
```

```
labels =

    'Other'    'Early'    'USA'
    'Four'     'Mid'      'Europe'
         []    'Late'     'Japan'
```

The first column of `labels` corresponds to the data in `cyl4`, and indicates that row `2` of `table` contains data on cars with four cylinders. The second column of `labels` corresponds to the data in `when`, and indicates that column `3` of `table` contains data on cars made during the late period. The third column of `labels` corresponds to the data in `org`, and indicates that location `1` of the third dimension of `table` contains data on cars made in the USA.

Therefore, `table(2,3,1)` contains the number of four-cylinder cars made in the USA during the late period.

```
table(2,3,1)
```

```
ans =

    38
```

The data contains 38 four-cylinder cars made in the USA during the late period.

Generate Contingency Table Using `crosstab`

Load the hospital data.

```
load hospital
```

The `hospital` dataset array contains data on 100 hospital patients, including last name, gender, age, weight, smoking status, and systolic and diastolic blood pressure measurements.

To determine whether smoking status is independent of gender, use `crosstab` to create a 2-by-2 contingency table of smokers and nonsmokers, grouped by gender.

```
[tbl,chi2,p,labels] = crosstab(hospital.Sex, hospital.Smoker)
```

```
tbl =

    40    13
    26    21


chi2 =

    4.5083


p =

    0.0337


labels =

    'Female'    '0'
    'Male'      '1'
```

The rows of the resulting contingency table `tbl` correspond to the patient's gender, with row 1 containing data for females and row 2 containing data for males. The columns correspond to the patient's smoking status, with column 1 containing data for nonsmokers and column 2 containing data for smokers. The returned result `chi2 =`

`4.5083` is the value of the chi-squared test statistic for a Pearson's chi-squared test of independence. The returned value `p = 0.0337` is an approximate *p*-value based on the chi-squared distribution.

Input Arguments

`x1` — Input vector
vector of grouping variables

Input vector, specified as a vector of grouping variables. All input vectors, including x1, x2, ..., `xn`, must be the same length.

Data Types: `single` | `double` | `char` | `logical`

`x2` — Input vector
vector of grouping variables

Input vector, specified as a vector of grouping variables. All input vectors, including x1, x2, ..., `xn`, must be the same length.

Data Types: `single` | `double` | `char` | `logical`

`x1,...,xn` — Input vectors
vectors of grouping variables

Input vectors, specified as vectors of grouping variables. If you use this syntax to specify more than two input vectors, then `crosstab` generates a multi-dimensional cross-tabulation table. All input vectors, including x1, x2, ..., `xn`, must be the same length.

Data Types: `single` | `double` | `char` | `logical`

Output Arguments

`tbl` — Cross-tabulation table
matrix of integer values

Cross-tabulation table, returned as a matrix of integer values.

If you specify two input vectors, x1 and x2, then tbl is an *m*-by-*n* matrix, where *m* is the number of distinct values in x1 and *n* is the number of distinct values in x2.

If you specify three or more input vectors, then `tbl(i,j,...,n)` is a count of indices where `grp2idx(x1)` is `i`, `grp2idx(x2)` is `j`, `grp2idx(x3)` is `k`, and so on.

`chi2` — Chi-square statistic
positive scalar value

Chi-square statistic, returned as a positive scalar value. The null hypothesis is that the proportion in any entry of `tbl` is the product of the proportions in each dimension.

`p` — *p*-Value
scalar value in the range `[0,1]`

p-value for the chi-square test statistic, returned as a scalar value in the range `[0,1]`. `crosstab` tests that `tbl` is independent in each dimension.

`labels` — Data labels
cell array

Data labels, returned as a cell array. The entries in the first column are labels for the rows of `tbl`, the entries in the second column are labels for the columns, and so on, for a multi-dimensional `tbl`.

More About

Algorithms

`crosstab` uses `grp2idx` to assign a positive integer to each distinct value. `tbl(i,j)` is a count of indices where `grp2idx(x1)` is `i` and `grp2idx(x2)` is `j`. The numerical order of `grp2idx(x1)` and `grp2idx(x2)` order rows and columns of `tbl`, respectively.

In this case, the returned value of `tbl(i,j,...,n)` is a count of indices where `grp2idx(x1)` is `i`, `grp2idx(x2)` is `j`, `grp2idx(x3)` is `k`, and so on.

- "Grouping Variables" on page 2-52

See Also
`grp2idx` | `tabulate`

crossval

Loss estimate using cross validation

Syntax

```
vals = crossval(fun,X)
vals = crossval(fun,X,Y,...)
mse = crossval('mse',X,y,'Predfun',predfun)
mcr = crossval('mcr',X,y,'Predfun',predfun)
val = crossval(criterion,X1,X2,...,y,'Predfun',predfun)
vals = crossval(...,'name',value)
```

Description

`vals = crossval(fun,X)` performs 10-fold cross validation for the function `fun`, applied to the data in `X`.

`fun` is a function handle to a function with two inputs, the training subset of `X`, `XTRAIN`, and the test subset of `X`, `XTEST`, as follows:

```
testval = fun(XTRAIN,XTEST)
```

Each time it is called, `fun` should use `XTRAIN` to fit a model, then return some criterion `testval` computed on `XTEST` using that fitted model.

`X` can be a column vector or a matrix. Rows of `X` correspond to observations; columns correspond to variables or features. Each row of `vals` contains the result of applying `fun` to one test set. If `testval` is a non-scalar value, `crossval` converts it to a row vector using linear indexing and stored in one row of `vals`.

`vals = crossval(fun,X,Y,...)` is used when data are stored in separate variables `X`, `Y`, ... All variables (column vectors, matrices, or arrays) must have the same number of rows. `fun` is called with the training subsets of `X`, `Y`, ... , followed by the test subsets of `X`, `Y`, ... , as follows:

```
testvals = fun(XTRAIN,YTRAIN,...,XTEST,YTEST,...)
```

`mse = crossval('mse',X,y,'Predfun',predfun)` returns `mse`, a scalar containing a 10-fold cross validation estimate of mean-squared error for the function `predfun`. `X` can

be a column vector, matrix, or array of predictors. `y` is a column vector of response values. `X` and `y` must have the same number of rows.

`predfun` is a function handle called with the training subset of `X`, the training subset of `y`, and the test subset of `X` as follows:

```
yfit = predfun(XTRAIN,ytrain,XTEST)
```

Each time it is called, `predfun` should use `XTRAIN` and `ytrain` to fit a regression model and then return fitted values in a column vector `yfit`. Each row of `yfit` contains the predicted values for the corresponding row of `XTEST`. `crossval` computes the squared errors between `yfit` and the corresponding response test set, and returns the overall mean across all test sets.

`mcr = crossval('mcr',X,y,'Predfun',predfun)` returns `mcr`, a scalar containing a 10-fold cross validation estimate of misclassification rate (the proportion of misclassified samples) for the function `predfun`. The matrix `X` contains predictor values and the vector `y` contains class labels. `predfun` should use `XTRAIN` and `YTRAIN` to fit a classification model and return `yfit` as the predicted class labels for `XTEST`. `crossval` computes the number of misclassifications between `yfit` and the corresponding response test set, and returns the overall misclassification rate across all test sets.

`val = crossval(`*`criterion`*`,X1,X2,...,y,'Predfun',predfun)`, where *`criterion`* is `'mse'` or `'mcr'`, returns a cross validation estimate of mean-squared error (for a regression model) or misclassification rate (for a classification model) with predictor values in `X1`, `X2`, ... and, respectively, response values or class labels in `y`. `X1`, `X2`, ... and `y` must have the same number of rows. `predfun` is a function handle called with the training subsets of `X1`, `X2`, ..., the training subset of `y`, and the test subsets of `X1`, `X2`, ..., as follows:

```
yfit=predfun(X1TRAIN,X2TRAIN,...,ytrain,X1TEST,X2TEST,...)
```

`yfit` should be a column vector containing the fitted values.

`vals = crossval(...,'`*`name`*`,`*`value`*`)` specifies one or more optional parameter name/value pairs from the following table. Specify *`name`* inside single quotes.

Name	Value
`holdout`	A scalar specifying the ratio or the number of observations `p` for holdout cross validation. When `0 < p < 1`, approximately `p*n` observations for the test set are randomly selected. When

Name	Value
	`p` is an integer, `p` observations for the test set are randomly selected.
`kfold`	A scalar specifying the number of folds `k` for `k`-fold cross validation.
`leaveout`	Specifies leave-one-out cross validation. The value must be `1`.
`mcreps`	A positive integer specifying the number of Monte-Carlo repetitions for validation. Ifthe first input of `crossval` is `'mse'` or `'mcr'`, `crossval` returns the mean of mean-squared error or misclassification rate across all of the Monte-Carlo repetitions. Otherwise, `crossval` concatenates the values `vals` from all of the Monte-Carlo repetitions along the first dimension.
`partition`	An object `c` of the `cvpartition` class, specifying the cross validation type and partition.
`stratify`	A column vector `group` specifying groups for stratification. Both training and test sets have roughly the same class proportions as in `group`. `NaN`s or empty strings in `group` are treated as missing values, and the corresponding rows of the data are ignored.
`options`	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the `options` structure with `statset`. Option fields: • `UseParallel` — Set to `true` to compute in parallel. Default is `false`. • `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `crossval` uses the default stream.

Only one of `kfold`, `holdout`, `leaveout`, or `partition` can be specified, and `partition` cannot be specified with `stratify`. If both `partition` and `mcreps` are specified,

the first Monte-Carlo repetition uses the partition information in the `cvpartition` object, and the `repartition` method is called to generate new partitions for each of the remaining repetitions. If no cross validation type is specified, the default is 10-fold cross validation.

Note: When using cross validation with classification algorithms, stratification is preferred. Otherwise, some test sets may not include observations from all classes.

Examples

Example 1

Compute mean-squared error for regression using 10-fold cross validation:

```
load('fisheriris');
y = meas(:,1);
X = [ones(size(y,1),1),meas(:,2:4)];

regf=@(XTRAIN,ytrain,XTEST)(XTEST*regress(ytrain,XTRAIN));

cvMse = crossval('mse',X,y,'predfun',regf)
cvMse =
    0.1015
```

Example 2

Compute misclassification rate using stratified 10-fold cross validation:

```
load('fisheriris');
y = species;
X = meas;
cp = cvpartition(y,'k',10); % Stratified cross-validation

classf = @(XTRAIN, ytrain,XTEST)(classify(XTEST,XTRAIN,...
ytrain));

cvMCR = crossval('mcr',X,y,'predfun',classf,'partition',cp)
cvMCR =
    0.0200
```

Example 3

Compute the confusion matrix using stratified 10-fold cross validation:

```
load('fisheriris');
y = species;
X = meas;
order = unique(y); % Order of the group labels
cp = cvpartition(y,'k',10); % Stratified cross-validation

f = @(xtr,ytr,xte,yte)confusionmat(yte,...
classify(xte,xtr,ytr),'order',order);

cfMat = crossval(f,X,y,'partition',cp);
cfMat = reshape(sum(cfMat),3,3)
cfMat =
    50     0     0
     0    48     2
     0     1    49
```

`cfMat` is the summation of 10 confusion matrices from 10 test sets.

More About

- “Grouping Variables” on page 2-52

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*. New York: Springer, 2001.

See Also

`cvpartition`

crossval

Class: ClassificationDiscriminant

Cross-validated discriminant analysis classifier

Syntax

```
cvmodel = crossval(obj)
cvmodel = crossval(obj,Name,Value)
```

Description

`cvmodel = crossval(obj)` creates a partitioned model from `obj`, a fitted discriminant analysis classifier. By default, `crossval` uses 10-fold cross validation on the training data to create `cvmodel`.

`cvmodel = crossval(obj,Name,Value)` creates a partitioned model with additional options specified by one or more Name,Value pair arguments.

Tips

- Assess the predictive performance of `obj` on cross-validated data using the "kfold" methods and properties of cvmodel, such as `kfoldLoss`.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'`

Object of class `cvpartition`, created by the `cvpartition` function. `crossval` splits the data into subsets with `cvpartition`.

Use only one of these options at a time: `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`.

Default: [ ]

`'Holdout'`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. Use only one of these options at a time: `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`.

`'KFold'`

Number of folds to use in a cross-validated classifier, a positive integer.

Use only one of these options at a time: `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`.

Default: 10

`'Leaveout'`

Set to `'on'` for leave-one-out cross validation.

Use only one of these options at a time: `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`.

Examples

Create a classification model for the Fisher iris data, and then create a cross-validation model. Evaluate the quality the model using `kfoldLoss`.

```
load fisheriris
```

```
obj = fitcdiscr(meas,species);
cvmodel = crossval(obj);
L = kfoldLoss(cvmodel)

L =
    0.0200
```

Alternatives

You can create a cross-validation classifier directly from the data, instead of creating a discriminant analysis classifier followed by a cross-validation classifier. To do so, include one of these options in `fitcdiscr`: `'CrossVal'`, `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`.

See Also

`kfoldEdge` | `kfoldfun` | `kfoldLoss` | `kfoldMargin` | `fitcdiscr` | `crossval` | `kfoldPredict`

How To

- “Discriminant Analysis” on page 15-3

crossval

Class: ClassificationECOC

Cross-validated, error-correcting output code multiclass model

Syntax

```
CVMdl = crossval(Mdl)
CVMdl = crossval(Mdl,Name,Value)
```

Description

`CVMdl = crossval(Mdl)` returns a cross-validated (partitioned), error-correcting output codes (ECOC) multiclass model (`CVMdl`) from a trained ECOC model (`Mdl`).

By default, `crossval` uses 10-fold cross validation on the training data to create `CVMdl`.

`CVMdl = crossval(Mdl,Name,Value)` returns a partitioned ECOC model with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the number of folds or a holdout sample proportion.

Tips

Assess the predictive performance of `Mdl` on cross-validated data using the kfold functions and properties of CVMdl, such as `kfoldLoss`.

Input Arguments

`Mdl` — ECOC multiclass model

`ClassificationECOC` model

ECOC multiclass model, specified as a `ClassificationECOC` model returned by `fitcecoc`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'` — Cross-validation partition

`[ ]` (default) | `cvpartition` partition object

Cross-validation partition, specified as the comma-separated pair consisting of `'CVPartition'` and a `cvpartition` partition object as created by `cvpartition`. The partition object specifies the type of cross-validation, and also the indexing for training and validation sets.

If you specify `CVPartition`, then you cannot specify any of Holdout, KFold, or Leaveout.

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). If you specify `'Holdout',`*p*, then the software:

1. Randomly reserves *p*`*100`% of the data as validation data, and trains the model using the rest of the data
2. Stores the compact, trained model in CVMdl`.Trained`

If you specify `Holdout`, then you cannot specify any of CVPartition, KFold, or Leaveout.

Example: `'Holdout',0.1`

Data Types: `double | single`

`'KFold'` — Number of folds

10 (default) | positive integer value

Number of folds to use in a cross-validated classifier, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value. If you specify, e.g., `'KFold',`*k*, then the software:

1. Randomly partitions the data into *k* sets

2 For each set, reserves the set as validation data, and trains the model using the other $k - 1$ sets

3 Stores the k compact, trained models in the cells of a k-by-1 cell vector in CVMdl.Trained

If you specify KFold, then you cannot specify any of CVPartition, Holdout, or Leaveout.

Example: 'KFold',8

Data Types: double

'Leaveout' — Leave-one-out cross-validation flag

'off' (default) | 'on'

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of 'Leaveout' and 'on' or 'off'. If you specify 'Leaveout','on', then, for each of the n observations, where n is size(Mdl.X,1), the software:

1 Reserves the observation as validation data, and trains the model using the other $n - 1$ observations

2 Stores the n compact, trained models in CVMdl.Trained

If you specify Leaveout, then you cannot specify CVPartition, Holdout, or KFold.

Example: 'Leaveout','on'

Data Types: char

'Options' — Estimation options

[ ] (default) | structure array returned by statset

Estimation options, specified as the comma-separated pair consisting of 'Options' and a structure array returned by statset.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify 'Options',statset('UseParallel',1).

Output Arguments

CVMdl — Cross-validated ECOC model

ClassificationPartitionedECOC model

Cross-validated ECOC model, returned as a `ClassificationPartitionedECOC` model.

Examples

Cross Validate an ECOC Classifier

Train a one-versus-one ECOC classifier using binary SVM learners.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
rng(1); % For reproducibility
```

Create an SVM template. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1)
```

```
t =

Fit template for classification SVM.

                    Alpha: [0x1 double]
          BoxConstraint: []
              CacheSize: []
          CachingMethod: ''
    DeltaGradientTolerance: []
           GapTolerance: []
           KKTTolerance: []
         IterationLimit: []
         KernelFunction: ''
            KernelScale: []
           KernelOffset: []
     KernelPolynomialOrder: []
                NumPrint: []
                      Nu: []
        OutlierFraction: []
        ShrinkagePeriod: []
                 Solver: ''
        StandardizeData: 1
      SaveSupportVectors: []
```

```
    VerbosityLevel: []
            Method: 'SVM'
              Type: 'classification'
```

`t` is an SVM template. All of its properties are empty, except for `StandardizeData`, `Method`, and `Type`. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier. It is good practice to specify the class order.

```
Mdl = fitcecoc(X,Y,'Learners',t,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationECOC` classifier. You can access its properties using dot notation.

Cross validate `Mdl` using 10-fold cross validation.

```
CVMdl = crossval(Mdl);
```

`CVMdl` is a `ClassificationPartitionedECOC` cross-validated ECOC classifier.

Estimate the generalization error.

```
oosLoss = kfoldLoss(CVMdl)
```

```
oosLoss =

    0.0400
```

The out-of-sample classification error is 4%, which indicates that the ECOC classifier generalizes fairly well.

Cross Validate an ECOC Classifier Using Parallel Computing

Consider the `arrhythmia` data set. There are 16 classes in the study, 13 of which are represented in the data. The first class indicates that the subject did not have arrhythmia, and the last class indicates that the subject's arrhythmia state was not recorded. Suppose that the other classes are ordinal levels indicating the severity of arrhythmia.

Train an ECOC classifier with a custom coding design specified by the description of the classes.

Load the `arrhythmia` data set.

```
load arrhythmia
Y = categorical(Y);
K = unique(Y); % Number of distinct classes
```

Construct a coding matrix that describes the nature of the classes.

```
OrdMat = designecoc(11,'ordinal');
nOM = size(OrdMat);
class1VSOrd = [1; -ones(11,1); 0];
class1VSClass16 = [1; zeros(11,1); -1];
OrdVSClass16 = [0; ones(11,1); -1];
Coding = [class1VSOrd class1VSClass16 OrdVSClass16,...
    [zeros(1,nOM(2)); OrdMat; zeros(1,nOM(2))]];
```

Train an ECOC classifier using the custom coding design (`Coding`) and parallel computing. Specify to use an ensemble of 50 classification trees boosted using GentleBoost.

```
t = templateEnsemble('GentleBoost',50,'Tree');
options = statset('UseParallel',1);
Mdl = fitcecoc(X,Y,'Coding',Coding,'Learners',t,'Options',options);
```

`Mdl` is a `ClassificationECOC` model. You can access its properties using dot notation.

Cross validate `Mdl` using 8-fold cross validation and parallel computing.

```
rng(1); % For reproducibility
CVMdl = crossval(Mdl,'Options',options,'KFold',8);
```

```
Warning: One or more folds do not contain points from all the groups.
```

Since some of the classes have low relative frequency, some of the folds do not train using observations from those classes. `CVMdl` is a `ClassificationPartitionedECOC` cross-validated ECOC model.

Estimate the generalization error using parallel computing.

```
oosLoss = kfoldLoss(CVMdl,'Options',options)
```

```
oosLoss =
```

```
0.3208
```

The out-of-sample classification error is 32%, which indicates that this model does not generalize well. To improve the model, try training using a different boosting method, such as RobustBoost, or a different algorithm altogether, such as SVM.

- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

Alternatives

Instead of training an ECOC model and then cross validating it, you can create a cross-validated ECOC model directly using `fitcecoc` and by specifying any of these name-value pair arguments: CrossVal, CVPartition, Holdout, Leaveout, or KFold.

See Also

`ClassificationECOC` | `ClassificationPartitionedECOC` | `CompactClassificationECOC` | `cvpartition` | `fitcecoc` | `statset`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

crossval

Class: ClassificationEnsemble

Cross validate ensemble

Syntax

```
cvens = crossval(ens)
cvens = crossval(ens,Name,Value)
```

Description

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a classification ensemble. Default is 10-fold cross validation.

`cvens = crossval(ens,Name,Value)` creates a cross-validated ensemble with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'cvpartition'`

A partition of class `cvpartition`. Sets the partition for cross validation.

Use no more than one of the name-value pairs `cvpartition`, `holdout`, `kfold`, or `leaveout`.

`'holdout'`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'kfold'`

Number of folds for cross validation, a numeric positive scalar.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'leaveout'`

If `'on'`, use leave-one-out cross validation.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'nprint'`

Printout frequency, a positive integer scalar. Use this parameter to observe the training of cross-validation folds.

Default: `'off'`, meaning no printout

Output Arguments

`cvens`

A cross-validated classification ensemble of class `ClassificationPartitionedEnsemble`.

Alternatives

You can create a cross-validation ensemble directly from the data, instead of creating an ensemble followed by a cross-validation ensemble. To do so, include one of these

five options in `fitensemble`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Examples

Create a cross-validated classification model for the Fisher iris data, and assess its quality using the `kfoldLoss` method.

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)

L =
    0.0467
```

See Also

`ClassificationPartitionedEnsemble` | `cvpartition`

crossval

Class: ClassificationKNN

Cross-validated *k*-nearest neighbor classifier

Syntax

```
cvmodel = crossval(mdl)
cvmodel = crossval(mdl,Name,Value)
```

Description

`cvmodel = crossval(mdl)` creates a partitioned model from `mdl`, a fitted KNN classification model. By default, `crossval` uses 10-fold cross validation on the training data to create `cvmodel`.

`cvmodel = crossval(mdl,Name,Value)` creates a partitioned model with additional options specified by one or more Name,Value pair arguments.

Tips

- Assess the predictive performance of `mdl` on cross-validated data using the "kfold" methods and properties of cvmodel, such as `kfoldLoss`.

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class

`ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'`

Object of class `cvpartition`, created by the `cvpartition` function. `crossval` splits the data into subsets with `cvpartition`.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'Holdout'`

Holdout validation tests the specified fraction of the data, and uses the remaining data for training. Specify a numeric scalar from `0` to `1`. Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'KFold'`

Number of folds to use in a cross-validated tree, a positive integer.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Default: 10

`'Leaveout'`

Set to `'on'` for leave-one-out cross validation.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Output Arguments

`cvmodel`

Partitioned model of class `ClassificationPartitionedModel`.

Examples

Cross-Validated *K*-Nearest Neighbor Model

Construct a cross-validated k-nearest neighbor model, and assess classification performance using the model.

Load the data.

```
load fisheriris
X = meas;
Y = species;
```

Construct a classifier for nearest neighbors.

```
mdl = fitcknn(X,Y);
```

Construct a cross-validated classifier.

```
cvmdl = crossval(mdl)
```

```
cvmdl =

classreg.learning.partition.ClassificationPartitionedModel:
      CrossValidatedModel: 'KNN'
           PredictorNames: {'x1'  'x2'  'x3'  'x4'}
    CategoricalPredictors: []
             ResponseName: 'Y'
          NumObservations: 150
                    KFold: 10
                Partition: [1x1 cvpartition]
               ClassNames: {'setosa'  'versicolor'  'virginica'}
           ScoreTransform: 'none'
```

Find the cross-validated loss of the classifier.

```
cvmdlloss = kfoldLoss(cvmdl)
```

```
cvmdlloss =

    0.0400
```

The cross-validated loss is less than 5%. You can expect `mdl` to have a similar error rate.

- "Examine the Quality of a KNN Classifier" on page 16-29
- "Modify a KNN Classifier" on page 16-30

Alternatives

You can create a cross-validated model directly from the data, instead of creating a model followed by a cross-validated model. To do so, include one of these options in `fitcknn`: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

See Also

`ClassificationKNN` | `ClassificationPartitionedModel` | `crossval` | `fitcknn` | `kfoldEdge` | `kfoldfun` | `kfoldLoss` | `kfoldMargin` | `kfoldPredict`

More About

- "Classification Using Nearest Neighbors" on page 16-8

crossval

Class: ClassificationNaiveBayes

Cross-validated naive Bayes classifier

Syntax

```
CVMdl = crossval(Mdl)
CVMdl = crossval(Mdl,Name,Value)
```

Description

`CVMdl = crossval(Mdl)` returns a partitioned naive Bayes classifier (`CVSMdl`) from a trained naive Bayes classifier (`Mdl`).

By default, `crossval` uses 10-fold cross validation on the training data to create `CVMdl`.

`CVMdl = crossval(Mdl,Name,Value)` returns a partitioned naive Bayes classifier with additional options specified by one or more Name,Value pair arguments.

For example, you can specify a holdout sample proportion.

Tips

Assess the predictive performance of `Mdl` on cross-validated data using the "kfold" function and properties of CVMdl, such as `kfoldLoss`.

Input Arguments

`Mdl` — Fully trained naive Bayes classifier

`ClassificationNaiveBayes` model

A fully trained naive Bayes classifier, specified as a `ClassificationNaiveBayes` model trained by `fitcnb`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'` — Cross-validation partition

`[ ]` (default) | `cvpartition` partition object

Cross-validation partition, specified as the comma-separated pair consisting of `'CVPartition'` and a `cvpartition` partition object as created by `cvpartition`. The partition object specifies the type of cross-validation, and also the indexing for training and validation sets.

If you specify `CVPartition`, then you cannot specify any of Holdout, KFold, or Leaveout.

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). If you specify `'Holdout',`*p*, then the software:

1. Randomly reserves *p*`*100`% of the data as validation data, and trains the model using the rest of the data
2. Stores the compact, trained model in CVMdl`.Trained`

If you specify `Holdout`, then you cannot specify any of CVPartition, KFold, or Leaveout.

Example: `'Holdout',0.1`

Data Types: `double | single`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated classifier, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value. If you specify, e.g., `'KFold',`*k*, then the software:

1. Randomly partitions the data into *k* sets

2 For each set, reserves the set as validation data, and trains the model using the other $k - 1$ sets

3 Stores the k compact, trained models in the cells of a k-by-1 cell vector in CVMdl.Trained

If you specify KFold, then you cannot specify any of CVPartition, Holdout, or Leaveout.

Example: 'KFold',8

Data Types: double

'Leaveout' — Leave-one-out cross-validation flag

'off' (default) | 'on'

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of 'Leaveout' and 'on' or 'off'. If you specify 'Leaveout','on', then, for each of the n observations, where n is size(Mdl.X,1), the software:

1 Reserves the observation as validation data, and trains the model using the other $n - 1$ observations

2 Stores the n compact, trained models in CVMdl.Trained

If you specify Leaveout, then you cannot specify CVPartition, Holdout, or KFold.

Example: 'Leaveout','on'

Data Types: char

Output Arguments

CVMdl — Cross-validated naive Bayes classifier

ClassificationPartitionedModel model

Cross-validated naive Bayes classifier, returned as a ClassificationPartitionedModel model.

Examples

Cross Validate a Naive Bayes Classifier Using crossval

Load the ionosphere data set.

```
load ionosphere
X = X(:,3:end); % Remove first two predictors for stability
rng(1);         % For reproducibility
```

Train a naive Bayes classifier. It is good practice to define the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
Mdl = fitcnb(X,Y,'ClassNames',{'b','g'});
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier. `'b'` is the negative class and `'g'` is the positive class.

Cross validate the classifier using 10-fold cross validation.

```
CVMdl = crossval(Mdl)
FirstModel = CVMdl.Trained{1}
```

```
CVMdl =

  classreg.learning.partition.ClassificationPartitionedModel
    CrossValidatedModel: 'NaiveBayes'
         PredictorNames: {1x32 cell}
           ResponseName: 'Y'
        NumObservations: 351
                  KFold: 10
              Partition: [1x1 cvpartition]
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'



FirstModel =

  classreg.learning.classif.CompactClassificationNaiveBayes
            PredictorNames: {1x32 cell}
              ResponseName: 'Y'
                ClassNames: {'b'  'g'}
            ScoreTransform: 'none'
         DistributionNames: {1x32 cell}
    DistributionParameters: {2x32 cell}
```

`CVMdl` is a `ClassificationPartitionedModel` cross-validated classifier. The software:

1. Randomly partitions the data into 10, equally sized sets.
2. Trains a naive Bayes classifier on nine of the sets.
3. Repeats steps 1 and 2 $k = 10$ times. It excludes one partition each time, and trains on the other nine partitions.
4. Combines generalization statistics for each fold.

`FirstModel` is the first of the 10 trained classifiers. It is a `CompactClassificationNaiveBayes` model.

You can estimate the generalization error by passing `CVMdl` to `kfoldLoss`.

Specify a Holdout-Sample Proportion for Naive Bayes Cross Validation

By default, `crossval` uses 10-fold cross validation to cross validate a naive Bayes classifier. You have several other options, such as specifying a different number of folds or holdout-sample proportion. This example shows how to specify a holdout-sample proportion.

Load the `ionosphere` data set.

```
load ionosphere
X = X(:,3:end); % Remove first two predictors for stability
rng(1);         % For reproducibility
```

Train a naive Bayes classifier. Assume that each predictor is conditionally, normally distributed given its label. It is good practice to define the class order.

```
Mdl = fitcnb(X,Y,'ClassNames',{'b','g'});
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier. `'b'` is the negative class and `'g'` is the positive class.

Cross validate the classifier by specifying a 30% holdout sample.

```
CVMdl = crossval(Mdl,'Holdout',0.30)
TrainedModel = CVMdl.Trained{1}
```

```
CVMdl =
```

```
  classreg.learning.partition.ClassificationPartitionedModel
    CrossValidatedModel: 'NaiveBayes'
         PredictorNames: {1x32 cell}
           ResponseName: 'Y'
        NumObservations: 351
                  KFold: 1
              Partition: [1x1 cvpartition]
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'


TrainedModel =

  classreg.learning.classif.CompactClassificationNaiveBayes
            PredictorNames: {1x32 cell}
              ResponseName: 'Y'
                ClassNames: {'b'  'g'}
            ScoreTransform: 'none'
          DistributionNames: {1x32 cell}
    DistributionParameters: {2x32 cell}
```

`CVMdl` is a `ClassificationPartitionedModel`. `TrainedModel` is a `CompactClassificationNaiveBayes` classifier trained using 70% of the data.

Estimate the generalization error.

```
kfoldLoss(CVMdl)
```

```
ans =

    0.2571
```

The out-of-sample misclassification error is approximately 2.6%.

Alternatives

Instead of creating a naive Bayes classifier followed by a cross-validation classifier, create a cross-validated classifier directly using `fitcnb` and by specifying any of these

name-value pair arguments: `'CrossVal'`, `'CVPartition'`, `'Holdout'`, `'Leaveout'`, or `'KFold'`.

See Also

`ClassificationNaiveBayes` | `ClassificationPartitionedModel` | `CompactClassificationNaiveBayes` | `fitcnb` | `kfoldLoss`

crossval

Class: ClassificationSVM

Cross-validated support vector machine classifier

Syntax

```
CVSVMModel = crossval(SVMModel)
CVSVMModel = crossval(SVMModel,Name,Value)
```

Description

`CVSVMModel = crossval(SVMModel)` returns a cross-validated (partitioned) support vector machine classifier (`CVSVMModel`) from a trained SVM classifier (`SVMModel`).

By default, `crossval` uses 10-fold cross validation on the training data to create `CVSVMModel`.

`CVSVMModel = crossval(SVMModel,Name,Value)` returns a partitioned SVM classifier with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the number of folds or holdout sample proportion.

Tips

Assess the predictive performance of `SVMModel` on cross-validated data using the "kfold" methods and properties of CVSVMModel, such as `kfoldLoss`.

Input Arguments

`SVMModel` — Full, trained SVM classifier

`ClassificationSVM` classifier

Full, trained SVM classifier, specified as a `ClassificationSVM` model trained using `fitcsvm`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'` — Cross-validation partition

`[ ]` (default) | `cvpartition` partition object

Cross-validation partition, specified as the comma-separated pair consisting of `'CVPartition'` and a `cvpartition` partition object as created by `cvpartition`. The partition object specifies the type of cross-validation, and also the indexing for training and validation sets.

If you specify `CVPartition`, then you cannot specify any of Holdout, KFold, or Leaveout.

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). If you specify `'Holdout',`*p*, then the software:

1. Randomly reserves *p*`*100`% of the data as validation data, and trains the model using the rest of the data
2. Stores the compact, trained model in CVMdl`.Trained`

If you specify `Holdout`, then you cannot specify any of CVPartition, KFold, or Leaveout.

Example: `'Holdout',0.1`

Data Types: `double | single`

`'KFold'` — Number of folds

10 (default) | positive integer value

Number of folds to use in a cross-validated classifier, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value. If you specify, e.g., `'KFold',`*k*, then the software:

1. Randomly partitions the data into *k* sets

2 For each set, reserves the set as validation data, and trains the model using the other $k - 1$ sets

3 Stores the k compact, trained models in the cells of a k-by-1 cell vector in CVMdl.Trained

If you specify KFold, then you cannot specify any of CVPartition, Holdout, or Leaveout.

Example: 'KFold',8

Data Types: double

'Leaveout' — Leave-one-out cross-validation flag

'off' (default) | 'on'

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of 'Leaveout' and 'on' or 'off'. If you specify 'Leaveout','on', then, for each of the n observations, where n is size(Mdl.X,1), the software:

1 Reserves the observation as validation data, and trains the model using the other $n - 1$ observations

2 Stores the n compact, trained models in CVMdl.Trained

If you specify Leaveout, then you cannot specify CVPartition, Holdout, or KFold.

Example: 'Leaveout','on'

Data Types: char

Output Arguments

CVSVMModel — Cross-validated SVM classifier

ClassificationPartitionedModel classifier

Cross-validated SVM classifier, returned as a ClassificationPartitionedModel classifier.

Examples

Cross Validate an SVM Classifier Using crossval

Load the ionosphere data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM classifier. It is good practice to standardize the predictors and define the class order.

```
SVMModel = fitcsvm(X,Y,'Standardize',true,'ClassNames',{'b','g'});
```

`SVMModel` is a trained `ClassificationSVM` classifier. `'b'` is the negative class and `'g'` is the positive class.

Cross validate the classifier using 10-fold cross validation.

```
CVSVMModel = crossval(SVMModel)
FirstModel = CVSVMModel.Trained{1}
```

```
CVSVMModel =

  classreg.learning.partition.ClassificationPartitionedModel
    CrossValidatedModel: 'SVM'
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
        NumObservations: 351
                  KFold: 10
              Partition: [1x1 cvpartition]
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'



FirstModel =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
                  Alpha: [78x1 double]
                   Bias: -0.2209
       KernelParameters: [1x1 struct]
                     Mu: [1x34 double]
                  Sigma: [1x34 double]
         SupportVectors: [78x34 double]
```

```
    SupportVectorLabels: [78x1 double]
```

`CVSVMModel` is a `ClassificationPartitionedModel` cross-validated classifier. The software:

1. Randomly partitions the data into 10, equally sized sets.
2. Trains an SVM classifier on nine of the sets.
3. Repeats steps 1 and 2 $k = 10$ times. It leaves out one of the partitions each time, and trains on the other nine partitions.
4. Combines generalization statistics for each fold.

`FirstModel` is the first of the 10 trained classifiers. It is a `CompactClassificationSVM` classifier.

You can estimate the generalization error by passing `CVSVMModel` to `kfoldLoss`.

Specify a Holdout-Sample Proportion for SVM Cross Validation

By default, `crossval` uses 10-fold cross validation to cross validate an SVM classifier. You have several other options, such as specifying a different number of folds or holdout sample proportion. This example shows how to specify a holdout-sample proportion.

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM classifier. It is good practice to standardize the predictors and define the class order.

```
SVMModel = fitcsvm(X,Y,'Standardize',true,'ClassNames',{'b','g'});
```

`SVMModel` is a trained `ClassificationSVM` classifier. `'b'` is the negative class and `'g'` is the positive class.

Cross validate the classifier by specifying a 15% holdout sample.

```
CVSVMModel = crossval(SVMModel,'Holdout',0.15)
TrainedModel = CVSVMModel.Trained{1}
```

```
CVSVMModel =

  classreg.learning.partition.ClassificationPartitionedModel
    CrossValidatedModel: 'SVM'
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
        NumObservations: 351
                  KFold: 1
              Partition: [1x1 cvpartition]
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'


TrainedModel =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
             ClassNames: {'b'  'g'}
         ScoreTransform: 'none'
                  Alpha: [74x1 double]
                   Bias: -0.2952
       KernelParameters: [1x1 struct]
                     Mu: [1x34 double]
                  Sigma: [1x34 double]
         SupportVectors: [74x34 double]
    SupportVectorLabels: [74x1 double]
```

`CVSVMModel` is a `ClassificationPartitionedModel`. `TrainedModel` is a `CompactClassificationSVM` classifier trained using 85% of the data.

Estimate the generalization error.

```
kfoldLoss(CVSVMModel)
```

```
ans =

    0.0769
```

The out-of-sample misclassification error is approximately 8%.

Alternatives

Instead of training an SVM classifier and then cross-validating it, you can create a cross-validated classifier directly using `fitcsvm` and by specifying any of these name-value pair arguments: `'CrossVal'`, `'CVPartition'`, `'Holdout'`, `'Leaveout'`, or `'KFold'`.

See Also

`ClassificationPartitionedModel` | `ClassificationSVM` | `CompactClassificationSVM` | `cvpartition` | `fitcsvm`

crossval

Class: ClassificationTree

Cross-validated decision tree

Syntax

```
cvmodel = crossval(model)
cvmodel = crossval(model,Name,Value)
```

Description

`cvmodel = crossval(model)` creates a partitioned model from `model`, a fitted classification tree. By default, `crossval` uses 10-fold cross validation on the training data to create `cvmodel`.

`cvmodel = crossval(model,Name,Value)` creates a partitioned model with additional options specified by one or more Name,Value pair arguments.

Tips

- Assess the predictive performance of `model` on cross-validated data using the "kfold" methods and properties of cvmodel, such as `kfoldLoss`.

Input Arguments

`model`

A classification model, produced using `fitctree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'`

Object of class `cvpartition`, created by the `cvpartition` function. `crossval` splits the data into subsets with `cvpartition`.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'Holdout'`

Holdout validation tests the specified fraction of the data, and uses the remaining data for training. Specify a numeric scalar from `0` to `1`. Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'KFold'`

Number of folds to use in a cross-validated tree, a positive integer.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Default: 10

`'Leaveout'`

Set to `'on'` for leave-one-out cross validation.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Output Arguments

`cvmodel`

Partitioned model of class `ClassificationPartitionedModel`.

Examples

Create a Cross-Validation Model

Create a classification model for the ionosphere data, then create a cross-validation model. Evaluate the quality the model using `kfoldLoss`.

```
load ionosphere
tree = fitctree(X,Y);
cvmodel = crossval(tree);
L = kfoldLoss(cvmodel)

L =
    0.1168
```

Alternatives

You can create a cross-validation tree directly from the data, instead of creating a decision tree followed by a cross-validation tree. To do so, include one of these five options in `fitctree`: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

See Also

`fitctree` | `crossval`

crossval

Class: RegressionEnsemble

Cross validate ensemble

Syntax

```
cvens = crossval(ens)
cvens = crossval(ens,Name,Value)
```

Description

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a regression ensemble. Default is 10-fold cross validation.

`cvens = crossval(ens,Name,Value)` creates a cross-validated ensemble with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'cvpartition'`

A partition of class `cvpartition`. Sets the partition for cross validation.

Use no more than one of the name-value pairs `cvpartition`, `holdout`, `kfold`, and `leaveout`.

`'holdout'`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'kfold'`

Number of folds for cross validation, a numeric positive scalar.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'leaveout'`

If `'on'`, use leave-one-out cross-validation.

Use no more than one of the name-value pairs `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'nprint'`

Printout frequency, a positive integer scalar. Use this parameter to observe the training of cross-validation folds.

Default: `'off'`, meaning no printout

Output Arguments

`cvens`

A cross-validated classification ensemble of class `RegressionPartitionedEnsemble`.

Alternatives

You can create a cross-validation ensemble directly from the data, instead of creating an ensemble followed by a cross-validation ensemble. To do so, include one of these

five options in `fitensemble`: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Examples

Create a cross-validated classification model for the `carsmall` data, and assess its quality using the `kfoldLoss` method:

```
X = [Acceleration Displacement Horsepower Weight];
rens = fitensemble(X,MPG,'LSBoost',100,'Tree');
cvens = crossval(rens);
L = kfoldLoss(cvens)

L =
   21.9868
```

See Also

`RegressionPartitionedEnsemble` | `cvpartition`

crossval

Class: RegressionTree

Cross-validated decision tree

Syntax

```
cvmodel = crossval(model)
cvmodel = crossval(model,Name,Value)
```

Description

`cvmodel = crossval(model)` creates a partitioned model from `model`, a fitted regression tree. By default, `crossval` uses 10-fold cross validation on the training data to create `cvmodel`.

`cvmodel = crossval(model,Name,Value)` creates a partitioned model with additional options specified by one or more Name,Value pair arguments.

Tips

- Assess the predictive performance of `model` on cross-validated data using the "kfold" methods and properties of cvmodel, such as `kfoldLoss`.

Input Arguments

`model`

A regression model, produced using `fitrtree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'`

Object of class `cvpartition`, created by the `cvpartition` function. `crossval` splits the data into subsets with `cvpartition`.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Default: `[ ]`

`'Holdout'`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'KFold'`

Number of folds to use in a cross-validated tree, a positive integer.

Use only one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Default: 10

`'Leaveout'`

Set to `'on'` for leave-one-out cross-validation.

Output Arguments

`cvmodel`

A partitioned model of class `RegressionPartitionedModel`.

Examples

Create a regression model of the `carsmall` data, and assess its accuracy with `kfoldLoss`:

```
load carsmall
X = [Acceleration Displacement Horsepower Weight];
tree = fitrtree(X,MPG);
cvtree = crossval(tree);
L = kfoldLoss(cvtree)

L =
   25.2432
```

Alternatives

You can create a cross-validation tree directly from the data, instead of creating a decision tree followed by a cross-validation tree. To do so, include one of these five options in `fitrtree`: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

See Also

`fitrtree` | `crossval`

cutcategories

Class: classregtree

Cut categories

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
C = cutcategories(t)
C = cutcategories(t,nodes)
```

Description

`C = cutcategories(t)` returns an *n*-by-2 cell array `C` of the categories used at branches in the decision tree `t`, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `C{i,1}`, and the right child is chosen if `x` is among those listed in `C{i,2}`. Both columns of `C` are empty for branch nodes based on continuous predictors and for leaf nodes.

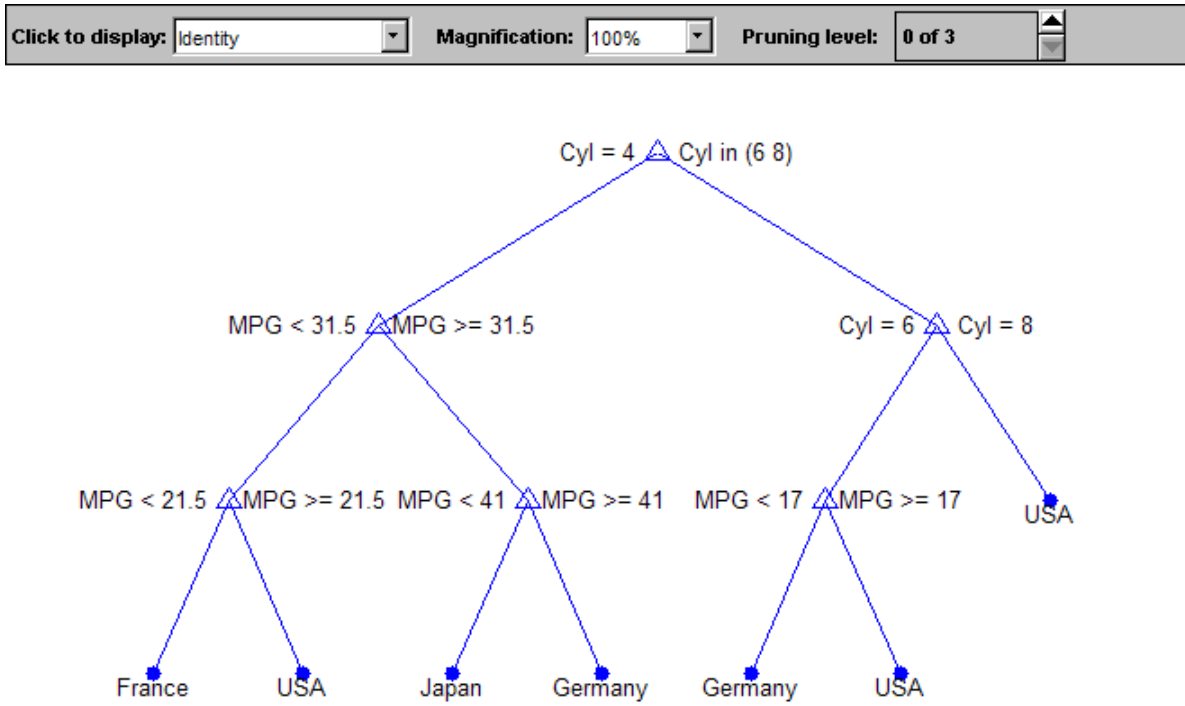
`C = cutcategories(t,nodes)` takes a vector `nodes` of node numbers and returns the categories for the specified nodes.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
                 'names',{'MPG' 'Cyl'},'cat',2)
```

```
t =
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA
view(t)
```




```
C = cutcategories(t)
C =
    [4]    [1x2 double]
```

```
     []              []
    [6]    [         8]
     []              []
     []              []
     []              []
     []              []
     []              []
     []              []
     []              []
     []              []
     []              []
     []              []
C{1,2}
ans =
     6     8
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `cuttype` | `cutpoint` | `cutvar`

cutpoint

Class: classregtree

Decision tree cut point values

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
v = cutpoint(t)
v = cutpoint(t,nodes)
```

Description

`v = cutpoint(t)` returns an *n*-element vector `v` of the values used as cut points in the decision tree `t`, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `x < v(i)` and the right child is chosen if `x >= v(i)`. `v` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

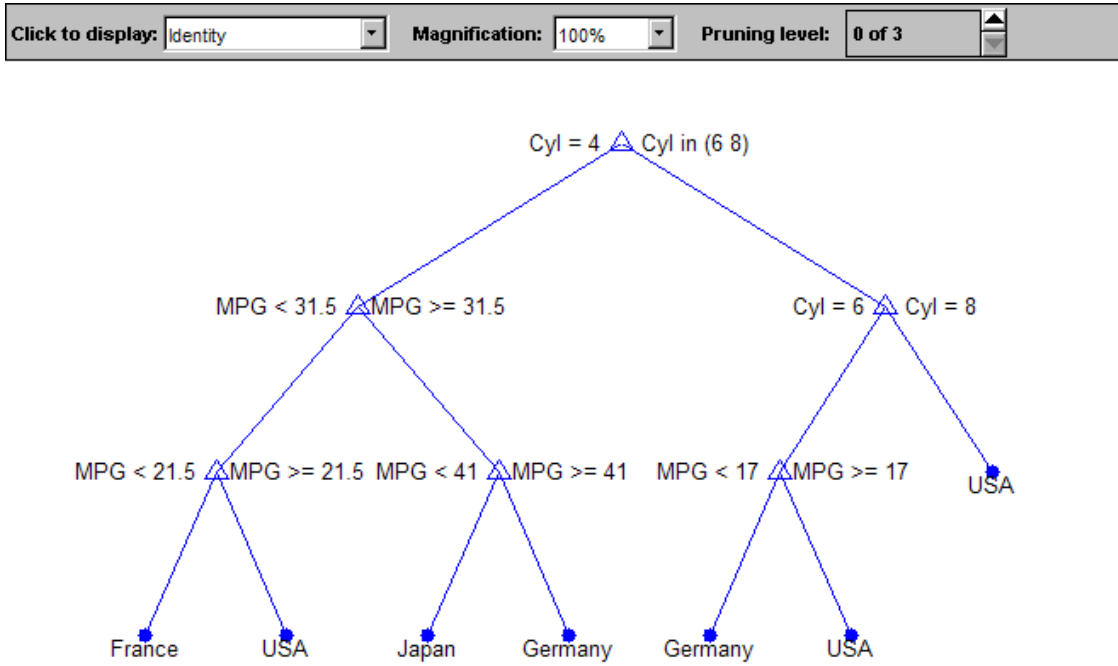
`v = cutpoint(t,nodes)` takes a vector `nodes` of node numbers and returns the cut points for the specified nodes.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
                 'names',{'MPG' 'Cyl'},'cat',2)
t =
```

```
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA

view(t)
```




```
v = cutpoint(t)
v =
       NaN
   31.5000
       NaN
```

```
21.5000
41.0000
17.0000
    NaN
    NaN
    NaN
    NaN
    NaN
    NaN
    NaN
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `cuttype` | `cutcategories` | `cutvar`

cuttype

Class: classregtree

Cut types

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
c = cuttype(t)
c = cuttype(t,nodes)
```

Description

`c = cuttype(t)` returns an *n*-element cell array `c` indicating the type of cut at each node in the tree `t`, where *n* is the number of nodes. For each node `i`, `c{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

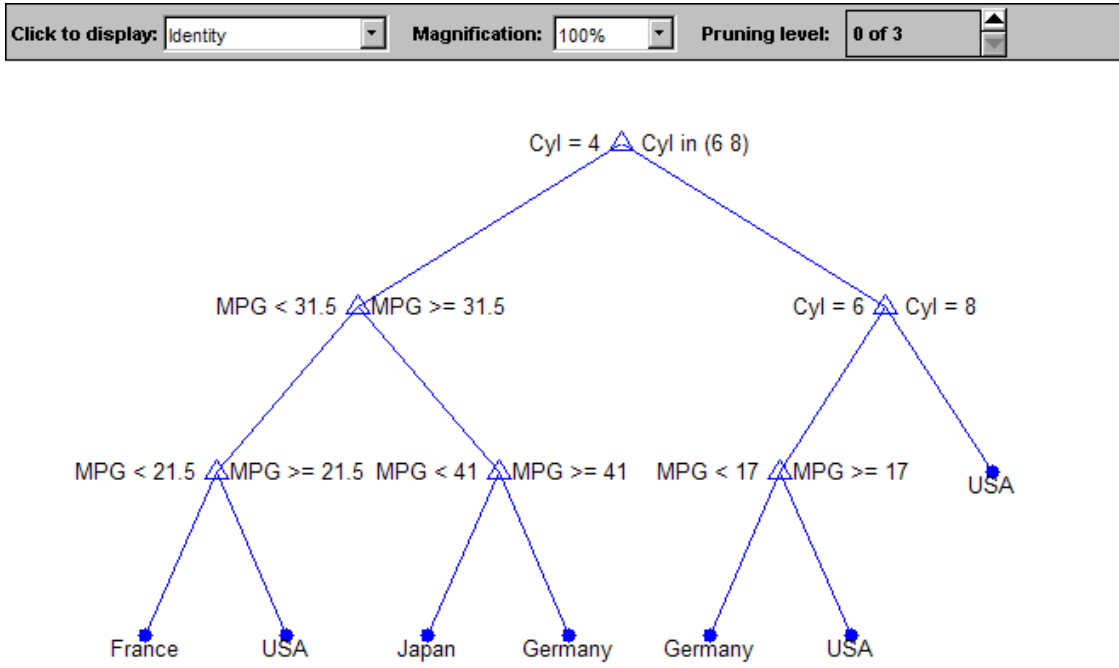
`cutvar` returns the cut points for `'continuous'` cuts, and `cutcategories` returns the set of categories.

`c = cuttype(t,nodes)` takes a vector `nodes` of node numbers and returns the cut types for the specified nodes.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
                 'names',{'MPG' 'Cyl'},'cat',2)
t =
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA
view(t)
```




```
c = cuttype(t)
```

```
c =
    'categorical'
    'continuous'
    'categorical'
    'continuous'
    'continuous'
    'continuous'
    ''
    ''
    ''
    ''
    ''
    ''
    ''
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `cutvar` | `numnodes` | `cutcategories`

cutvar

Class: classregtree

Cut variable names

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
v = cutvar(t)
v = cutvar(t,nodes)
[v,num] = cutvar(...)
```

Description

`v = cutvar(t)` returns an *n*-element cell array `v` of the names of the variables used for branching in each node of the tree `t`, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `v` contains an empty string.

`v = cutvar(t,nodes)` takes a vector `nodes` of node numbers and returns the cut variables for the specified nodes.

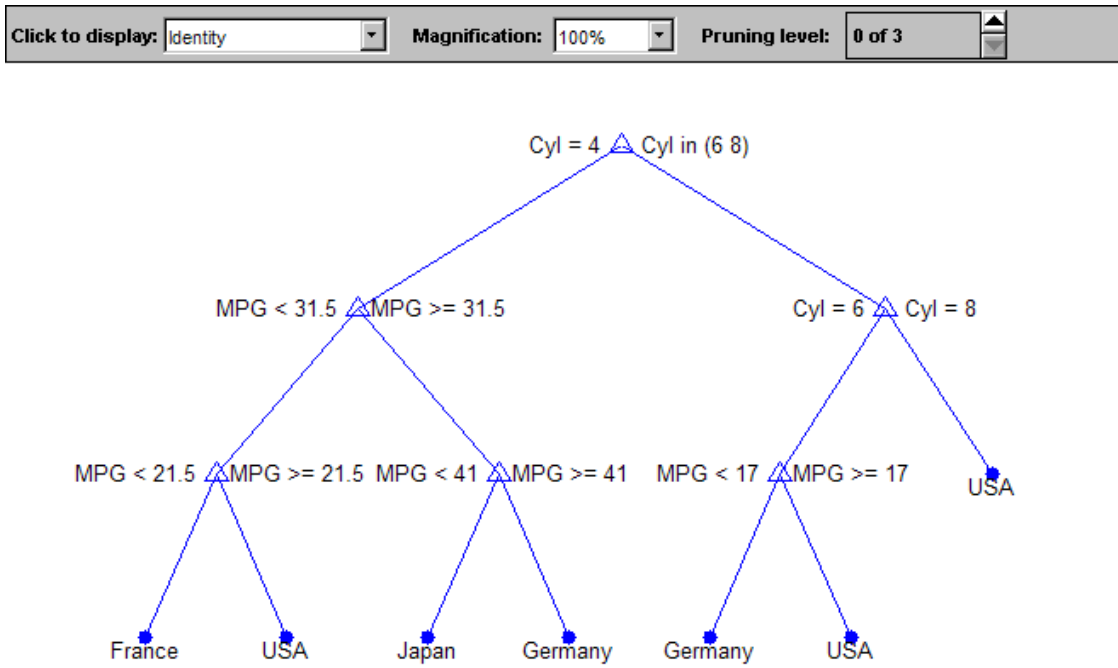
`[v,num] = cutvar(...)` also returns a vector `num` containing the number of each variable.

Examples

Create a classification tree for car data:

```
load carsmall

t = classregtree([MPG Cylinders],Origin,...
```

```
                'names',{'MPG' 'Cyl'},'cat',2)
t =
Decision tree for classification
 1  if Cyl=4 then node 2 elseif Cyl in {6 8} then node 3 else USA
 2  if MPG<31.5 then node 4 elseif MPG>=31.5 then node 5 else USA
 3  if Cyl=6 then node 6 elseif Cyl=8 then node 7 else USA
 4  if MPG<21.5 then node 8 elseif MPG>=21.5 then node 9 else USA
 5  if MPG<41 then node 10 elseif MPG>=41 then node 11 else Japan
 6  if MPG<17 then node 12 elseif MPG>=17 then node 13 else USA
 7  class = USA
 8  class = France
 9  class = USA
10  class = Japan
11  class = Germany
12  class = Germany
13  class = USA

view(t)
```




```
[v,num] = cutvar(t)
v =
    'Cyl'
```

```
    'MPG'
    'Cyl'
    'MPG'
    'MPG'
    'MPG'
    ''
    ''
    ''
    ''
    ''
    ''
    ''
num =
     2
     1
     2
     1
     1
     1
     0
     0
     0
     0
     0
     0
     0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `children` | `numnodes`

cvloss

Class: ClassificationTree

Classification error by cross validation

Syntax

```
E = cvloss(tree)
[E,SE] = cvloss(tree)
[E,SE,Nleaf] = cvloss(tree)
[E,SE,Nleaf,BestLevel] = cvloss(tree)
[E,...] = cvloss(tree,Name,Value)
```

Description

`E = cvloss(tree)` returns the cross-validated classification error (loss) for `tree`, a classification tree.

`[E,SE] = cvloss(tree)` returns the standard error of `E`.

`[E,SE,Nleaf] = cvloss(tree)` returns the number of leaves of tree.

`[E,SE,Nleaf,BestLevel] = cvloss(tree)` returns the optimal pruning level for tree.

`[E,...] = cvloss(tree,Name,Value)` cross validates with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`tree`

A classification tree produced by `fitctree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `ClassificationTree.cvloss` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`ClassificationTree.cvloss` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

`'TreeSize'`

One of the following strings:

- `'se'` — `cvloss` uses the smallest tree whose cost is within one standard error of the minimum cost.
- `'min'` — `cvloss` uses the minimal cost tree.

Default: `'se'`

`'KFold'`

Number of cross-validation samples, a positive integer.

Default: 10

Output Arguments

E

The cross-validation classification error (loss). A vector or scalar depending on the setting of the `Subtrees` name-value pair.

SE

The standard error of `E`. A vector or scalar depending on the setting of the `Subtrees` name-value pair.

Nleaf

Number of leaf nodes in tree. Leaf nodes are terminal nodes, which give classifications, not splits. A vector or scalar depending on the setting of the `Subtrees` name-value pair.

BestLevel

By default, a scalar representing the largest pruning level that achieves a value of `E` within `SE` of the minimum error. If you set `TreeSize` to `'min'`, `BestLevel` is the smallest value in `Subtrees`.

Examples

Compute the Cross-Validation Error

Compute the cross-validation error for a default classification tree.

Load the `ionosphere` data set.

```
load ionosphere
```

Grow a classification tree using the entire data set.

```
Mdl = fitctree(X,Y);
```

Compute the cross-validation error.

```
rng(1); % For reproducibility
E = cvloss(Mdl)
```

```
E =

    0.1111
```

`E` is the 10-fold misclassification error.

Find the Best Pruning Level Using Cross Validation

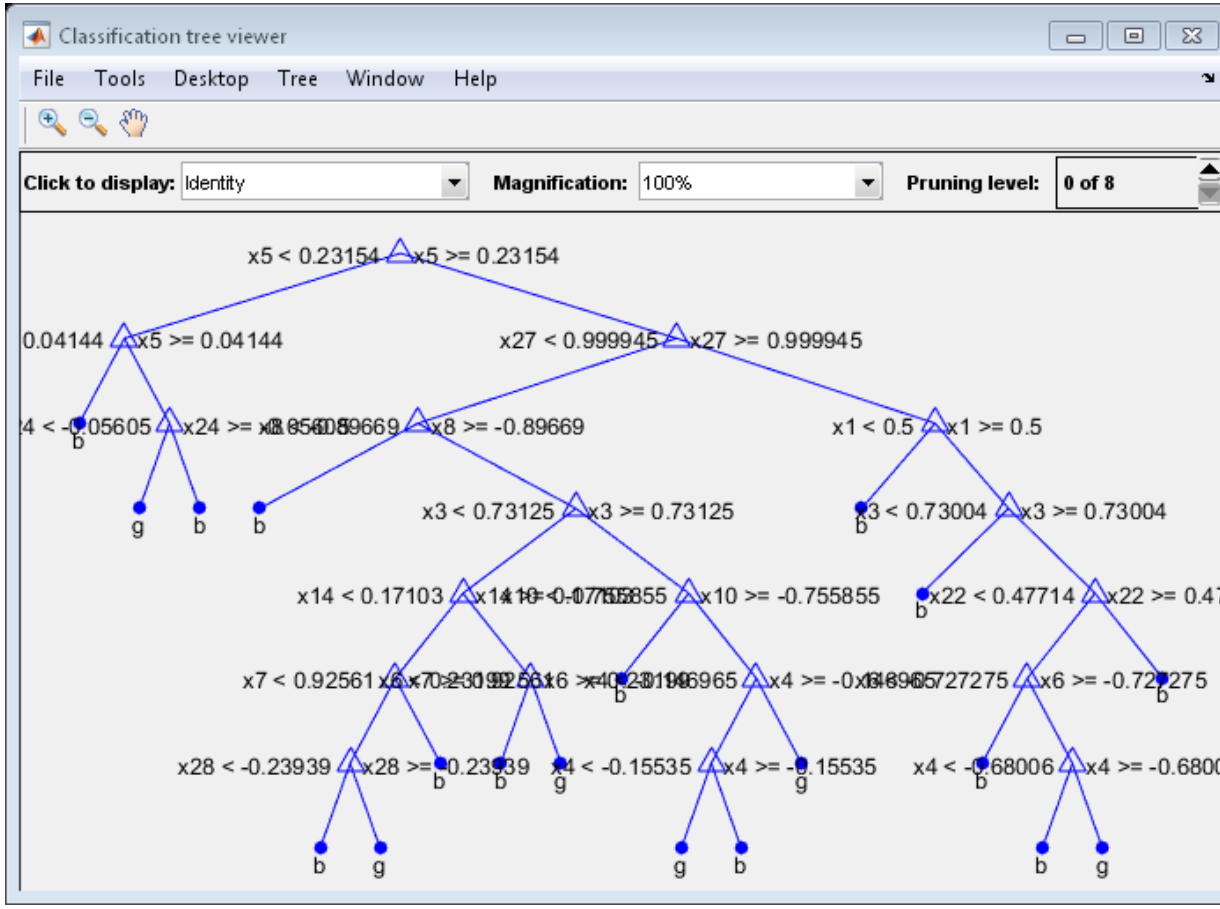
Apply *k*-fold cross validation to find the best level to prune a classification tree for all of its subtrees.

Load the `ionosphere` data set.

```
load ionosphere
```

Grow a classification tree using the entire data set. View the resulting tree.

```
Mdl = fitctree(X,Y);
view(Mdl,'Mode','graph')
```



Compute the 5-fold cross-validation error for each subtree except for the highest pruning level. Specify to return the best pruning level over all subtrees.

```
rng(1); % For reproducibility
m = max(Mdl.PruneList) - 1
[E,~,~,bestLevel] = cvloss(Mdl,'SubTrees',0:m,'KFold',5)
```

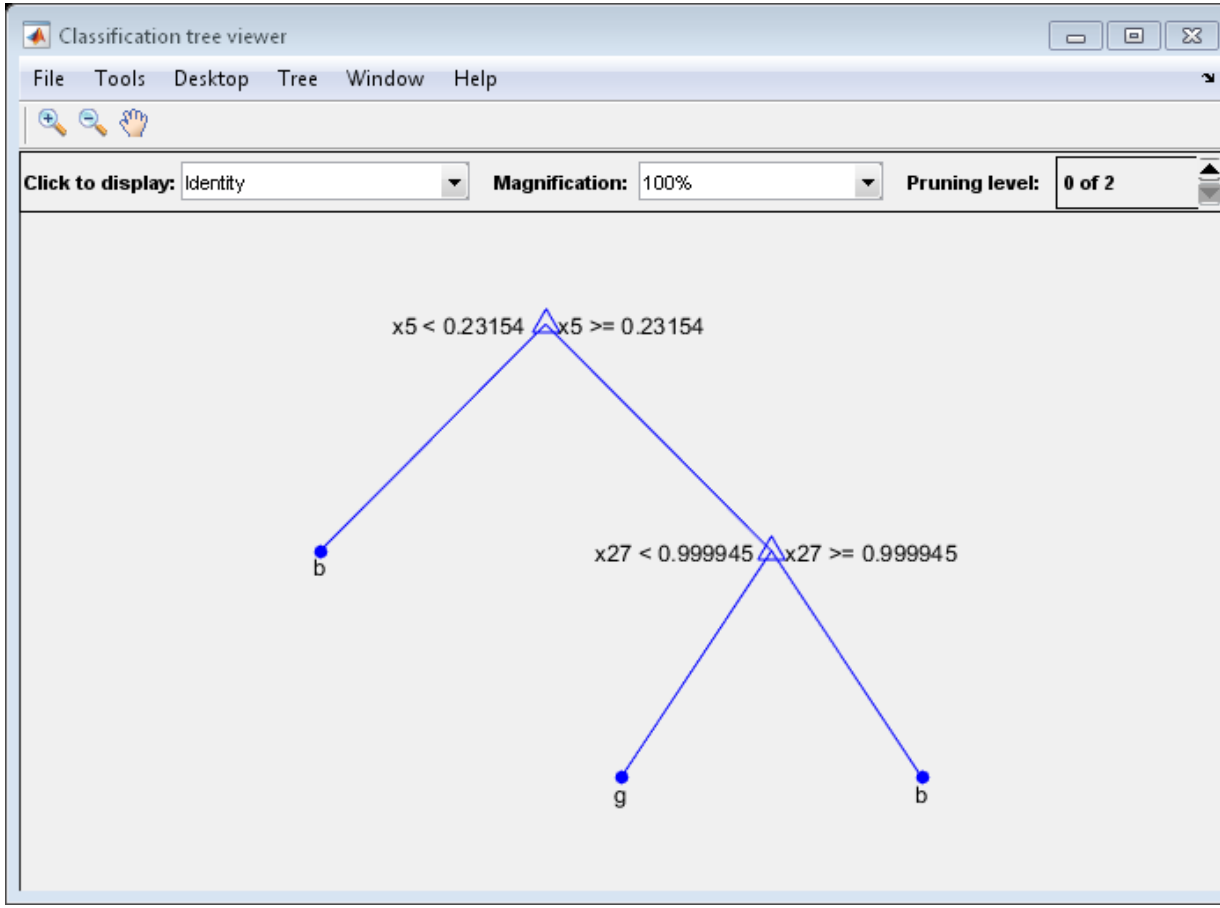
```
m =

     7
```

```
E =

    0.1368
    0.1339
    0.1311
    0.1339
    0.1339
    0.1254
    0.0997
    0.1738


bestLevel =

     6
```

Of the 7 pruning levels, the best pruning level is 6.

Prune the tree to the best level. View the resulting tree.

```
MdlPrune = prune(Mdl,'Level',bestLevel);
view(MdlPrune,'Mode','graph')
```



Alternatives

You can construct a cross-validated tree model with `crossval`, and call `kfoldLoss` instead of `cvloss`. If you are going to examine the cross-validated tree more than once, then the alternative can save time.

However, unlike `cvloss`, `kfoldLoss` does not return SE,Nleaf, or BestLevel. `kfoldLoss` also does not allow you to examine any error other than the classification error.

See Also

`fitctree` | `crossval` | `kfoldLoss` | `loss`

cvloss

Class: RegressionTree

Regression error by cross validation

Syntax

```
E = cvloss(tree)
[E,SE] = cvloss(tree)
[E,SE,Nleaf] = cvloss(tree)
[E,SE,Nleaf,BestLevel] = cvloss(tree)
[E,...] = cvloss(tree,Name,Value)
```

Description

`E = cvloss(tree)` returns the cross-validated regression error (loss) for `tree`, a regression tree.

`[E,SE] = cvloss(tree)` returns the standard error of `E`.

`[E,SE,Nleaf] = cvloss(tree)` returns the number of leaves (terminal nodes) in `tree`.

`[E,SE,Nleaf,BestLevel] = cvloss(tree)` returns the optimal pruning level for tree.

`[E,...] = cvloss(tree,Name,Value)` cross validates with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`tree`

A regression tree produced by `fitrtree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `RegressionTree.cvloss` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`RegressionTree.cvloss` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

`'TreeSize'`

One of the following strings:

- `'se'` — `cvloss` uses the smallest tree whose cost is within one standard error of the minimum cost.
- `'min'` — `cvloss` uses the minimal cost tree.

Default: `'se'`

`'KFold'`

Number of cross-validation samples, a positive integer.

Default: 10

Output Arguments

`E`

The cross-validation mean squared error (loss). A vector or scalar depending on the setting of the `Subtrees` name-value pair.

`SE`

The standard error of `E`. A vector or scalar depending on the setting of the `Subtrees` name-value pair.

`Nleaf`

Number of leaf nodes in tree. Leaf nodes are terminal nodes, which give responses, not splits. A vector or scalar depending on the setting of the `Subtrees` name-value pair.

`BestLevel`

By default, a scalar representing the largest pruning level that achieves a value of `E` within `SE` of the minimum error. If you set `TreeSize` to `'min'`, `BestLevel` is the smallest value in `Subtrees`.

Examples

Compute the Cross-Validation Error

Compute the cross-validation error for a default regression tree.

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
X = [Displacement Horsepower Weight];
```

Grow a regression tree using the entire data set.

```
Mdl = fitrtree(X,MPG);
```

Compute the cross-validation error.

```
rng(1); % For reproducibility
E = cvloss(Mdl)
```

```
E =

   25.7383
```

`E` is the 10-fold weighted, averge MSE (weighted by number of test observations in the folds).

Find the Best Pruning Level Using Cross Validation

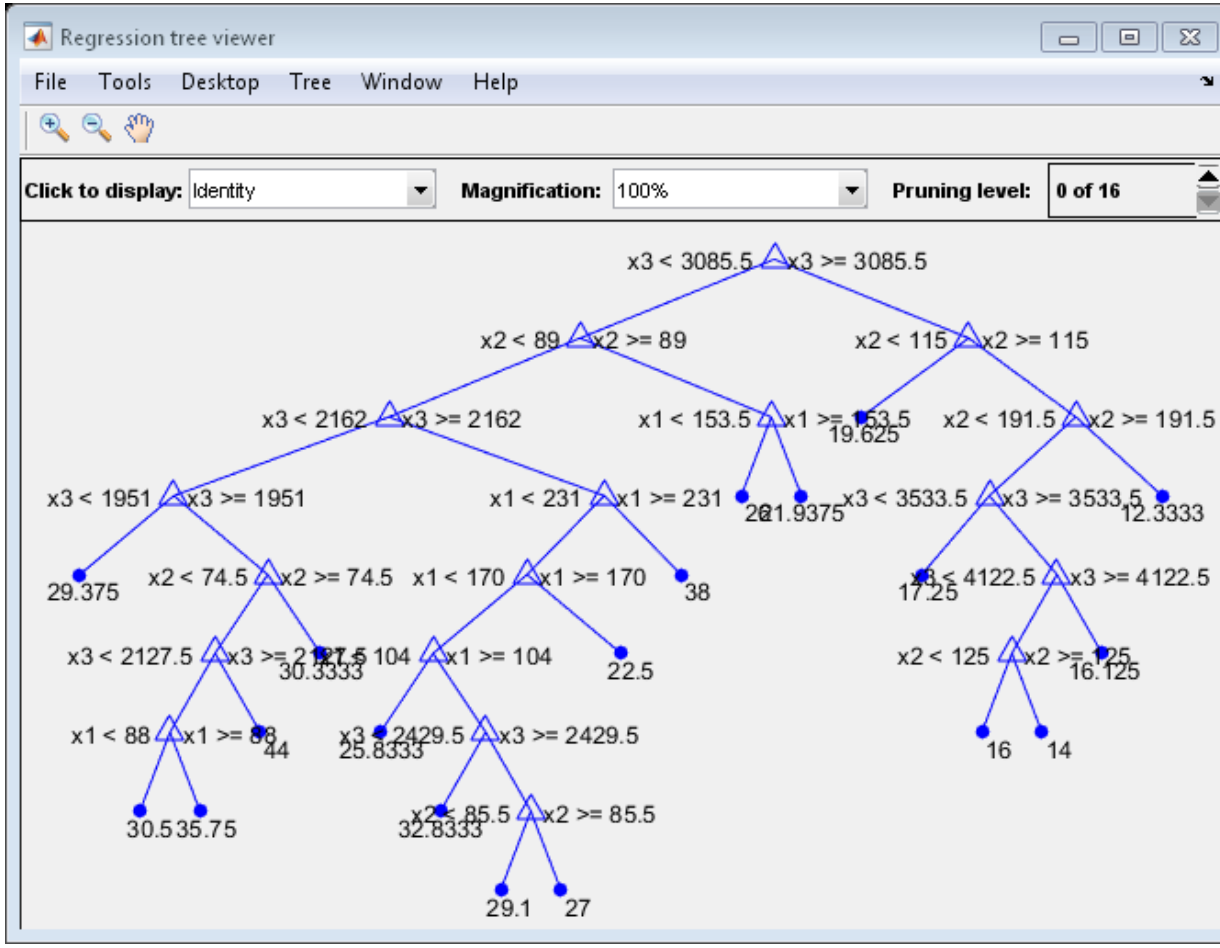
Apply *k*-fold cross validation to find the best level to prune a regression tree for all of its subtrees.

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
X = [Displacement Horsepower Weight];
```

Grow a regression tree using the entire data set. View the resulting tree.

```
Mdl = fitrtree(X,MPG);
view(Mdl,'Mode','graph')
```



Compute the 5-fold cross-validation error for each subtree except for the first two lowest and highest pruning level. Specify to return the best pruning level over all subtrees.

```
rng(1); % For reproducibility
m = max(Mdl.PruneList) - 1
[~,~,~,bestLevel] = cvloss(Mdl,'SubTrees',2:m,'KFold',5)
```

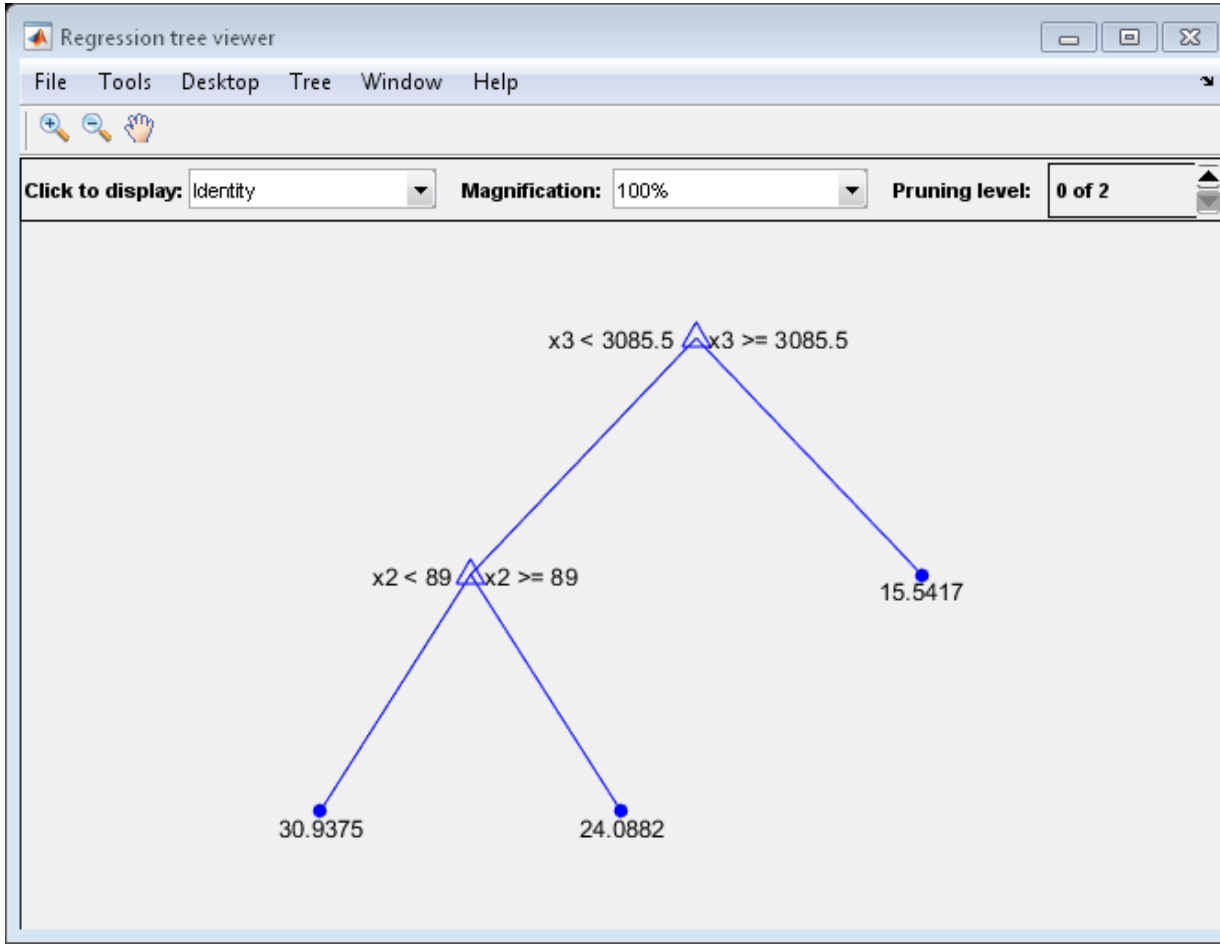
```
m =

    15
```

```
bestLevel =

    14
```

Of the 15 pruning levels, the best pruning level is 14.

Prune the tree to the best level. View the resulting tree.

```
MdlPrune = prune(Mdl,'Level',bestLevel);
view(MdlPrune,'Mode','graph')
```



Alternatives

You can construct a cross-validated tree model with `crossval`, and call `kfoldLoss` instead of `cvloss`. If you are going to examine the cross-validated tree more than once, then the alternative can save time.

However, unlike `cvloss`, `kfoldLoss` does not return SE, Nleaf, or BestLevel.

See Also

`crossval` | `loss` | `kfoldLoss` | `fitrtree`

cvpartition class

Data partitions for cross validation

Description

An object of the `cvpartition` class defines a random partition on a set of data of a specified size. Use this partition to define test and training sets for validating a statistical model using cross validation.

Construction

.cvpartition	Create cross validation partition for data

Methods

disp	Display `cvpartition` object
display	Display `cvpartition` object
repartition	Repartition data for cross-validation
test	Test indices for cross-validation
training	Training indices for cross-validation

Properties

NumObservations	Number of observations (including observations with missing `group` values)

NumTestSets	Number of test sets
TestSize	Size of each test set
TrainSize	Size of each training set
Type	Type of partition

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Use a 10-fold stratified cross validation to compute the misclassification error for `classify` on iris data.

```
load('fisheriris');
CVO = cvpartition(species,'k',10);
err = zeros(CVO.NumTestSets,1);
for i = 1:CVO.NumTestSets
    trIdx = CVO.training(i);
    teIdx = CVO.test(i);
    ytest = classify(meas(teIdx,:),meas(trIdx,:),...
   species(trIdx,:));
    err(i) = sum(~strcmp(ytest,species(teIdx)));
end
cvErr = sum(err)/sum(CVO.TestSize);
```

See Also

`crossval`

How To

- “Grouping Variables” on page 2-52

cvpartition

Class: cvpartition

Create cross validation partition for data

Syntax

```
c = cvpartition(n,'KFold',k)
c = cvpartition(group,'KFold',k)
c = cvpartition(n,'HoldOut',p)
c = cvpartition(group,'HoldOut',p)
c = cvpartition(n,'LeaveOut')
c = cvpartition(n,'resubstitution')
```

Description

`c = cvpartition(n,'KFold',k)` constructs an object `c` of the `cvpartition` class defining a random partition for `k`-fold cross validation on `n` observations. The partition divides the observations into `k` disjoint subsamples (or *folds*), chosen randomly but with roughly equal size. The default value of `k` is `10`.

`c = cvpartition(group,'KFold',k)` creates a random partition for a stratified `k`-fold cross validation. `group` is a numeric vector, categorical array, string array, or cell array of strings indicating the class of each observation. Each subsample has roughly equal size and roughly the same class proportions as in `group`. `cvpartition` treats `NaN`s or empty strings in `group` as missing values.

`c = cvpartition(n,'HoldOut',p)` creates a random partition for holdout validation on `n` observations. This partition divides the observations into a training set and a test (or *holdout*) set. The parameter `p` must be a scalar. When `0 < p < 1`, `cvpartition` randomly selects approximately `p*n` observations for the test set. When `p` is an integer, `cvpartition` randomly selects `p` observations for the test set. The default value of `p` is `1/10`.

`c = cvpartition(group,'HoldOut',p)` randomly partitions observations into a training set and a test set with stratification, using the class information in `group`; that is, both training and test sets have roughly the same class proportions as in `group`.

`c = cvpartition(n,'LeaveOut')` creates a random partition for leave-one-out cross validation on `n` observations. Leave-one-out is a special case of `'KFold'`, in which the number of folds equals the number of observations.

`c = cvpartition(n,'resubstitution')` creates an object `c` that does not partition the data. Both the training set and the test set contain all of the original `n` observations.

Examples

Use stratified 10-fold cross validation to compute misclassification rate:

```
load fisheriris;
y = species;
c = cvpartition(y,'k',10);

fun = @(xT,yT,xt,yt)(sum(~strcmp(yt,classify(xt,xT,yT))));

rate = sum(crossval(fun,meas,y,'partition',c))...
           /sum(c.TestSize)
rate =
    0.0200
```

See Also

`crossval` | `repartition`

How To

- “Grouping Variables” on page 2-52

cvshrink

Class: ClassificationDiscriminant

Cross-validate regularization of linear discriminant

Syntax

```
err = cvshrink(obj)
[err,gamma] = cvshrink(obj)
[err,gamma,delta] = cvshrink(obj)
[err,gamma,delta,numpred] = cvshrink(obj)
[err,...] = cvshrink(obj,Name,Value)
```

Description

`err = cvshrink(obj)` returns a vector of cross-validated classification error values for differing values of the regularization parameter Gamma.

`[err,gamma] = cvshrink(obj)` also returns the vector of Gamma values.

`[err,gamma,delta] = cvshrink(obj)` also returns the vector of Delta values.

`[err,gamma,delta,numpred] = cvshrink(obj)` returns the vector of number of nonzero predictors for each setting of the parameters Gamma and Delta.

`[err,...] = cvshrink(obj,Name,Value)` cross validates with additional options specified by one or more Name,Value pair arguments.

Tips

- Examine the `err` and `numpred` outputs to see the tradeoff between cross-validated error and number of predictors. When you find a satisfactory point, set the corresponding `gamma` and `delta` properties in the model using dot notation. For example, if `(i,j)` is the location of the satisfactory point, set

  ```
  obj.Gamma = gamma(i);
  ```

```
obj.Delta = delta(i,j);
```

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'delta'`

- Scalar `delta` — `cvshrink` uses this value of `delta` with every value of `gamma` for regularization.
- Row vector `delta` — For each `i` and `j`, `cvshrink` uses `delta(j)` with `gamma(i)` for regularization.
- Matrix `delta` — The number of rows of `delta` must equal the number of elements in `gamma`. For each `i` and `j`, `cvshrink` uses `delta(i,j)` with `gamma(i)` for regularization.

Default: `0`

`'gamma'`

Vector of Gamma values for cross-validation.

Default: `0:0.1:1`

`'NumDelta'`

Number of Delta intervals for cross-validation. For every value of Gamma, `cvshrink` cross-validates the discriminant using `NumDelta + 1` values of Delta, uniformly spaced from zero to the maximal Delta at which all predictors are eliminated for this value of Gamma. If you set `delta`, `cvshrink` ignores `NumDelta`.

Default: 0

`'NumGamma'`

Number of Gamma intervals for cross-validation. `cvshrink` cross-validates the discriminant using `NumGamma + 1` values of Gamma, uniformly spaced from `MinGamma` to `1`. If you set `gamma`, `cvshrink` ignores `NumGamma`.

Default: 10

`'verbose'`

Verbosity level, an integer from `0` to `2`. Higher values give more progress messages.

Default: 0

Output Arguments

`err`

Numeric vector or matrix of errors. `err` is the misclassification error rate, meaning the average fraction of misclassified data over all folds.

- If `delta` is a scalar (default), `err(i)` is the misclassification error rate for `obj` regularized with `gamma(i)`.
- If `delta` is a vector, `err(i,j)` is the misclassification error rate for `obj` regularized with `gamma(i)` and `delta(j)`.
- If `delta` is a matrix, `err(i,j)` is the misclassification error rate for `obj` regularized with `gamma(i)` and `delta(i,j)`.

`gamma`

Vector of Gamma values used for regularization. See “Gamma and Delta” on page 22-1027.

`delta`

Vector or matrix of Delta values used for regularization. See “Gamma and Delta” on page 22-1027.

- If you give a scalar for the `delta` name-value pair, the output `delta` is a row vector the same size as `gamma`, with entries equal to the input scalar.
- If you give a row vector for the `delta` name-value pair, the output `delta` is a matrix with the same number of columns as the row vector, and with the number of rows equal to the number of elements of `gamma`. The output `delta(i,j)` is equal to the input `delta(j)`.
- If you give a matrix for the `delta` name-value pair, the output `delta` is the same as the input matrix. The number of rows of `delta` must equal the number of elements in `gamma`.

`numpred`

Numeric vector or matrix containing the number of predictors in the model at various regularizations. `numpred` has the same size as `err`.

- If `delta` is a scalar (default), `numpred(i)` is the number of predictors for `obj` regularized with `gamma(i)` and `delta`.
- If `delta` is a vector, `numpred(i,j)` is the number of predictors for `obj` regularized with `gamma(i)` and `delta(j)`.
- If `delta` is a matrix, `numpred(i,j)` is the number of predictors for `obj` regularized with `gamma(i)` and `delta(i,j)`.

Definitions

Gamma and Delta

Regularization is the process of finding a small set of predictors that yield an effective predictive model. For linear discriminant analysis, there are two parameters, γ and δ, that control regularization as follows. `cvshrink` helps you select appropriate values of the parameters.

Let Σ represent the covariance matrix of the data X, and let $\hat{X}$ be the centered data (the data X minus the mean by class). Define

$$D = \mathrm{diag}\left(\hat{X}^T * \hat{X}\right).$$

The regularized covariance matrix $\tilde{\Sigma}$ is

$$\tilde{\Sigma} = (1-\gamma)\Sigma + \gamma D.$$

Whenever $\gamma \geq$ `MinGamma`, $\tilde{\Sigma}$ is nonsingular.

Let μ_k be the mean vector for those elements of X in class k, and let μ_0 be the global mean vector (the mean of the rows of X). Let C be the correlation matrix of the data X, and let $\tilde{C}$ be the regularized correlation matrix:

$$\tilde{C} = (1-\gamma)C + \gamma I,$$

where I is the identity matrix.

The linear term in the regularized discriminant analysis classifier for a data point x is

$$(x-\mu_0)^T \tilde{\Sigma}^{-1}(\mu_k - \mu_0) = \left[(x-\mu_0)^T D^{-1/2}\right]\left[\tilde{C}^{-1}D^{-1/2}(\mu_k - \mu_0)\right].$$

The parameter δ enters into this equation as a threshold on the final term in square brackets. Each component of the vector $\left[\tilde{C}^{-1}D^{-1/2}(\mu_k - \mu_0)\right]$ is set to zero if it is smaller in magnitude than the threshold δ. Therefore, for class k, if component j is thresholded to zero, component j of x does not enter into the evaluation of the posterior probability.

The `DeltaPredictor` property is a vector related to this threshold. When $\delta \geq$ `DeltaPredictor(i)`, all classes k have

$$\left|\tilde{C}^{-1}D^{-1/2}(\mu_k - \mu_0)\right| \leq \delta.$$

Therefore, when $\delta \geq$ `DeltaPredictor(i)`, the regularized classifier does not use predictor `i`.

Examples

Regularize Data with Many Predictors

Regularize a discriminant analysis classifier, and view the tradeoff between the number of predictors in the model and the classification accuracy.

Create a linear discriminant analysis classifier for the `ovariancancer` data. Set the `SaveMemory` and `FillCoeffs` options to keep the resulting model reasonably small.

```
load ovariancancer
obj = fitcdiscr(obs,grp,...
    'SaveMemory','on','FillCoeffs','off');
```

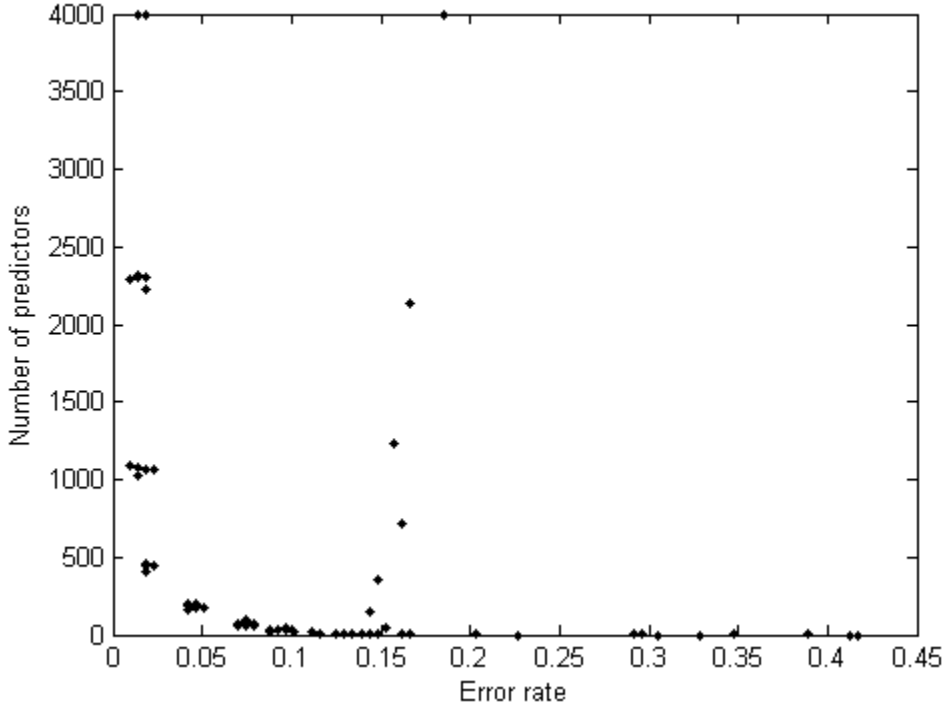
Use 10 levels of `Gamma` and 10 levels of `Delta` to search for good parameters. This search is time-consuming. Set `Verbose` to `1` to view the progress.

```
rng('default') % for reproducibility
[err,gamma,delta,numpred] = cvshrink(obj,...
    'NumGamma',9,'NumDelta',9,'Verbose',1);
```

```
Done building cross-validated model.
Processing Gamma step 1 out of 10.
Processing Gamma step 2 out of 10.
Processing Gamma step 3 out of 10.
Processing Gamma step 4 out of 10.
Processing Gamma step 5 out of 10.
Processing Gamma step 6 out of 10.
Processing Gamma step 7 out of 10.
Processing Gamma step 8 out of 10.
Processing Gamma step 9 out of 10.
Processing Gamma step 10 out of 10.
```

Plot the classification error rate against the number of predictors.

```
plot(err,numpred,'k.')
xlabel('Error rate');
ylabel('Number of predictors');
```



- "Regularize a Discriminant Analysis Classifier" on page 15-21

See Also

`ClassificationDiscriminant` | `fitcdiscr`

More About

- "Discriminant Analysis" on page 15-3

cvshrink

Class: RegressionEnsemble

Cross validate shrinking (pruning) ensemble

Syntax

```
vals = cvshrink(ens)
[vals,nlearn] = cvshrink(ens)
[vals,nlearn] = cvshrink(ens,Name,Value)
```

Description

`vals = cvshrink(ens)` returns an `L`-by-`T` matrix with cross-validated values of the mean squared error. `L` is the number of `lambda` values in the `ens.Regularization` structure. `T` is the number of threshold values on weak learner weights. If `ens` does not have a `Regularization` property filled in by the `regularize` method, pass a lambda name-value pair.

`[vals,nlearn] = cvshrink(ens)` returns an `L`-by-`T` matrix of the mean number of learners in the cross-validated ensemble.

`[vals,nlearn] = cvshrink(ens,Name,Value)` cross validates with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble, created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'cvpartition'`

A partition created with `cvpartition` to use in a cross-validated tree. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'holdout'`

Holdout validation tests the specified fraction of the data, and uses the rest of the data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated tree: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'kfold'`

Number of folds to use in a cross-validated tree, a positive integer. If you do not supply a cross-validation method, `cvshrink` uses 10-fold cross validation. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

Default: 10

`'lambda'`

Vector of nonnegative regularization parameter values for lasso. If empty, `cvshrink` does not perform cross validation.

Default: [ ]

`'leaveout'`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time: `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.

`'threshold'`

Numeric vector with lower cutoffs on weights for weak learners. `cvshrink` discards learners with weights below `threshold` in its cross-validation calculation.

Default: 0

Output Arguments

`vals`

`L`-by-`T` matrix with cross-validated values of the mean squared error. `L` is the number of values of the regularization parameter `'lambda'`, and `T` is the number of `'threshold'` values on weak learner weights.

`nlearn`

`L`-by-`T` matrix with cross-validated values of the mean number of learners in the cross-validated ensemble.`L` is the number of values of the regularization parameter `'lambda'`, and `T` is the number of `'threshold'` values on weak learner weights.

Examples

Create a regression ensemble for predicting mileage from the `carsmall` data. Cross validate the ensemble for three values each of `lambda` and `threshold`.

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression');
[vals nlearn] = cvshrink(ens,'lambda',[.01 .1 1],...
    'threshold',[0 .01 .1])

vals =
   20.0949   19.9007  131.6316
   20.0924   19.8431  128.0989
   19.9759   19.7987  119.5574

nlearn =
   13.3000   11.6000    3.5000
   13.2000   11.5000    3.6000
   13.4000   11.4000    3.9000
```

Clearly, setting a threshold of `0.1` leads to unacceptable errors, while a threshold of `0.01` gives similar errors to a threshold of `0`. The mean number of learners with a threshold of `0.1` is about `11.5`, whereas the mean number is about `13.2` when the threshold is `0`.

See Also

`regularize` | `shrink`

datasample

Randomly sample from data, with or without replacement

Syntax

```
y = datasample(data,k)
y = datasample(data,k,dim)
[y,idx] = datasample(data,k,...)
[y,...] = datasample(s,data,k,...)
[y,...] = datasample(data,k,Name,Value)
[y,...] = datasample(data,k,dim,Name,Value)
```

Description

`y = datasample(data,k)` returns `k` observations sampled uniformly at random, with replacement, from the data in `data`.

`y = datasample(data,k,dim)` returns a sample taken along dimension `dim` of `data`.

`[y,idx] = datasample(data,k,...)` returns an index vector indicating which values `datasample` sampled from `data`.

`[y,...] = datasample(s,data,k,...)` uses the random number stream `s` to generate random numbers.

`[y,...] = datasample(data,k,Name,Value)` or `[y,...] = datasample(data,k,dim,Name,Value)` samples with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`data`

Vector, matrix, *N*-dimensional array, table, or dataset array representing the data from which to sample. By default, `datasample` regards the rows of a `data` matrix, or the first

nonsingleton dimension of a `data` array, as data elements. Change this behavior with the dim argument.

`k`

Positive integer, the number of samples.

`dim`

Integer specifying the dimension on which to take samples. For example, if `data` is a matrix and `dim` is `2`, `y` contains a selection of columns in `data`. If `data` is a table or dataset array and `dim` is `2`, `y` contains a selection of variables in `data`. Use `dim` to ensure sampling along a specific dimension regardless of whether `data` is a vector, matrix or *N*-dimensional array.

Default: `1`

`s`

Random number stream. Create `s` using `rng` or `RandStream`.

Default: The global random number stream

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Replace'`

Select the sample with replacement if `Replace` is `true`, or without replacement if `Replace` is `false`. If `Replace` is `false`, k must not be larger than the number of data elements in data.

Default: `true`

`'Weights'`

Vector with the same number of elements as data elements in data, and with nonnegative elements. Sample with probability proportional to the elements of `Weights`.

Default: `ones(datasize,1)`, where `datasize` is the number of data elements in data

Output Arguments

`y`

- If data is a vector, `y` is a vector containing k elements selected from `data`.
- If data is a matrix, `y` is a matrix containing k rows selected from `data`. Or, if dim = `2`, `y` is a matrix containing k columns selected from `data`
- If data is an *N*-dimensional array, `datasample` samples along its first non-singleton dimension. Or, if you give a dim name-value pair, `datasample` samples along the dimension dim.

When the sample is taken with replacement (default), `y` can contain repeated observations from `data`. Set the Replace name-value pair to `false` to sample without replacement.

`idx`

Vector of indices indicating which elements `datasample` chose from data to create y. For example:

- If `data` is a vector, `y = data(idx)`.
- If `data` is a matrix, `y = data(idx,:)`.

Examples

Draw five unique values from the integers `1:10`.

```
y = datasample(1:10,5,'Replace',false)
```

```
y =
     6     3     7     8     5
```

Generate a random sequence of the characters `ACGT`, with replacement, according to specified probabilities.

```
seq = datasample('ACGT',48,'Weights',[0.15 0.35 0.35 0.15])
```

```
seq =
```

```
CTTCGACTGTGAGTGGGCGCGACAAGGCTACCGGCCCGGGCGGCACTC
```

Select a random subset of columns from a data matrix.

```
X = randn(10,1000);
Y = datasample(X,5,2,'Replace',false)

Y =
    0.7007    0.3382    2.1298   -0.1891    0.5026
    0.6520   -0.6693   -0.1961   -0.9915    1.9107
    0.1785    0.6640    2.3247   -1.1735   -1.0020
    1.6760    2.6102   -0.8902   -0.7735    1.8676
   -0.3251   -0.6415   -0.2572   -0.1629   -1.0523
    0.1011    0.9323   -1.3088   -0.4477    0.8036
   -0.5767   -0.5778   -0.8556    0.8672   -0.0727
   -0.0615   -0.9084    0.9020   -0.4185   -1.9520
    0.7256   -1.1228    0.7558    1.2691    2.4997
   -1.2273    0.5754   -0.8755   -0.8224   -1.2066
```

Resample observations from a dataset array to create a bootstrap replicate dataset.

```
load hospital
y = datasample(hospital,size(hospital,1));
```

Use the second output to sample “in parallel" from two data vectors.

```
x1 = randn(100,1);
x2 = randn(100,1);
[y1,idx] = datasample(x1,10);
y2 = x2(idx);
```

Alternatives

You can use `randi` or `randperm` to generate indices for random sampling with or without replacement, respectively. However, `datasample` can be more convenient because it samples directly from your data. `datasample` also allows weighted sampling.

More About

Tips

- To sample random integers with replacement from a range, use `randi`.

- To sample random integers without replacement, use `randperm` or `datasample`.
- To randomly sample from data, with or without replacement, use `datasample`.

Algorithms

`datasample` uses `randperm`, `rand`, or `randi` to generate random values. Therefore, `datasample` changes the state of the MATLAB global random number generator. Control the random number generator using `rng`.

For selecting weighted samples without replacement, `datasample` uses the algorithm of Wong and Easton [1].

References

[1] Wong, C. K. and M. C. Easton. *An Efficient Method for Weighted Sampling Without Replacement*. SIAM Journal of Computing 9(1), pp. 111–113, 1980.

See Also

`rand` | `randi` | `randperm` | `RandStream` | `rng`

dataset class

Arrays for statistical data

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

Dataset arrays are used to collect heterogeneous data and metadata including variable and observation names into a single container variable. Dataset arrays are suitable for storing column-oriented or tabular data that are often stored as columns in a text file or in a spreadsheet, and can accommodate variables of different types, sizes, units, etc.

Dataset arrays can contain different kinds of variables, including numeric, logical, character, categorical, and cell. However, a dataset array is a different class than the variables that it contains. For example, even a dataset array that contains only variables that are double arrays cannot be operated on as if it were itself a double array. However, using dot subscripting, you can operate on variable in a dataset array as if it were a workspace variable.

You can subscript dataset arrays using parentheses much like ordinary numeric arrays, but in addition to numeric and logical indices, you can use variable and observation names as indices.

Construction

Use the `dataset` constructor to create a dataset array from variables in the MATLAB workspace. You can also create a dataset array by reading data from a text or spreadsheet file. You can access each variable in a dataset array much like fields in a structure, using dot subscripting. See the following section for a list of operations available for dataset arrays.

.dataset	Construct dataset array

Methods

cat	Concatenate dataset arrays
cellstr	Create cell array of strings from dataset array
dataset2cell	Convert dataset array to cell array
dataset2struct	Convert dataset array to structure
datasetfun	Apply function to dataset array variables
disp	Display dataset array
display	Display dataset array
double	Convert dataset variables to double array
end	Last index in indexing expression for dataset array
export	Write dataset array to file
get	Access dataset array properties
horzcat	Horizontal concatenation for dataset arrays
intersect	Set intersection for dataset array observations

isempty	True for empty dataset array
ismember	Dataset array elements that are members of set
ismissing	Find dataset array elements with missing values
join	Merge observations
length	Length of dataset array
ndims	Number of dimensions of dataset array
numel	Number of elements in dataset array
replacedata	Replace dataset variables
replaceWithMissing	Insert missing data indicators into a dataset array
set	Set and display properties
setdiff	Set difference for dataset array observations
setxor	Set exclusive or for dataset array observations
single	Convert dataset variables to single array
size	Size of dataset array
sortrows	Sort rows of dataset array

stack	Stack data from multiple variables into single variable
subsasgn	Subscripted assignment to dataset array
subsref	Subscripted reference for dataset array
summary	Print summary of dataset array
union	Set union for dataset array observations
unique	Unique observations in dataset array
unstack	Unstack data from single variable into multiple variables
vertcat	Vertical concatenation for dataset arrays

Properties

A dataset array `D` has properties that store metadata (information about your data). Access or assign to a property using `P = D.Properties.PropName` or `D.Properties.PropName = P`, where `PropName` is one of the following:

Description	String describing data set
DimNames	Two-element cell array of strings giving names of dimensions of data set
ObsNames	Cell array of nonempty, distinct strings giving names of observations in data set
Units	Units of variables in data set

UserData	Variable containing additional information associated with data set
VarDescription	Cell array of strings giving descriptions of variables in data set
VarNames	Cell array giving names of variables in data set

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Load a dataset array from a .mat file and create some simple subsets:

```
load hospital
h1 = hospital(1:10,:)
h2 = hospital(:,{'LastName' 'Age' 'Sex' 'Smoker'})

% Access and modify metadata
hospital.Properties.Description
hospital.Properties.VarNames{4} = 'Wgt'

% Create a new dataset variable from an existing one
hospital.AtRisk = hospital.Smoker | (hospital.Age > 40)

% Use individual variables to explore the data
boxplot(hospital.Age,hospital.Sex)
h3 = hospital(hospital.Age<30,...
   {'LastName' 'Age' 'Sex' 'Smoker'})

% Sort the observations based on two variables
h4 = sortrows(hospital,{'Sex','Age'})
```

See Also

`tdfread` | `textscan` | `xlsread`

How To

- “Dataset Arrays” on page 2-132

dataset

Class: dataset

Construct dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
A = dataset(varspec,'ParamName',Value)
A = dataset('File',filename,'ParamName',Value)
A = dataset('XLSFile',filename,'ParamName',Value)
A = dataset('XPTFile',xptfilename,'ParamName',Value)
```

Description

`A = dataset(varspec,'ParamName',Value)` creates dataset array `A` using the workspace variable input method *`varspec`* and one or more optional name/value pairs (see Parameter Name/Value Pairs).

The input method *`varspec`* can be one or more of the following:

- *`VAR`* — a workspace variable. `dataset` uses the workspace name for the variable name in `A`. To include multiple variables, specify *`VAR_1`*,*`VAR_2`*,...,*`VAR_N`*. Variables can be arrays of any size, but all variables must have the same number of rows. `VAR` can also be an expression. In this case, `dataset` creates a default name automatically.
- {*`VAR`*,*`name`*} — a workspace variable, *`VAR`* and a variable name, *`name`* . `dataset` uses *`name`* as the variable name. To include multiple variables and names, specify {*`VAR_1`*,*`name_1`*}, {*`VAR_2`*,*`name_2`*},..., {*`VAR_N`*,*`name_N`*}.

- {*VAR*,*name_1*,...,*name_m*} — an *m*-columned workspace variable, *VAR*. `dataset` uses the names *name_1*, ..., *name_m* as variable names. You must include a name for every column in `VAR`. Each column becomes a separate variable in `A`.

You can combine these input methods to include as many variables and names as needed. Names must be valid, unique MATLAB identifier strings. For example input combinations, see Examples. For optional name/value pairs see Inputs.

To convert numeric arrays, cell arrays, structure arrays, or tables to dataset arrays, you can also use (respectively):

- `mat2dataset`
- `cell2dataset`
- `struct2dataset`
- `table2dataset`

Note: Dataset arrays may contain built-in types or array objects as variables. Array objects must implement each of the following:

- Standard MATLAB parenthesis indexing of the form `var(i,...)`, where `i` is a numeric or logical vector corresponding to rows of the variable
- A `size` method with a `dim` argument
- A `vertcat` method

`A = dataset('File',filename,'ParamName',Value)` creates dataset array `A` from column-oriented data in the text file specified by the string `filename`. Variables in `A` are of type `double` if data in the corresponding column of the file, following the column header, are entirely numeric; otherwise the variables in `A` are cell arrays of strings. `dataset` converts empty fields to either `NaN` (for a numeric variable) or the empty string (for a string-valued variable). `dataset` ignores insignificant white space in the file. You cannot specify both a file and workspace variables as input. See Name/Value Pairs for more information.

`A = dataset('XLSFile',filename,'ParamName',Value)` creates dataset array `A` from column-oriented data in the Excel spreadsheet specified by the string `filename`. Variables in `A` are of type `double` if data in the corresponding column of the spreadsheet, following the column header, are entirely numeric; otherwise the variables in `A` are cell arrays of strings. See Name/Value Pairs for more information.

`A = dataset('XPTFile',xptfilename,'ParamName',Value)` creates a dataset array from a SAS® XPORT format file. Variable names from the XPORT format file are preserved. Numeric data types in the XPORT format file are preserved but all other data types are converted to cell arrays of strings. The XPORT format allows for 28 missing data types. `dataset` represents these in the file by an upper case letter, `'.'` or `'_'`. `dataset` converts all missing data to `NaN` values in `A`. See Name/Value Pairs for more information.

Parameter Name/Value Pairs

Specify one or more of the following name/value pairs when constructing a dataset:

`'VarNames'`

A cell array `{name_1,...,name_m}` naming the `m` variables in `A` with the specified variable names. Names must be valid, unique MATLAB identifier strings. The number of names must equal the number of variables in `A`. You cannot use the `VarNames` parameter if you provide names for individual variables using `{VAR,name}` pairs. To specify `VarNames` when using a file as input, set `ReadVarNames` to `false`.

`'ObsNames'`

A cell array `{name_1,...,name_n}` naming the `n` observations in `A` with the specified observation names. The names need not be valid MATLAB identifier strings, but must be unique. The number of names must equal the number of observations (rows) in `A`. To specify `ObsNames` when using a file as input, set `ReadObsNames` to `false`.

Name/value pairs available when using text files as inputs:

`'Delimiter'`

A string indicating the character separating columns in the file. Values are

- `'\t'` (tab, the default when no `format` is specified)
- `' '` (space, the default when a `format` is specified)
- `','` (comma)
- `';'` (semicolon)
- `'|'` (bar)

`'Format'`

A format string, as accepted by `textscan`. `dataset` reads the file using `textscan`, and creates variables in `A` according to the conversion specifiers in the format string. You may also provide any name/value pairs accepted by `textscan`. Using the `Format` parameter is much faster for large files. If `ReadObsNames` is `true`, the `format` string should include a format specifier for the first column of the file.

`'HeaderLines'`

Numeric value indicating the number of lines to skip at the beginning of a file.

Default: `0`

`'TreatAsEmpty'`

Specifies strings to treat as the empty string in a numeric column. Values may be a character string or a cell array of strings. The parameter applies only to numeric columns in the file; `dataset` does not accept numeric literals such as `'-99'`.

Name/value pairs available when using text files or Excel spreadsheets as inputs:

`'ReadVarNames'`

A logical value indicating whether (`true`) or not (`false`) to read variable names from the first row of the file. The default is `true`. If `ReadVarNames` is `true`, variable names in the column headers of the file or range (if using an Excel spreadsheet) cannot be empty.

`'ReadObsNames'`

A logical value indicating whether (`true`) or not (`false`) to read observation names from the first column of the file or range (if using an Excel spreadsheet). The default is `false`. If `ReadObsNames` and `ReadVarNames` are both `true`, `dataset` saves the header of the first column in the file or range as the name of the first dimension in `A.Properties.DimNames`.

When reading from an `XPT` format file, the `ReadObsNames` parameter name/value pair determines whether or not to try to use the first variable in the file as observation names. Specify as a logical value (default `false`). If the contents of the first variable are not valid observation names then `dataset` reads the variable into a variable of the dataset array and does not set the observation names.

Name/value pairs available when using Excel spreadsheets as input:

`'Sheet'`

A positive scalar value of type `double` indicating the sheet number, or a quoted string indicating the sheet name.

`'Range'`

A string of the form `'C1:C2'` where `C1` and `C2` are the names of cells at opposing corners of a rectangular region to be read, as for `xlsread`. By default, the rectangular region extends to the right-most column containing data. If the spreadsheet contains empty columns between columns of data, or if the spreadsheet contains figures or other non-tabular information, specify a range that contains only data.

Examples

Create a dataset array from workspace variables, including observation names:

```
load cereal
cereal = dataset(Calories,Protein,Fat,Sodium,Fiber,Carbo,...
   Sugars,'ObsNames',Name)
cereal.Properties.VarDescription = Variables(4:10,2);
```

Create a dataset array from a single, multi-columned workspace variable, designating variable names for each column:

```
load cities
categories = cellstr(categories);
cities = dataset({ratings,categories{:}},...
   'ObsNames',cellstr(names))
```

Load data from a text or spreadsheet file

```
patients = dataset('File','hospital.dat',...
   'Delimiter',',','ReadObsNames',true)
patients2 = dataset('XLSFile','hospital.xls',...
   'ReadObsNames',true)
```

1. Load patient data from the CSV file `hospital.dat` and store the information in a `dataset` array with observation names given by the first column in the data (patient identification):

```
patients = dataset('file','hospital.dat', ...
             'format','%s%s%s%f%f%f%f%f%f%f%f', ...
             'Delimiter',',','ReadObsNames',true);
```

You can also load the data without specifying a format string. `dataset` will automatically create `dataset` variables that are either `double` arrays or cell arrays of strings, depending on the contents of the file:

```
patients = dataset('file','hospital.dat',...
                   'delimiter',',',...
                   'ReadObsNames',true);
```

2. Make the {0,1}-valued variable `smoke` nominal, and change the labels to `'No'` and `'Yes'`:

```
patients.smoke = nominal(patients.smoke,{'No','Yes'});
```

3. Add new levels to `smoke` as placeholders for more detailed histories of smokers:

```
patients.smoke = addlevels(patients.smoke,...
                 {'0-5 Years','5-10 Years','LongTerm'});
```

4. Assuming the nonsmokers have never smoked, relabel the `'No'` level:

```
patients.smoke = setlabels(patients.smoke,'Never','No');
```

5. Drop the undifferentiated `'Yes'` level from `smoke`:

```
patients.smoke = droplevels(patients.smoke,'Yes');
```

```
Warning: OLDLEVELS contains categorical levels that
were present in A, caused some array elements to have
undefined levels.
```

Note that smokers now have an undefined level.

6. Set each smoker to one of the new levels, by observation name:

```
patients.smoke('YPL-320') = '5-10 Years';
```

See Also

`cell2dataset` | `mat2dataset` | `struct2dataset` | `tdfread` | `textscan` | `xlsread`

More About

- "Dataset Arrays" on page 2-132

dataset2cell

Class: dataset

Convert dataset array to cell array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
C = dataset2cell(D)
```

Description

`C = dataset2cell(D)` converts the dataset array `D` to a cell array `C`. Each variable of `D` becomes a column in `C`. If `D` is an `M`-by-`N` array, then `C` is `(M+1)`-by-`N`, with the variable names of `D` in the first row. If `D` contains observation names, then `C` is `(M+1)`-by-`(N+1)`, with the observation names in the first column.

See Also

`dataset` | `cell2dataset` | `dataset.export`

More About

- “Dataset Arrays” on page 2-132

dataset2struct

Class: dataset

Convert dataset array to structure

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
S = dataset2struct(D)
S = dataset2struct(D,'AsScalar',true)
```

Description

`S = dataset2struct(D)` converts a dataset array to a structure array. Each variable of D becomes a field in S. If D is an *M*-by-*N* dataset array, then S is *M*-by-1 and has *N* fields. If D contains observation names, then S contains those names in the additional field `ObsNames`.

`S = dataset2struct(D,'AsScalar',true)` converts a dataset array to a scalar structure. Each variable of D becomes a field in S. If D is an *M*-by-*N* dataset array, then S has *N* fields, each of which as *M* rows. If D contains observation names, then S contains those names in the additional field `ObsNames`.

Input Arguments

`D`

M-by-*N* dataset array.

Output Arguments

S

M-by-1 structure array, with *N* fields. If the input dataset array contains observation names, then `S` has an additional field `ObsNames`.

If you specify `'AsScalar',true`, then `S` is a scalar structure, with *N* fields, each with *M* rows.

Examples

Convert Dataset Array to Structure Array

Load sample dataset array.

```
load('hospital')
```

Create a dataset array, `D`, that has only a subset of the observations and variables.

```
D = hospital(1:8,{'LastName','Sex','Age'});
size(D)
```

```
ans =

     8     3
```

The dataset array `D` has 8 observations and 3 variables.

Convert `D` to a structure array.

```
S = dataset2struct(D)
```

```
S =

8x1 struct array with fields:
    ObsNames
    LastName
    Sex
    Age
```

The structure is `8x1`, corresponding to the 8 observations in the dataset array. `S` also has the field `ObsNames`, since `D` had observation names.

Display the field data for the first element of S.

```
S(1)
```

```
ans =

    ObsNames: 'YPL-320'
    LastName: 'SMITH'
         Sex: [1x1 nominal]
         Age: 38
```

This information corresponds to the first observation (row) of the dataset array.

Convert Dataset Array to Scalar Structure

Load sample dataset array.

```
load('hospital')
```

Create a dataset array, D, that has only a subset of the observations and variables.

```
D = hospital(1:8,{'LastName','Sex','Age'});
size(D)
```

```
ans =

     8     3
```

The dataset array D has 8 observations and 3 variables.

Convert D to a scalar structure array.

```
S = dataset2struct(D,'AsScalar',true)
```

```
S =

    ObsNames: {8x1 cell}
    LastName: {8x1 cell}
         Sex: [8x1 nominal]
         Age: [8x1 double]
```

The data in the fields of the scalar structure is 8x1, corresponding to the 8 observations in the dataset array. S also has the field ObsNames, since D had observation names.

Display the data for the field LastName.

```
S.LastName

ans =

    'SMITH'
    'JOHNSON'
    'WILLIAMS'
    'JONES'
    'BROWN'
    'DAVIS'
    'MILLER'
    'WILSON'
```

The structure field `LastName` contains all of the data that was in the original dataset array variable, `LastName`.

See Also

`dataset` | `dataset2cell` | `struct2dataset`

More About

- “Dataset Arrays” on page 2-132

dataset2table

Convert dataset array to table

Syntax

```
t = dataset2table(ds)
```

Description

`t = dataset2table(ds)` converts a dataset array to a table.

Examples

Convert a Dataset Array to a Table

Load the sample data, which contains nutritional information for 77 cereals.

```
load cereal;
```

Create a dataset array containing the calorie, protein, fat, and name data for the first five cereals. Label the variables.

```
Calories = Calories(1:5);
Protein = Protein(1:5);
Fat = Fat(1:5);
Name = Name(1:5);

cereal = dataset(Calories,Protein,Fat,'ObsNames',Name)
cereal.Properties.VarDescription = Variables(4:6,2);
```

```
cereal =

                            Calories    Protein    Fat
    100% Bran                70         4          1
    100% Natural Bran       120         3          5
    All-Bran                 70         4          1
    All-Bran with Extra Fiber 50        4          0
    Almond Delight          110         2          2
```

Convert the dataset array to a table.

```
t = dataset2table(cereal)
```

```
t =

                              Calories    Protein    Fat
                              --------    -------    ---
    100% Bran                  70         4          1
    100% Natural Bran         120         3          5
    All-Bran                   70         4          1
    All-Bran with Extra Fiber  50         4          0
    Almond Delight            110         2          2
```

Input Arguments

ds — Input dataset array

dataset array

Input dataset array to convert to a table, specified as a dataset array. Each variable in ds becomes a variable in the output table t.

Output Arguments

t — Output table

table

Output table, returned as a table. The table can store metadata such as descriptions, variable units, variable names, and row names. For more information, see `Table Properties`.

More About

- "Array Dimensions"
- "Dataset Arrays" on page 2-132

See Also

`dataset | table`

datasetfun

Class: dataset

Apply function to dataset array variables

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
b = datasetfun(fun,A)
[b,c,...] = datasetfun(fun,A)
[b,...] = datasetfun(fun,A,...,'UniformOutput',false)
[b,...] = datasetfun(fun,A,...,'DatasetOutput',true)
[b,...] = datasetfun(fun,A,...,'DataVars',vars)
[b,...] = datasetfun(fun,A,...,'ObsNames',obsnames)
[b,...] = datasetfun(fun,A,...,'ErrorHandler',efun)
```

Description

`b = datasetfun(fun,A)` applies the function specified by `fun` to each variable of the dataset array `A`, and returns the results in the vector `b`. The *i*th element of `b` is equal to `fun` applied to the *i*th dataset variable of `A`. `fun` is a function handle to a function that takes one input argument and returns a scalar value. `fun` must return values of the same class each time it is called, and `datasetfun` concatenates them into the vector `b`. The outputs from `fun` must be one of the following types: numeric, logical, character, structure, or cell.

To apply functions that return results that are nonscalar or of different sizes and types, use the `'UniformOutput'` or `'DatasetOutput'` parameters described below.

Do not rely on the order in which `datasetfun` computes the elements of `b`, which is unspecified.

If `fun` is bound to more than one built-in function or file, (that is, if it represents a set of overloaded functions), `datasetfun` follows MATLAB dispatching rules in calling the function. (See "Function Precedence Order".)

`[b,c,...] = datasetfun(fun,A)`, where `fun` is a function handle to a function that returns multiple outputs, returns vectors `b`, `c`, ..., each corresponding to one of the output arguments of `fun`. `datasetfun` calls `fun` each time with as many outputs as there are in the call to `datasetfun`. `fun` may return output arguments having different classes, but the class of each output must be the same each time `fun` is called.

`[b,...] = datasetfun(fun,A,...,'UniformOutput',false)` allows you to specify a function `fun` that returns values of different sizes or types. `datasetfun` returns a cell array (or multiple cell arrays), where the *i*th cell contains the value of `fun` applied to the *i*th dataset variable of `A`. Setting `'UniformOutput'` to `true` is equivalent to the default behavior.

`[b,...] = datasetfun(fun,A,...,'DatasetOutput',true)` specifies that the output(s) of `fun` are returned as variables in a dataset array (or multiple dataset arrays). `fun` must return values with the same number of rows each time it is called, but it may return values of any type. The variables in the output dataset array(s) have the same names as the variables in the input. Setting `'DatasetOutput'` to `false` (the default) specifies that the type of the output(s) from `datasetfun` is determined by `'UniformOutput'`.

`[b,...] = datasetfun(fun,A,...,'DataVars',vars)` allows you to apply `fun` only to the dataset variables in `A` specified by `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

`[b,...] = datasetfun(fun,A,...,'ObsNames',obsnames)` specifies observation names for the dataset output when `'DatasetOutput'` is `true`.

`[b,...] = datasetfun(fun,A,...,'ErrorHandler',efun)`, where `efun` is a function handle, specifies the MATLAB function to call if the call to `fun` fails. The error-handling function is called with the following input arguments:

- A structure with the fields `identifier`, `message`, and `index`, respectively containing the identifier of the error that occurred, the text of the error message, and the linear index into the input array(s) at which the error occurred

- The set of input arguments at which the call to the function failed

The error-handling function should either re-throw an error, or return the same number of outputs as `fun`. These outputs are then returned as the outputs of `datasetfun`. If `'UniformOutput'` is true, the outputs of the error handler must also be scalars of the same type as the outputs of `fun`. For example, the following code could be saved in a file as the error-handling function:

```
function [A,B] = errorFunc(S,varargin)

warning(S.identifier,S.message);
A = NaN;
B = NaN;
```

If an error-handling function is not specified, the error from the call to `fun` is rethrown.

Examples

Work With Datasets Using Function Handles

Use function handles to compute the mean and plot a histogram of selected variables in a dataset array.

Load the sample data.

```
load hospital
```

Use `datasetfun` to compute the means of the `Weight` and `BloodPressure` variables, and store the results in a dataset array.

```
stats = datasetfun(@mean,hospital,...
        'DataVars',{'Weight','BloodPressure'},...
        'UniformOutput',false)


stats =

    [154]    [1x2 double]
```

The variable `BloodPressure` contains two columns: One for the systolic measurement, and one for the diastolic measurement.

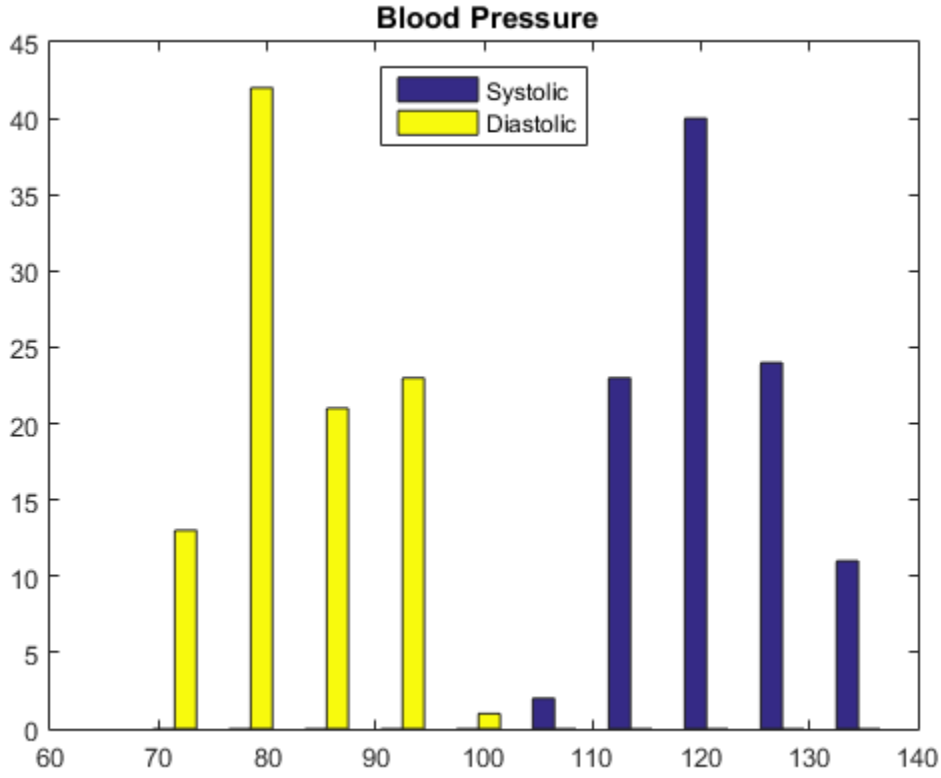
Display the mean of the blood pressure variable.

```
stats{2}
```

```
ans =

  122.7800   82.9600
```

Plot a histogram of the blood pressure variable.

```
datasetfun(@hist,hospital,...
           'DataVars','BloodPressure',...
           'UniformOutput',false);
title('{\bf Blood Pressure}')
legend('Systolic','Diastolic','Location','N')
```



See Also

`grpstats`

daugment

D-optimal augmentation

Syntax

```
dCE2 = daugment(dCE,mruns)
[dCE2,X] = daugment(dCE,mruns)
[dCE2,X] = daugment(dCE,mruns,model)
[dCE2,X] = daugment(...,param1,val1,param2,val2,...)
```

Description

`dCE2 = daugment(dCE,mruns)` uses a coordinate-exchange algorithm to *D*-optimally add `mruns` runs to an existing experimental design `dCE` for a linear additive model.

`[dCE2,X] = daugment(dCE,mruns)` also returns the design matrix `X` associated with the augmented design.

`[dCE2,X] = daugment(dCE,mruns,model)` uses the linear regression model specified in `model`. `model` is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n – 1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Alternatively, `model` can be a matrix specifying polynomial terms of arbitrary order. In this case, `model` should have one column for each factor and one row for each term in

the model. The entries in any row of *model* are powers for the factors in the columns. For example, if a model has factors X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

[dCE2,X] = daugment(...,*param1*,*val1*,*param2*,*val2*,...) specifies additional parameter/value pairs for the design. Valid parameters and their values are listed in the following table.

Parameter	Value
'bounds'	Lower and upper bounds for each factor, specified as a 2-by-nfactors matrix, where nfactors is the number of factors. Alternatively, this value can be a cell array containing nfactors elements, each element specifying the vector of allowable values for the corresponding factor.
'categorical'	Indices of categorical predictors.
'display'	Either 'on' or 'off' to control display of the iteration counter. The default is 'on'.
'excludefun'	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with nfactors columns, where nfactors is the number of factors, and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the ith row S should be excluded.
'init'	Initial design as an mruns-by-nfactors matrix, where nfactors is the number of factors. The default is a randomly selected set of points.
'levels'	Vector of number of levels for each factor.
'maxiter'	Maximum number of iterations. The default is 10.
'options'	The value is a structure that contains options specifying whether to compute multiple tries in parallel, and specifying how to use random numbers when generating the starting points for the tries. Create the options structure with statset. Applicable statset parameters are: • 'UseParallel' — If true and if a parpool of the Parallel Computing Toolbox is open, compute in parallel. If the Parallel

Parameter	Value

	Computing Toolbox is not installed, or a `parpool` is not open, computation occurs in serial mode. Default is `false`, meaning serial computation.
	• `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
	• `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `daugment` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
	  • You have an open Parallel pool
	  • `UseParallel` is `true`
	  • `UseSubstreams` is `false`
	In that case, use a cell array the same size as the Parallel pool.

`'tries'`	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is `1`.

Note: The `daugment` function augments an existing design using a coordinate-exchange algorithm; the `'start'` parameter of the `candexch` function provides the same functionality using a row-exchange algorithm.

Examples

The following eight-run design is adequate for estimating main effects in a four-factor model:

```
dCEmain = cordexch(4,8)
dCEmain =
     1    -1    -1     1
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
```

```
     1     1     1     1
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
```

To estimate the six interaction terms in the model, augment the design with eight additional runs:

```
dCEinteraction = daugment(dCEmain,8,'interaction')
dCEinteraction =
     1    -1    -1     1
    -1    -1     1     1
    -1     1    -1     1
     1     1     1    -1
     1     1     1     1
    -1     1    -1    -1
     1    -1    -1    -1
    -1    -1     1    -1
    -1     1     1     1
    -1    -1    -1    -1
     1    -1     1    -1
     1     1    -1     1
    -1     1     1    -1
     1     1    -1    -1
     1    -1     1     1
     1     1     1    -1
```

The augmented design is full factorial, with the original eight runs in the first eight rows.

See Also

`dcovary` | `cordexch` | `candexch`

dcovary

D-optimal design with fixed covariates

Syntax

```
dCV = dcovary(nfactors,fixed)
[dCV,X] = dcovary(nfactors,fixed)
[dCV,X] = dcovary(nfactors,fixed,model)
[dCV,X] = daugment(...,param1,val1,param2,val2,...)
```

Description

`dCV = dcovary(nfactors,fixed)` uses a coordinate-exchange algorithm to generate a *D*-optimal design for a linear additive model with `nfactors` factors, subject to the constraint that the model include the fixed covariate factors in `fixed`. The number of runs in the design is the number of rows in `fixed`. The design `dCV` augments `fixed` with initial columns for treatments of the model terms.

`[dCV,X] = dcovary(nfactors,fixed)` also returns the design matrix `X` associated with the design.

`[dCV,X] = dcovary(nfactors,fixed,model)` uses the linear regression model specified in *`model`*. *`model`* is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n – 1, n)

4 The squared terms in order 1, 2, ..., *n*

Other models use a subset of these terms, in the same order.

Alternatively, *`model`* can be a matrix specifying polynomial terms of arbitrary order. In this case, *`model`* should have one column for each factor and one row for each term in the model. The entries in any row of *`model`* are powers for the factors in the columns. For example, if a model has factors `X1`, `X2`, and `X3`, then a row `[0 1 2]` in *`model`* specifies the term `(X1.^0).*(X2.^1).*(X3.^2)`. A row of all zeros in *`model`* specifies a constant term, which can be omitted.

`[dCV,X] = daugment(...,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` specifies additional parameter/value pairs for the design. Valid parameters and their values are listed in the following table.

Parameter	Value
`'bounds'`	Lower and upper bounds for each factor, specified as a `2`-by-`nfactors` matrix. Alternatively, this value can be a cell array containing `nfactors` elements, each element specifying the vector of allowable values for the corresponding factor.
`'categorical'`	Indices of categorical predictors.
`'display'`	Either `'on'` or `'off'` to control display of the iteration counter. The default is `'on'`.
`'excludefun'`	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with `nfactors` columns and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the ith row S should be excluded.
`'init'`	Initial design as an `mruns`-by-`nfactors` matrix. The default is a randomly selected set of points.
`'levels'`	Vector of number of levels for each factor.
`'maxiter'`	Maximum number of iterations. The default is `10`.
`'options'`	The value is a structure that contains options specifying whether to compute multiple tries in parallel, and specifying how to use random numbers when generating the starting points for the tries. Create the options structure with `statset`. Applicable `statset` parameters are:

Parameter	Value

	• `'UseParallel'` — If `true` and if a `parpool` of the Parallel Computing Toolbox is open, compute in parallel. If the Parallel Computing Toolbox is not installed, or a `parpool` is not open, computation occurs in serial mode. Default is `false`, meaning serial computation.
	• `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
	• `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `dcovary` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
	  • You have an open Parallel pool
	  • `UseParallel` is `true`
	  • `UseSubstreams` is `false`
	  In that case, use a cell array the same size as the Parallel pool.

`'tries'`	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is `1`.

Examples

Example 1

Suppose you want a design to estimate the parameters in a three-factor linear additive model, with eight runs that necessarily occur at different times. If the process experiences temporal linear drift, you may want to include the run time as a variable in the model. Produce the design as follows:

```
time = linspace(-1,1,8)';
[dCV1,X] = dcovary(3,time,'linear')
dCV1 =
   -1.0000    1.0000    1.0000   -1.0000
```

```
    1.0000   -1.0000   -1.0000   -0.7143
   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000   -1.0000    1.0000   -0.1429
    1.0000    1.0000   -1.0000    0.1429
   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    0.7143
   -1.0000   -1.0000    1.0000    1.0000
X =
    1.0000   -1.0000    1.0000    1.0000   -1.0000
    1.0000    1.0000   -1.0000   -1.0000   -0.7143
    1.0000   -1.0000   -1.0000   -1.0000   -0.4286
    1.0000    1.0000   -1.0000    1.0000   -0.1429
    1.0000    1.0000    1.0000   -1.0000    0.1429
    1.0000   -1.0000    1.0000   -1.0000    0.4286
    1.0000    1.0000    1.0000    1.0000    0.7143
    1.0000   -1.0000   -1.0000    1.0000    1.0000
```

The column vector `time` is a fixed factor, normalized to values between ±1. The number of rows in the fixed factor specifies the number of runs in the design. The resulting design `dCV` gives factor settings for the three controlled model factors at each time.

Example 2

The following example uses the `dummyvar` function to block an eight-run experiment into 4 blocks of size 2 for estimating a linear additive model with two factors:

```
fixed = dummyvar([1 1 2 2 3 3 4 4]);
dCV2 = dcovary(2,fixed(:,1:3),'linear')
dCV2 =
   1   1   1   0   0
  -1  -1   1   0   0
  -1   1   0   1   0
   1  -1   0   1   0
   1   1   0   0   1
  -1  -1   0   0   1
  -1   1   0   0   0
   1  -1   0   0   0
```

The first two columns of `dCV2` contain the settings for the two factors; the last three columns are dummy variable codings for the four blocks.

See Also

`daugment` | `cordexch` | `dummyvar`

DefaultYfit property

Class: TreeBagger

Default value returned by `predict` and `oobPredict`

Description

The `DefaultYfit` property controls what predicted value `TreeBagger` returns when no prediction is possible, for example when the `oobPredict` method needs to predict for an observation that is in-bag for all trees in the ensemble.

For classification, you can set this property to either `''` or `'MostPopular'`. If you choose `'MostPopular'` (default), the property value becomes the name of the most probable class in the training data.

For regression, you can set this property to any numeric scalar. The default is the mean of the response for the training data.

If you set this property to `''` for classification or `NaN` for regression, `TreeBagger` excludes the in-bag observations from computation of the out-of-bagerror and margin.

See Also

`Predict` | `oobPredict` | `OOBIndices`

delete

Class: qrandstream

Delete handle object

Syntax

```
delete(h)
```

Description

`delete(h)` deletes the handle object `h`, where `h` is a scalar handle. The `delete` method deletes a handle object but does not clear the handle from the workspace. A deleted handle is no longer valid.

See Also

`clear` | `isvalid` | `qrandstream`

DeltaCritDecisionSplit property

Class: TreeBagger

Split criterion contributions for each predictor

Description

The `DeltaCritDecisionSplit` property is a numeric array of size 1-by-`Nvars` of changes in the split criterion summed over splits on each variable, averaged across the entire ensemble of grown trees.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

dendrogram

Dendrogram plot

Syntax

```
dendrogram(tree)
dendrogram(tree,Name,Value)

dendrogram(tree,P)
dendrogram(tree,P,Name,Value)

H = dendrogram( ___ )
[H,T,outperm] = dendrogram( ___ )
```

Description

`dendrogram(tree)` generates a dendrogram plot of the hierarchical binary cluster tree. A dendrogram consists of many *U*-shaped lines that connect data points in a hierarchical tree. The height of each *U* represents the distance between the two data points being connected.

- If there are 30 or fewer data points in the original data set, then each leaf in the dendrogram corresponds to one data point.
- If there are more than 30 data points, then `dendrogram` collapses lower branches so that there are 30 leaf nodes. As a result, some leaves in the plot correspond to more than one data point.

`dendrogram(tree,Name,Value)` uses additional options specified by one or more name-value pair arguments.

`dendrogram(tree,P)` generates a dendrogram plot with no more than `P` leaf nodes. If there are more than `P` data points in the original data set, then `dendrogram` collapses the lower branches of the tree. As a result, some leaves in the plot correspond to more than one data point.

`dendrogram(tree,P,Name,Value)` uses additional options specified by one or more name-value pair arguments.

`H = dendrogram( ___ )` generates a dendrogram plot and returns a vector of line handles. You can use any of the input arguments from the previous syntaxes.

`[H,T,outperm] = dendrogram( ___ )` also returns a vector containing the leaf node number for each object in the original data set, `T`, and a vector giving the order of the node labels of the leaves as shown in the dendrogram, `outperm`.

- It is useful to return `T` when the number of leaf nodes, P, is less than the total number of data points, so that some leaf nodes in the display correspond to multiple data points.
- The order of the node labels given in `outperm` is from left to right for a horizontal dendrogram, and from bottom to top for a vertical dendrogram.

Examples

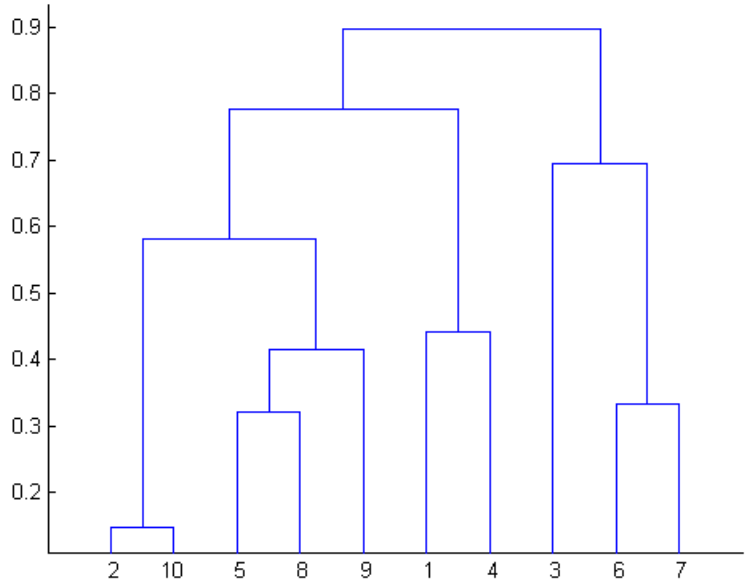
Plot Dendrogram

Generate sample data.

```
rng('default') % For reproducibility
X = rand(10,3);
```

Create a hierarchical binary cluster tree using `linkage`. Then, plot the dendrogram using the default options.

```
tree = linkage(X,'average');

figure()
dendrogram(tree)
```



Specify Dendrogram Leaf Node Order

Generate sample data.

```
rng('default') % For reproducibility
X = rand(10,3);
```

Create a hierarchical binary cluster tree using `linkage`.

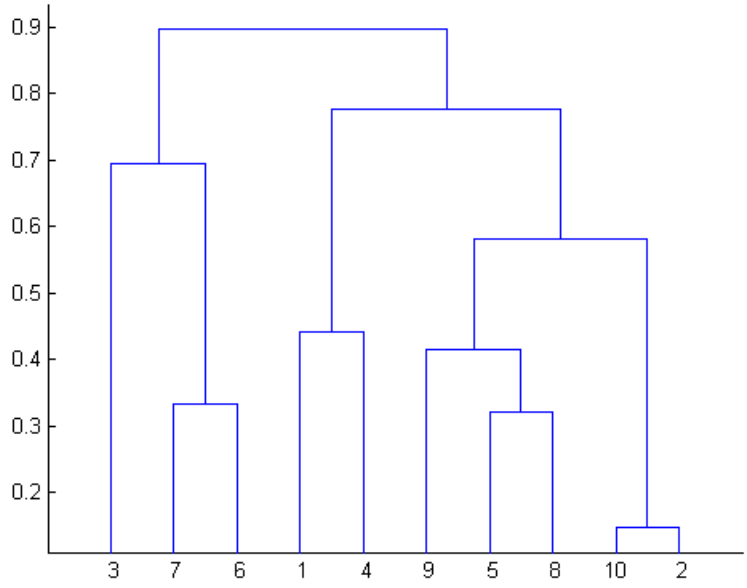
```
tree = linkage(X,'average');

D = pdist(X);
leafOrder = optimalleaforder(tree,D)
```

```
leafOrder =

     3     7     6     1     4     9     5     8    10     2
```

Plot the dendrogram using an optimal leaf order.

```
figure()
```

```
dendrogram(tree,'Reorder',leafOrder)
```



The order of the leaf nodes in the dendrogram plot corresponds—from left to right—to the permutation in `leafOrder`.

Specify Number of Nodes in Dendrogram Plot

Generate sample data.

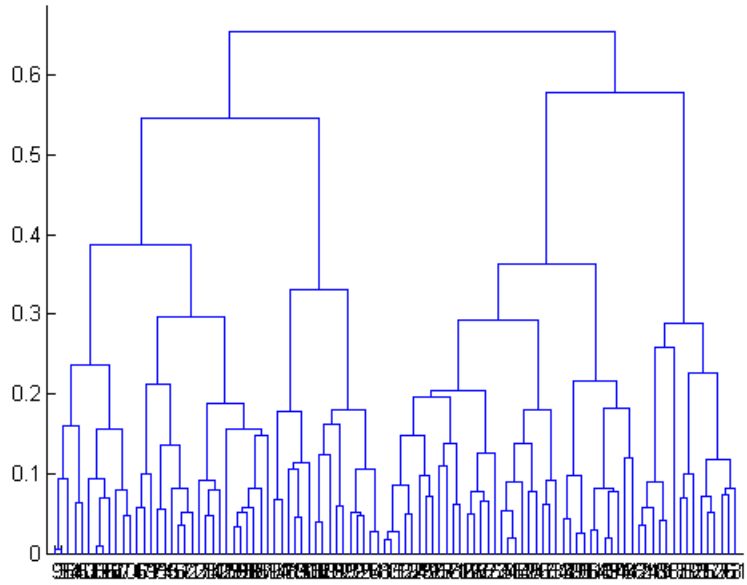
```
rng('default') % For reproducibility
X = rand(100,2);
```

There are 100 data points in the original data set, `X`.

Create a hierarchical binary cluster tree using `linkage`. Then, plot the dendrogram for the complete tree (100 leaf nodes) by setting the input argument `P` equal to `0`.

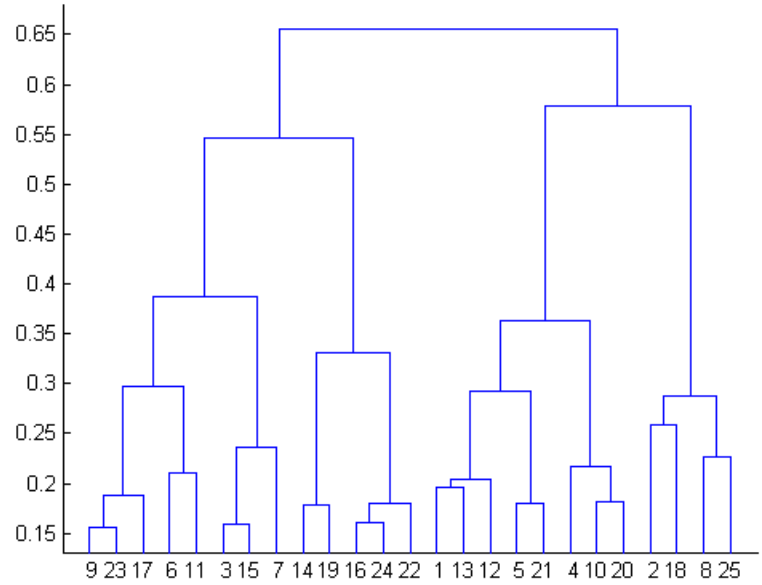
```
tree = linkage(X,'average');
```

```
figure()
dendrogram(tree,0)
```



Now, plot the dendrogram with only 25 leaf nodes. Return the mapping of the original data points to the leaf nodes shown in the plot.

```
figure()
[~,T] = dendrogram(tree,25);
```



List the original data points that are in leaf node 7 of the dendrogram plot.

```
find(T==7)
```

```
ans =

     7
    33
    60
    70
    74
    76
    86
```

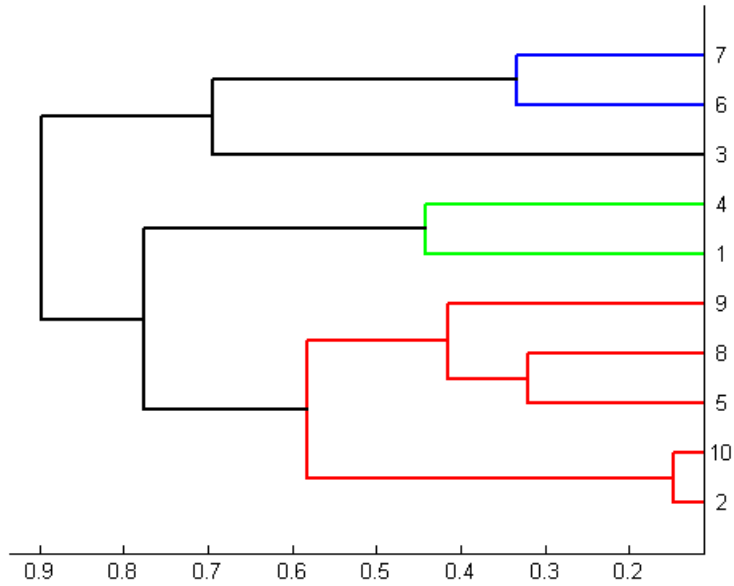
Change Dendrogram Orientation and Line Width

Generate sample data.

```
rng('default') % For reproducibility
X = rand(10,3);
```

Create a hierarchical binary cluster tree using `linkage`. Then, plot the dendrogram with a vertical orientation, using the default color threshold. Return handles to the lines so you can change the dendrogram line widths.

```
tree = linkage(X,'average');

figure()
H = dendrogram(tree,'Orientation','left','ColorThreshold','default');
set(H,'LineWidth',2)
```



Input Arguments

`tree` — Hierarchical binary cluster tree

matrix returned by `linkage`

Hierarchical binary cluster tree, specified as an $(M-1)$-by-3 matrix that you generate using `linkage`, where M is the number of data points in the original data set.

`P` — Maximum number of leaf nodes

30 (default) | positive integer value

Maximum number of leaf nodes to include in the dendrogram plot, specified as a positive integer value.

- If there are `P` or fewer data points in the original data set, then each leaf in the dendrogram corresponds to one data point.
- If there are more than `P` data points, then `dendrogram` collapses lower branches so that there are `P` leaf nodes. As a result, some leaves in the plot correspond to more than one data point.

  If you do not specify `P`, then `dendrogram` uses 30 as the maximum number of leaf nodes. To display the complete tree, set `P` equal to `0`.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Orientation','left','Reorder',myOrder` specifies a vertical dendrogram with leaves in the order specified by `myOrder`.

`'Reorder'` — Order of leaf nodes

vector

Order of leaf nodes in the dendrogram plot, specified as the comma-separated pair consisting of `'Reorder'` and a vector giving the order of nodes in the complete tree. The order vector must be a permutation of the vector `1:M`, where *M* is the number of data points in the original data set. Specify the order from left to right for horizontal dendrograms, and from bottom to top for vertical dendrograms.

If *M* is greater than the number of leaf nodes in the dendrogram plot, P (by default, P is 30), then you can only specify a permutation vector that does not separate the groups of leaves that correspond to collapsed nodes.

Example:

Data Types: `single` | `double`

`'CheckCrossing'` — Indicator for whether to check for crossing branches

`true` (default) | `false`

Indicator for whether to check for crossing branches in the dendrogram plot, specified as the comma-separated pair consisting of `'CheckCrossing'` and either `true` or `false`. This option is only useful when you specify a value for Reorder.

When `CheckCrossing` has the value `true`, `dendrogram` issues a warning if the order of the leaf nodes causes crossing branches in the plot. If the dendrogram plot does not show a complete tree (because the number of data points in the original data set is greater than P), `dendrogram` only issues a warning when the order of the leaf nodes causes branch to cross in the dendrogram as shown in the plot. That is, there is no warning if the order causes crossing branches in the complete tree but not in the dendrogram as shown in the plot.

Data Types: `logical`

`'ColorThreshold'` — Threshold for unique colors

`'default'` | scalar value in the range `(0,max(tree(:,3)))`

Threshold for unique colors in the dendrogram plot, specified as the comma-separated pair consisting of `'ColorThreshold'` and either the string `'default'` or a scalar value in the range `(0,max(tree(:,3)))`. If `ColorThreshold` has the value *T*, then `dendrogram` assigns a unique color to each group of nodes in the dendrogram whose linkage is less than *T*.

- If `ColorThreshold` has the value `'default'`, then the threshold, *T*, is 70% of the maximum linkage, `0.7*max(tree(:,3))`.
- If you do not specify a value for `ColorThreshold`, or if you specify a threshold outside the range `(0,max(tree(:,3)))`, then `dendrogram` uses only one color for the dendrogram plot.

`'Orientation'` — Orientation of dendrogram

`'top'` (default) | `'bottom'` | `'left'` | `'right'`

Orientation of the dendrogram in the figure window, specified as the comma-separated pair consisting of `'Orientation'` and one of these strings:

`'top'`	Top to bottom

`'bottom'`	Bottom to top
`'left'`	Left to right
`'right'`	Right to left

Data Types: `char`

`'Labels'` — Label for each data point
character array | cell array of strings

Label for each data point in the original data set, specified as the comma-separated pair consisting of `'Labels'` and a character array or cell array of strings. `dendrogram` labels any leaves in the dendrogram plot containing a single data point with that data point's label.

Data Types: `char | cell`

Output Arguments

`H` — Handles to lines
vector

Handles to lines in the dendrogram plot, returned as a vector.

`T` — Leaf node numbers
column vector

Leaf node numbers for each data point in the original data set, returned as a column vector of length *M*, where *M* is the number of data points in the original data set.

When there are fewer than P data points in the original data (`P` is 30, by default), all data points are displayed in the dendrogram, with each node containing a single data point. In this case, `T` is the identity map, `T = (1:M)'`.

`T` is useful when P is less than the total number of data points. That is, when some leaf nodes in the dendrogram display correspond to multiple data points. For example, to find out which data points are contained in leaf node `k` of the dendrogram plot, use `find(T==k)`.

`outperm` — Permutation of node labels
vector

Permutation of the node labels of the leaves of the dendrogram as shown in the plot, returned as a row vector. `outperm` gives the order from left to right for a horizontal dendrogram, and from bottom to top for a vertical dendrogram. If there are P leaves in the dendrogram plot, `outperm` is a permutation of the vector `1:P`.

See Also

`cluster` | `clusterdata` | `cophenet` | `inconsistent` | `linkage` | `pdist` | `silhouette`

Description property

Class: dataset

String describing data set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

`Description` is a string describing the data set. The default is an empty string.

designecoc

Coding matrix for reducing error-correcting output code to binary

Syntax

```
M = designecoc(K,name)
M = designecoc(K,name,Name,Value)
```

Description

`M = designecoc(K,name)` returns the coding matrix `M` that reduces the error-correcting output code (ECOC) design specified by `name` and `K` classes to a binary problem. `M` has `K` rows and L columns, with each row corresponding to a class and each column corresponding to a binary learner. `name` and `K` determine the value of L.

You can view or customize `M`, and then specify it as the coding matrix for training an ECOC multiclass classifier using `fitcecoc`.

`M = designecoc(K,name,Name,Value)` returns the coding matrix with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the number of trials when generating a dense or sparse, random coding matrix.

Examples

Train ECOC Classifiers Using a Custom Coding Design

Consider the `arrhythmia` data set. There are 16 classes in the study, 13 of which are represented in the data. The first class indicates that the subject did not have arrhythmia, and the last class indicates that the subject's arrhythmia state was not recorded. Suppose that the other classes are ordinal levels indicating the severity of arrhythmia. Train an ECOC classifier using a custom coding design specified by the description of the classes.

Load the `arrhythmia` data set.

```
load arrhythmia
K = 13; % Number of distinct classes
```

Construct a coding matrix that describes the nature of the classes.

```
OrdMat = designecoc(11,'ordinal');
nOM = size(OrdMat);
class1VSOrd = [1; -ones(11,1); 0];
class1VSClass16 = [1; zeros(11,1); -1];
OrdVSClass16 = [0; ones(11,1); -1];
Coding = [class1VSOrd class1VSClass16 OrdVSClass16,...
    [zeros(1,nOM(2)); OrdMat; zeros(1,nOM(2))]]
```

```
Coding =

     1     1     0     0     0     0     0     0     0     0     0     0     0
    -1     0     1    -1    -1    -1    -1    -1    -1    -1    -1    -1    -1
    -1     0     1     1    -1    -1    -1    -1    -1    -1    -1    -1    -1
    -1     0     1     1     1    -1    -1    -1    -1    -1    -1    -1    -1
    -1     0     1     1     1     1    -1    -1    -1    -1    -1    -1    -1
    -1     0     1     1     1     1     1    -1    -1    -1    -1    -1    -1
    -1     0     1     1     1     1     1     1    -1    -1    -1    -1    -1
    -1     0     1     1     1     1     1     1     1    -1    -1    -1    -1
    -1     0     1     1     1     1     1     1     1     1    -1    -1    -1
    -1     0     1     1     1     1     1     1     1     1     1    -1    -1
    -1     0     1     1     1     1     1     1     1     1     1     1    -1
    -1     0     1     1     1     1     1     1     1     1     1     1     1
     0    -1    -1     0     0     0     0     0     0     0     0     0     0
```

Train an ECOC classifier using the custom coding design `Coding` and specify that the binary learners are decision trees.

```
Mdl = fitcecoc(X,Y,'Coding',Coding,'Learner','Tree');
```

Estimate the in-sample classification error.

```
genErr = resubLoss(Mdl)
```

```
genErr =

    0.1460
```

Choose Among Several Random Coding Designs

If you request a random coding matrix by specifying `sparserandom` or `denserandom`, then, by default, `designecoc` generates 10,000 random matrices. Then, it chooses the matrix with the largest, minimal, pair-wise row distances based on the Hamming measure. You can specify to generate more matrices to increase the chance of obtaining a better one, or you can generate several coding matrices, and then see which performs best.

Load the `arrhythmia` data set. Reserve the observations classified into class 16 (i.e., those that do not have an arrhythmia classification) as new data.

```
load arrhythmia
oosIdx = Y == 16;
isIdx = ~oosIdx;
Y = categorical(Y(isIdx));
tabulate(Y)
K = numel(unique(Y));
```

```
  Value    Count   Percent
      1      245     56.98%
      2       44     10.23%
      3       15      3.49%
      4       15      3.49%
      5       13      3.02%
      6       25      5.81%
      7        3      0.70%
      8        2      0.47%
      9        9      2.09%
     10       50     11.63%
     14        4      0.93%
     15        5      1.16%
```

Generate four random coding design matrices such that the first two are dense and the second two are sparse. Specify to find the best out of 20,000 variates.

```
rng(1); % For reproducibility

Coding = cell(4,1); % Preallocate for coding matrices
CodingTypes = {'denserandom','denserandom','sparserandom','sparserandom'};
for j = 1:4;
    Coding{j} = designecoc(K,CodingTypes{j},'NumTrials',2e4);
```

```
end
```

`Coding` is a 4-by-1 cell array, where each cell is a coding design matrix. The matrices have `K` rows, but the number of columns (i.e., binary learners) might vary.

Train and cross validate ECOC classifiers using the 15-fold cross validation. Specify that each ECOC classifier be trained using a classification tree, and the random coding matrix stored in `Coding`.

```
Mdl = cell(4,1); % Preallocate for the ECOC classifiers
for j = 1:4;
    Mdl{j} = fitcecoc(X(isIdx,:),Y,'Learners','tree',...
        'Coding',Coding{j},'KFold',15);
end
```

```
Warning: One or more folds do not contain points from all the groups.
Warning: One or more folds do not contain points from all the groups.
Warning: One or more folds do not contain points from all the groups.
Warning: One or more folds do not contain points from all the groups.
```

`Mdl` is a 4-by-1 cell array of `ClassificationPartitionedECOC` models. Several classes have low relative frequency in the data, and so there is a chance that, during cross validation, some in-sample folds will not train using observations from those classes.

Estimate the 15-fold classification error for each classifier.

```
genErr = nan(4,1);
for j = 1:4;
    genErr(j) = kfoldLoss(Mdl{j});
end

genErr
```

```
genErr =

    0.2279
    0.2163
    0.2116
    0.2256
```

Though the generalization error is still high, the best performing model, based solely on the out-of-sample classification error, is the model that used the coding design `Coding{3}`.

You can try to improve the generalization error by tuning some parameters of the binary learners. For example, you can specify to use the twoing rule or deviance for the split criterion, rather than the default Gini's diversity index. You might also specify to use surrogate splits since there are missing values in the data.

Input Arguments

K — Number of classes

positive integer

Number of classes, specified as a positive integer.

`K` specifies the number of rows of the coding matrix M.

Data Types: `single` | `double`

name — Coding design name

`'binarycomplete'` | `'denserandom'` | `'onevsall'` | `'onevsone'` | `'sparserandom'` | ...

Coding design name, specified as a string. This table summarizes the available coding schemes.

Value	Number of Binary Learners	Description
`'allpairs'` and `'onevsone'`	$K(K-1)/2$	For each binary learner, one class is positive, another is negative, and the software ignores the rest. This design exhausts all combinations of class pair assignments.
`'binarycomplete'`	$2^{(K-1)}-1$	This design partitions the classes into all binary combinations, and does not ignore any classes. For each binary learner, all class assignments are `-1` and `1` with at least one positive and negative class in the assignment.

Value	Number of Binary Learners	Description
`'denserandom'`	Random, but approximately $10 \log_2 K$	For each binary learner, the software randomly assigns classes into positive or negative classes, with at least one of each type. For more details, see "Random Coding Design Matrices" on page 22-1542.
`'onevsall'`	K	For each binary learner, one class is positive and the rest are negative. This design exhausts all combinations of positive class assignments.
`'ordinal'`	$K - 1$	For the first binary learner, the first class is negative, and the rest positive. For the second binary learner, the first two classes are negative, the rest positive, and so on.
`'sparserandom'`	Random, but approximately $15 \log_2 K$	For each binary learner, the software randomly assigns classes as positive or negative with probability 0.25 for each, and ignores classes with probability 0.5. For more details, see "Random Coding Design Matrices" on page 22-1542.
`'ternarycomplete'`	$\left(3^K - 2^{(K+1)} + 1\right)/2$	This design partitions the classes into all ternary combinations. All class assignments are `0`, `-1`, and `1` with at least one positive and one negative class in the assignment.

Data Types: `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'NumTrials',1000` specifies to generate `1000` random matrices.

`'NumTrials'` — Number of random coding matrices to generate

`10000` (default) | positive integer

Number of random coding matrices to generate, specified as the comma-separated pair consisting of `'NumTrials'` and a positive integer.

The software:

- Generates `NumTrials` matrices, and selects the one with the maximal, pair-wise row distance.
- Ignores `NumTrials` for all values of `name` except `'denserandom'` and `'sparserandom'`.

Example: `'NumTrials',1000`

Data Types: `single | double`

Output Arguments

`M` — Coding matrix

numeric matrix

Coding matrix that reduces an ECOC scheme to binary, returned as a numeric matrix. `M` has K rows and L columns, where L is the number of binary learners. Each row corresponds to a class and each column corresponds to a binary learner.

The elements of `M` are `-1`, `0`, or `1`, and the value corresponds to a dichotomous class assignment. This table describes the meaning of `M(i,j)`, that is, the class that learner `j` assigns to observations in class `i`.

Value	Dichotomous Class Assignment
-1	Negative class
0	Before training, learner `j` removes observations in class `i` from the data set.
1	Positive class

The binary learners for designs `denserandom`, `binarycomplete`, and `onevsall` do not assign `0` to observations in any class.

More About

Tips

- The number of binary learners grows with the number of classes. For a problem with many classes, the `binarycomplete` and `ternarycomplete` coding designs are not efficient. However:
  - If $K \leq 4$, then use `ternarycomplete` coding design rather than `sparserandom`.
  - If $K \leq 5$, then use `binarycomplete` coding design rather than `denserandom`.

  You can display the coding design matrix of a trained ECOC classifier by entering `Mdl.CodingMatrix` into the Command Window.
- You should form a coding matrix using intimate knowledge of the application, and taking into account computational constraints. If you have sufficient computational power and time, then try several coding matrices and choose the one with the best performance (e.g., check the confusion matrices for each model using `confusionmat`).

Algorithms

Custom Coding Design Matrices

Custom coding matrices must have a certain form. The software validates custom coding matrices by ensuring:

- Every element is -1, 0, or 1.
- Every column contains as least one -1 and one 1.
- For all distinct column vectors u and v, $u \neq v$ and $u \neq -v$.

- All rows vectors are unique.
- The matrix can separate any two classes. That is, you can travel from any row to any other row following these rules:
  - You can move vertically from 1 to -1 or -1 to 1.
  - You can move horizontally from a nonzero element to another nonzero element.
  - You can use a column of the matrix for a vertical move only once.

  If it is not possible to move from row i to row j using these rules, then classes i and j cannot be separated by the design. For example, in the coding design

$$\begin{bmatrix} 1 & 0 \\ -1 & 0 \\ 0 & 1 \\ 0 & -1 \end{bmatrix}$$

  classes 1 and 2 cannot be separated from classes 3 and 4 (that is, you cannot move horizontally from the -1 in row 2 to column 2 since there is a 0 in that position). Therefore, the software rejects this coding design.

Random Coding Design Matrices

For a given number of classes, e.g., K, the software generates random coding design matrices as follows.

1. The software generates one of the following:
   a. Dense random — The software sets each element of the K-by-L_d coding design matrix with a 1 or a -1 with equal probability, where $L_d \approx \lceil 10 \log_2 K \rceil$.
   b. Sparse random — The software sets each element of the K-by-L_s coding design matrix with a 1, with probability 0.25, a -1 with probability 0.25, and a 0 with probability 0.5, where $L_s \approx \lceil 15 \log_2 K \rceil$.
2. If a column does not contain at least one 1 and at least one -1, then the software removes that column.
3. For distinct columns u and v, if $u = v$ or $u \neq -v$, then the software removes v from the coding design matrix.

The software randomly generates 10,000 matrices by default, and retains the matrix with the largest, minimal pair-wise row distance based on the Hamming measure ([4]) given by

$$\Delta(k_1,k_2)=0.5\sum_{l=1}^{L}\left|m_{k_1l}\right|\left|m_{k_2l}\right|\left|m_{k_1l}-m_{k_2l}\right|,$$

where m_{k_jl} is an element of coding design matrix j.

References

[1] Fürnkranz, Johannes. “Round Robin Classification.” *J. Mach. Learn. Res.*, Vol. 2, 2002, pp. 721–747.

[2] Escalera, S., O. Pujol, and P. Radeva. “Separability of ternary codes for sparse designs of error-correcting output codes.” *Pattern Recog. Lett.*, Vol. 30, Issue 3, 2009, pp. 285–297.

See Also

`ClassificationECOC` | `fitcecoc`

devianceTest

Class: GeneralizedLinearModel

Analysis of deviance

Syntax

```
tbl = devianceTest(mdl)
```

Description

`tbl = devianceTest(mdl)` returns an analysis of deviance table for the `mdl` generalized linear model. `tbl` gives the result of a test of whether the fitted model fits significantly better than a constant model.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

Output Arguments

`tbl`

Table containing two rows and four columns.

- The first row relates to a constant model.
- The second row relates to the full model in `mdl`.
- The columns are:

`Deviance`	Deviance is twice the difference between the log likelihoods of the corresponding

	model (`mdl` or constant) and the saturated model. The test statistic for the deviance test is twice the difference between the log likelihoods of the tested model mdl and the constant model. For more information, see Deviance.
`DFE`	Error degrees of freedom. It is the number of observations minus the number of parameters in the corresponding model.
`chi2Stat`	F statistic or Chi-squared statistic, depending on whether the dispersion is estimated (F statistic) or not (Chi-squared statistic) • *Chi-squared statistic* is the difference between the deviance of the constant model and the deviance of the full model. • *F statistic* is the difference between the deviance of the constant model and the deviance of the full model, divided by the estimated dispersion.
`pValue`	*p*-value associated with the test. It is the Chi-squared statistic with (number of coefficients in the model minus one) degrees of freedom, or *F* statistic with (number of coefficients in the model minus one) numerator degrees of freedom, and DFE denominator degrees of freedom.

Definitions

Deviance

Deviance of a model M_1 is twice the difference between the loglikelihood of that model and the saturated model, M_S. The saturated model is the model with the maximum number of parameters that can be estimated. For example, if there are n observations y_i,

$i = 1, 2, ..., n$, with potentially different values for $X_i^T\beta$, then you can define a saturated model with n parameters. Let $L(b,y)$ denote the maximum value of the likelihood function for a model. Then the deviance of model M_1 is

$$-2\left(\log L(b_1, y) - \log L(b_S, y)\right),$$

where b_1 are the estimated parameters for model M_1 and b_S are the estimated parameters for the saturated model. The deviance has a chi-square distribution with $n - p$ degrees of freedom, where n is the number of parameters in the saturated model and p is the number of parameters in model M_1.

If M_1 and M_2 are two different generalized linear models, then the fit of the models can be assessed by comparing the deviances D_1 and D_2 of these models. The difference of the deviances is

$$\begin{aligned} D = D_2 - D_1 &= -2\left(\log L(b_2, y) - \log L(b_S, y)\right) + 2\left(\log L(b_1, y) - \log L(b_S, y)\right) \\ &= -2\left(\log L(b_2, y) - \log L(b_1, y)\right). \end{aligned}$$

Asymptotically, this difference has a chi-square distribution with degrees of freedom v equal to the number of parameters that are estimated in one model but fixed (typically at 0) in the other. That is, it is equal to the difference in the number of parameters estimated in M_1 and M_2. You can get the p-value for this test using `1 - chi2cdf(D,V)`, where $D = D_2 - D_1$.

Examples

Deviance Test

Perform a deviance test on a generalized linear model.

Construct a generalized linear model.

```
rng('default') % for reproducibility
X = randn(100,5);
mu = exp(X(:,[1 4 5])*[.4;.2;.3]);
y = poissrnd(mu);
mdl = fitglm(X,y,'linear','Distribution','poisson');
```

Test whether the model differs from a constant in a statistically significant way.

```
tbl = devianceTest(mdl)
```

```
tbl =

                                    Deviance    DFE
                                    ________    ___

    log(y) ~ 1                      128.58      99
    log(y) ~ 1 + x1 + x2 + x3 + x4 + x5    83.726      94


                                    chi2Stat
                                    ________

    log(y) ~ 1
    log(y) ~ 1 + x1 + x2 + x3 + x4 + x5    44.858


                                      pValue
                                    __________

    log(y) ~ 1
    log(y) ~ 1 + x1 + x2 + x3 + x4 + x5    1.5502e-08
```

The *p*-value is very small, indicating that the model significantly differs from a constant.

See Also

`GeneralizedLinearModel`

More About

- “Generalized Linear Models” on page 10-12

designMatrix

Class: GeneralizedLinearMixedModel

Fixed- and random-effects design matrices

Syntax

```
D = designMatrix(glme)
D = designMatrix(glme,'Fixed')

D = designMatrix(glme,'Random')
Dsub = designMatrix(glme,'Random',gnumbers)
[Dsub,gnames] = designMatrix(glme,'Random',gnumbers)
```

Description

`D = designMatrix(glme)` or `D = designMatrix(glme,'Fixed')` returns the fixed-effects design matrix for the generalized linear mixed-effects model glme.

`D = designMatrix(glme,'Random')` returns the random-effects design matrix for the generalized linear mixed-effects model glme.

`Dsub = designMatrix(glme,'Random',gnumbers)` returns a subset of the random-effects design matrix for the generalized linear mixed-effects model glme that corresponds to the grouping variables indicated by gnumbers.

`[Dsub,gnames] = designMatrix(glme,'Random',gnumbers)` also returns the grouping variable names that correspond to gnumbers.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

`gnumbers` — Grouping variable numbers

array of integer values

Grouping variable numbers, specified as an array of integer values containing elements in the range [1,*R*], where *R* is the length of the cell array that contains the grouping variables for the generalized linear mixed-effects model glme.

For example, you can specify the grouping variables g_1, g_3, and g_r as `[1,3,r]`.

Data Types: `single` | `double`

Output Arguments

`D` — Design matrix

matrix

Design matrix of a generalized linear mixed-effects model glme returned as one of the following:

- Fixed-effects design matrix — *n*-by-*p* matrix consisting of the fixed-effects design matrix of glme, where *n* is the number of observations and *p* is the number of fixed-effects terms.
- Random-effects design matrix — *n*-by-*k* matrix, consisting of the random-effects design matrix of glme. Here, *k* is equal to `length(B)`, where `B` is the random-effects coefficients vector of generalized linear mixed-effects model glme. The random-effects design matrix is returned as a sparse matrix. For more information about sparse matrices, see "Full and Sparse Matrices".

  If glme has *R* grouping variables g_1, g_2, ..., g_R, with levels m_1, m_2, ..., m_R, respectively, and if q_1, q_2, ..., q_R are the lengths of the random-effects vectors that are associated with g_1, g_2, ..., g_R, respectively, then `B` is a column vector of length $q_1*m_1 + q_2*m_2 + ... + q_R*m_R$.

  `B` is made by concatenating the empirical Bayes predictors of random effects vectors corresponding to each level of each grouping variable as `[`g_1`level`$_1$`; `g_1`level`$_2$`; ...; `g_1`level`$_{m_1}$`; `g_2`level`$_1$`; `g_2`level`$_2$`; ...; `g_2`level`$_{m_2}$`; ...; `g_R`level`$_1$`; `g_R`level`$_2$`; ...; `g_R`level`$_{m_R}$`]'`.

Data Types: `single` | `double`

`Dsub` — Submatrix of random-effects design matrix

matrix

Submatrix of random-effects design matrix that corresponds to the grouping variables specified by gnumbers, returned as an n-by-k matrix, where k is length of the column vector `Bsub`.

`Bsub` contains the concatenated empirical Bayes predictors of random-effects vectors, corresponding to each level of the grouping variables, specified by gnumbers.

If, for example, gnumbers is `[1,3,r]`, this corresponds to the grouping variables g_1, g_3, and g_r. Then, `Bsub` contains the empirical Bayes predictors of random-effects vectors corresponding to each level of the grouping variables g_1, g_3, and g_r, such as

$[g_1level_1;\ g_1level_2;\ ...;\ g_1level_{m_1};\ g_3level_1;\ g_3level_2;\ ...;\ g_3level_{m_3};\ g_rlevel_1;\ g_rlevel_2;\ ...;\ g_rlevel_{m_r}]'$.

Thus, `Dsub*Bsub` represents the contribution of all random effects corresponding to grouping variables g_1, g_3, and g_r to the response of `glme`.

If gnumbers is empty, then `Dsub` is the full random-effects design matrix.

Data Types: `single | double`

`gnames` — Names of grouping variables

k-by-1 cell array

Names of grouping variables corresponding to the integers in gnumbers if the design type is `'Random'`, returned as a k-by-1 cell array. If the design type is `'Fixed'`, then `gnames` is an empty matrix `[]`.

Data Types: `cell`

Examples

Obtain Fixed- and Random-Effects Design Matrices

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

```
load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Extract the fixed-effects design matrix and display rows 1 through 10.

```
Dfe = designMatrix(glme,'Fixed');
disp(Dfe(1:10,:))
```

```
    1.0000         0    0.1834    0.2259    1.0000         0
    1.0000         0    0.3035    0.0725         0    1.0000
    1.0000         0    0.0717    0.1630    1.0000         0
    1.0000         0    0.1069    0.0809   -1.0000   -1.0000
    1.0000         0    0.0241    0.0319    1.0000         0
    1.0000         0    0.1214    0.1114         0    1.0000
    1.0000         0    0.0033    0.0553    1.0000         0
    1.0000         0    0.2350    0.0616    1.0000         0
    1.0000         0    0.0488    0.0177         0    1.0000
    1.0000         0    0.1148    0.0105    1.0000         0
```

Column 1 of the fixed-effects design matrix `Dfe` contains the constant term. Column 2, 3, and 4 contain the `newprocess`, `time_dev`, and `temp_dev` terms, respectively. Columns 5 and 6 contain dummy variables for `supplier_C` and `supplier_B`, respectively.

Extract the random-effects design matrix and display rows 1 through 10.

```
Dre = designMatrix(glme,'Random');
disp(Dre(1:10,:))
```

```
   (1,1)        1
   (2,1)        1
   (3,1)        1
```

```
   (4,1)        1
   (5,1)        1
   (6,2)        1
   (7,2)        1
   (8,2)        1
   (9,2)        1
  (10,2)        1
```

Convert the sparse matrix `Dre` to a full matrix and display rows 1 through 10.

```
>> full(Dre(1:10,:))

ans =

  Columns 1 through 10

     1     0     0     0     0     0     0     0     0     0
     1     0     0     0     0     0     0     0     0     0
     1     0     0     0     0     0     0     0     0     0
     1     0     0     0     0     0     0     0     0     0
     1     0     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0

  Columns 11 through 20

     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     0     0     0
```

Each column corresponds to a level of the grouping variable `factory`.

See Also

`fitglme` | `fitted` | `GeneralizedLinearMixedModel` | `residuals` | `response`

designMatrix

Class: LinearMixedModel

Fixed- and random-effects design matrices

Syntax

```
D = designMatrix(lme)
D = designMatrix(lme,'Fixed')

D = designMatrix(lme,'Random')
Dsub = designMatrix(lme,'Random',gnumbers)
[Dsub,gnames] = designMatrix(lme,'Random',gnumbers)
```

Description

`D = designMatrix(lme)` or `D = designMatrix(lme,'Fixed')` returns the fixed-effects design matrix for the linear mixed-effects model lme.

`D = designMatrix(lme,'Random')` returns the random-effects design matrix for the linear mixed-effects model lme.

`Dsub = designMatrix(lme,'Random',gnumbers)` returns a subset of the random-effects design matrix for the linear mixed-effects model lmecorresponding to the grouping variables indicated by the integers in gnumbers.

`[Dsub,gnames] = designMatrix(lme,'Random',gnumbers)` also returns the grouping variable names corresponding to the integers in `gnumbers`.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

`gnumbers` — Grouping variable numbers

integer array

Grouping variable numbers, specified as an integer array, where R is the length of the cell array that contains the grouping variables for the linear mixed-effects model `lme`.

For example, you can specify the grouping variables g_1, g_3, and g_r as follows.

Example: `[1,3,r]`

Data Types: `double | single`

Output Arguments

`D` — Design matrix

matrix

Design matrix of a linear mixed-effects model `lme` returned as one of the following:

- Fixed-effects design matrix — n-by-p matrix consisting of the fixed-effects design of `lme`, where n is the number of observations and p is the number of fixed-effects terms.
- Random-effects design matrix — n-by-k matrix, consisting of the random-effects design matrix of `lme`. Here, k is equal to `length(B)`, where `B` is the random-effects coefficients vector of linear mixed-effects model `lme`.

  If `lme` has R grouping variables g_1, g_2, ..., g_R, with levels m_1, m_2, ..., m_R, respectively, and if q_1, q_2, ..., q_R are the lengths of the random-effects vectors that are associated with g_1, g_2, ..., g_R, respectively, then `B` is a column vector of length $q_1*m_1 + q_2*m_2 + ... + q_R*m_R$.

  `B` is made by concatenating the best linear unbiased predictors of random-effects vectors corresponding to each level of each grouping variable as `[`g_1`level`$_1$`; `g_1`level`$_2$`; ...; `g_1`level`$_{m_1}$`; `g_2`level`$_1$`; `g_2`level`$_2$`; ...; `g_2`level`$_{m_2}$`; ...; `g_R`level`$_1$`; `g_R`level`$_2$`; ...; `g_R`level`$_{m_R}$`]'`.

Data Types: `single | double`

`Dsub` — Submatrix of random-effects design matrix

matrix

Submatrix of random-effects design matrix corresponding to the grouping variables indicated by the integers in gnumbers, returned as an n-by-k matrix, where k is length of the column vector `Bsub`.

`Bsub` contains the concatenated best linear unbiased predictors (BLUPs) of random-effects vectors, corresponding to each level of the grouping variables, specified by gnumbers.

If, for example, gnumbers is `[1,3,r]`, this corresponds to the grouping variables g_1, g_3, and g_r. Then, `Bsub` contains the concatenated BLUPs of random-effects vectors corresponding to each level of the grouping variables g_1, g_3, and g_r, such as

$[g_1level_1; g_1level_2; ...; g_1level_{m_1}; g_3level_1; g_3level_2; ...; g_3level_{m_3}; g_rlevel_1; g_rlevel_2; ...; g_rlevel_{m_r}]'$.

Thus, `Dsub*Bsub` represents the contribution of all random effects corresponding to grouping variables g_1, g_3, and g_r to the response of `lme`.

If gnumbers is empty, then `Dsub` is the full random-effects design matrix.

Data Types: `single | double`

`gnames` — Names of grouping variables

k-by-1 cell array

Names of grouping variables corresponding to the integers in gnumbers if the design type is `'Random'`, returned as a k-by-1 cell array. If the design type is `'Fixed'`, then `gnames` is an empty matrix `[]`.

Data Types: `cell`

Examples

Display Fixed- and Random-Effects Design Matrices

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data shows the deviations from the target quality characteristic measured from the products that 5 operators manufacture during three different shifts, morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the deviation of the quality characteristics from the target value. This is simulated data.

`Shift` and `Operator` are nominal variables.

```
shift.Shift = nominal(shift.Shift);
shift.Operator = nominal(shift.Operator);
```

Fit a linear mixed-effects model with a random intercept grouped by operator to assess if performance significantly differs according to the time of the shift.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)');
```

Display the fixed-effects design matrix.

```
designMatrix(lme)
```

```
ans =

     1     1     0
     1     0     0
     1     0     1
     1     1     0
     1     0     0
     1     0     1
     1     1     0
     1     0     0
     1     0     1
     1     1     0
     1     0     0
     1     0     1
     1     1     0
     1     0     0
     1     0     1
```

The column of 1s represents the constant term in the model. `fitlme` takes the evening shift as the reference group and creates two dummy variables to represent the morning and night shifts, respectively.

Display the random-effects design matrix.

```
designMatrix(lme,'random')
```

```
ans =

   (1,1)        1
   (2,1)        1
   (3,1)        1
   (4,2)        1
   (5,2)        1
   (6,2)        1
   (7,3)        1
   (8,3)        1
   (9,3)        1
  (10,4)        1
  (11,4)        1
  (12,4)        1
  (13,5)        1
  (14,5)        1
  (15,5)        1
```

The first number, i, in the (i,j) indices corresponds to the observation number, and j corresponds to the level of the grouping variable, `Operator`, i.e., the operator number.

Show the full display of the random-effects design matrix.

```
full(designMatrix(lme,'random'))
```

```
ans =

     1     0     0     0     0
     1     0     0     0     0
     1     0     0     0     0
     0     1     0     0     0
     0     1     0     0     0
     0     1     0     0     0
     0     0     1     0     0
     0     0     1     0     0
     0     0     1     0     0
     0     0     0     1     0
     0     0     0     1     0
     0     0     0     1     0
     0     0     0     0     1
     0     0     0     0     1
```

```
     0     0     0     0     1
```

Each column corresponds to a level of the grouping variable, `Operator`.

Random-Effects Design Matrix of Multiple Grouping Variables

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Store and examine the full random-effects design matrix.

```
D = full(designMatrix(lme,'random'));
```

The first three columns of matrix `D` contain the indicator variables `fitlme` creates for the three levels (`Loamy`, `Silty`, `Sandy`, respectively) of the first grouping variable, `Soil`. The next 15 columns contain the indicator variables created for the second grouping variable, `Tomato` nested under `Soil`. These are basically the elementwise

products of the dummy variables representing the levels of `Soil` (`Loamy`, `Silty`, and `Sandy`, respectively) and the levels of `Tomato` (`Cherry`, `Grape`, `Heirloom`, `Plum`, `Vine`, respectively).

Subset of the Random-Effects Design Matrix

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Compute the random-effects design matrix for the second grouping variable, and display the first 12 rows.

```
[Dsub,gname]  = designMatrix(lme,'random',2);
full(Dsub(1:12,:))

ans =
```

```
     0     0     0     0     0     0     0     0     0     0     1     0     0     0
     0     0     0     0     0     0     0     0     0     0     1     0     0     0
     0     0     0     0     0     0     0     0     0     0     1     0     0     0
     0     0     0     0     0     0     0     0     0     0     1     0     0     0
     0     1     0     0     0     0     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0     0     0     0     0     0     0
     0     0     0     0     0     0     0     1     0     0     0     0     0     0
     0     0     0     0     0     0     0     1     0     0     0     0     0     0
     0     0     0     0     0     0     0     1     0     0     0     0     0     0
     0     0     0     0     0     0     0     1     0     0     0     0     0     0
```

`Dsub` contains the dummy variables created for the second grouping variable, that is, tomato nested under soil. These are the elementwise products of the dummy variables representing the levels of `Soil` (`Loamy`, `Silty`, `Sandy`, respectively) and the levels of `Tomato` (`Cherry`, `Grape`, `Heirloom`, `Plum`, `Vine`, respectively).

Display the name of the grouping variable.

```
gname
```

```
gname =

    'Soil:Tomato'
```

See Also

`fitlmematrix` | `fitted` | `LinearMixedModel`

dfittool

Open Distribution Fitting app

This page contains programmatic syntax information for the Distribution Fitting app. For general usage information, see Distribution Fitting.

Syntax

```
dfittool
dfittool(y)
dfittool(y,cens)
dfittool(y,cens,freq)
dfittool(y,cens,freq,dsname)
```

Description

`dfittool` opens the Distribution Fitting app, or brings focus to the app if it is already open.

`dfittool(y)` opens the Distribution Fitting app populated with the data specified by the vector y.

`dfittool(y,cens)` uses the vector cens to specify whether each observation in y is censored.

`dfittool(y,cens,freq)` uses the vector freq to specify the frequency of each element of y.

`dfittool(y,cens,freq,dsname)` creates a data set with the name dsname, using the data vector, y, censoring indicator, cens, and frequency vector, freq.

Examples

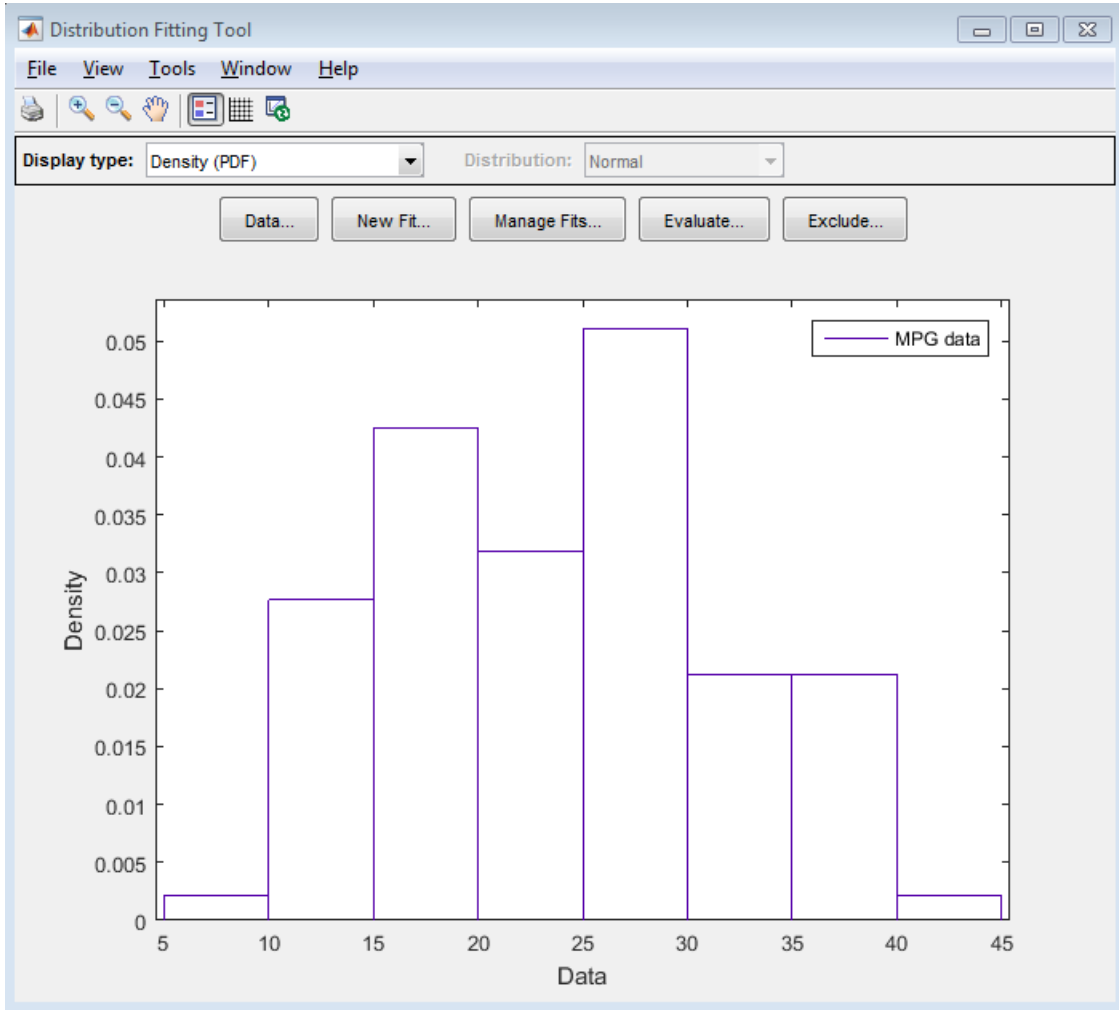
Open Distribution Fitting App with Existing Data

Load the `carsmall` sample data.

```
load carsmall
```

Open the Distribution Fitting app using the `MPG` miles per gallon data.

```
dfittool(MPG)
```



The Distribution Fitting app opens, populated with the `MPG` data, and displays the density (PDF) plot. You can use the app to display different plots and fit distributions to this data.

Open Distribution Fitting App with Censoring Data

Load the sample data.

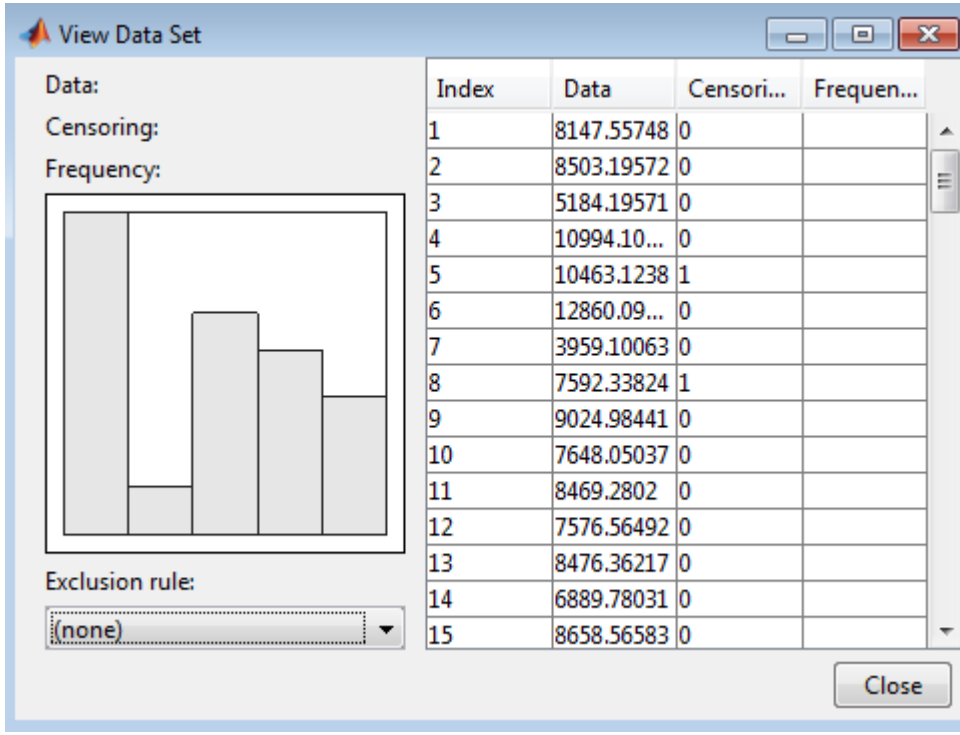
```
load(fullfile(matlabroot,'examples','stats','lightbulb.mat'))
```

The first column of the data contains the lifetime (in hours) of two types of light bulbs. The second column contains information about the type of light bulb. 1 indicates fluorescent bulbs, and 0 indicates the incandescent bulb. The third column contains censoring information. 1 indicates censored data, and 0 indicates the exact failure time. This is simulated data.

Open the Distribution Fitting app using the first column of `lightbulb` as the input data, and the third column as the censoring data. Name the data `lifetime`.

```
dfittool(lightbulb(:,1),lightbulb(:,3),[],'lifetime')
```

To open the Data dialog box, click **Data**. In the **Manage data sets** pane, click to highlight the `lifetime` data set row. Finally, to open the View Data Set dialog, click **View**. The lifetime data appears in the second column and the corresponding censoring indicator appears in the third column.



Index	Data	Censori...	Frequen...
1	8147.55748	0	
2	8503.19572	0	
3	5184.19571	0	
4	10994.10...	0	
5	10463.1238	1	
6	12860.09...	0	
7	3959.10063	0	
8	7592.33824	1	
9	9024.98441	0	
10	7648.05037	0	
11	8469.2802	0	
12	7576.56492	0	
13	8476.36217	0	
14	6889.78031	0	
15	8658.56583	0	

- "Fit a Distribution Using the Distribution Fitting App" on page 5-101

Input Arguments

y — Input data

array of scalar values | variable representing an array of scalar values

Input data, specified as an array of scalar values or a variable representing an array of such values.

Data Types: `single` | `double`

cens — Censoring indicator

`zeros(n)` (default) | vector of 0 and 1 values

Censoring indicator, specified as a vector of 0 and 1 values. The length of cens must be equal to the length of y. If `y(j)` is censored, then `(cens(j)==1)`. If `y(j)` is not

censored, then `(cens(j)==0)`. If cens is omitted or empty, then no y values are censored.

If you have frequency data (freq) but not censoring data (cens), then you must specify empty brackets ([ ]) for cens.

Data Types: `single | double`

`freq` — Frequency data

`ones(n)` (default) | vector of scalar values

Frequency data, specified as a vector of scalar values. The length of freq must be equal to the length of y. If freq is omitted or empty, then all y values have a frequency of 1.

If you have frequency data (freq) but not censoring data (cens), then you must specify empty brackets ([ ]) for cens.

Data Types: `single | double`

`dsname` — Data set name

string

Data set name, specified as a string enclosed in single quotes.

If you want to specify a data set name, but do not have censoring data (cens) or frequency data (freq), then you must specify empty brackets ([ ]) for both freq and cens.

Example: `'MyData'`

Data Types: `char`

More About

- "Model Data Using the Distribution Fitting App" on page 5-74
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

See Also

`fitdist | makedist`

Dimensions property

Class: qrandset

Number of dimensions

Description

Number of dimensions in the point set. The `Dimensions` property of a point set contains a positive integer that indicates the number of dimensions for which the points have values. For example, a point set with `Dimensions=5` produces points that each have five values.

Set this property by specifying the number of dimensions when constructing a new point set. After construction, you cannot change the value. The default number of dimensions is 2.

DimNames property

Class: dataset

Two-element cell array of strings giving names of dimensions of data set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

A two-element cell array of strings giving the names of the two dimensions of the data set. The default is `{'Observations' 'Variables'}`.

discardSupportVectors

Class: CompactClassificationECOC

Discard support vectors of linear support vector machine binary learners

Syntax

```
Mdl = discardSupportVectors(MdlSV)
```

Description

`Mdl = discardSupportVectors(MdlSV)` returns a trained error-correcting output codes (ECOC) model (`Mdl`) containing at least one linear, support vector machine (SVM) binary learner. `Mdl` is similar to the trained ECOC model `MdlSV`, except:

- The `Alpha`, `SupportVectors`, and `SupportVectorLabels` properties of all linear SVM binary learners are empty (`[]`).
- If you display any linear SVM binary learners stored in the cell array of trained models `Mdl.BinaryLearners`, the software lists the `Beta` property instead of `Alpha`.

Tip

For linear, SVM binary learners, and for efficiency, `fitcecoc` empties the properties `Alpha`, `SupportVectorLabels`, and `SupportVectors`. `fitcecoc` lists `Beta`, rather than `Alpha`, in the model display.

To store `Alpha`, `SupportVectorLabels`, and `SupportVectors`, pass a linear, SVM template that specifies storing support vectors to `fitcecoc`. For example, enter:

```
t = templateSVM('SaveSupportVectors','on')
Mdl = fitcecoc(X,Y,'Learners',t);
```

You can subsequently remove the support vectors and related values by passing the resulting `ClassificationECOC` model to `discardSupportVectors`.

Input Arguments

`MdlSV` — Trained ECOC model

`ClassificationECOC` model | `CompactClassificationECOC` model

Trained ECOC model containing at least one linear, SVM binary learner, specified as a `ClassificationECOC` or `CompactClassificationECOC` model.

Output Arguments

`Mdl` — Trained ECOC model

`ClassificationECOC` model | `CompactClassificationECOC` model

Trained ECOC model, returned as a `ClassificationECOC` or `CompactClassificationECOC` model. `Mdl` is the same type as MdlSV.

The properties `Alpha`, `SupportVectorLabels`, and `SupportVectors` of all linear, SVM binary learners in the cell array `Mdl.BinaryLearners` are empty. The software lists the property `Beta` when you display any linear, SVM binary learner, and does not list `Alpha`.

Examples

Retain and Discard Support Vectors of SVM Binary Learners

By default, `fitcecoc` empties the `Alpha`, `SupportVectorLabels`, and `SupportVectors` properties of the linear, SVM binary learners stored in the `BinaryLearners` property of the trained ECOC model. You can retain the support vectors and related values, and then discard them from the model.

Load Fisher's iris data set.

```
load fisheriris
rng(1); % For reproducibility
```

Train an ECOC model using the entire data set. Specify retaining the support vectors by passing in the appropriate SVM template.

```
t = templateSVM('SaveSupportVectors',true);
```

```
MdlSV = fitcecoc(meas,species,'Learners',t);
```

`Mdl` is a trained `ClassificationECOC` model. By default, `fitcecoc` uses linear, SVM binary learners. It implements a one-versus-one coding design, which requires three binary learners for three-class learning.

Access the estimated α values using dot notation.

```
alpha = cell(3,1);
alpha{1} = MdlSV.BinaryLearners{1}.Alpha;
alpha{2} = MdlSV.BinaryLearners{2}.Alpha;
alpha{3} = MdlSV.BinaryLearners{3}.Alpha;
alpha
```

```
alpha =

    [ 3x1 double]
    [ 3x1 double]
    [23x1 double]
```

`alpha` is a 3-by-1 cell array that stores the estimated values of α.

Discard the support vectors and related values from the ECOC model.

```
Mdl = discardSupportVectors(MdlSV);
```

`Mdl` is similar to `MdlSV`, except that the `Alpha`, `SupportVectorLabels`, and `SupportVectors` of all linear SVM binary learners are empty ([ ]).

```
areAllEmpty = @(x)isempty([x.Alpha x.SupportVectors x.SupportVectorLabels]);
cellfun(areAllEmpty,Mdl.BinaryLearners)
```

```
ans =

     1
     1
     1
```

Compare the sizes of the two ECOC models.

```
vars = whos('MdlSV','Mdl');
```

```
100*(1 - vars(1).bytes/vars(2).bytes)
```

```
ans =

    5.3485
```

`Mdl` is about 5% smaller than `MdlSV`.

Reduce your memory footprint by compacting `Mdl`, and then clearing `MdlSV` and `Mdl` from the workspace.

```
CMdl = compact(Mdl);
clear MdlSV Mdl;
```

Predict the label for a random row of the training data using the more efficient SVM model.

```
idx = randsample(size(meas,1),1)
predictedLabel = predict(CMdl,meas(idx,:))
trueLabel = species(idx)
```

```
idx =

    63


predictedLabel =

    'versicolor'


trueLabel =

    'versicolor'
```

Algorithms

For each linear, SVM binary learner in an ECOC model, `predict` and `resubPredict` estimate SVM scores [$f(x)$] using

$$f(x) = \beta' x + \beta_0,$$

β is the `Beta` property and β_0 is the `Bias` property of the binary learners. You can access these properties for each linear, SVM binary learner in the cell array `Mdl.BinaryLearners`. For more details on the SVM score calculation, see "Support Vector Machines for Binary Classification" on page 22-1613.

See Also

`ClassificationECOC` | `ClassificationSVM` | `CompactClassificationECOC` | `discardSupportVectors` | `fitcecoc` | `fitcsvm` | `templateSVM`

Introduced in R2015a

discardSupportVectors

Class: CompactClassificationSVM

Discard support vectors for linear support vector machine models

Syntax

```
Mdl = discardSupportVectors(MdlSV)
```

Description

`Mdl = discardSupportVectors(MdlSV)` returns the trained, linear support vector machine (SVM) model `Mdl`, which is similar to the trained, linear SVM model `MdlSV`, except:

- The `Alpha`, `SupportVectors`, and `SupportVectorLabels` properties are empty ([ ]).
- If you display `Mdl`, the software lists the `Beta` property instead of `Alpha`.

Tips

For a trained, linear SVM model, the `SupportVectors` property is an n_{sv}-by-p matrix. n_{sv} is the number of support vectors (at most the training sample size) and p is the number of predictors or features. The `Alpha` and `SupportVectorLabels` properties are vectors with n_{sv} elements. These properties can be large for complex data sets containing many observations or examples. However, the `Beta` property is a vector with p elements.

If the trained SVM model has many support vectors, use `discardSupportVectors` to reduce the amount of disk space that the trained, linear SVM model consumes. You can display the size of the support vector matrix by entering `size(MdlSV.SupportVectors)`.

Input Arguments

`MdlSV` — Trained, linear SVM model

`ClassificationSVM` model | `CompactClassificationSVM` model

Trained, linear SVM model, specified as a `ClassificationSVM` or `CompactClassificationSVM` model.

If the field `MdlSV.KernelParameters.Function` is not `'linear'` (i.e., `MdlSV` is not a linear SVM model), the software returns an error.

Output Arguments

`Mdl` — Trained, linear SVM model

`ClassificationSVM` model | `CompactClassificationSVM` model

Trained, linear SVM model, returned as a `ClassificationSVM` or `CompactClassificationSVM` model. `Mdl` is the same type as MdlSV.

The properties `Alpha`, `SupportVectorLabels`, and `SupportVectors` of `Mdl` are empty. The software lists the property `Beta` in its display, and does not list `Alpha`.

Examples

Discard Support Vectors

To use less disk space, you can discard the support vectors and other related parameters from a trained, linear SVM.

Load the `ionosphere` data set.

```
load ionosphere
```

Train a linear SVM model using the entire data set.

```
MdlSV = fitcsvm(X,Y)
numSV = size(MdlSV.SupportVectors,1)
p = size(X,2)
```

```
MdlSV =

  ClassificationSVM
      PredictorNames: {1x34 cell}
        ResponseName: 'Y'
          ClassNames: {'b'  'g'}
      ScoreTransform: 'none'
     NumObservations: 351
               Alpha: [103x1 double]
                Bias: -3.8828
    KernelParameters: [1x1 struct]
      BoxConstraints: [351x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [351x1 logical]
              Solver: 'SMO'


numSV =

   103


p =

    34
```

By default, `fitcsvm` trains a linear SVM model for two-class learning. The software lists `Alpha` in the display. There are 103 support vectors and 34 predictors. If you discard the support vectors, the resulting model consumes less memory.

Discard the support vectors and other related parameters.

```
Mdl = discardSupportVectors(MdlSV)
Mdl.Alpha
Mdl.SupportVectors
Mdl.SupportVectorLabels
```

```
Mdl =

  ClassificationSVM
      PredictorNames: {1x34 cell}
        ResponseName: 'Y'
```

```
          ClassNames: {'b'  'g'}
      ScoreTransform: 'none'
     NumObservations: 351
                Beta: [34x1 double]
                Bias: -3.8828
    KernelParameters: [1x1 struct]
      BoxConstraints: [351x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [351x1 logical]
              Solver: 'SMO'


ans =

     []


ans =

     []


ans =

     []
```

The software lists `Beta` in the display instead of `Alpha`. The `Alpha`, `SupportVectors`, and `SupportVectorLabels` properties are empty.

Compare the sizes of the models.

```
vars = whos('MdlSV','Mdl');
100*(1 - vars(1).bytes/vars(2).bytes)
```

```
ans =

   20.5535
```

`Mdl` is about 20% smaller than `MdlSV`.

Remove `MdlSV` from the workspace.

```
clear MdlSV
```

Reduce Memory Consumption of SVM Models

`predict` accepts compacted SVM models, and, for linear SVM models, does not require the `Alpha`, `SupportVectors`, and `SupportVectorLabels` properties to predict labels for new observations. If your training set is large, consider compacting the SVM model, and then discarding the stored support vectors and other related estimates.

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM model using default options.

```
MdlSV = fitcsvm(X,Y);
```

`MdlSV` is a `ClassificationSVM` model containing nonempty values for its `Alpha`, `SupportVectors`, and `SupportVectorLabels` properties.

Reduce the size of the SVM model by discarding the training data, support vectors, and related estimates.

```
CMdlSV = compact(MdlSV);                % Discard training data
CMdl = discardSupportVectors(CMdlSV);  % Discard support vectors
```

`CMdl` is a `CompactClassificationSVM` model.

Compare the sizes of the SVM models `MdlSV` and `CMdl`.

```
vars = whos('MdlSV','CMdl');
100*(1 - vars(1).bytes/vars(2).bytes)
```

```
ans =

   97.4447
```

The compacted model consumes much less memory than the full model.

Predict the label for a random row of the training data using the more efficient SVM model.

```
idx = randsample(size(X,1),1)
predictedLabel = predict(CMdl,X(idx,:))
trueLabel = Y(idx)
```

```
idx =

   147


predictedLabel =

    'b'


trueLabel =

    'b'
```

Algorithms

`predict` and `resubPredict` estimate SVM scores [$f(x)$], and subsequently labels and estimates posterior probabilities using

$$f(x) = \beta' x + \beta_0,$$

β is `Mdl.Beta` and β_0 is `Mdl.Bias`. For more details, see "Support Vector Machines for Binary Classification" on page 22-1613.

See Also

`ClassificationECOC` | `ClassificationSVM` | `CompactClassificationSVM` | `discardSupportVectors` | `fitcsvm` | `templateSVM`

Introduced in R2015a

disp

Class: classregtree

Display `classregtree` object

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
display(t)
```

Description

`display(t)` prints the `classregtree` object `t`.

See Also

`classregtree` | `view`

disp

Class: cvpartition

Display `cvpartition` object

Syntax

```
disp(c)
```

Description

`disp(c)` prints the `cvpartition` object `c`.

See Also

`cvpartition`

disp

Class: dataset

Display dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
disp(ds)
```

Description

`disp(ds)` prints the dataset array `ds`, including variable names and observation names (if present), without printing the dataset name. In all other ways it's the same as leaving the semicolon off an expression.

For numeric or categorical variables that are 2-D and have three or fewer columns, `disp` prints the actual data using either short g, long g, or bank format, depending on the current command line setting. Otherwise, `disp` prints the size and type of each dataset element.

For character variables that are 2-D and 10 or fewer characters wide, `disp` prints quoted strings. Otherwise, `disp` prints the size and type of each dataset element.

For cell variables that are 2-D and have three or fewer columns, `disp` prints the contents of each cell (or its size and type if too large). Otherwise, `disp` prints the size of each dataset element.

For time series variables, `disp` prints columns for both the time and the data. If the variable is 2-D and has three or fewer columns, `disp` prints the actual data Otherwise, `disp` prints the size and type of each dataset element.

For other types of variables, `disp` prints the size and type of each dataset element.

See Also

`dataset` | `display` | `format`

disp

Class: GeneralizedLinearModel

Display generalized linear regression model

Syntax

```
disp(mdl)
```

Description

`disp(mdl)` displays the `mdl` linear model.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

Examples

Display a Generalized Linear Regression Model

Create and display a generalized linear regression model.

Create a generalized linear regression model of Poisson data.

```
X = 2 + randn(100,1);
mu = exp(1 + X/2);
y = poissrnd(mu);
mdl = fitglm(X,y,...
    'y ~ x1','distr','poisson');
```

Display the model.

```
disp(mdl)
```

```
Generalized Linear regression model:
    log(y) ~ 1 + x1
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)     0.9581     0.090294    10.611    2.6519e-26
    x1             0.51027     0.033738    15.124    1.1179e-51


100 observations, 98 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 221, p-value = 5.77e-50
```

Alternatives

Enter *`mdl`* at the command line to obtain a display, where *`mdl`* is the name of your model.

See Also

`GeneralizedLinearModel`

More About

- “Generalized Linear Models” on page 10-12

disp

Class: GeneralizedLinearMixedModel

Display generalized linear mixed-effects model

Syntax

```
disp(glme)
```

Description

`disp(glme)` displays fitted generalized linear mixed-effects model glme.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Definitions

Akaike and Bayesian Information Criteria

The *Akaike information criterion* (AIC) is $AIC = -2\log L_M + 2(param)$.

$\log L_M$ depends on the method used to fit the model.

- If you use `'Laplace'` or `'ApproximateLaplace'`, then $\log L_M$ is the maximized log likelihood.
- If you use `'MPL'`, then $\log L_M$ is the maximized log likelihood of the pseudo data from the final pseudo likelihood iteration.
- If you use `'REMPL'`, then $\log L_M$ is the maximized restricted log likelihood of the pseudo data from the final pseudo likelihood iteration.

param is the total number of parameters estimated in the model. For most GLME models, *param* is equal to $nc + p + 1$, where nc is the total number of parameters in the random-effects covariance, excluding the residual variance, and p is the number of fixed-effects coefficients. However, if the dispersion parameter is fixed at 1.0 for binomial or Poisson distributions, then *param* is equal to $(nc + p)$.

The *Bayesian information criterion* (BIC) is $BIC = -2*\log L_M + \ln(n_{eff})(param)$.

$\log L_M$ depends on the method used to fit the model.

- If you use `'Laplace'` or `'ApproximateLaplace'`, then $\log L_M$ is the maximized log likelihood.
- If you use `'MPL'`, then $\log L_M$ is the maximized log likelihood of the pseudo data from the final pseudo likelihood iteration.
- If you use `'REMPL'`, then $\log L_M$ is the maximized restricted log likelihood of the pseudo data from the final pseudo likelihood iteration.

n_{eff} is the effective number of observations.

- If you use `'MPL'`, `'Laplace'`, or `'ApproximateLaplace'`, then $n_{eff} = n$, where n is the number of observations.
- If you use `'REMPL'`, then $n_{eff} = n - p$.

param is the total number of parameters estimated in the model. For most GLME models, *param* is equal to $nc + p + 1$, where nc is the total number of parameters in the random-effects covariance, excluding the residual variance, and p is the number of fixed-effects coefficients. However, if the dispersion parameter is fixed at 1.0 for binomial or Poisson distributions, then *param* is equal to $(nc + p)$.

A lower value of deviance indicates a better fit. As the value of deviance decreases, both AIC and BIC tend to decrease. Both AIC and BIC also include penalty terms based on the number of parameters estimated, p. So, when the number of parameters increase, the values of AIC and BIC tend to increase as well. When comparing different models, the model with the lowest AIC or BIC value is considered as the best fitting model.

For models fitted using `'MPL'` and `'REMPL'`, AIC and BIC are based on the log likelihood (or restricted log likelihood) of pseudo data from the final pseudo likelihood iteration. Therefore, a direct comparison of AIC and BIC values between models fitted using `'MPL'` and `'REMPL'` is not appropriate.

Examples

Display a Generalized Linear Mixed-Effects Model

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Display the model.

```
disp(glme)
```

```
glme =


Generalized linear mixed-effects model fit by ML

Model information:
    Number of observations             100
    Fixed effects coefficients           6
    Random effects coefficients         20
    Covariance parameters                1
```

```
    Distribution                    Poisson
    Link                            Log
    FitMethod                       Laplace

Formula:
    defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1 | factory)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    416.35    434.58    -201.17          402.35

Fixed effects coefficients (95% CIs):
    Name                 Estimate     SE          tStat       DF    pValue
    '(Intercept)'           1.4689     0.15988      9.1875    94    9.8194e-15
    'newprocess'          -0.36766     0.17755     -2.0708    94      0.041122
    'time_dev'            -0.094521    0.82849    -0.11409    94       0.90941
    'temp_dev'             -0.28317     0.9617    -0.29444    94       0.76907
    'supplier_C'          -0.071868    0.078024     -0.9211    94       0.35936
    'supplier_B'           0.071072     0.07739     0.91836    94       0.36078


    Lower        Upper
       1.1515       1.7864
     -0.72019    -0.015134
      -1.7395       1.5505
      -2.1926       1.6263
     -0.22679     0.083051
    -0.082588      0.22473

Random effects covariance parameters:
Group: factory (20 Levels)
    Name1               Name2               Type         Estimate
    '(Intercept)'       '(Intercept)'       'std'        0.31381

Group: Error
    Name                      Estimate
    'sqrt(Dispersion)'        1
```

The `Model information` table displays the total number of observations in the sample data (100), the number of fixed- and random-effects coefficients (6 and 20, respectively), and the number of covariance parameters (1). It also indicates that the response variable has a `Poisson` distribution, the link function is `Log`, and the fit method is `Laplace`.

`Formula` indicates the model specification using Wilkinson's notation.

The `Model fit statistics` table displays statistics used to assess the goodness of fit of the model. This includes the Akaike information criterion (`AIC`), Bayesian information criterion (`BIC`) values, log likelihood (`LogLikelihood`), and deviance (`Deviance`) values.

The `Fixed effects coefficients` table indicates that `fitglme` returned 95% confidence intervals. It contains one row for each fixed-effects predictor, and each column contains statistics corresponding to that predictor. Column 1 (`Name`) contains the name of each fixed-effects coefficient, column 2 (`Estimate`) contains its estimated value, and column 3 (`SE`) contains the standard error of the coefficient. Column 4 (`tStat`) contains the *t*-statistic for a hypothesis test that the coefficient is equal to 0. Column 5 (`DF`) and column 6 (`pValue`) contain the degrees of freedom and *p*-value that correspond to the *t*-statistic, respectively. The last two columns (`Lower` and `Upper`) display the lower and upper limits, respectively, of the 95% confidence interval for each fixed-effects coefficient.

`Random effects covariance parameters` displays a table for each grouping variable (here, only `factory`), including its total number of levels (20), and the type and estimate of the covariance parameter. Here, `std` indicates that `fitglme` returns the standard deviation of the random effect associated with the factory predictor, which has an estimated value of 0.31381. It also displays a table containing the error parameter type (here, the square root of the dispersion parameter), and its estimated value of 1.

The standard display generated by `fitglme` does not provide confidence intervals for the random-effects parameters. To compute and display these values, use `covarianceParameters`.

See Also

`covarianceParameters` | `fitglme` | `GeneralizedLinearMixedModel`

disp

Class: gmdistribution

Display Gaussian mixture distribution object

Syntax

```
disp(obj)
```

Description

`disp(obj)` prints a text representation of the `gmdistribution` object, `obj`, without printing the object name. In all other ways it's the same as leaving the semicolon off an expression.

See Also

`gmdistribution` | `display`

disp

Class: LinearModel

Display linear regression model

Syntax

```
display(mdl)
```

Description

`display(mdl)` displays the `mdl` linear model.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

Examples

Display a Linear Regression Model

Create and display a linear regression model.

Create a linear regression model.

```
X = randn(100,5);
y = X*[1;2;3;4;5] + 6 + randn(100,1);
mdl = fitlm(X,y);
```

Display the model.

```
disp(mdl)
```

```
Linear regression model:
```

```
    y ~ 1 + x1 + x2 + x3 + x4 + x5

Estimated Coefficients:
                   Estimate    SE         tStat     pValue
    (Intercept)    6.0806      0.11393    53.371    4.2509e-72
    x1             1.1181       0.1154    9.6894    8.4046e-16
    x2             2.0903      0.11378    18.372    7.2209e-33
    x3             3.0926      0.10725    28.836    1.7967e-48
    x4             3.9343      0.11489    34.244    6.9609e-55
    x5             4.9538      0.10799    45.873    3.8195e-66


Number of observations: 100, Error degrees of freedom: 94
Root Mean Squared Error: 1.08
R-squared: 0.979,  Adjusted R-Squared 0.978
F-statistic vs. constant model: 891, p-value = 1.59e-77
```

Alternatives

Enter *`mdl`* at the command line to obtain a display, where *`mdl`* is the name of your model.

See Also

`LinearModel`

How To

- "Linear Regression" on page 9-11
- "Stepwise Regression" on page 9-124
- "Robust Regression — Reduce Outlier Effects" on page 9-128

disp

Class: LinearMixedModel

Display linear mixed-effects model

Syntax

```
display(lme)
```

Description

`display(lme)` displays the fitted linear mixed-effects model `lme`.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Examples

Randomized Block Design

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The dataset array shows the absolute deviations from the target quality characteristic measured from the products that five operators manufacture during three shifts, morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the absolute deviation of the quality characteristics from the target value. This is simulated data.

`Shift` and `Operator` are nominal variables.

```
shift.Shift = nominal(shift.Shift);
shift.Operator = nominal(shift.Operator);
```

Fit a linear mixed-effects model with a random intercept grouped by operator to assess if performance significantly differs according to the time of the shift.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)');
```

Display the model.

```
disp(lme)
```

```
Linear mixed-effects model fit by ML

Model information:
    Number of observations             15
    Fixed effects coefficients          3
    Random effects coefficients         5
    Covariance parameters               2

Formula:
    QCDev ~ 1 + Shift + (1 | Operator)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    59.012    62.552    -24.506          49.012

Fixed effects coefficients (95% CIs):
    Name                   Estimate    SE         tStat       DF    pValue       Lower
    '(Intercept)'           3.1196     0.88681      3.5178    12    0.0042407     1.187
    'Shift_Morning'        -0.3868     0.48344     -0.80009   12      0.43921    -1.440
    'Shift_Night'           1.9856     0.48344      4.1072    12    0.0014535    0.9322

Random effects covariance parameters (95% CIs):
Group: Operator (5 Levels)
```

```
    Name1               Name2               Type         Estimate    Lower      Upper
    '(Intercept)'       '(Intercept)'       'std'        1.8297      0.94915    3.527

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.76439     0.49315    1.1848
```

This display includes the model performance statistics, Akaike information criterion (AIC), Bayesian information criterion (BIC), loglikelihood, and deviance.

The fixed-effects coefficients table includes the names and estimates of the coefficients in the first two columns. The third column `SE` shows the standard errors of the coefficients. The column `tStat` includes the *t*-statistic values that correspond to each coefficient. `DF` is the residual degrees of freedom, and the `pValue` is the *p*-value that corresponds to the corresponding *t*-statistic value. The columns `Lower` and `Upper` display the lower and upper limits of a 95% confidence interval for each fixed-effects coefficient.

The first table for the random effects shows the types and the estimates of the random effects covariance parameters, with the lower and upper limits of a 95% confidence interval for each parameter. The display also shows the name of the grouping variable, operator, and the total number of levels, 5.

The second table for the random effects shows the estimate of the observation error, with the lower and upper limits of a 95% confidence interval.

Definitions

Akaike and Bayesian Information Criteria

Akaike information criterion (AIC) is $AIC = -2*\log L_M + 2*(nc + p + 1)$, where $\log L_M$ is the maximized log likelihood (or maximized restricted log likelihood) of the model, and $nc + p + 1$ is the number of parameters estimated in the model. p is the number of fixed-effects coefficients, and nc is the total number of parameters in the random-effects covariance excluding the residual variance.

Bayesian information criterion (BIC) is $BIC = -2*\log L_M + \ln(n_{eff})*(nc + p + 1)$, where $\log L_M$ is the maximized log likelihood (or maximized restricted log likelihood) of the model, n_{eff} is the effective number of observations, and $(nc + p + 1)$ is the number of parameters estimated in the model.

- If the fitting method is maximum likelihood (ML), then $n_{eff} = n$, where n is the number of observations.
- If the fitting method is restricted maximum likelihood (REML), then $n_{eff} = n - p$.

A lower value of deviance indicates a better fit. As the value of deviance decreases, both AIC and BIC tend to decrease. Both AIC and BIC also include penalty terms based on the number of parameters estimated, p. So, when the number of parameters increase, the values of AIC and BIC tend to increase as well. When comparing different models, the model with the lowest AIC or BIC value is considered as the best fitting model.

Deviance

`LinearMixedModel` computes the deviance of model M as minus two times the loglikelihood of that model. Let L_M denote the maximum value of the likelihood function for model M. Then, the deviance of model M is

$$-2 * \log L_M .$$

A lower value of deviance indicates a better fit. Suppose M_1 and M_2 are two different models, where M_1 is nested in M_2. Then, the fit of the models can be assessed by comparing the deviances Dev_1 and Dev_2 of these models. The difference of the deviances is

$$Dev = Dev_1 - Dev_2 = 2\left(\log LM_2 - \log LM_1\right).$$

Usually, the asymptotic distribution of this difference has a chi-square distribution with degrees of freedom v equal to the number of parameters that are estimated in one model but fixed (typically at 0) in the other. That is, it is equal to the difference in the number of parameters estimated in M_1 and M_2. You can get the p-value for this test using `1 - chi2cdf(Dev,V)`, where $Dev = Dev_2 - Dev_1$.

However, in mixed-effects models, when some variance components fall on the boundary of the parameter space, the asymptotic distribution of this difference is more complicated. For example, consider the hypotheses

H_0: $D = \begin{pmatrix} D_{11} & 0 \\ 0 & 0 \end{pmatrix}$, D is a q-by-q symmetric positive semidefinite matrix.

H_1: D is a (q+1)-by-(q+1) symmetric positive semidefinite matrix.

That is, H_1 states that the last row and column of D are different from zero. Here, the bigger model M_2 has $q + 1$ parameters and the smaller model M_1 has q parameters. And Dev has a 50:50 mixture of χ^2_q and $\chi^2_{(q+1)}$ distributions (Stram and Lee, 1994).

References

[1] Hox, J. *Multilevel Analysis, Techniques and Applications*. Lawrence Erlbaum Associates, Inc., 2002.

[2] Stram D. O. and J. W. Lee. "Variance components testing in the longitudinal mixed-effects model". *Biometrics*, Vol. 50, 4, 1994, pp. 1171–1177.

See Also

`fitlme` | `fitlmematrix` | `LinearMixedModel`

disp

Class: NaiveBayes

Display `NaiveBayes` classifier object

Syntax

```
disp(nb)
```

Description

`disp(nb)` prints a text representation of the `NaiveBayes` object `nb`, without printing the object name. In all other ways it's the same as leaving the semicolon off an expression.

See Also

`NaiveBayes` | `display`

disp

Class: NonLinearModel

Display nonlinear regression model

Syntax

```
disp(mdl)
```

Description

`disp(mdl)` displays the `mdl` nonlinear model at the command line.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

Examples

Display a Nonlinear Regression Model

Create and display a nonlinear regression model.

Load the `reaction` data, and specify both a model function and starting values for the iterations.

```
load reaction
modelfun = 'rate~(b1*x2-x3/b5)/(1+b2*x1+b3*x2+b4*x3)';
beta0 = [1 .05 .02 .1 2];
```

Create a model of the data.

```
mdl = fitnlm(reactants,rate,modelfun,beta0);
```

Display the model.

```
disp(mdl)
```

```
Nonlinear regression model:
    rate ~ (b1*x2 - x3/b5)/(1 + b2*x1 + b3*x2 + b4*x3)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1      1.2526     0.86701    1.4447    0.18654
    b2    0.062776    0.043561    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075157    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.193
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. constant model: 1.81e+03, p-value = 7.36e-12
```

Alternatives

Enter *mdl* at the command line to obtain a display, where *mdl* is the name of your model.

See Also

`NonLinearModel`

More About

- “Nonlinear Regression” on page 11-2

disp

Class: piecewisedistribution

Display piecewisedistribution object

Syntax

```
disp(A)
```

Description

`disp(A)` prints a text representation of the piecewisedistribution object `A`, without printing the object name. In all other ways it's the same as leaving the semicolon off an expression.

See Also

`piecewisedistribution`

disp

Class: qrandset

Display qrandset object

Syntax

```
disp(p)
```

Description

`disp(p)` displays the properties of the quasi-random point set `s`, without printing the variable name. `disp` prints out the number of dimensions and points in the point-set, and follows this with the list of all property values for the object.

See Also

`qrandset`

disp

Class: qrandstream

Display `qrandstream` object

Syntax

```
disp(q)
```

Description

`disp(q)` displays the quasi-random stream `q`, without printing the variable name. `disp` prints the type and number of dimensions in the stream, and follows it with the list of point set properties.

See Also

`qrandstream`

display

Class: classregtree

Display `classregtree` object

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
display(t)
display(A)
```

Description

`display(t)` prints the `classregtree` object `t`. `classregtree` calls`display` when a you do not use a semicolon to terminate a statement.

`display(A)` prints the categorical array A. `categorical` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`classregtree` | `prune` | `test` | `eval`

display

Class: cvpartition

Display `cvpartition` object

Syntax

```
display(c)
```

Description

`display(c)` prints the `cvpartition` object `c`. `cvpartition` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`cvpartition`

display

Class: dataset

Display dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
display(ds)
```

Description

`display(ds)` prints the dataset array `ds`, including variable names and observation names (if present). `dataset` calls`display` when a you do not use a semicolon to terminate a statement

For numeric or categorical variables that are 2-D and have three or fewer columns, `display` prints the actual data. Otherwise, `display` prints the size and type of each dataset element.

For character variables that are 2-D and 10 or fewer characters wide, `display` prints quoted strings. Otherwise, `display` prints the size and type of each dataset element.

For cell variables that are 2-D and have three or fewer columns, `display` prints the contents of each cell (or its size and type if too large). Otherwise, `display` prints the size of each dataset element.

For time series variables, `display` prints columns for both the time and the data. If the variable is 2-D and has three or fewer columns, `display` prints the actual data. Otherwise, `display` prints the size and type of each dataset element.

For other types of variables, `display` prints the size and type of each dataset element.

See Also

`dataset` | `display` | `format`

display

Class: gmdistribution

Display Gaussian mixture distribution object

Syntax

```
display(obj)
```

Description

`display(obj)` prints a text representation of the `gmdistribution` object `obj`. `gmdistribution` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`gmdistribution` | `disp`

display

Class: NaiveBayes

Display `NaiveBayes` classifier object

Syntax

```
display(nb)
```

Description

`display(nb)` prints a text representation of the `NaiveBayes` object `nb`. `NaiveBayes` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`NaiveBayes` | `display`

display

Class: piecewisedistribution

Display piecewisedistribution object

Syntax

```
display(A)
```

Description

`display(A)` prints a text representation of the piecewisedistribution object `A`, without printing the object name. `piecewisedistribution` calls`display` when a you do not use a semicolon to terminate a statement.

See Also

`piecewisedistribution`

DistName property

Class: ProbDist

Read-only string containing probability distribution name of ProbDist object

Description

`DistName` is a read-only property of the `ProbDist` class. `DistName` is a string containing the type of distribution used to create the object.

Values

Possible values are:

- `'kernel'`
- `'beta'`
- `'binomial'`
- `'birnbaumsaunders'`
- `'exponential'`
- `'extreme value'`
- `'gamma'`
- `'generalized extreme value'`
- `'generalized pareto'`
- `'inversegaussian'`
- `'logistic'`
- `'loglogistic'`
- `'lognormal'`
- `'nakagami'`
- `'negative binomial'`
- `'normal'`
- `'poisson'`

- `'rayleigh'`
- `'rician'`
- `'tlocationscale'`
- `'weibull'`

Use this information to view and compare the type of distribution used to create distribution objects.

Dist property

Class: NaiveBayes

Distribution names

Description

The `Dist` property is a string or a 1-by-`NDims` cell array of strings indicating the types of distributions for all the features. If all the features use the same type of distribution, `Dist` is a single string. Otherwise `Dist(j)` indicates the distribution type used for the `j`th feature.

The valid strings for this property are the following:

`'normal'`	Normal distribution.
`'kernel'`	Kernel smoothing density estimate.
`'mvmn'`	Multivariate multinomial distribution.
`'mn'`	Multinomial bag-of-tokens model.

DistributionName property

Class: gmdistribution

Type of distribution

Description

The string `'gaussian mixture distribution'`.

disttool

Interactive density and distribution plots

Syntax

```
disttool
```

Description

`disttool` is a graphical interface for exploring the effects of changing parameters on the plot of a cdf or pdf.

See Also

`randtool` | `dfittool`

double

Class: dataset

Convert dataset variables to double array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
b = double(A)
b = double(a,vars)
```

Description

`b = double(A)` returns the contents of the dataset `A`, converted to one double array. The classes of the variables in the dataset must support the conversion.

`b = double(a,vars)` returns the contents of the dataset variables specified by `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

See Also

`dataset` | `single` | `replacedata`

droplevels

Drop levels from a nominal or ordinal array

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
B = droplevels(A)
B = droplevels(A,oldlevels)
```

Description

`B = droplevels(A)` drops unused levels from the nominal or ordinal array A. The array B has the same size, type, and values as A, but has a list of potential levels that includes only those present in some element of A.

`B = droplevels(A,oldlevels)` removes the specified levels oldlevels from A.

`droplevels` removes levels, but does not remove elements. Elements of B that correspond to elements of A having levels in oldlevels all have an undefined level.

Examples

Drop Levels From an Ordinal Array

Bin patient ages into ordinal levels corresponding to 10-year intervals.

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
```

```
A = ordinal(hospital.Age,labels,[],edges);
getlabels(A)
```

```
ans =

  Columns 1 through 8

    '0s'    '10s'    '20s'    '30s'    '40s'    '50s'    '60s'    '70s'

  Columns 9 through 10

    '80s'    '90s'
```

Drop any levels that have no patients in them.

```
A = droplevels(A);
getlabels(A)
```

```
ans =

    '20s'    '30s'    '40s'    '50s'
```

- “Add and Drop Category Levels” on page 2-21

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

`oldlevels` — Levels to remove

cell array of strings | 2-D character matrix

Levels to remove from the `nominal` or `ordinal` array, specified as a cell array of strings or 2-D character matrix.

Data Types: `char` | `cell`

Output Arguments

B — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, returned as a `nominal` or `ordinal` array object.

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`addlevels` | `mergelevels` | `nominal` | `ordinal` | `reorderlevels`

dummyvar

Create dummy variables

Syntax

```
D = dummyvar(group)
```

Description

`D = dummyvar(group)` returns a matrix `D` containing zeros and ones, whose columns are dummy variables for the grouping variable `group`. Columns of `group` represent categorical predictor variables, with values indicating categorical levels. Rows of `group` represent observations across variables.

`group` can be a numeric vector or categorical column vector representing levels within a single variable, a cell array containing one or more grouping variables, or a numeric matrix or cell array of categorical column vectors representing levels within multiple variables. If `group` is a numeric vector or matrix, values in any column must be positive integers in the range from `1` to the number of levels for the corresponding variable. In this case, `dummyvars` treats each column as a separate numeric grouping variable. With multiple grouping variables, the sets of dummy variable columns are in the same order as the grouping variables in `group`.

The order of the dummy variable columns in `D` matches the order of the groups defined by `group`. When `group` is a categorical vector, the groups and their order match the output of the `getlabels(group)` method. When `group` is a numeric vector, `dummyvar` assumes that the groups and their order are `1:max(group)`. In this respect, `dummyvars` treats a numeric grouping variable differently than `grp2idx`.

If `group` is n-by-p, `D` is n-by-S, where S is the sum of the number of levels in each of the columns of `group`. The number of levels s in any column of `group` is the maximum positive integer in the column or the number of categorical levels. Levels are considered distinct if they appear in different columns of `group`, even if they have the same value. Columns of `D` are, from left to right, dummy variables created from the first column of `group`, followed by dummy variables created from the second column of `group`, etc.

`dummyvar` treats `NaN` values or undefined categorical levels in `group` as missing data and returns `NaN` values in `D`.

Dummy variables are used in regression analysis and ANOVA to indicate values of categorical predictors.

Note: If a column of 1s is introduced in the matrix `D`, the resulting matrix `X = [ones(size(D,1),1) D]` will be rank deficient. The matrix `D` itself will be rank deficient if `group` has multiple columns. This is because dummy variables produced from any column of `group` always sum to a column of 1s. Regression and ANOVA calculations often address this issue by eliminating one dummy variable (implicitly setting the coefficients for dropped columns to zero) from each group of dummy variables produced by a column of `group`.

Examples

Suppose you are studying the effects of two machines and three operators on a process. Use `group` to organize predictor data on machine-operator combinations:

```
machine = [1 1 1 1 2 2 2 2]';
operator = [1 2 3 1 2 3 1 2]';
group = [machine operator]
group =
     1     1
     1     2
     1     3
     1     1
     2     2
     2     3
     2     1
     2     2
```

Use `dummyvar` to create dummy variables for a regression or ANOVA calculation:

```
D = dummyvar(group)
D =
     1     0     1     0     0
     1     0     0     1     0
     1     0     0     0     1
     1     0     1     0     0
     0     1     0     1     0
```

```
     0     1     0     0     1
     0     1     1     0     0
     0     1     0     1     0
```

The first two columns of `D` represent observations of machine `1` and machine `2`, respectively; the remaining columns represent observations of the three operators.

More About

- "Grouping Variables" on page 2-52
- "Dummy Indicator Variables" on page 2-55
- "Regression with Categorical Covariates" on page 2-58

See Also

`regress` | `anova1`

dwtest

Durbin-Watson test

Syntax

```
p = dwtest(r,x)
p = dwtest(r,x,Name,Value)
[p,d] = dwtest(___)
```

Description

`p = dwtest(r,x)` returns the *p*-value for the Durbin-Watson test of the null hypothesis that the residuals from a linear regression are uncorrelated. The alternative hypothesis is that there is autocorrelation among the residuals.

`p = dwtest(r,x,Name,Value)` returns the *p*-value for the Durbin-Watson test with additional options specified by one or more name-value pair arguments. For example, you can conduct a one-sided test or calculate the *p*-value using a normal approximation.

`[p,d] = dwtest(___)` also returns the Durbin-Watson test statistic, d, using any of the input arguments from the previous syntaxes.

Examples

Test Residuals For Correlation

Load the sample census data.

```
load census
```

Create a design matrix using the census date (`cdate`) as the predictor. Add a column of `1` values to include a constant term.

```
n = length(cdate);
x = [ones(n,1),cdate];
```

Fit a linear regression to the data.

```
[b,bint,r] = regress(pop,x);
```

Test the null hypothesis that there is no autocorrelation among the residuals, `r`.

```
[p,d] = dwtest(r,x)
```

```
p =

     0


d =

    0.1308
```

The returned value `p = 0` indicates rejection of the null hypothesis at the 5% significance level.

One-Sided Hypothesis Test

Load the sample census data.

```
load census
```

Create a design matrix using the census date (`cdate`) as the predictor. Add a column of `1` values to include a constant term.

```
n = length(cdate);
x = [ones(n,1),cdate];
```

Fit a linear regression to the data.

```
[b,bint,r] = regress(pop,x);
```

Test the null hypothesis that there is no autocorrelation among regression residuals, against the alternative hypothesis that the autocorrelation is greater than zero.

```
[p,d] = dwtest(r,x,'Tail','right')
```

```
p =

     0
```

```
d =

    0.1308
```

The returned value `p = 0` indicates rejection of the null hypothesis at the 5% significance level, in favor of the alternative hypothesis that the autocorrelation among residuals is greater than zero.

Input Arguments

x — Design matrix

matrix

Design matrix for a linear regression, specified as a matrix. Include a column of `1` values in the design matrix so the model contains a constant term.

Data Types: `single` | `double`

r — Regression residuals

vector

Regression residuals, specified as a vector. Obtain r by performing a linear regression using a function such as `regress`, or by using the backslash operator.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Method','approximate'` specifies a right-tailed hypothesis test and calculates the p-value using a normal approximation.

'Method' — Computation method for *p*-value

`'exact'` | `'approximate'`

Computation method for the *p*-value, specified as the comma-separated pair consisting of `'Method'` and one of the following.

`'exact'`	Calculate an exact *p*-value using the Pan algorithm. This is the default if the sample size is less than 400.
`'approximate'`	Calculate the *p*-value using a normal approximation. This is the default if the sample size is 400 or larger.

Example: `'Method','exact'`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternate hypothesis that autocorrelation among the residuals is not zero.
`'right'`	Test the alternative hypothesis that autocorrelation among the residuals is greater than zero.
`'left'`	Test the alternative hypothesis that autocorrelation among the residuals is less than zero.

Example: `'Tail','right'`

Output Arguments

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

d — Test statistic

nonnegative scalar value

Test statistic of the hypothesis test, returned as a nonnegative scalar value.

More About

Durbin-Watson Test

The Durbin-Watson test is used to test the null hypothesis that linear regression residuals are uncorrelated, against the alternative that autocorrelation exists.

The test statistic for the Durbin-Watson test is

$$d = \frac{\sum_{t=2}^{T} (e_t - e_{t-1})^2}{\sum_{t=1}^{T} e_t^2},$$

where T is the number of observations, and e_t is the residual at time t.

The p-value of the Durbin-Watson test is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. A significantly small p-value casts doubt on the validity of the null hypothesis and indicates correlation among residuals. The p-value can be calculated exactly using the Pan algorithm. Alternatively, the p-value can be estimated using a normal approximation.

See Also

`regress`

dwtest

Class: LinearModel

Durbin-Watson test of linear model

Syntax

```
P = dwtest(mdl)
[P,DW] = dwtest(mdl)
[P,DW] = dwtest(mdl,method)
[P,DW] = dwtest(mdl,method,tail)
```

Description

`P = dwtest(mdl)` returns the *p*-value of the Durbin-Watson test on the `mdl` linear model.

`[P,DW] = dwtest(mdl)` returns the Durbin-Watson statistic.

`[P,DW] = dwtest(mdl,method)` specifies the method `dwtest` uses to compute the *p*-value.

`[P,DW] = dwtest(mdl,method,tail)` specifies the alternative hypothesis.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`method`

Algorithm for computing the *p*-value:

- `'exact'` — Calculates an exact *p*-value using Pan's algorithm.
- `'approximate'` — Calculates the *p*-value using a normal approximation.

Default: `'exact'` when the sample size is less than `400`, `'approximate'` otherwise

`tail`

`dwtest` tests whether `mdl` has no serial correlation against one of these alternative hypotheses:

Tail	Alternative Hypothesis
`'both'`	Serial correlation is not 0.
`'right'`	Serial correlation is greater than 0 (right-tailed test).
`'left'`	Serial correlation is less than 0 (left-tailed test).

Default: `'both'`

Output Arguments

`P`

p-value of the test, a scalar. `dwtest` tests if the residuals are uncorrelated, against the alternative that there is autocorrelation among them. Small values of `P` indicate that the residuals are correlated.

`DW`

Value of the Durbin-Watson statistic, a scalar.

Definitions

Durbin-Watson Statistic

Let r be the vector of residuals (in `mdl.residuals.response`). The Durbin-Watson statistic is

$$DW = \frac{\sum_{i=1}^{n-1} (r_{i+1} - r_i)^2}{\sum_{i=1}^{n} r_i^2}.$$

Examples

Test Residuals for Autocorrelation

Examine whether the residuals from a fitted model of census data over time have autocorrelated residuals.

Load the census data and create a linear model.

```
load census
mdl = fitlm(cdate,pop);
```

Find the *p*-value of the Durbin-Watson autocorrelation test.

```
P = dwtest(mdl)
```

```
P =

     0
```

There is significant autocorrelation in the residuals.

Algorithms

Approximate calculation of the *p*-value uses a normal approximation [1]. Exact calculation uses Pan's algorithm [2].

References

[1] Durbin, J., and G. S. Watson. *Testing for Serial Correlation in Least Squares Regression I.* Biometrika 37, pp. 409–428, 1950.

[2] Farebrother, R. W. *Pan's Procedure for the Tail Probabilities of the Durbin-Watson Statistic.* Applied Statistics 29, pp. 224–227, 1980.

See Also

`LinearModel`

How To

- “Linear Regression” on page 9-11

ecdf

Empirical cumulative distribution function

Syntax

```
[f,x] = ecdf(y)
[f,x] = ecdf(y,Name,Value)
[f,x,flo,fup] = ecdf( ___ )

ecdf( ___ )
ecdf(ax, ___ )
```

Description

`[f,x] = ecdf(y)` returns the empirical cumulative distribution function (cdf), `f`, evaluated at the points in `x`, using the data in the vector `y`.

In survival and reliability analysis, this empirical cdf is called the Kaplan-Meier estimate. And the data might correspond to survival or failure times.

`[f,x] = ecdf(y,Name,Value)` returns the empirical function values, `f`, evaluated at the points in `x`, with additional options specified by one or more `Name,Value` pair arguments.

For example, you can specify the type of function to evaluate or which data is censored.

`[f,x,flo,fup] = ecdf( ___ )` also returns the 95% lower and upper confidence bounds for the evaluated function values. You can use any of the input arguments in the previous syntaxes.

`ecdf` computes the confidence bounds using Greenwood's formula. They are not simultaneous confidence bounds.

`ecdf( ___ )` plots the evaluated function.

`ecdf(ax, ___ )` plots the evaluated function using axes with the handle, `ax`, instead of the current axes returned by `gca`.

Examples

Compute Empirical Cumulative Distribution Function

Compute the Kaplan-Meier estimate of the cumulative distribution function (cdf) for simulated survival data.

Generate survival data from a Weibull distribution with parameters 3 and 1.

```
rng default;  % for reproducibility
failuretime = random('wbl',3,1,15,1);
```

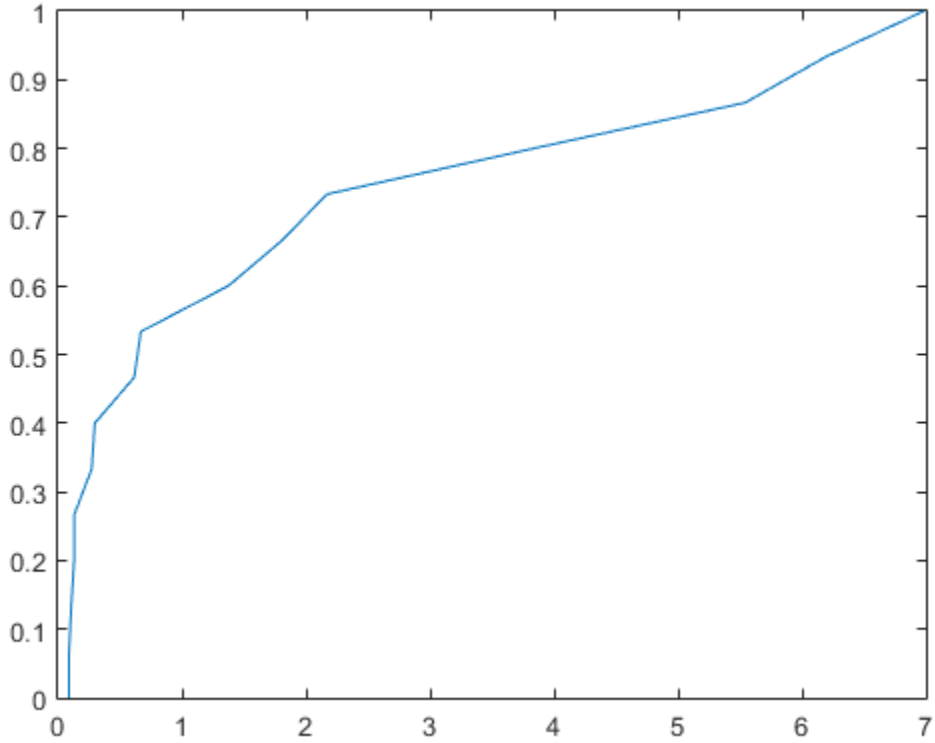
Compute the Kaplan-Meier estimate of the cdf for survival data.

```
[f,x] = ecdf(failuretime);
[f,x]
```

```
ans =

         0    0.0895
    0.0667    0.0895
    0.1333    0.1072
    0.2000    0.1303
    0.2667    0.1313
    0.3333    0.2718
    0.4000    0.2968
    0.4667    0.6147
    0.5333    0.6684
    0.6000    1.3749
    0.6667    1.8106
    0.7333    2.1685
    0.8000    3.8350
    0.8667    5.5428
    0.9333    6.1910
    1.0000    6.9825
```

Plot the estimated cdf.

```
figure()
plot(x,f)
```



Empirical Hazard Function of Right-Censored Data

Compute and plot the hazard function of simulated right-censored survival data.

Generate failure times from a Birnbaum-Saunders distribution.

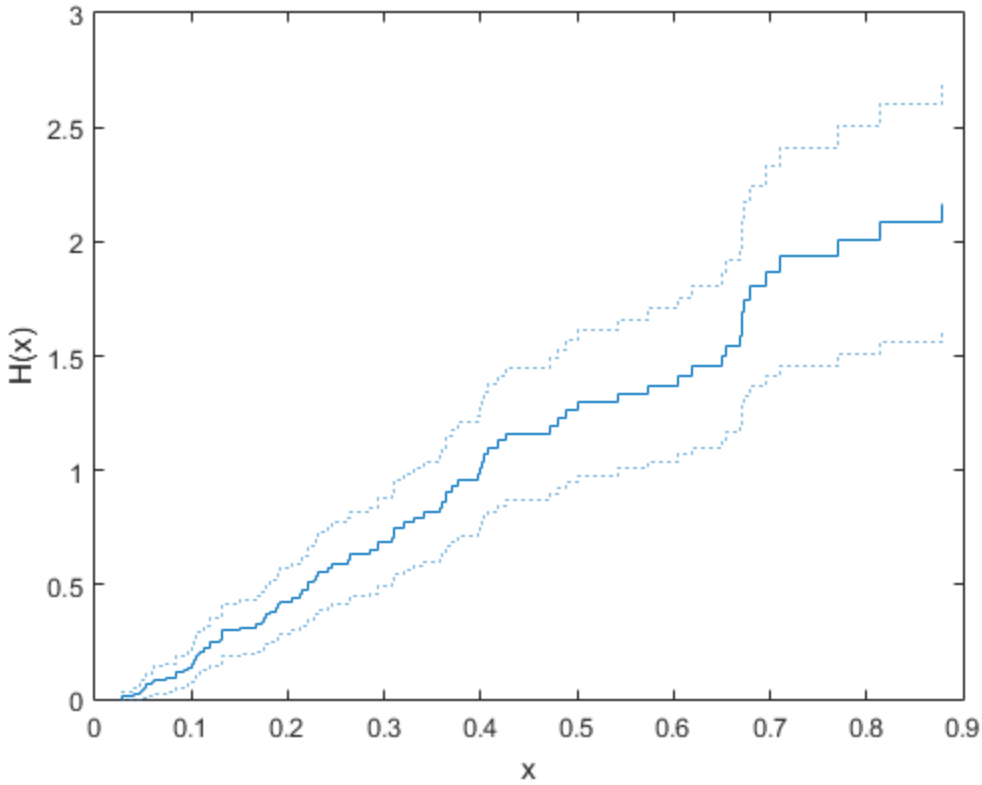
```
rng default  % for reproducibility
failuretime = random('birnbaumsaunders',0.3,1,100,1);
```

Assuming that the end of the study is at time 0.9, generate a logical array that indicates simulated failure times that are larger than 0.9 as censored data, and store this information in a vector.

```
T = 0.9;
cens = (failuretime>T);
```

Plot the empirical hazard function for the data.

```
ecdf(failuretime,'function','cumulative hazard',...
'censoring',cens,'bounds','on');
```



Compare Empirical Cumulative Distribution Function (CDF) with Known CDF

Generate right-censored survival data and compare the empirical cumulative distribution function (cdf) with the known cdf.

Generate failure times from an exponential distribution with mean failure time of 15.

```
rng default  % for reproducibility
y = exprnd(15,75,1);
```

Generate drop-out times from an exponential distribution with mean failure time of 30.

```
d = exprnd(30,75,1);
```

Generate the observed failure times. They are the minimum of the generated failure times and the drop-out times.

```
t = min(y,d);
```

Create a logical array that indicates generated failure times that are larger than the drop-out times. The data for which this is true are censored.

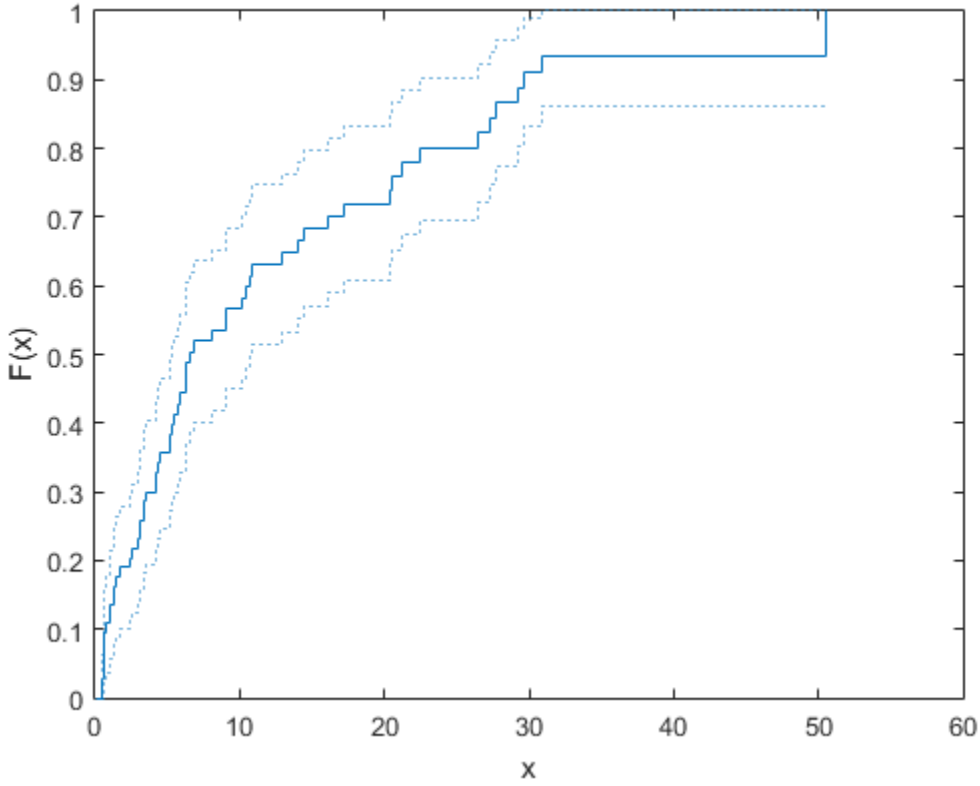
```
censored = (y>d);
```

Compute the empirical cdf and confidence bounds.

```
[f,x,flo,fup] = ecdf(t,'censoring',censored);
```

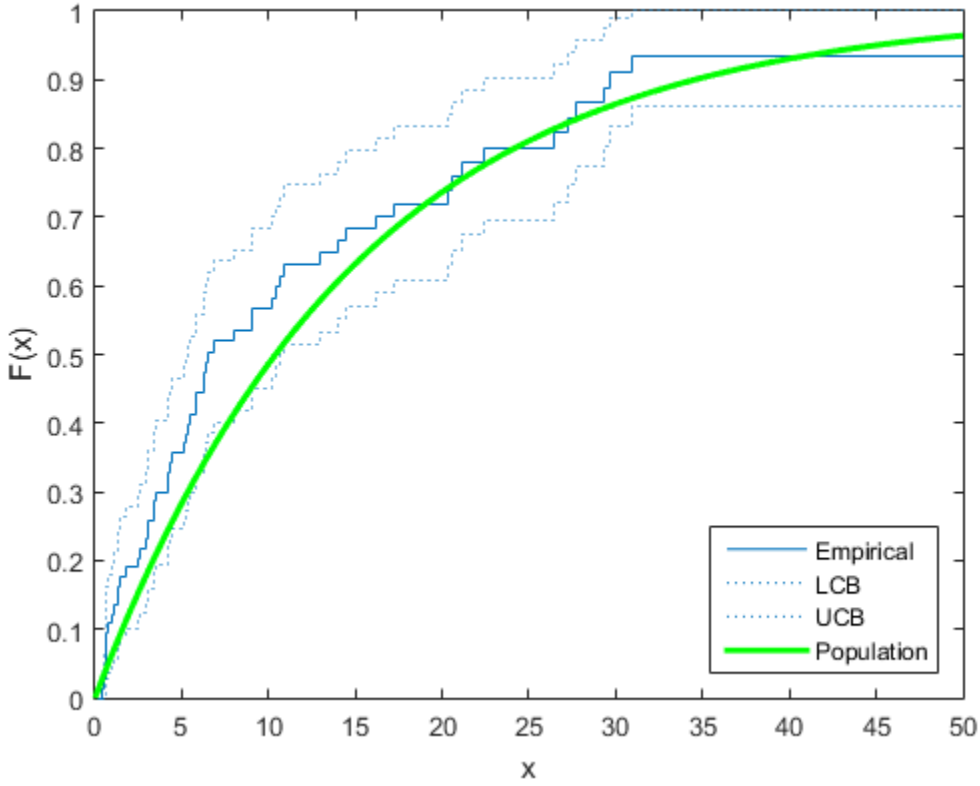
Plot the cdf and confidence bounds.

```
figure()
ecdf(t,'censoring',censored,'bounds','on');
hold on
```



Superimpose a plot of the known population cdf.

```
xx = 0:.1:max(t);
yy = 1-exp(-xx/15);
plot(xx,yy,'g-','LineWidth',2)
axis([0 50 0 1])
legend('Empirical','LCB','UCB','Population',...
       'Location','SE')
hold off
```



Empirical Survivor Function with 99% Confidence Bounds

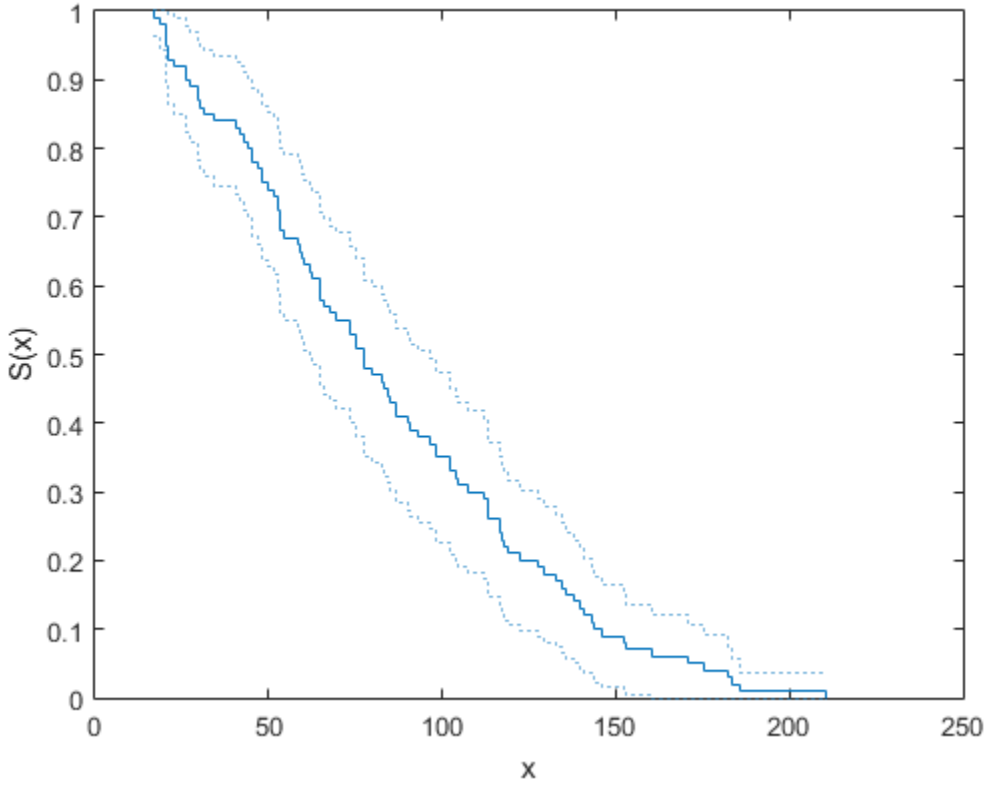
Generate survival data and plot the empirical survivor function with 99% confidence bounds.

Generate lifetime data from a Weibull distribution with parameters 100 and 2.

```
rng default  % for reproducibility
R = wblrnd(100,2,100,1);
```

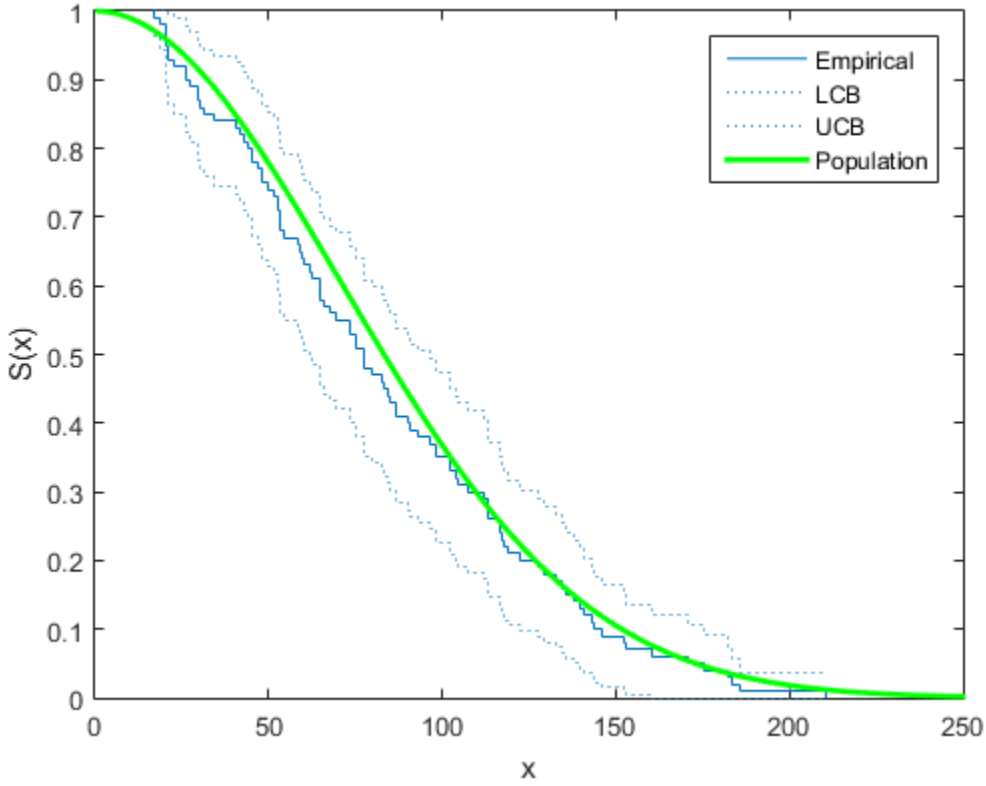
Plot the survivor function for the data with 99% confidence bounds.

```
ecdf(R,'function','survivor','alpha',0.01,'bounds','on')
hold on
```



Fit the Weibull survivor function.

```
x = 1:1:250;
wblsurv = 1-cdf('weibull',x,100,2);
plot(x,wblsurv,'g-','LineWidth',2)
legend('Empirical','LCB','UCB','Population',...
'Location','NE')
```



The survivor function based on the actual distribution is within the confidence bounds.

Input Arguments

y — Input data

column vector

Input data, specified as a column vector. For example, in survival or reliability analysis, data might be survival or failure times for each item or individual.

Data Types: `single` | `double`

ax — Axes handle

handle

Axes handle for the figure `ecdf` plots to, specified as a handle.

For instance, if `h` is a handle for a figure, then `ecdf` can plot to that figure as follows.

Example: `ecdf(h,x)`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'censoring',c,'function','cumulative hazard','alpha',0.025,'bounds','on'` specifies that `ecdf` returns the cumulative hazard function and plots the 97.5% confidence bounds, accounting for the censored data specified by vector `c`.

'censoring' — Indicator of censored data

array of 0s (default) | vector of 0s and 1s

Indicator of censored data, specified as the comma-separated pair including `'censoring'` and a Boolean array of the same size as x. Enter `1` for observations that are right-censored and `0` for observations that are fully observed. Default is all observations are fully observed.

For instance, if vector `cdata`stores the censored data information, you can enter the censoring information as follows.

Example: `'censoring',cdata`

Data Types: `logical`

'frequency' — Frequency of observations

array of 1s (default) | vector of nonnegative scalars

Frequency of observations, specified as the comma-separated pair consisting of `'frequency'` and a vector containing nonnegative integer counts. This vector is the same size as the vector x. The `j`th element of this vector gives the number of times the `j`th element of x was observed. Default is one observation per element of x.

For instance, if `failurefreq` is a vector of frequencies, then you can enter it as follows.

Example: `'frequency',failurefreq`

Data Types: `single | double`

`'alpha'` — Confidence level

0.05 (default) | scalar value in the range (0,1)

Confidence level for the confidence interval of the evaluated function, specified as the comma-separated pair consisting of `'alpha'` and a scalar value between in the range (0,1). Default is 0.05 for 95% confidence. For a given value `alpha`, the confidence level is `100(1-alpha)`%.

For instance, for a 99% confidence interval, you can specify the alpha value as follows.

Example: `'alpha',0.01`

Data Types: `single | double`

`'function'` — Type of function returned

`'cdf'` (default) | `'survivor'` | `'cumulative hazard'`

Type of function that `ecdf` evaluates and returns, specified as the comma-separated pair consisting of `'function'` and one of the following.

`'cdf'`	Default. Cumulative distribution function.
`'survivor'`	Survivor function.
`'cumulative hazard'`	Cumulative hazard function.

Example: `'function','cumulative hazard'`

Data Types: `char`

`'bounds'` — Indicator for including bounds

`'off'` (default) | `'on'`

Indicator for including bounds, specified as the comma-separated pair consisting of `'bounds'` and one of the following.

`'off'`	Default. Specify to omit bounds.
`'on'`	Specify to include bounds.

Note: This name-value argument is used only for plotting.

Example: `'bounds','on'`

Data Types: `char`

Output Arguments

`f` — Function values

column vector

Function values evaluated at the points in x, returned as a column vector.

`x` — Distinct observed points

column vector

Distinct observed points in data vector y, returned as a column vector.

`flo` — Lower confidence bound

column vector

Lower confidence bound for the evaluated function, returned as a column vector. `ecdf` computes the confidence bounds using Greenwood's formula. They are not simultaneous confidence bounds.

`fup` — Upper confidence bound

column vector

Upper confidence bound for the evaluated function, returned as a column vector. `ecdf` computes the confidence bounds using Greenwood's formula. They are not simultaneous confidence bounds.

More About

Greenwood's Formula

Approximation for the variance of Kaplan-Meier estimator.

The variance estimate is given by

$$V\left(S\left(t\right)\right) = S^2\left(t\right) \sum_{t_i<T} \frac{d_i}{r_i\left(r_i - d_i\right)},$$

where r_i is the number at risk at time t_i, and d_i is the number of failures at time t_i.

References

[1] Cox, D. R., and D. Oakes. *Analysis of Survival Data*. London: Chapman & Hall, 1984.

[2] Lawless, J. F. *Statistical Models and Methods for Lifetime Data*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 2003.

See Also

`cdfplot` | `ecdfhist`

ecdfhist

Histogram based on empirical cumulative distribution function

Syntax

```
[n,c] = ecdfhist(f,x)
[n,c] = ecdfhist(f,x,m)

n = ecdfhist(f,x,centers)

ecdfhist( ___ )
```

Description

`[n,c] = ecdfhist(f,x)` returns the heights, `n`, of histogram bars for 10 equally spaced bins and the position of the bin centers, `c`.

`ecdfhist` computes the bar heights from the increases in the empirical cumulative distribution function, `f`, at evaluation points, `x`. It normalizes the bar heights so that the area of the histogram is equal to 1. In contrast, `histogram` produces bars with heights representing bin counts.

`[n,c] = ecdfhist(f,x,m)` returns the histogram bars using `m` bins.

`n = ecdfhist(f,x,centers)` returns the heights of the histogram bars with bin centers specified by `centers`.

`ecdfhist( ___ )` plots the histogram bars.

Examples

Return Histogram Bar Heights and Bin Centers

Compute the histogram bar heights based on the empirical cumulative distribution function.

Generate failure times from a Birnbaum-Saunders distribution.

```
rng('default') % for reproducibility
failuretime = random('birnbaumsaunders',0.3,1,100,1);
```

Assuming that the end of the study is at time 0.9, mark the generated failure times that are larger than 0.9 as censored data and store that information in a vector.

```
T = 0.9;
cens = (failuretime>T);
```

Compute the empirical cumulative distribution function for the data.

```
[f,x] = ecdf(failuretime,'censoring',cens);
```

Now, find the bar heights of the histogram using the cumulative distribution function estimate.

```
[n,c] = ecdfhist(f,x);
[n' c']
```

```
ans =

    2.3529    0.0715
    1.7647    0.1565
    1.4117    0.2415
    1.5294    0.3265
    1.0588    0.4115
    0.4706    0.4965
    0.4706    0.5815
    0.9412    0.6665
    0.2353    0.7515
    0.2353    0.8365
```

Return Bar Heights and Bin Centers for a Given Number of Bins

Compute the bar heights for six bins using the empirical cumulative distribution function and also return the bin centers.

Generate failure times from a Birnbaum-Saunders distribution.

```
rng('default') % for reproducibility
failuretime = random('birnbaumsaunders',0.3,1,100,1);
```

Assuming that the end of the study is at time 0.9, mark the generated failure times that are larger than 0.9 as censored data and store that information in a vector.

```
T = 0.9;
cens = (failuretime>T);
```

First, compute the empirical cumulative distribution function for the data.

```
[f,x] = ecdf(failuretime,'censoring',cens);
```

Now, estimate the histogram with six bins using the cumulative distribution function estimate.

```
[n,c] = ecdfhist(f,x,6);
[n' c']
```

```
ans =

    1.9764    0.0998
    1.7647    0.2415
    1.1294    0.3831
    0.4235    0.5248
    0.7764    0.6665
    0.2118    0.8081
```

Draw Histogram for Given Bin Centers

Draw the histogram of the empirical cumulative distribution histogram for specified bin centers.

Generate failure times from a Birnbaum-Saunders distribution.

```
rng default;  % For reproducibility
failuretime = random('birnbaumsaunders',0.3,1,100,1);
```

Assuming that the end of the study is at time 0.9, mark the generated failure times that are larger than 0.9 as censored data and store that information in a vector.

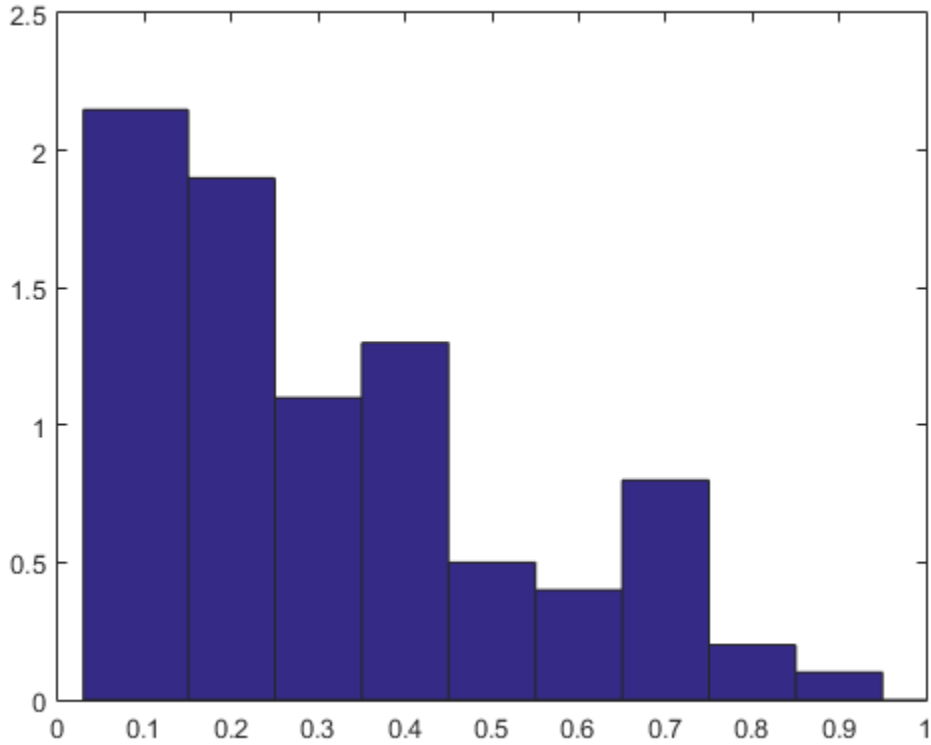
```
T = 0.9;
cens = (failuretime>T);
```

Define bin centers.

```
centers = 0.1:0.1:1;
```

Compute the empirical cumulative distribution function for the data and draw the histogram for specified bin centers.

```
[f,x] = ecdf(failuretime,'censoring',cens);
ecdfhist(f,x,centers)
axis([0 1 0 2.5])
```



Compare Histogram with Known Probability Distribution Function

Generate right-censored survival data and compare the histogram from cumulative distribution function with the known probability distribution function.

Generate failure times from an exponential distribution with mean failure time of 15.

```
rng default; % For reproducibility
y = exprnd(15,75,1);
```

Generate drop-out times from an exponential distribution with mean failure time of 30.

```
d = exprnd(30,75,1);
```

Record the minimum of these times as the observed failure times.

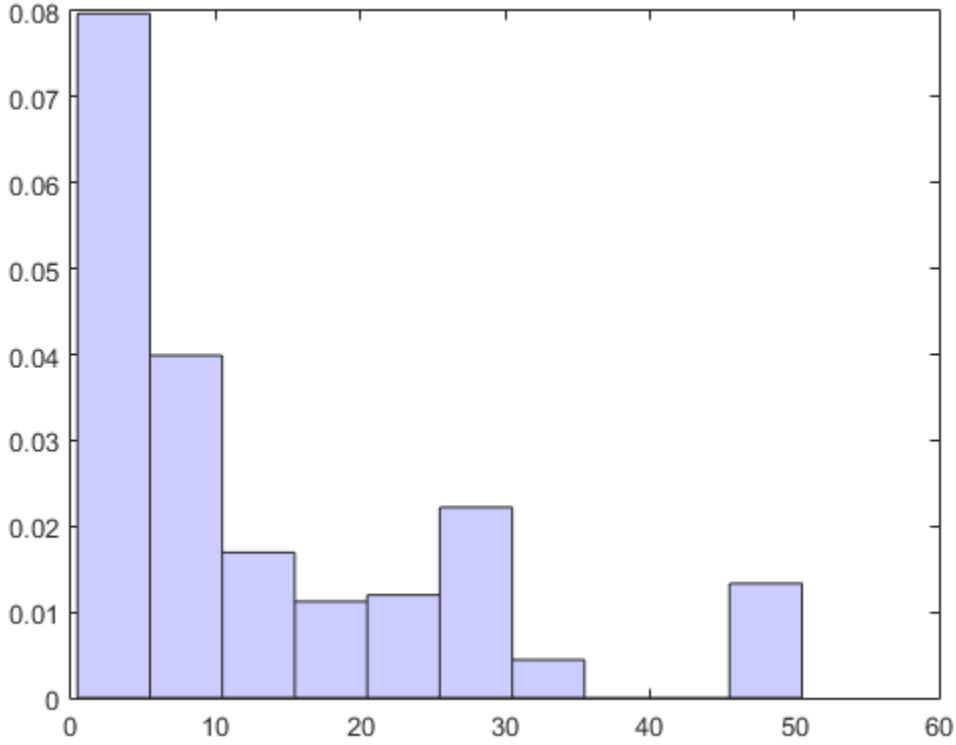
```
t = min(y,d);
```

Generate censoring by finding the generated failure times that are greater than the drop-out times.

```
censored = (y>d);
```

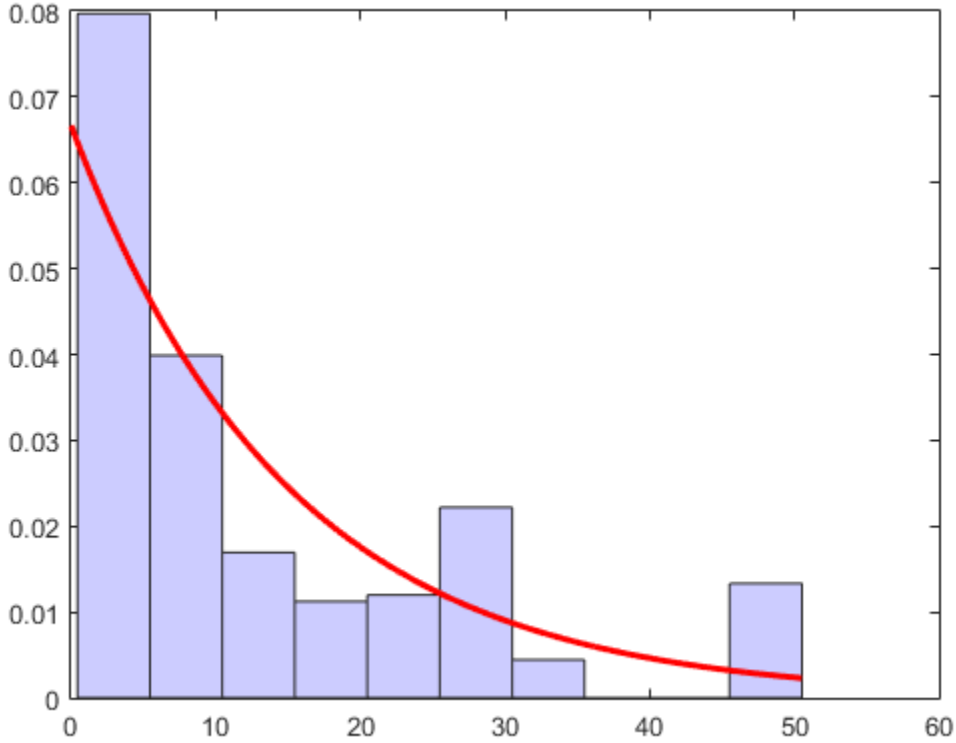
Calculate the empirical cdf and plot a histogram using the empirical cumulative distribution function.

```
[f,x] = ecdf(t,'censoring',censored);
ecdfhist(f,x)
h = findobj(gca,'Type','patch');
h.FaceColor = [.8 .8 1];
hold on
```



Superimpose a plot of the known population pdf.

```
xx = 0:.1:max(t);
yy = exp(-xx/15)/15;
plot(xx,yy,'r-','LineWidth',2)
hold off
```



Input Arguments

`f` — Empirical cdf values

vector

Empirical cdf values at given evaluation points, x, specified as a vector.

For instance, you can use `ecdf` to obtain the empirical cdf values and enter them in `ecdfhist` as follows.

Example: `[f,x] = ecdf(failure); ecdfhist(f,x);`

Data Types: `single | double`

x — Evaluation points

vector

Evaluation points at which empirical cdf values, `f`, are calculated, specified as a vector.

For instance, you can use `ecdf` to obtain the empirical cdf values and enter them in `ecdfhist` as follows.

Example: `[f,x] = ecdf(failure); ecdfhist(f,x);`

Data Types: `single | double`

m — Number of bins

scalar

Number of bins, specified as a scalar.

For instance, you can draw a histogram with 8 bins as follows.

Example: `ecdfhist(f,x,8)`

Data Types: `single | double`

centers — Center points of bins

vector

Center points of bins, specified as a vector.

Example: `centers = 2:2:10; ecdfhist(f,x,centers);`

Data Types: `single | double`

Output Arguments

n — Heights of histogram bars

row vector

Heights of histogram bars `ecdfhist` calculates based on the empirical cdf values, returned as a row vector.

c — Position of bin centers

row vector

Position of bin centers, returned as a row vector.

More About

- "Nonparametric and Empirical Probability Distributions" on page 5-40

See Also

`ecdf` | `histc` | `histogram`

edge

Class: ClassificationKNN

Edge of k-nearest neighbor classifier

Syntax

```
E = edge(mdl,X,Y)
E = edge(mdl,X,Y,Name,Value)
```

Description

`E = edge(mdl,X,Y)` returns the classification edge for `mdl` with data `X` and classification `Y`.

`E = edge(mdl,X,Y,Name,Value)` computes the edge with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

`X` — Matrix of predictor values

matrix

Matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y` — Categorical variables
categorical array | cell array of strings | character array | logical vector | numeric vector

A categorical array, cell array of strings, character array, logical vector, or a numeric vector with the same number of rows as `X`. Each row of `Y` represents the classification of the corresponding row of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'weights'`

Observation weights, a numeric vector of length `size(X,1)`. If you supply `weights`, `edge` computes weighted classification edge.

Default: `ones(size(X,1))`

Output Arguments

`E`

Classification edge, a scalar that is the mean classification margin (see “Margin” on page 22-1211).

Definitions

Edge

The *edge* is the mean value of the classification *margin*.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

Margin is a column vector with the same number of rows as `X`.

Score

The *score* of a classification is the posterior probability of the classification. The posterior probability is the number of neighbors that have that classification, divided by the number of neighbors. For a more detailed definition that includes weights and prior probabilities, see "Posterior Probability" on page 22-3654.

Examples

Edge Calculation

Construct a k-nearest neighbor classifier for the Fisher iris data, where $k = 5$.

Load the data.

```
load fisheriris
X = meas;
Y = species;
```

Construct a classifier for five-nearest neighbors.

```
mdl = fitcknn(X,Y,'NumNeighbors',5);
```

Examine the edge of the classifier for minimum, mean, and maximum observations classified `'setosa'`, `'versicolor'`, and `'virginica'` respectively.

```
NewX = [min(X);mean(X);max(X)];
Y = {'setosa';'versicolor';'virginica'};
E = edge(mdl,NewX,Y)
```

```
E =

     1
```

The classifier has no doubt that the `Y` entries are correct classifications (all five nearest neighbors of each `NewX` point classify as the corresponding `Y` entry).

See Also

`ClassificationKNN` | `fitcknn` | `loss` | `margin`

More About

- "Classification Using Nearest Neighbors" on page 16-8

edge

Class: CompactClassificationDiscriminant

Classification edge

Syntax

```
E = edge(obj,X,Y)
E = edge(obj,X,Y,Name,Value)
```

Description

`E = edge(obj,X,Y)` returns the classification edge for `obj` with data `X` and classification `Y`.

`E = edge(obj,X,Y,Name,Value)` computes the edge with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `fitcdiscr`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

`Y`

Class labels, with the same data type as exists in `obj`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'weights'`

Observation weights, a numeric vector of length `size(X,1)`. If you supply weights, `edge` computes the weighted classification edge.

Default: `ones(size(X,1))`

Output Arguments

`E`

Edge, a scalar representing the weighted average value of the margin.

Definitions

Edge

The *edge* is the weighted mean value of the classification *margin*. The weights are class prior probabilities. If you supply additional weights, those weights are normalized to sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

The classification margin is a column vector with the same number of rows as in the matrix X. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 15-7.

Examples

Compute the classification edge and margin for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries:

```
load fisheriris
X = meas(:,1:2);
obj = fitcdiscr(X,species);
E = edge(obj,X,species)

E =
    0.4980

M = margin(obj,X,species);
M(end-10:end)

ans =
    0.6551
    0.4838
    0.6551
   -0.5127
    0.5659
    0.4611
    0.4949
    0.1024
    0.2787
   -0.1439
   -0.4444
```

The classifier trained on all the data is better:

```
obj = fitcdiscr(meas,species);
E = edge(obj,meas,species)

E =
    0.9454
```

```
M = margin(obj,meas,species);
M(end-10:end)

ans =
    0.9983
    1.0000
    0.9991
    0.9978
    1.0000
    1.0000
    0.9999
    0.9882
    0.9937
    1.0000
    0.9649
```

See Also

`predict` | `ClassificationDiscriminant` | `fitcdiscr` | `loss` | `margin`

How To

- "Discriminant Analysis" on page 15-3

edge

Class: CompactClassificationECOC

Classification edge for error-correcting output code mutliclass classifiers

Syntax

```
e = edge(Mdl,X,Y)
e = edge(Mdl,X,Y,Name,Value)
```

Description

`e = edge(Mdl,X,Y)` returns the classification edge (`e`) for the error-correcting output code (ECOC) multiclass classifier `Mdl` using predictor data `X` and class labels `Y`. Each row of `X` and `Y` is an observation.

`e = edge(Mdl,X,Y,Name,Value)` computes the classification edge with additional options specified by one or more Name,Value pair arguments.

For example, specify a decoding scheme, binary learner loss function, or verbosity level.

Input Arguments

`Mdl` — ECOC multiclass classifier

`ClassificationECOC` model | `CompactClassificationECOC` model

ECOC multiclass classifier, specified as a `ClassificationECOC` or `CompactClassificationECOC` model. You can create a:

- `ClassificationECOC` model by training the ECOC classifier using `fitcecoc`
- `CompactClassificationECOC` model by passing a `ClassificationECOC` classifier to `compact`

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also called an instance or example), and each column corresponds to one variable (also known as a feature). The variables composing the columns of `X` should be the same as the variables that trained the `Mdl` classifier.

The length of `Y` and the number of rows of `X` must be equal.

If you trained `Mdl` specifying to standardize the predictor data, then the software standardizes the columns of `X` using the corresponding means and standard deviations that the software stored in `Mdl.BinaryLearner{j}.Mu` and `Mdl.BinaryLearner{j}.Sigma` for learner `j`.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `Mdl.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	$\{-1,1\}$	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	$[0,1]$	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `Mdl.CodingMatrix`.
  - `s` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.
  - L is the number of binary learners.

  For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`

- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single` | `double`

`'Weights'` — Observation weights

`ones(size(X,1))` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector. `Weights` need the same length as the number of rows of `X`, i.e., `size(X,1)`. The software normalizes `Weights` to sum up to the value of the prior probability in the respective class.

If you supply weights, `edge` computes the weighted classification edge.

Output Arguments

`e` — Classification edge

scalar

Classification edge, returned as a scalar. `e` represents the (weighted) mean of the classification margins.

Definitions

Classification Edge

The *classification edge* is the weighted mean of the *classification margins*.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margin

The *classification margins* are, for each observation, the difference between the negative loss for the positive class and maximal negative loss among the negative classes. If the margins are on the same scale, then they serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [4].

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left| m_{kj} \right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$

Value	Description	Score Domain	$g(y_j,s_j)$
`'linear'`	Linear	$(-\infty,\infty)$	$(1-y_js_j)/2$
`'quadratic'`	Quadratic	$[0,1]$	$[1-y_j(2s_j-1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Estimate the Test-Sample Edge of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify a 30% holdout sample. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'Holdout',0.30,'Learners',t,'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

Estimate the test-sample edge.

```
e = edge(CMdl,XTest,YTest)
```

```
e =

    0.4573
```

The estimated test sample margin average is approximately 0.45.

Estimate the Test-Sample Weighted Margin Mean of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Suppose that the observations were measured sequentially, and that the last 75 observations were better quality due to a technology upgrade. One way to incorporate this advancement is to weigh the better quality observations more than the other observations.

Define a weight vector that weighs the better quality observations two times the other observations.

```
n = size(X,1);
weights = [ones(n-75,1);2*ones(75,1)];
```

Train an ECOC model using SVM binary classifiers and specify a 30% holdout sample and the weighting scheme. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'Holdout',0.30,'Learners',t,...
    'Weights',weights,'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
wTest = weights(testInds,:);
```

`CVMdl` is a trained `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` classifier that the software trained using the training set.

Estimate the test-sample weighted edge using the weighting scheme.

```
e = edge(CMdl,XTest,YTest,'Weights',wTest)
```

```
e =

    0.4798
```

The test sample weighted average margin is approximately 0.48.

Select ECOC Model Features by Comparing Test-Sample Edges

The classifier edge measures the average of the classifier margins. One way to perform feature selection is to compare test-sample edges from multiple models. Based solely on this criterion, the classifier with the highest edge is the best classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Partition the data set into training and test sets. Specify a 30% holdout sample for testing.

```
Partition = cvpartition(Y,'Holdout',0.30);
testInds = test(Partition); % Indices for the test set
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`Partition` defines the data set partition.

Define these two data sets:

- `fullX` contains all predictors.
- `partX` contains the petal dimensions.

```
fullX = X;
partX = X(:,3:4);
```

Train an ECOC model using SVM binary classifiers for each predictor set, and specify the partition definition. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(fullX,Y,'CVPartition',Partition,'Learners',t,...
    'ClassNames',classOrder);
PCVMdl = fitcecoc(partX,Y,'CVPartition',Partition,'Learners',t,...
    'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};
PCMdl = PCVMdl.Trained{1};
```

`CVMdl` and `PCVMdl` are `ClassificationPartitionedECOC` models. They contain the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

Estimate the test sample edge for each classifier.

```
fullEdge = edge(CMdl,XTest,YTest)
partEdge = edge(PCMdl,XTest(:,3:4),YTest)
```

```
fullEdge =

    0.4573


partEdge =

    0.4839
```

`PCMdl` achieves an edge that resembles the more complex model `CMdl`.

- “Quick Start Parallel Computing for Statistics and Machine Learning Toolbox” on page 21-2

Tip

To compare margins or edges of several classifiers, use template objects to specify a common score transform function among the classifiers when you train them using `fitcecoc`.

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q., X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `CompactClassificationECOC` | `fitcecoc` | `margin` | `predict` | `resubEdge`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

edge

Class: CompactClassificationEnsemble

Classification edge

Syntax

```
E = edge(ens,X,Y)
E = edge(ens,X,Y,Name,Value)
```

Description

`E = edge(ens,X,Y)` returns the classification edge for `ens` with data `X` and classification `Y`.

`E = edge(ens,X,Y,Name,Value)` computes the edge with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A classification ensemble constructed with `fitensemble`, or a compact classification ensemble constructed with `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `ens`.

`Y`

Class labels, with the same data type as exists in `ens`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `ens.NumTrained`. `edge` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'mode'`

String representing the meaning of the output E:

- `'ensemble'` — `E` is a scalar value, the edge for the entire ensemble.
- `'individual'` — `E` is a vector with one element per trained learner.
- `'cumulative'` — `E` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

`'UseObsForLearner'`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of X.
- `T` is the number of weak learners in ens.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of X.

Default: `true(N,T)`

`'weights'`

Observation weights, a numeric vector of length `size(X,1)`. If you supply weights, `edge` computes weighted classification edge.

Default: `ones(size(X,1))`

Output Arguments

E

The classification edge, a vector or scalar depending on the setting of the `mode` name-value pair. Classification edge is weighted average classification margin.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix X.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in ens`.Prior`. If you supply weights in the `weights` name-value pair, those weights are used instead of class probabilities.

Examples

Make a boosted ensemble classifier for the `ionosphere` data, and find the classification edge for the last few rows:

```
load ionosphere
ens = fitensemble(X,Y,'AdaboostM1',100,'Tree');
E = edge(ens,X(end-10:end,:),Y(end-10:end))

E =
    8.3310
```

See Also

margin | edge

edge

Class: CompactClassificationNaiveBayes

Classification edge for naive Bayes classifiers

Syntax

```
e = edge(Mdl,X,Y)
e = edge(Mdl,X,Y,Name,Value)
```

Description

`e = edge(Mdl,X,Y)` returns the classification edge (`e`) for the naive Bayes classifier `Mdl` using predictor data `X` and class labels `Y`.

`e = edge(Mdl,X,Y,Name,Value)` computes the classification edge with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`Mdl` — Naive Bayes classifier

`ClassificationNaiveBayes` model | `CompactClassificationNaiveBayes` model

Naive Bayes classifier, specified as a `ClassificationNaiveBayes` model or `CompactClassificationNaiveBayes` model returned by `fitcnb` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained `Mdl`.

The length of `Y` and the number of rows of `X` must be equal.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `Mdl.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector.

The size of `Weights` must be equal to the number of rows of X. The software weighs the observations in each row of X with the corresponding weight in `Weights`.

If you do not specify your own loss function, then the software normalizes `Weights` to add up to `1`.

Data Types: `double`

Output Arguments

`e` — Classification edge

scalar

Classification edge, returned as a scalar. If you supply Weights, then `e` is the weighted classification edge.

Definitions

Classification Edge

The *classification edge* is the weighted mean of the classification margins.

If you supply weights, then the software normalizes them to sum to the prior probability of their respective class. The software uses the normalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margins

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.

- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

$$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Score

The naive Bayes *score* is the class posterior probability given the observation.

Examples

Estimate the Test Sample Edge of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);      % For reproducibility
```

Train a naive Bayes classifier. Specify a 30% holdout sample for testing. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
CVMdl = fitcnb(X,Y,'Holdout',0.30,...
    'ClassNames',{'setosa','versicolor','virginica'});
CMdl = CVMdl.Trained{1};          % Extract trained, compact classifier
testInds = test(CVMdl.Partition); % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds);
```

`CVMdl` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Estimate the test sample edge.

```
e = edge(CMdl,XTest,YTest)
```

```
e =

    0.8244
```

The estimated test sample margin average is approximately `0.82`. This indicates that, on average, the test sample difference between the estimated posterior probability for the predicted class and the posterior probability for the class with the next lowest posterior probability is approximately 0.82. This indicates that the classifier labels with high confidence.

Estimate the Test Sample Weighted Margin Mean of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);
```

Suppose that the setosa iris measurements are lower quality because they were measured with an older technology. One way to incorporate this is to weigh the setosa iris measurements less than the other observations.

Define a weight vector that weighs the better quality observations twice the other observations.

```
n = size(X,1);
idx = strcmp(Y,'setosa');
weights = ones(size(X,1),1);
weights(idx) = 0.5;
```

Train a naive Bayes classifier. Specify the weighting scheme and a 30% holdout sample for testing. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
CVMdl = fitcnb(X,Y,'Weights',weights,'Holdout',0.30,...
    'ClassNames',{'setosa','versicolor','virginica'});
CMdl = CVMdl.Trained{1};          % Extract trained, compact classifier
testInds = test(CVMdl.Partition); % Extract the test indices
XTest = X(testInds,:);
```

```
YTest = Y(testInds);
wTest = weights(testInds);
```

`CVMdl` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Estimate the test sample weighted edge using the weighting scheme.

```
e = edge(CMdl,XTest,YTest,'Weights',wTest)
```

```
e =

    0.7893
```

The test sample weighted average margin is approximately 0.79. This indicates that, on average, the test sample difference between the estimated posterior probability for the predicted class and the posterior probability for the class with the next lowest posterior probability is approximately 0.79. This indicates that the classifier labels with high confidence.

Select Naive Bayes Classifier Features by Comparing Test Sample Edges

The classifier edge measures the average of the classifier margins. One way to perform feature selection is to compare test sample edges from multiple models. Based solely on this criterion, the classifier with the highest edge is the best classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);
```

Partition the data set into training and test sets. Specify a 30% holdout sample for testing.

```
Partition = cvpartition(Y,'Holdout',0.30);
testInds = test(Partition); % Indices for the test set
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`Partition` defines the data set partition.

Define these two data sets:

- `fullX` contains all predictors.
- `partX` contains the last two predictors.

```
fullX = X;
partX = X(:,3:4);
```

Train naive Bayes classifiers for each predictor set. Specify the partition definition.

```
FCVMdl = fitcnb(fullX,Y,'CVPartition',Partition);
PCVMdl = fitcnb(partX,Y,'CVPartition',Partition);
FCMdl = FCVMdl.Trained{1};
PCMdl = PCVMdl.Trained{1};
```

`FCVMdl` and `PCVMdl` are `ClassificationPartitionedModel` classifiers. They contain the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Estimate the test sample edge for each classifier.

```
fullEdge = edge(FCMdl,XTest,YTest)
partEdge = edge(PCMdl,XTest(:,3:4),YTest)
```

```
fullEdge =

    0.8244


partEdge =

    0.8420
```

The test-sample edges of the classifiers are nearly the same. However, the model trained using two predictors (`PCMdl`) is less complex.

References

[1] Hu, Q., X. Che, L. Zhang, and D. Yu. “Feature Evaluation and Selection Based on Neighborhood Soft Margin.” *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `fitcnb` | `loss` | `margin` | `predict` | `resubEdge` | `resubLoss`

More About

- "Naive Bayes Classification" on page 15-31

edge

Class: CompactClassificationSVM

Classification edge for support vector machine classifiers

Syntax

```
e = edge(SVMModel,X,Y)
e = edge(SVMModel,X,Y,Name,Value)
```

Description

`e = edge(SVMModel,X,Y)` returns the classification edge (`e`) for the support vector machine (SVM) classifier `SVMModel` using predictor data `X` and class labels `Y`.

`e = edge(SVMModel,X,Y,Name,Value)` computes the classification edge with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`SVMModel` — SVM classifier

`ClassificationSVM` classifier | `CompactClassificationSVM` classifier

SVM classifier, specified as a `ClassificationSVM` classifier or `CompactClassificationSVM` classifier returned by `fitcsvm` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained the `SVMModel` classifier.

The length of `Y` and the number of rows of `X` must be equal.

If you set `'Standardize',true` in `fitcsvm` to train `SVMModel`, then the software standardizes the columns of `X` using the corresponding means in `SVMModel.Mu` and standard deviations in `SVMModel.Sigma`.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `SVMModel.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Weights'` — Observation weights

`ones(size(X,1))` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector. `Weights` must have the same length as the number of rows of `X`, i.e., `size(X,1)`.

If you supply weights, `edge` computes the weighted classification edge.

Output Arguments

`e` — Classification edge

scalar

Classification edge, returned as a scalar. `e` represents the (weighted) mean of the classification margins.

Definitions

Classification Edge

The *edge* is the weighted mean of the *classification margins*.

The weights are the prior class probabilities. If you supply weights, then the software normalizes them to sum to the prior probabilities in the respective classes. The software uses the renormalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margins

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j,x) = x_j'x$ (the linear kernel), then the score function reduces to

$$f(x) = (x / s)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Examples

Estimate the Test Sample Edge of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM classifier. Specify a 15% holdout sample for testing. It is good practice to specify the class order and standardize the data.

```
CVSVMModel = fitcsvm(X,Y,'Holdout',0.15,'ClassNames',{'b','g'},...
    'Standardize',true);
CompactSVMModel = CVSVMModel.Trained{1}; % Extract trained, compact classifier
testInds = test(CVSVMModel.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVSVMModel` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Estimate the test sample edge.

```
e = edge(CompactSVMModel,XTest,YTest)
```

```
e =

    5.0765
```

The estimated test sample margin average is approximately 5.

Estimate the Test Sample Weighted Margin Mean of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

```
rng(1); % For reproducibility
```

Suppose that the observations were measured sequentially, and that the last 150 observations were better quality due to a technology upgrade. One way to incorporate this advancement is to weigh the better quality observations more than the other observations.

Define a weight vector that weighs the better quality observations two times the other observations.

```
n = size(X,1);
weights = [ones(n-150,1);2*ones(150,1)];
```

Train an SVM classifier. Specify the weighting scheme and a 15% holdout sample for testing. It is good practice to specify the class order and standardize the data.

```
CVSVMModel = fitcsvm(X,Y,'Weights',weights,'Holdout',0.15,...
    'ClassNames',{'b','g'},'Standardize',true);
CompactSVMModel = CVSVMModel.Trained{1};
testInds = test(CVSVMModel.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
wTest = weights(testInds,:);
```

`CVSVMModel` is a trained `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Estimate the test sample weighted edge using the weighting scheme.

```
e = edge(CompactSVMModel,XTest,YTest,'Weights',wTest)
```

```
e =

    4.8341
```

The test sample weighted average margin is approximately 5.

Select SVM Classifier Features by Comparing Test Sample Edges

The classifier edge measures the average of the classifier margins. One way to perform feature selection is to compare test sample edges from multiple models. Based solely on this criterion, the classifier with the highest edge is the best classifier.

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Partition the data set into training and test sets. Specify a 15% holdout sample for testing.

```
Partition = cvpartition(Y,'Holdout',0.15);
testInds = test(Partition); % Indices for the test set
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`Partition` defines the data set partition.

Define these two data sets:

- `fullX` contains all predictors (except the removed column of 0s).
- `partX` contains the last 20 predictors.

```
fullX = X;
partX = X(:,end-20:end);
```

Train SVM classifiers for each predictor set. Specify the partition definition.

```
FullCVSVMModel = fitcsvm(fullX,Y,'CVPartition',Partition);
PartCVSVMModel = fitcsvm(partX,Y,'CVPartition',Partition);
FCSVMModel = FullCVSVMModel.Trained{1};
PCSVMModel = PartCVSVMModel.Trained{1};
```

`FullCVSVMModel` and `PartCVSVMModel` are `ClassificationPartitionedModel` classifiers. They contain the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Estimate the test sample edge for each classifier.

```
fullEdge = edge(FCSVMModel,XTest,YTest)
partEdge = edge(PCSVMModel,XTest(:,end-20:end),YTest)
```

```
fullEdge =

    2.8319
```

```
partEdge =

    1.5540
```

The edge for the classifier trained on the complete data set is greater, suggesting that the classifier trained using all of the predictors is better.

Algorithms

For binary classification, the software defines the margin for observation j, m_j, as

$$m_j = 2y_j f(x_j),$$

where $y_j \in \{-1,1\}$, and $f(x_j)$ is the predicted score of observation j for the positive class. However, the literature commonly uses $m_j = y_j f(x_j)$ to define the margin.

References

[1] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[2] Hu, Q, X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm` | `loss` | `margin` | `predict` | `resubEdge`

edge

Class: CompactClassificationTree

Classification edge

Syntax

```
E = edge(tree,X,Y)
E = edge(tree,X,Y,Name,Value)
```

Description

`E = edge(tree,X,Y)` returns the classification edge for `tree` with data `X` and classification `Y`.

`E = edge(tree,X,Y,Name,Value)` computes the edge with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

A classification tree created by `fitctree`, or a compact classification tree created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `tree`.

`Y`

Class labels, with the same data type as exists in `tree`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'weights'`

Observation weights, a numeric vector of length `size(X,1)`. If you supply weights, `edge` computes weighted classification edge.

Default: `ones(size(X,1))`

Output Arguments

`E`

The edge, a scalar representing the weighted average value of the margin.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as the matrix X.

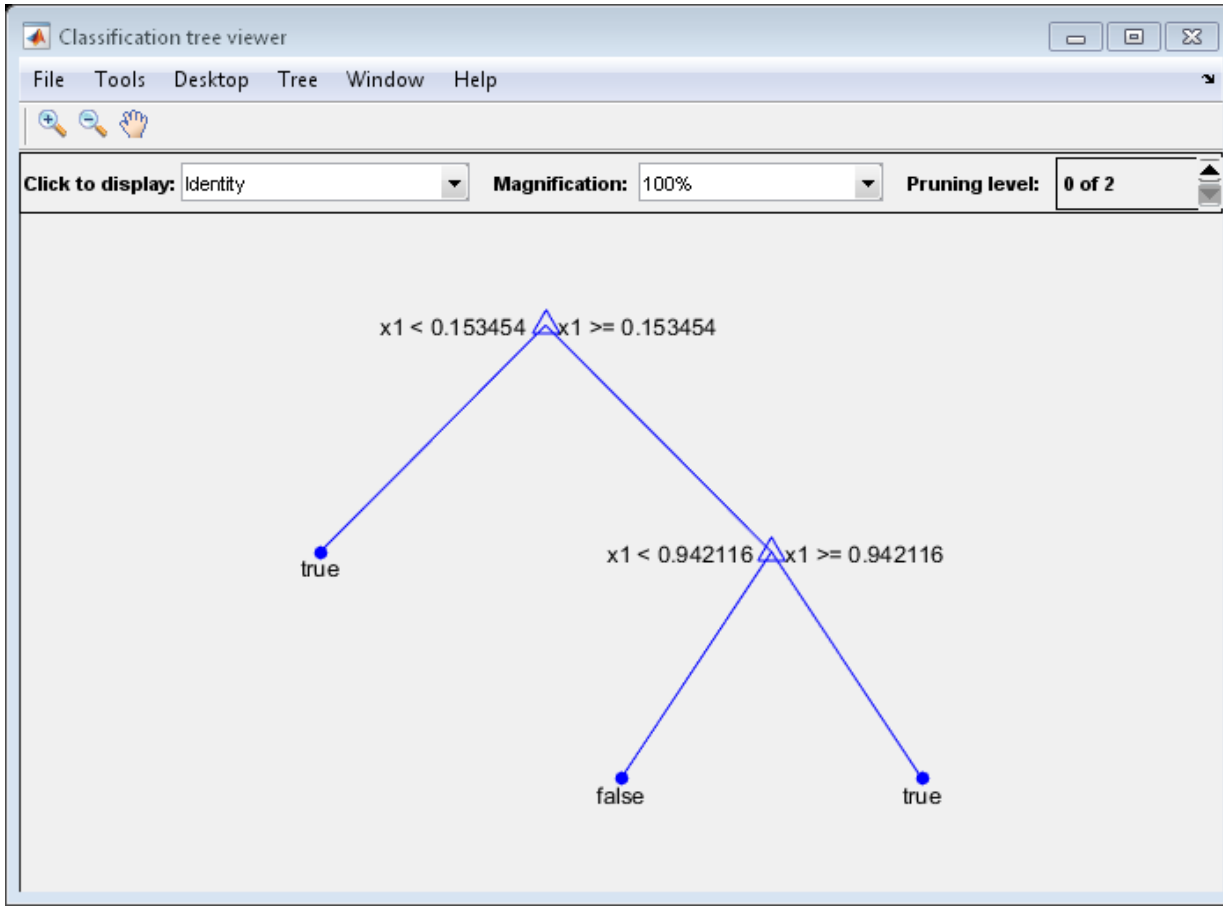
Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

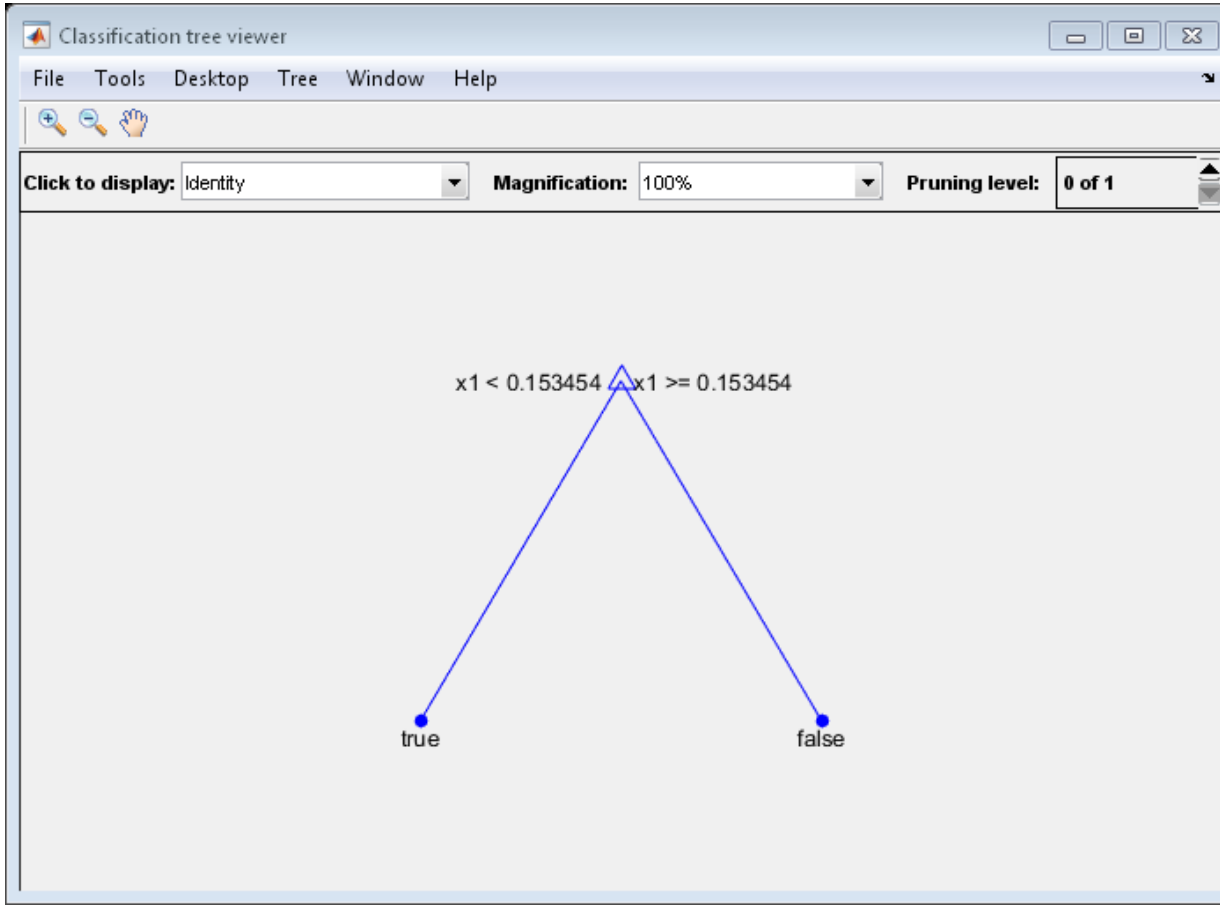
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in tree`.Prior`. If you supply weights in the `weights` name-value pair, those weights are normalized to sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Examples

Compute the classification margin and edge for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries:

```
load fisheriris
X = meas(:,1:2);
tree = fitctree(X,species);
E = edge(tree,X,species)

E =
    0.6299

M = margin(tree,X,species);
```

```
M(end-10:end)

ans =
    0.1111
    0.1111
    0.1111
   -0.2857
    0.6364
    0.6364
    0.1111
    0.7500
    1.0000
    0.6364
    0.2000
```

The classification tree trained on all the data is better.

```
tree = fitctree(meas,species);
E = edge(tree,meas,species)

E =
    0.9384

M = margin(tree,meas,species);
M(end-10:end)

ans =
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
```

See Also

`margin` | `predict` | `fitctree` | `loss`

end

Class: dataset

Last index in indexing expression for dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
end(A,k,n)
```

Description

`end(A,k,n)` is called for indexing expressions involving the dataset `A` when `end` is part of the `k`-th index out of `n` indices. For example, the expression `A(end-1,:)` calls `A`'s `end` method with `end(A,1,2)`.

See Also

`size`

end

Class: qrandset

Last index in indexing expression for point set

Syntax

```
end(p,k,n)
```

Description

`end(p,k,n)` is called for indexing expressions involving the point set `p` when `end` is part of the `k`-th index out of `n` indices. For example, the expression `p(end-1,:)` calls `p`'s `end` method with `end(p,1,2)`.

See Also

`qrandset`

epsilon

Class: RepeatedMeasuresModel

Epsilon adjustment for repeated measures anova

Syntax

```
tbl = epsilon(rm)
tbl = epsilon(rm,C)
```

Description

`tbl = epsilon(rm)` returns the epsilon adjustment factors for repeated measures model rm.

`tbl = epsilon(rm,C)` returns the epsilon adjustment factors for the test based on the contrast matrix `C`.

Tips

- The `mauchly` method tests for sphericity.
- The `ranova` method contains *p*-values based on each epsilon value.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`C` — Contrasts

matrix

Contrasts, specified as a matrix. The default value of C is the Q factor in a QR decomposition of the matrix M, where M is defined so that Y*M is the difference between all successive pairs of columns of the repeated measures matrix Y.

Data Types: `single | double`

Output Arguments

`tbl` — Epsilon adjustment factors

table

Epsilon adjustment factors for the repeated measures model rm, returned as a table. `tbl` contains four different adjustments for `epsilon`.

Correction	Definition
`Uncorrected`	No adjustments, epsilon = 1
`Greenhouse-Geiser`	Greenhouse-Geiser approximation
`Huynh-Feldt`	Huynh-Feldt approximation
`Lower bound`	Lower bound on the *p*-value

For details, see “Compound Symmetry Assumption and Epsilon Corrections” on page 8-79.

Data Types: `table`

Examples

Epsilon Corrections for Repeated Measures ANOVA

Load the sample data.

```
load fisheriris
```

The column vector, `species` consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
```

```
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform repeated measures analysis of variance.

```
ranovatbl = ranova(rm)
```

```
ranovatbl =

                          SumSq     DF      MeanSq       F          pValue       pValu
                          ______    ___    _________    ______    ____________    _____

    Measurements          1656.3     3       552.09    6873.3              0        0
    species:Measurements  282.47     6       47.078     586.1    1.4271e-206        0
    Error                 35.423   441    0.080324
```

`ranova` computes the last three *p*-values using Greenhouse-Geisser, Huynh-Feldt, and lower bound corrections, respectively.

Display the epsilon correction values.

```
epsilon(rm)
```

```
ans =

                        epsilon
                        _______

    Uncorrected               1
    Greenhouse-Geisser  0.75179
    Huynh-Feldt         0.77448
    Lower bound         0.33333
```

You can check the compound symmetry (sphericity) assumption using the `mauchly` method.

Algorithms

`ranova` computes the regular *p*-value (in the `pValue` column of the `rmanova` table) using the *F*-statistic cumulative distribution function:

p-value = 1 – fcdf(F,v_1,v_2).

When the compound symmetry assumption is not satisfied, `ranova` uses a correction factor epsilon, ε, to compute the corrected p-values as follows:
p-value_corrected = 1 – fcdf(F,ε*v_1,ε*v_2).

The `epsilon` method returns the epsilon adjustment values.

See Also

`fitrm` | `mauchly` | `ranova`

More About

- “Compound Symmetry Assumption and Epsilon Corrections” on page 8-79
- “Mauchly’s Test of Sphericity” on page 8-81

evcdf

Extreme value cumulative distribution function

Syntax

```
p = evcdf(x,mu,sigma)
[p,plo,pup] = evcdf(x,mu,sigma,pcov,alpha)
[p,plo,pup] = evcdf(___,'upper')
```

Description

`p = evcdf(x,mu,sigma)` returns the cumulative distribution function (cdf) for the type 1 extreme value distribution, with location parameter `mu` and scale parameter `sigma`, at each of the values in `x`. `x`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `mu` and `sigma` are `0` and `1`, respectively.

`[p,plo,pup] = evcdf(x,mu,sigma,pcov,alpha)` returns confidence bounds for `p` when the input parameters `mu` and `sigma` are estimates. `pcov` is a 2-by-2 covariance matrix of the estimated parameters. `alpha` has a default value of `0.05`, and specifies `100(1 - alpha)`% confidence bounds. `plo` and `pup` are arrays of the same size as `p`, containing the lower and upper confidence bounds.

`[p,plo,pup] = evcdf(___,'upper')` returns the complement of the type 1 extreme value distribution cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities. You can use the `'upper'` argument with any of the previous syntaxes.

The function `evcdf` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\frac{X-\hat{\mu}}{\hat{\sigma}}$$

and then transforming those bounds to the scale of the output `P`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov`

from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X` and subtracting the resulting distribution values from `1`. See "Extreme Value Distribution" on page B-39 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

More About

- "Extreme Value Distribution" on page B-39

See Also

`cdf` | `evpdf` | `evinv` | `evstat` | `evfit` | `evlike` | `evrnd`

evfit

Extreme value parameter estimates

Syntax

```
parmhat = evfit(data)
[parmhat,parmci] = evfit(data)
[parmhat,parmci] = evfit(data,alpha)
[...] = evfit(data,alpha,censoring)
[...] = evfit(data,alpha,censoring,freq)
[...] = evfit(data,alpha,censoring,freq,options)
```

Description

`parmhat = evfit(data)` returns maximum likelihood estimates of the parameters of the type 1 extreme value distribution given the data in the vector `data`. `parmhat(1)` is the location parameter, μ, and `parmhat(2)` is the scale parameter, σ.

`[parmhat,parmci] = evfit(data)` returns 95% confidence intervals for the parameter estimates on the μ and σ parameters in the 2-by-2 matrix `parmci`. The first column of the matrix of the extreme value fit contains the lower and upper confidence bounds for the parameter μ, and the second column contains the confidence bounds for the parameter σ.

`[parmhat,parmci] = evfit(data,alpha)` returns 100(1 - `alpha`)% confidence intervals for the parameter estimates, where `alpha` is a value in the range `[0 1]` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = evfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly.

`[...] = evfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq` of the same size as `data`. Typically, `freq` contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = evfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. You can create `options` using the function `statset`. Enter `statset('evfit')` to see the names and default values of the parameters that `evfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X`. See "Extreme Value Distribution" on page B-39 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

More About

- "Extreme Value Distribution" on page B-39

See Also

`mle` | `evlike` | `evpdf` | `evcdf` | `evinv` | `evstat` | `evrnd`

evinv

Extreme value inverse cumulative distribution function

Syntax

```
X = evinv(P,mu,sigma)
[X,XLO,XUP] = evinv(P,mu,sigma,pcov,alpha)
```

Description

`X = evinv(P,mu,sigma)` returns the inverse cumulative distribution function (cdf) for a type 1 extreme value distribution with location parameter `mu` and scale parameter `sigma`, evaluated at the values in `P`. `P`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `mu` and `sigma` are `0` and `1`, respectively.

`[X,XLO,XUP] = evinv(P,mu,sigma,pcov,alpha)` produces confidence bounds for `X` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` is a scalar that specifies 100(1 – `alpha`)% confidence bounds for the estimated parameters, and has a default value of 0.05. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

The function `evinv` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\hat{\mu} + \hat{\sigma} q$$

where q is the `P`th quantile from an extreme value distribution with parameters $\mu = 0$ and $\sigma = 1$. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X`. See “Extreme Value Distribution” on page

B-39 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

See Also

`icdf` | `evcdf` | `evpdf` | `evstat` | `evfit` | `evlike` | `evrnd`

eq

Class: qrandstream

Test handle equality

Syntax

```
h1 == h2
tf = eq(h1, h2)
```

Description

`h1 == h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise equality result. If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = eq(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `gt` | `le` | `ne` | `ge` | `lt`

error

Class: CompactTreeBagger

Error (misclassification probability or MSE)

Syntax

```
err = error(B,X,Y)
err = error(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`err = error(B,X,Y)` computes the misclassification probability (for classification trees) or mean squared error (MSE, for regression trees) for each tree, for predictors `X` given true response `Y`. For classification, `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. For regression, `Y` must be a numeric vector. `err` is a vector with one error measure for each of the `NTrees` trees in the ensemble `B`.

`err = error(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `error` computes cumulative errors and `err` is a vector of length `NTrees`, where the first element gives error from `trees(1)`, second element gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `err` is a vector of length `NTrees`, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `err` is a scalar showing the cumulative error for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'`

	mode, the first element gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`TreeBagger.error`

error

Class: TreeBagger

Error (misclassification probability or MSE)

Syntax

```
err = error(B,X,Y)
err = error(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`err = error(B,X,Y)` computes the misclassification probability for classification trees or mean squared error (MSE) for regression trees for each tree, for predictors `X` given true response `Y`. For classification, `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. For regression, `Y` must be a numeric vector. `err` is a vector with one error measure for each of the `NTrees` trees in the ensemble `B`.

`err = error(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `error` computes cumulative errors and `err` is a vector of length `NTrees`, where the first element gives error from `trees(1)`, second element gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `err` is a vector of length `NTrees`, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `err` is a scalar showing the cumulative error for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'`

	mode, the first element gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`CompactTreeBagger.error`

eval

Class: classregtree

Predicted responses

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
yfit = eval(t,X)
yfit = eval(t,X,s)
[yfit,nodes] = eval(...)
[yfit,nodes,cnums] = eval(...)
[...] = t(X)
[...] = t(X,s)
```

Description

`yfit = eval(t,X)` takes a classification or regression tree `t` and a matrix `X` of predictors, and produces a vector `yfit` of predicted response values. For a regression tree, `yfit(i)` is the fitted response value for a point having the predictor values `X(i,:)`. For a classification tree, `yfit(i)` is the class into which the tree assigns the point with data `X(i,:)`.

`yfit = eval(t,X,s)` takes an additional vector `s` of pruning levels, with 0 representing the full, unpruned tree. `t` must include a pruning sequence as created by `classregtree` or by `prune`. If `s` has k elements and `X` has n rows, the output `yfit` is an n-by-k matrix, with the `j`th column containing the fitted values produced by the `s(j)` subtree. `s` must be sorted in ascending order.

To compute fitted values for a tree that is not part of the optimal pruning sequence, first use `prune` to prune the tree.

`[yfit,nodes] = eval(...)` also returns a vector `nodes` the same size as `yfit` containing the node number assigned to each row of `X`. Use `view` to display the node numbers for any node you select.

`[yfit,nodes,cnums] = eval(...)` is valid only for classification trees. It returns a vector `cnum` containing the predicted class numbers.

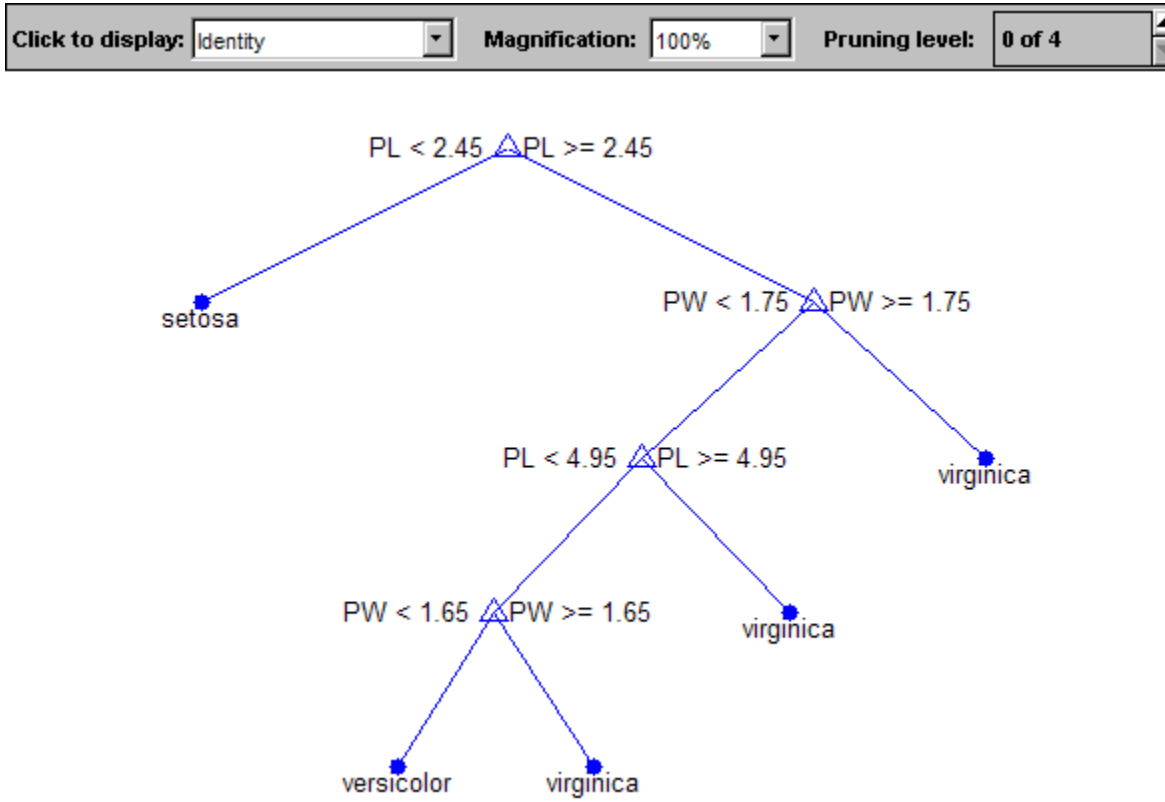
`NaN` values in `X` are treated as missing. If `eval` encounters a missing value when it attempts to evaluate the split rule at a branch node, it cannot determine whether to proceed to the left or right child node. Instead, it sets the corresponding fitted value equal to the fitted value assigned to the branch node.

`[...] = t(X)` or `[...] = t(X,s)` also invoke `eval`.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```



Find assigned class names:

```
sfit = eval(t,meas);
```

Compute that proportion is correctly classified:

```
pct = mean(strcmp(sfit,species))
pct =
    0.9800
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `test` | `view` | `prune`

evalclusters

Evaluate clustering solutions

Syntax

```
eva = evalclusters(x,clust,criterion)
eva = evalclusters(x,clust,criterion,Name,Value)
```

Description

`eva = evalclusters(x,clust,criterion)` creates a clustering evaluation object containing data used to evaluate the optimal number of data clusters.

`eva = evalclusters(x,clust,criterion,Name,Value)` creates a clustering evaluation object using additional options specified by one or more name-value pair arguments.

Examples

Evaluate the Clustering Solution Using Calinski-Harabasz Criterion

Evaluate the optimal number of clusters using the Calinski-Harabasz clustering evaluation criterion.

Load the sample data.

```
load fisheriris;
```

The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Evaluate the optimal number of clusters using the Calinski-Harabasz criterion. Cluster the data using `kmeans`.

```
rng('default');  % For reproducibility
eva = evalclusters(meas,'kmeans','CalinskiHarabasz','KList',[1:6])
```

```
eva =

  CalinskiHarabaszEvaluation with properties:

    NumObservations: 150
       InspectecedK: [1 2 3 4 5 6]
    CriterionValues: [1x6 double]
           OptimalK: 3
```

The `OptimalK` value indicates that, based on the Calinski-Harabasz criterion, the optimal number of clusters is three.

Evaluate a Matrix of Clustering Solutions

Use an input matrix of proposed clustering solutions to evaluate the optimal number of clusters.

Load the sample data.

```
load fisheriris;
```

The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Use `kmeans` to create an input matrix of proposed clustering solutions for the sepal length measurements, using 1, 2, 3, 4, 5, and 6 clusters.

```
clust = zeros(size(meas,1),6);
for i=1:6
clust(:,i) = kmeans(meas,i,'emptyaction','singleton',...
        'replicate',5);
end
```

Each row of `clust` corresponds to one sepal length measurement. Each of the six columns corresponds to a clustering solution containing 1 to 6 clusters.

Evaluate the optimal number of clusters using the Calinski-Harabasz criterion.

```
eva = evalclusters(meas,clust,'CalinskiHarabasz')
```

```
eva =

  CalinskiHarabaszEvaluation with properties:
```

```
    NumObservations: 150
         InspectedK: [1 2 3 4 5 6]
    CriterionValues: [NaN 513.9245 561.6278 530.7658 459.5058 473.6577]
           OptimalK: 3
```

The `OptimalK` value indicates that, based on the Calinski-Harabasz criterion, the optimal number of clusters is three.

Specify Clustering Algorithm with a Function Handle

Use a function handle to specify the clustering algorithm, then evaluate the optimal number of clusters.

Load the sample data.

```
load fisheriris;
```

The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Use a function handle to specify the clustering algorithm.

```
myfunc = @(X,K)(kmeans(X, K, 'emptyaction','singleton',...
    'replicate',5));
```

Evaluate the optimal number of clusters for the sepal length data using the Calinski-Harabasz criterion.

```
eva = evalclusters(meas,myfunc,'CalinskiHarabasz',...
    'klist',[1:6])

eva =

  CalinskiHarabaszEvaluation with properties:

    NumObservations: 150
         InspectedK: [1 2 3 4 5 6]
    CriterionValues: [NaN 513.9245 561.6278 530.7658 459.5058 473.6577]
           OptimalK: 3
```

The `OptimalK` value indicates that, based on the Calinski-Harabasz criterion, the optimal number of clusters is three.

- “Clustering Using Gaussian Mixture Models” on page 14-29

Input Arguments

x — Input data

matrix

Input data, specified as an N-by-P matrix. N is the number of observations, and P is the number of variables.

Data Types: `single` | `double`

clust — Clustering algorithm

`'kmeans'` | `'linkage'` | `'gmdistribution'` | matrix of clustering solutions | function handle

Clustering algorithm, specified as one of the following.

`'kmeans'`	Cluster the data in x using the `kmeans` clustering algorithm, with `'EmptyAction'` set to `'singleton'` and `'Replicates'` set to `5`.
`'linkage'`	Cluster the data in x using the `clusterdata` agglomerative clustering algorithm, with `'Linkage'` set to `'ward'`.
`'gmdistribution'`	Cluster the data in x using the `gmdistribution` Gaussian mixture distribution algorithm, with `'SharedCov'` set to `true` and `'Replicates'` set to `5`.

If `Criterion` is `'CalinskiHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can specify a clustering algorithm using the `function_handle` (`@`) operator. The function must be of the form `C = clustfun(DATA,K)`, where `DATA` is the data to be clustered, and `K` is the number of clusters. The output of `clustfun` must be one of the following:

- A vector of integers representing the cluster index for each observation in `DATA`. There must be `K` unique values in this vector.
- A numeric n-by-K matrix of score for n observations and K classes. In this case, the cluster index for each observation is determined by taking the largest score value in each row.

If `Criterion` is `'CalinskiHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can also specify `clust` as a n-by-K matrix containing the proposed clustering solutions. n is the number of observations in the sample data, and K is the number of proposed

clustering solutions. Column *j* contains the cluster indices for each of the *N* points in the *j*th clustering solution.

`criterion` — Clustering evaluation criterion
`'CalinskiHarabasz' | 'DaviesBouldin' | 'gap' | 'silhouette'`

Clustering evaluation criterion, specified as one of the following.

`'CalinskiHarabasz'`	Create a `CalinskiHarabaszEvaluation` clustering evaluation object containing Calinski-Harabasz index values.
`'DaviesBouldin'`	Create a `DaviesBouldinEvaluation` cluster evaluation object containing Davies-Bouldin index values.
`'gap'`	Create a `GapEvaluation` cluster evaluation object containing gap criterion values.
`'silhouette'`	Create a `SilhouetteEvaluation` cluster evaluation object containing silhouette values.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'KList',[1:5],'Distance','cityblock'` specifies to test 1, 2, 3, 4, and 5 clusters using the sum of absolute differences distance measure.

For All Criteria

`'KList'` — List of number of clusters to evaluate
vector

List of number of clusters to evaluate, specified as the comma-separated pair consisting of `'KList'` and a vector of positive integer values. You must specify `KList` when clust is

a clustering algorithm name string or a function handle. When criterion is `'gap'`, clust must be a string or a function handle, and you must specify KList.

Example: `'KList',[1:6]`

For Silhouette and Gap

`'Distance'` — Distance metric
`'sqEuclidean'` (default) | `'Euclidean'` | `'cityblock'` | vector | function | ...

Distance metric used for computing the criterion values, specified as the comma-separated pair consisting of `'Distance'` and one of the following.

`'sqEuclidean'`	Squared Euclidean distance
`'Euclidean'`	Euclidean distance
`'cityblock'`	Sum of absolute differences
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors)
`'correlation'`	One minus the sample correlation between points (treated as sequences of values)
`'Hamming'`	Percentage of coordinates that differ
`'Jaccard'`	Percentage of nonzero coordinates that differ

For detailed information about each distance metric, see `pdist`.

You can also specify a function for the distance metric by using the `function_handle` (`@`) operator. The distance function must be of the form `d2 = distfun(XI,XJ)`, where `XI` is a 1-by-n vector corresponding to a single row of the input matrix `X`, and `XJ` is an m_2-by-n matrix corresponding to multiple rows of `X`. `distfun` must return an m_2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

If `Criterion` is `'silhouette'`, you can also specify `Distance` as the output vector output created by the function `pdist`.

When `Clust` a string representing a built-in clustering algorithm, `evalclusters` uses the distance metric specified for `Distance` to cluster the data, except for the following:

- If `Clust` is `'linkage'`, and `Distance` is either `'sqEuclidean'` or `'Euclidean'`, then the clustering algorithm uses Euclidean distance and Ward linkage.

- If `Clust` is `'linkage'` and `Distance` is any other metric, then the clustering algorithm uses the specified distance metric and average linkage.

In all other cases, the distance metric specified for Distance must match the distance metric used in the clustering algorithm to obtain meaningful results.

Example: `'Distance','Euclidean'`

For Silhouette Only

`'ClusterPriors'` — Prior probabilities for each cluster

`'empirical'` (default) | `'equal'`

Prior probabilities for each cluster, specified as the comma-separated pair consisting of `'ClusterPriors'` and one of the following.

`'empirical'`	Compute the overall silhouette value for the clustering solution by averaging the silhouette values for all points. Each cluster contributes to the overall silhouette value proportionally to its size.
`'equal'`	Compute the overall silhouette value for the clustering solution by averaging the silhouette values for all points within each cluster, and then averaging those values across all clusters. Each cluster contributes equally to the overall silhouette value, regardless of its size.

Example: `'ClusterPriors','empirical'`

For Gap Only

`'B'` — Number of reference data sets

100 (default) | positive integer value

Number of reference data sets generated from the reference distribution ReferenceDistribution, specified as the comma-separated pair consisting of `'B'` and a positive integer value.

Example: `'B',150`

'ReferenceDistribution' — Reference data generation method

'PCA' (default) | 'uniform'

Reference data generation method, specified as the comma-separated pair consisting of 'ReferenceDistributions' and one of the following.

'PCA'	Generate reference data from a uniform distribution over a box aligned with the principal components of the data matrix x.
'uniform'	Generate reference data uniformly over the range of each feature in the data matrix x.

Example: 'ReferenceDistribution','uniform'

'SearchMethod' — Method for selecting optimal number of clusters

'globalMaxSE' (default) | 'firstMaxSE'

Method for selecting the optimal number of clusters, specified as the comma-separated pair consisting of 'SearchMethod' and one of the following.

'globalMaxSE'	Evaluate each proposed number of clusters in KList and select the smallest number of clusters satisfying $$\mathrm{Gap}(K) \geq GAPMAX - \mathrm{SE}(GAPMAX),$$ where K is the number of clusters, Gap(K) is the gap value for the clustering solution with K clusters, $GAPMAX$ is the largest gap value, and SE($GAPMAX$) is the standard error corresponding to the largest gap value.
'firstMaxSE'	Evaluate each proposed number of clusters in KList and select the smallest number of clusters satisfying $$\mathrm{Gap}(K) \geq \mathrm{Gap}(K+1) - \mathrm{SE}(K+1),$$ where K is the number of clusters, Gap(K) is the gap value for the clustering solution with K clusters, and SE(K + 1) is the standard error of the clustering solution with K + 1 clusters.

Example: `'SearchMethod','globalMaxSE'`

Output Arguments

`eva` — Clustering evaluation data

clustering evaluation object

Clustering evaluation data, returned as a clustering evaluation object.

More About

- "*k*-Means Clustering" on page 14-21
- "Hierarchical Clustering" on page 14-3
- "Gaussian Mixture Models" on page 5-150

See Also

`clustering.evaluation.CalinskiHarabaszEvaluation` | `clustering.evaluation.DaviesBouldinEvaluation` | `clustering.evaluation.GapEvaluation` | `clustering.evaluation.SilhouetteEvaluation`

evlike

Extreme value negative log-likelihood

Syntax

```
nlogL = evlike(params,data)
[nlogL,AVAR] = evlike(params,data)
[...] = evlike(params,data,censoring)
[...] = evlike(params,data,censoring,freq)
```

Description

`nlogL = evlike(params,data)` returns the negative of the log-likelihood for the type 1 extreme value distribution. `params(1)` is the tail location parameter, `mu`, and `params(2)` is the scale parameter, `sigma`. `nlogL` is a scalar.

`[nlogL,AVAR] = evlike(params,data)` returns the inverse of Fisher's information matrix, `AVAR`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `AVAR` are their asymptotic variances. `AVAR` is based on the observed Fisher's information, not the expected information.

`[...] = evlike(params,data,censoring)` accepts a Boolean vector of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = evlike(params,data,censoring,freq)` accepts a frequency vector of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `data`. See “Extreme Value Distribution” on page B-39 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

More About

- "Extreme Value Distribution" on page B-39

See Also

`evfit` | `evpdf` | `evcdf` | `evinv` | `evstat` | `evrnd`

evpdf

Extreme value probability density function

Syntax

```
Y = evpdf(X,mu,sigma)
```

Description

`Y = evpdf(X,mu,sigma)` returns the pdf of the type 1 extreme value distribution with location parameter `mu` and scale parameter `sigma`, evaluated at the values in `X`. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `mu` and `sigma` are `0` and `1`, respectively.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `X`. See “Extreme Value Distribution” on page B-39 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

More About

- “Extreme Value Distribution” on page B-39

See Also

`pdf` | `evcdf` | `evinv` | `evstat` | `evfit` | `evlike` | `evrnd`

evrnd

Extreme value random numbers

Syntax

```
R = evrnd(mu,sigma)
R = evrnd(mu,sigma,m,n,...)
R = evrnd(mu,sigma,[m,n,...])
```

Description

`R = evrnd(mu,sigma)` generates random numbers from the extreme value distribution with parameters specified by location parameter `mu` and scale parameter `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of R. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

`R = evrnd(mu,sigma,m,n,...)` or `R = evrnd(mu,sigma,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the extreme value distribution with parameters `mu` and `sigma`. `mu` and `sigma` can each be scalars or arrays of the same size as `R`.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima by negating `R`. See "Extreme Value Distribution" on page B-39 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

More About

- "Extreme Value Distribution" on page B-39

See Also

`random` | `evpdf` | `evcdf` | `evinv` | `evstat` | `evfit` | `evlike`

evstat

Extreme value mean and variance

Syntax

```
[M,V] = evstat(mu,sigma)
```

Description

`[M,V] = evstat(mu,sigma)` returns the mean of and variance for the type 1 extreme value distribution with location parameter `mu` and scale parameter `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other input. The default values for `mu` and `sigma` are `0` and `1`, respectively.

The type 1 extreme value distribution is also known as the Gumbel distribution. The version used here is suitable for modeling minima; the mirror image of this distribution can be used to model maxima. See "Extreme Value Distribution" on page B-39 for more details. If x has a Weibull distribution, then $X = \log(x)$ has the type 1 extreme value distribution.

More About

- "Extreme Value Distribution" on page B-39

See Also

`evpdf` | `evcdf` | `evinv` | `evfit` | `evlike` | `evrnd`

prob.ExponentialDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Exponential probability distribution object

Description

`prob.ExponentialDistribution` is an object consisting of parameters, a model description, and sample data for an exponential probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Exponential')` creates an exponential probability distribution object using the default parameter values.

`pd = makedist('Exponential','mu',mu)` creates an exponential probability distribution object using the specified parameter value.

Input Arguments

`mu` — Mean
1 (default) | positive scalar value

Mean of the exponential distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

`mu` — Mean
positive scalar value

Mean of the exponential distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The `(i,j)` element is the covariance between

the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters

proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Exponential Distribution

The exponential distribution is used to model events that occur randomly over time, and its main application area is studies of lifetimes. It is a special case of the gamma distribution with the shape parameter $a = 1$.

The exponential distribution uses the following parameters.

Parameter	Description	Support
`mu`	Mean	$\mu > 0$

The probability density function (pdf) is

$$f(x \mid \mu) = \frac{1}{\mu} e^{\frac{-x}{\mu}} \quad ; \quad x \geq 0 .$$

Examples

Create an Exponential Distribution Object Using Default Parameters

Create an exponential distribution object using the default parameter values.

```
pd = makedist('Exponential')
```

```
pd =

  ExponentialDistribution

  Exponential distribution
    mu = 1
```

Create an Exponential Distribution Object Using Specified Parameters

Create an exponential distribution object by specifying the parameter values.

```
pd = makedist('Exponential','mu',2)
```

```
pd =

  ExponentialDistribution

  Exponential distribution
    mu = 2
```

Compute the variance of the distribution.

```
v = var(pd)
```

```
v =

     4
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Exponential Distribution"
- Class Attributes
- Property Attributes

expcdf

Exponential cumulative distribution function

Syntax

```
p = expcdf(x,mu)
[p,plo,pup] = expcdf(x,mu,pcov,alpha)
[p,plo,pup] = expcdf(___,'upper')
```

Description

`p = expcdf(x,mu)` computes the exponential cdf at each of the values in `x` using the corresponding mean parameter `mu`. `x` and `mu` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `mu` must be positive.

`[p,plo,pup] = expcdf(x,mu,pcov,alpha)` produces confidence bounds for `Pp` when the input mean parameter `mu` is an estimate. `pcov` is the variance of the estimated `mu`. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `plo` and `pup` are arrays of the same size as `p` containing the lower and upper confidence bounds. The bounds are based on a normal approximation for the distribution of the log of the estimate of `mu`. If you estimate `mu` from a set of data, you can get a more accurate set of bounds by applying `expfit` to the data to get a confidence interval for `mu`, and then evaluating `expinv` at the lower and upper endpoints of that interval.

`[p,plo,pup] = expcdf(___,'upper')` returns the complement of the exponential cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities. You can use the `'upper'` argument with any of the prior syntaxes.

The exponential cdf is

$$p = F(x \mid u) = \int_0^x \frac{1}{\mu} e^{\frac{-t}{\mu}} dt = 1 - e^{\frac{-x}{\mu}}$$

The result, p, is the probability that a single observation from an exponential distribution will fall in the interval [0 x].

Examples

Compute the Exponential CDF

The following code shows that the median of the exponential distribution is μ`*log(2)`.

```
mu = 10:10:60;
p = expcdf(log(2)*mu,mu)
```

```
p =
  0.5000  0.5000  0.5000  0.5000  0.5000  0.5000
```

What is the probability that an exponential random variable is less than or equal to the mean, μ?

```
mu = 1:6;
x = mu;
p = expcdf(x,mu)
```

```
p =
  0.6321  0.6321  0.6321  0.6321  0.6321  0.6321
```

More About

- “Exponential Distribution” on page B-35

See Also

`cdf` | `exppdf` | `expinv` | `expstat` | `expfit` | `explike` | `exprnd`

expfit

Exponential parameter estimates

Syntax

```
muhat = expfit(data)
[muhat,muci] = expfit(data)
[muhat,muci] = expfit(data,alpha)
[...] = expfit(data,alpha,censoring)
[...] = expfit(data,alpha,censoring,freq)
```

Description

`muhat = expfit(data)` estimates the mean of an exponentially distributed sample `data`. Each entry of `muhat` corresponds to the data in a column of `data`.

`[muhat,muci] = expfit(data)` returns 95% confidence intervals for the mean parameter estimates in matrix `muci`. The first row of `muci` contains the lower bounds of the confidence intervals, and the second row contains the upper bounds.

`[muhat,muci] = expfit(data,alpha)` returns 100(1 - `alpha`)% confidence intervals for the parameter estimates, where `alpha` is a value in the range `[0 1]` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = expfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly. `data` must be a vector in order to pass in the argument `censoring`.

`[...] = expfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq` of the same size as `data`. Typically, `freq` contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

Examples

The following estimates the mean `mu` of exponentially distributed data, and returns a 95% confidence interval for the estimate:

```
mu = 3;
data = exprnd(mu,100,1); % Simulated data

[muhat,muci] = expfit(data)
muhat =
    2.7511
muci =
    2.2826
    3.3813
```

See Also

`mle` | `explike` | `exppdf` | `expcdf` | `expinv` | `expstat` | `exprnd`

ExhaustiveSearcher

Prepare exhaustive nearest neighbors searcher

Syntax

```
Mdl = ExhaustiveSearcher(X)
Mdl = ExhaustiveSearcher(X,Name,Value)
```

Description

`Mdl = ExhaustiveSearcher(X)` prepares an exhaustive nearest neighbors searcher (`Mdl`) to find the nearest neighbors of query data using the n-by-K numeric matrix of training data (`X`). `Mdl` is an `ExhaustiveSearcher` model object that stores the statistics and options required for an exhaustive nearest neighbors search. You can use `Mdl` to search the training data (`X`) for the nearest neighbors to the query data.

`Mdl = ExhaustiveSearcher(X,Name,Value)` prepares an exhaustive nearest neighbors searcher with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify a distance metric or distance metric parameters values.

Examples

Train Default Exhaustive Nearest Neighbors Searcher

Load Fisher's iris data set.

```
load fisheriris
X = meas;
[n,k] = size(X)
```

```
n =

   150
```

```
k =

     4
```

`X` has 150 observations and 4 predictors.

Prepare an exhaustive nearest neighbors searcher using the entire data set as training data.

```
Mdl = ExhaustiveSearcher(X)
```

```
Mdl =

  ExhaustiveSearcher with properties:

         Distance: 'euclidean'
    DistParameter: []
                X: [150x4 double]
```

`Mdl` is an `ExhaustiveSearcher` model object, and its properties appear in the Command Window. It contains information about the trained algorithm, such as the distance metric. You can alter property values using dot notation.

To search `X` for the nearest neighbors to a batch of query data, pass `Mdl` and the query data to `knnsearch` or `rangesearch`.

Specify the Mahalanobis Distance for Nearest Neighbor Search

Load Fisher's iris data. Focus on the petal dimensions.

```
load fisheriris
X = meas(:,[3 4]); % Predictors
```

Prepare an exhaustive, nearest neighbors searcher. Specify to use the Mahalanobis distance metric.

```
Mdl = createns(X,'NSMethod','exhaustive','Distance','mahalanobis')
```

```
Mdl =

  ExhaustiveSearcher with properties:

         Distance: 'mahalanobis'
    DistParameter: [2x2 double]
                X: [150x2 double]
```

`Mdl` is an `ExhaustiveSearcher` model object. Access properties of `Mdl` using dot notation. For example, use `Mdl.DistParameter` to access the Mahalanobis covariance parameter.

```
Mdl.DistParameter
```

```
ans =

    3.1163    1.2956
    1.2956    0.5810
```

You can pass query data and `Mdl` to:

- searcher.knnsearch to find indices and distances of nearest neighbors.
- searcher.rangesearch to find indices of all nearest neighbors within a distance that you specify.

Search for Nearest Neighbors of Query Data Using the Mahalanobis Distance

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(1);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
X = meas(~ismember(1:n,qIdx),:);
Y = meas(qIdx,:);
```

Prepare an exhaustive nearest neighbors searcher using the training data. Specify to use the Mahalanobis distance for finding nearest neighbors later.

```
Mdl = createns(X,'NSMethod','exhaustive','Distance','mahalanobis')
```

```
Mdl =

  ExhaustiveSearcher with properties:

         Distance: 'mahalanobis'
    DistParameter: [4x4 double]
                X: [145x4 double]
```

`Mdl` is an `ExhaustiveSearcher` model object. By default, the Mahalanobis metric parameter value is the estimated covariance matrix of the predictors (columns) in the training data. To display this value,use `Mdl.DistPatameter`.

```
Mdl.DistParameter
```

```
ans =

    0.6819   -0.0332    1.2526    0.5103
   -0.0332    0.1859   -0.3152   -0.1183
    1.2526   -0.3152    3.0638    1.2816
    0.5103   -0.1183    1.2816    0.5786
```

Find the indices of the training data (`Mdl.X`) that are the two nearest neighbors of each point in the query data (`Q`).

```
IdxNN = knnsearch(Mdl,Y,'K',2)
```

```
IdxNN =

    26    38
     6    21
     1    34
    84    76
    69   129
```

Each row of NN corresponds to a query data observation. The column order corresponds to the order of the nearest neighbors with respect to ascending distance. For example, using the Mahalanobis metric, the second nearest neighbor of `Q(3,:)` is `X(34,:)`.

Input Arguments

X — Training data

numeric matrix

Training data for an exhaustive nearest neighbor search, specified as a numeric matrix. X has n rows, each corresponding to an observation (i.e. an instance or example), and K columns, each corresponding to a predictor or feature.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Distance','mahalanobis','Cov',eye(3)` specifies to use the Mahalanobis distance when searching for nearest neighbors, and a 3-by-3 identity matrix for the covariance matrix in the Mahalanobis distance metric.

'Cov' — Covariance matrix for Mahalanobis distance metric

`nancov(X)` (default) | positive definite matrix

Covariance matrix for the Mahalanobis distance metric, specified as the comma-separated pair consisting of `'Cov'` and a positive definite matrix. `Cov` is a K-by-K matrix, where K is the number of columns of X. If you specify `Cov` and do not specify `'Distance','mahalanobis'`, then `ExhaustiveSearcher` throws an error.

Example: `'Cov',eye(3)`

Data Types: `double` | `single`

'Distance' — Distance metric

`'euclidean'` (default) | `'chebychev'` | `'cityblock'` | `'correlation'` | `'cosine'` | `'hamming'` | `'jaccard'` | `'mahalanobis'` | `'minkowski'` | `'seuclidean'` | `'spearman'` | custom distance function

Distance metric used to find nearest neighbors of query points, specified as a comma-separated pair consisting of `'Distance'` and a string or function handle.

This table describes the supported distance metrics specified by strings.

Value	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'cityblock'`	City block distance
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values)
`'cosine'`	One minus the cosine of the included angle between observations (row vectors)
`'euclidean'`	Euclidean distance
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ
`'minkowski'`	Minkowski distance
`'mahalanobis'`	Mahalanobis distance
`'seuclidean'`	Standardized Euclidean distance
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values)

For more details, see “Distance Metrics”.

You can specify a function handle for a custom distance metric using `@` (for example, `@distfun`). The custom distance function must:

- Have the form `function D2 = distfun(ZI, ZJ)`
- Take as arguments:
  - A 1-by-*K* vector `ZI` containing a single row from `X` or from the query points `Y`

- An m-by-K matrix `ZJ` containing multiple rows of `X` or `Y`

- Return an m-by-1 vector of distances `D2`, whose jth element is the distance between the observations `ZI` and `ZJ(j,:)`

The software does not use the distance metric for training the exhaustive searcher algorithm. Therefore, you can alter it after training by specifying a supported string or function handle for a custom function using dot notation.

Example: `'Distance','mahalanobis'`

Data Types: `char | function_handle`

`'P'` — Exponent for Minkowski distance metric

`2` (default) | positive scalar

Exponent for the Minkowski distance metric, specified as the comma-separated pair consisting of `'P'` and a positive scalar. If you specify `P` and do not specify `'Distance','minkowski'`, then the software throws an error.

Example: `'P',3`

Data Types: `double | single`

`'Scale'` — Scale parameter value for standard Euclidean distance metric

`nanstd(X)` (default) | nonnegative numeric vector

Scale parameter value for the standard Euclidean distance metric, specified as the comma-separated pair consisting of `'Scale'` and a nonnegative numeric vector. `Scale` has length K, where K is the number of columns of X.

The software scales each difference between the training and query data using the corresponding element of `Scale`. If you specify `Scale` and do not specify `'Distance','seuclidean'`, then `ExhaustiveSearcher` throws an error.

Example: `'Scale',quantile(X,0.75) - quantile(X,0.25)`

Data Types: `double | single`

Output Arguments

`Mdl` — Prepared exhaustive nearest neighbors searcher

`ExhaustiveSearcher` model object

Prepared exhaustive nearest neighbors searcher, returned as an `ExhaustiveSearcher` model object. To search the training data for the nearest neighbors of the query data, pass the query data and `Mdl` to `knnsearch` or `rangesearch`.

More About

- Using ExhaustiveSearcher Objects
- "*k*-Nearest Neighbor Search and Radius Search" on page 16-11
- "Distance Metrics"

See Also

`createns` | `knnsearch` | `rangesearch`

Introduced in R2010a

Using ExhaustiveSearcher Objects

Exhaustive nearest neighbors searcher

`ExhustiveSearcher` model objects store statistics and options for an exhaustive, nearest neighbors search. Statistics and options that you can store include the training data, the distance metric, and the parameter values of the distance metric. The exhaustive search algorithm finds the distance from each query observation to all n observations in the training data, which is an n-by-K numeric matrix.

Once you create an `ExhaustiveSearcher` model object, find neighboring points in the training data to the query data by performing a nearest neighbors search using `knnsearch` or a radius search using `rangesearch`. The exhaustive search algorithm is more efficient than the Kd-tree algorithm when K is large (i.e., $K \geq 10$), and it is more flexible than the Kd-tree algorithm with respect to distance metric choices. The algorithm also supports sparse data.

Examples

Train Default Exhaustive Nearest Neighbors Searcher

Load Fisher's iris data set.

```
load fisheriris
X = meas;
[n,k] = size(X)
```

```
n =

   150


k =

     4
```

`X` has 150 observations and 4 predictors.

Prepare an exhaustive nearest neighbors searcher using the entire data set as training data.

```
Mdl = ExhaustiveSearcher(X)


Mdl =

  ExhaustiveSearcher with properties:

        Distance: 'euclidean'
    DistParameter: []
                X: [150x4 double]
```

`Mdl` is an `ExhaustiveSearcher` model object, and its properties appear in the Command Window. It contains information about the trained algorithm, such as the distance metric. You can alter property values using dot notation.

To search `X` for the nearest neighbors to a batch of query data, pass `Mdl` and the query data to `knnsearch` or `rangesearch`.

Alter Properties of `ExhaustiveSearcher` Model

Load Fisher's iris data set.

```
load fisheriris
X = meas;
```

Train a default exhaustive searcher algorithm using the entire data set as training data.

```
Mdl = ExhaustiveSearcher(X)


Mdl =

  ExhaustiveSearcher with properties:

        Distance: 'euclidean'
    DistParameter: []
                X: [150x4 double]
```

Specify that the neighbor searcher use the Mahalanobis metric to compute the distances between the training and query data.

```
Mdl.Distance = 'mahalanobis'


Mdl =
```

```
  ExhaustiveSearcher with properties:

        Distance: 'mahalanobis'
    DistParameter: [4x4 double]
                X: [150x4 double]
```

Pass `Mdl` and the query data to either `knnsearch` or `rangesearch` to find the nearest neighbors to the points in the query data using the Mahalanobis distance.

Search for Nearest Neighbors of Query Data Using the Mahalanobis Distance

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(1);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
X = meas(~ismember(1:n,qIdx),:);
Y = meas(qIdx,:);
```

Prepare an exhaustive nearest neighbors searcher using the training data. Specify to use the Mahalanobis distance for finding nearest neighbors later.

```
Mdl = createns(X,'NSMethod','exhaustive','Distance','mahalanobis')
```

```
Mdl =

  ExhaustiveSearcher with properties:

        Distance: 'mahalanobis'
    DistParameter: [4x4 double]
                X: [145x4 double]
```

`Mdl` is an `ExhaustiveSearcher` model object. By default, the Mahalanobis metric parameter value is the estimated covariance matrix of the predictors (columns) in the training data. To display this value,use `Mdl.DistPatameter`.

```
Mdl.DistParameter
```

```
ans =

    0.6819   -0.0332    1.2526    0.5103
   -0.0332    0.1859   -0.3152   -0.1183
    1.2526   -0.3152    3.0638    1.2816
    0.5103   -0.1183    1.2816    0.5786
```

Find the indices of the training data (`Mdl.X`) that are the two nearest neighbors of each point in the query data (`Q`).

```
IdxNN = knnsearch(Mdl,Y,'K',2)
```

```
IdxNN =

    26    38
     6    21
     1    34
    84    76
    69   129
```

Each row of `NN` corresponds to a query data observation. The column order corresponds to the order of the nearest neighbors with respect to ascending distance. For example, using the Mahalanobis metric, the second nearest neighbor of `Q(3,:)` is `X(34,:)`.

Properties

`Distance` — Distance metric

`'cityblock'` | `'euclidean'` | `'mahalanobis'` | `'minkowski'` | `'seuclidean'` | custom distance function | ...

Distance metric used to find nearest neighbors of query points, specified as a string or function handle.

This table describes the supported distance metrics specified by strings.

Value	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference)
`'cityblock'`	City block distance

Value	Description
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values)
`'cosine'`	One minus the cosine of the included angle between observations (row vectors)
`'euclidean'`	Euclidean distance
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ
`'minkowski'`	Minkowski distance
`'mahalanobis'`	Mahalanobis distance
`'seuclidean'`	Standardized Euclidean distance
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values)

For more details, see “Distance Metrics”.

You can specify a function handle for a custom distance metric using `@` (for example, `@distfun`). A custom distance function must:

- Have the form `function D2 = distfun(ZI, ZJ)`
- Take as arguments:
  - A 1-by-*n* vector `ZI` containing a single row from `X` or from the query points `Y`
  - An *m*-by-*n* matrix `ZJ` containing multiple rows of `X` or `Y`
- Return an *m*-by-1 vector of distances `D2`, whose *j*th element is the distance between the observations `ZI` and `ZJ(`*j*`,:)`

The software does not use the distance metric for training the exhaustive searcher algorithm. Therefore, you can alter it after training by specifying a supported string or function handle for a custom function using dot notation. For example, to specify the Mahalanobis distance, enter `Mdl.Distance = 'mahalanobis'`.

Data Types: `char` | `function_handle`

`DistParameter` — Distance metric parameter values

`[]` | positive scalar

Distance metric parameter values, specified as empty (`[]`) or as a positive scalar.

This table describes the distance parameters of the supported distance metrics.

Distance Metric	Parameter Description
`'mahalanobis'`	A positive definite matrix representing the covariance matrix used for computing the Mahalanobis distances. By default, the software sets the covariance using `nancov(Mdl.X)`. You can alter the scale parameter using dot notation, e.g., `Mdl.DistParameter = CovNew`, where `CovNew` is a K-by-K positive definite numeric matrix.
`'minkowski'`	A positive scalar indicating the exponent of the Minkowski distances. By default, the exponent is `2`.
`'seuclidean'`	A positive, numeric vector indicating the values that the software uses to scale the predictors when computing the standardized Euclidean distances. By default, the software: 1 Estimates the standard deviation of each predictor (column) of `X` using `scale = nanstd(Mdl.X)`. 2 Scales each coordinate difference between the rows in `X` and the query matrix by dividing by the corresponding element of `scale`. You can alter the scale parameter using dot notation, e.g., `Mdl.DistParameter = sNew`, where `sNew` is a K-dimensional positive numeric vector.

If `Mdl.Distance` is not one of the parameters listed in this table, then `Mdl.DistParameter` is `[]`, which means that the specified distance metric formula has no parameters.

Data Types: `single` | `double`

`X` — Training data

numeric matrix

Training data that prepares the exhaustive searcher algorithm, specified as a numeric matrix. `X` has n rows, each corresponding to an observation (i.e., instance or example), and K columns, each corresponding to a predictor or feature.

Data Types: `single` | `double`

Object Functions

`knnsearch` `rangesearch`

Create Object

Create an `ExhaustiveSearcher` model object using `ExhaustiveSearcher` or `createns`.

See Also

`KDTreeSearcher`

More About

- "k-Nearest Neighbor Search and Radius Search" on page 16-11
- "Distance Metrics"

expinv

Exponential inverse cumulative distribution function

Syntax

```
X = expinv(P,mu)
[X,XLO,XUP] = expinv(X,mu,pcov,alpha)
```

Description

`X = expinv(P,mu)` computes the inverse of the exponential `cdf` with parameters specified by mean parameter `mu` for the corresponding probabilities in `P`. `P` and `mu` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `mu` must be positive and the values in `P` must lie on the interval [0 1].

`[X,XLO,XUP] = expinv(X,mu,pcov,alpha)` produces confidence bounds for `X` when the input mean parameter `mu` is an estimate. `pcov` is the variance of the estimated `mu`. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds. The bounds are based on a normal approximation for the distribution of the log of the estimate of `mu`. If you estimate `mu` from a set of data, you can get a more accurate set of bounds by applying `expfit` to the data to get a confidence interval for `mu`, and then evaluating `expinv` at the lower and upper end points of that interval.

The inverse of the exponential cdf is

$$x = F^{-1}(p \mid \mu) = -\mu \ln(1 - p)$$

The result, x, is the value such that an observation from an exponential distribution with parameter μ will fall in the range [0 x] with probability p.

Examples

Let the lifetime of light bulbs be exponentially distributed with μ = 700 hours. What is the median lifetime of a bulb?

```
expinv(0.50,700)
ans =
 485.2030
```

Suppose you buy a box of "700 hour" light bulbs. If 700 hours is the mean life of the bulbs, half of them will burn out in less than 500 hours.

More About

- "Exponential Distribution" on page B-35

See Also

`icdf` | `expcdf` | `exppdf` | `expstat` | `expfit` | `explike` | `exprnd`

explike

Exponential negative log-likelihood

Syntax

```
nlogL = explike(param,data)
[nlogL,avar] = explike(param,data)
[...] = explike(param,data,censoring)
[...] = explike(param,data,censoring,freq)
```

Description

`nlogL = explike(param,data)` returns the negative of the log-likelihood for the exponential distribution. `param` is the mean parameter, `mu`. `nlogL` is a scalar.

`[nlogL,avar] = explike(param,data)` returns the inverse of Fisher's information, `avar`, a scalar. If the input parameter value in `param` is the maximum likelihood estimate, `avar` is its asymptotic variance. `avar` is based on the observed Fisher's information, not the expected information.

`[...] = explike(param,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly.

`[...] = explike(param,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

More About

- “Exponential Distribution” on page B-35

See Also

`expcdf` | `exppdf` | `expstat` | `expfit` | `expinv` | `exprnd`

export

Class: dataset

Write dataset array to file

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
export(DS,'file',filename)
export(DS)
export(DS,'file',filename,'Delimiter',delim)
export(DS,'XLSfile',filename)
export(DS,'XPTFile',filename)
export(DS,...,'WriteVarNames',false)
export(DS,...,'WriteObsNames',false)
```

Description

`export(DS,'file',filename)` writes the dataset array `DS` to a tab-delimited text file, including variable names and observation names, if present. If the observation names exist, the name in the first column of the first line of the file is the first dimension name for the dataset (by default, `'Observations'`). `export` overwrites any existing file named `filename`.

`export(DS)` writes to a text file whose default name is the name of the dataset array `DS` appended by `'.txt'`. If `export` cannot construct the file name from the dataset array input, it writes to the file `'dataset.txt'`. `export` overwrites any existing file.

`export(DS,'file',filename,'Delimiter',delim)` writes the dataset array `DS` to a text file using the delimiter `delim`. `delim` must be one of the following:

- `' '` or `'space'`
- `'\t'` or `'tab'`
- `','` or `'comma'`
- `';'` or `'semi'`
- `'|'` or `'bar'`

`export(DS,'XLSfile',filename)` writes the dataset array `DS` to a Microsoft® Excel spreadsheet file, including variable names and observation names (if present). You can specify the `'Sheet'` and `'Range'` parameter name/value pairs, with parameter values as accepted by the `xlsread` function. Since `export` uses the `xlswrite` function internally, this syntax is only compatible with Microsoft Excel for Windows®, and does not work on a Mac. For more information, see `xlswrite`.

`export(DS,'XPTFile',filename)` writes the dataset array `DS` to a `SAS XPORT` format file. When writing to an `XPORT` format file, variables must be scalar valued. `export` saves observation names to a variable called `obsnames`, unless the `WriteObsNames` parameter described below is `false`. The `XPORT` format restricts the length of variable names to eight characters; longer variable names are truncated.

`export(DS,...,'WriteVarNames',false)` does not write the variable names to the text file. `export(DS,...,'WriteVarNames',true)` is the default, writing the names as column headings in the first line of the file.

`export(DS,...,'WriteObsNames',false)` does not write the observation names to the text file. `export(DS,...,'WriteObsNames',true)` is the default, writing the names as the first column of the file.

In some cases, `export` creates a text file that does not represent `A` exactly, as described below. If you use `dataset` to read the file back into MATLAB, the new dataset array may not have exactly the same contents as the original dataset array. Save `A` as a MAT-file if you need to import it again as a dataset array.

`export` writes out numeric variables using `long g format`, and categorical or character variables as unquoted strings.

For non-character variables with more than one column, `export` writes out multiple delimiter-separated fields on each line, and constructs suitable column headings for the first line of the file.

`export` writes out variables that have more than two dimensions as a single empty field in each line of the file.

For cell-valued variables, `export` writes out the contents of each cell only when the cell contains a single row, and writes out a single empty field otherwise.

In some cases, `export` creates a file that cannot be read back into MATLAB using `dataset`. Writing a dataset array that contains a cell-valued variable whose cell contents are not scalars results in a mismatch in the file between the number of fields on each line and the number of column headings on the first line. Writing a dataset array that contains a cell-valued variable whose cell contents are not all the same length results in a different number of fields on each line in the file. Therefore, if you might need to import a dataset array again, save it as a `.mat` file.

Examples

Move data between external text files and dataset arrays in the MATLAB workspace:

```
A = dataset('file','sat2.dat','delimiter',',')
A =
    Test                  Gender          Score
    'Verbal'              'Male'          470
    'Verbal'              'Female'        530
    'Quantitative'        'Male'          520
    'Quantitative'        'Female'        480

export(A(A.Score > 500,:),'file','HighScores.txt')

B = dataset('file','HighScores.txt','delimiter','\t')
B =
    Test                  Gender          Score
    'Verbal'              'Female'        530
    'Quantitative'        'Male'          520
```

See Also

`dataset`

exppdf

Exponential probability density function

Syntax

```
Y = exppdf(X,mu)
```

Description

`Y = exppdf(X,mu)` returns the pdf of the exponential distribution with mean parameter `mu`, evaluated at the values in `X`. `X` and `mu` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `mu` must be positive.

The exponential pdf is

$$y = f(x \mid \mu) = \frac{1}{\mu} e^{\frac{-x}{\mu}}$$

The exponential pdf is the gamma pdf with its first parameter equal to 1.

The exponential distribution is appropriate for modeling waiting times when the probability of waiting an additional period of time is independent of how long you have already waited. For example, the probability that a light bulb will burn out in its next minute of use is relatively independent of how many minutes it has already burned.

Examples

```
y = exppdf(5,1:5)
y =
  0.0067  0.0410  0.0630  0.0716  0.0736

y = exppdf(1:5,1:5)
```

```
y =
  0.3679   0.1839   0.1226   0.0920   0.0736
```

More About

- "Exponential Distribution" on page B-35

See Also

pdf | expcdf | expinv | expstat | expfit | explike | exprnd

exprnd

Exponential random numbers

Syntax

```
R = exprnd(mu)
R = exprnd(mu,m,n,...)
R = exprnd(mu,[m,n,...])
```

Description

`R = exprnd(mu)` generates random numbers from the exponential distribution with mean parameter `mu`. `mu` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `mu`.

`R = exprnd(mu,m,n,...)` or `R = exprnd(mu,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the exponential distribution with mean parameter `mu`. `mu` can be a scalar or an array of the same size as `R`.

Examples

```
n1 = exprnd(5:10)
n1 =
  7.5943  18.3400  2.7113  3.0936  0.6078  9.5841

n2 = exprnd(5:10,[1 6])
n2 =
  3.2752  1.1110  23.5530  23.4303  5.7190  3.9876

n3 = exprnd(5,2,3)
n3 =
  24.3339  13.5271  1.8788
   4.7932   4.3675  2.6468
```

More About

- “Exponential Distribution” on page B-35

See Also

`random` | `expcdf` | `exppdf` | `expstat` | `expfit` | `explike` | `expinv`

expstat

Exponential mean and variance

Syntax

```
[m,v] = expstat(mu)
```

Description

`[m,v] = expstat(mu)` returns the mean of and variance for the exponential distribution with parameters `mu`. `mu` can be a vectors, matrix, or multidimensional array. The mean of the exponential distribution is μ, and the variance is μ^2.

Examples

```
[m,v] = expstat([1 10 100 1000])
m =
      1     10     100     1000
v =
      1     100    10000   1000000
```

More About

- “Exponential Distribution” on page B-35

See Also

`expinv` | `expcdf` | `exppdf` | `expstat` | `expfit` | `explike` | `exprnd`

prob.ExtremeValueDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Extreme value probability distribution object

Description

`prob.ExtremeValueDistribution` is an object consisting of parameters, a model description, and sample data for an extreme value probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('ExtremeValue')` creates an extreme value probability distribution object using the default parameter values.

`pd = makedist('ExtremeValue','mu',mu,'sigma',sigma)` creates an extreme value probability distribution object using the specified parameter values.

Input Arguments

`mu` — Location parameter

0 (default) | scalar value

Location parameter of the extreme value distribution, specified as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

1 (default) | nonnegative scalar value

Scale parameter of the extreme value distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

Properties

`mu` — Location parameter

scalar value

Location parameter of the extreme value distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

nonnegative scalar value

Scale parameter of the extreme value distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object

pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Extreme Value Distribution

The extreme value distribution is appropriate for modeling the smallest value from a distribution whose tails decay exponentially fast, for example, the normal distribution. It can also model the largest value from a distribution, such as the normal or exponential distributions, by using the negative of the original values.

The extreme value distribution uses the following parameters.

Parameter	Description	Support
`mu`	Location parameter	$-\infty < \mu < \infty$
`sigma`	Scale parameter	$\sigma \geq 0$

The probability density function (pdf) is

$$f(x \mid \mu,\sigma) = \sigma^{-1} \exp\left(\frac{x-\mu}{\sigma}\right)\exp\left(-\exp\left(\frac{x-\mu}{\sigma}\right)\right) \quad ; \quad -\infty < x < \infty.$$

This form of the probability density function is suitable for modeling the minimum value. To model the maximum value, use the negative of the original values.

Examples

Create an Extreme Value Distribution Object Using Default Parameters

Create an extreme value distribution object using the default parameter values.

```
pd = makedist('ExtremeValue')
```

```
pd =

  ExtremeValueDistribution

  Extreme Value distribution
       mu = 0
    sigma = 1
```

Create an Extreme Value Distribution Object Using Specified Parameters

Create an extreme value distribution object by specifying the parameter values.

```
pd = makedist('ExtremeValue', 'mu',-1,'sigma',2)
```

```
pd =

  ExtremeValueDistribution

  Extreme Value distribution
       mu = -1
```

```
    sigma =  2
```

Compute the standard deviation for the distribution.

```
s = std(pd)
```

```
s =

    2.5651
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Extreme Value Distribution"
- Class Attributes
- Property Attributes

factoran

Factor analysis

Syntax

```
lambda = factoran(X,m)
[lambda,psi] = factoran(X,m)
[lambda,psi,T] = factoran(X,m)
[lambda,psi,T,stats] = factoran(X,m)
[lambda,psi,T,stats,F] = factoran(X,m)
[...] = factoran(...,param1,val1,param2,val2,...)
```

Definitions

`factoran` computes the maximum likelihood estimate (MLE) of the factor loadings matrix Λ in the factor analysis model

$$x = \mu + \Lambda f + e$$

where x is a vector of observed variables, μ is a constant vector of means, Λ is a constant d-by-m matrix of factor loadings, f is a vector of independent, standardized common factors, and e is a vector of independent specific factors. x, μ, and e are of length d. f is of length m.

Alternatively, the factor analysis model can be specified as

$$\mathrm{cov}(x) = \Lambda\Lambda^T + \Psi$$

where $\Psi = \mathrm{cov}(e)$ is a d-by-d diagonal matrix of specific variances.

Description

`lambda = factoran(X,m)` returns the maximum likelihood estimate, `lambda`, of the factor loadings matrix, in a common factor analysis model with `m` common factors. `X` is an `n`-by-`d` matrix where each row is an observation of `d` variables. The `(i,j)`th

element of the d-by-m matrix lambda is the coefficient, or loading, of the jth factor for the ith variable. By default, factoran calls the function rotatefactors to rotate the estimated factor loadings using the 'varimax' option.

[lambda,psi] = factoran(X,m) also returns maximum likelihood estimates of the specific variances as a column vector psi of length d.

[lambda,psi,T] = factoran(X,m) also returns the m-by-m factor loadings rotation matrix T.

[lambda,psi,T,stats] = factoran(X,m) also returns a structure stats containing information relating to the null hypothesis, H_0, that the number of common factors is m. stats includes the following fields:

Field	Description
loglike	Maximized log-likelihood value
dfe	Error degrees of freedom = ((d-m)^2 - (d+m))/2
chisq	Approximate chi-squared statistic for the null hypothesis
p	Right-tail significance level for the null hypothesis

factoran does not compute the chisq and p fields unless dfe is positive and all the specific variance estimates in psi are positive (see “Heywood Case” on page 22-1342 below). If X is a covariance matrix, then you must also specify the 'nobs' parameter if you want factoran to compute the chisq and p fields.

[lambda,psi,T,stats,F] = factoran(X,m) also returns, in F, predictions of the common factors, known as factor scores. F is an n-by-m matrix where each row is a prediction of m common factors. If X is a covariance matrix, factoran cannot compute F. factoran rotates F using the same criterion as for lambda.

[...] = factoran(...,*param1*,*val1*,*param2*,*val2*,...) enables you to specify optional parameter name/value pairs to control the model fit and the outputs. The following are the valid parameter/value pairs.

Parameter	Value	
'xtype'	Type of input in the matrix X. 'xtype' can be one of:	
	'data'	Raw data (default)
	'covariance'	Positive definite covariance or correlation matrix

Parameter	Value	
`'scores'`	Method for predicting factor scores. `'scores'` is ignored if `X` is not raw data.	
	`'wls'` `'Bartlett'`	Synonyms for a weighted least-squares estimate that treats `F` as fixed (`default`)
	`'regression'` `'Thomson'`	Synonyms for a minimum mean squared error prediction that is equivalent to a ridge regression
`'start'`	Starting point for the specific variances `psi` in the maximum likelihood optimization. Can be specified as:	
	`'random'`	Chooses `d` uniformly distributed values on the interval [0,1].
	`'Rsquared'`	Chooses the starting vector as a scale factor times `diag(inv(corrcoef(X)))` (default). For examples, see Jöreskog [2].
	Positive integer	Performs the given number of maximum likelihood fits, each initialized as with `'random'`. `factoran` returns the fit with the highest likelihood.
	Matrix	Performs one maximum likelihood fit for each column of the specified matrix. The `i`th optimization is initialized with the values from the `i`th column. The matrix must have `d` rows.
`'rotate'`	Method used to rotate factor loadings and scores. `'rotate'` can have the same values as the `'Method'` parameter of `rotatefactors`. See the reference page for `rotatefactors` for a full description of the available methods.	
	`'none'`	Performs no rotation.
	`'equamax'`	Special case of the orthomax rotation. Use the `'normalize'`, `'reltol'`, and `'maxit'` parameters to control the details of the rotation.

Parameter	Value	
	`'orthomax'`	Orthogonal rotation that maximizes a criterion based on the variance of the loadings. Use the `'coeff'`, `'normalize'`, `'reltol'`, and `'maxit'` parameters to control the details of the rotation.
	`'parsimax'`	Special case of the orthomax rotation (default). Use the `'normalize'`, `'reltol'`, and `'maxit'` parameters to control the details of the rotation.
	`'pattern'`	Performs either an oblique rotation (the default) or an orthogonal rotation to best match a specified pattern matrix. Use the `'type'` parameter to choose the type of rotation. Use the `'target'` parameter to specify the pattern matrix.
	`'procrustes'`	Performs either an oblique (the default) or an orthogonal rotation to best match a specified target matrix in the least squares sense. Use the `'type'` parameter to choose the type of rotation. Use `'target'` to specify the target matrix.
	`'promax'`	Performs an oblique procrustes rotation to a target matrix determined by `factoran` as a function of an orthomax solution. Use the `'power'` parameter to specify the exponent for creating the target matrix. Because `'promax'` uses `'orthomax'` internally, you can also specify the parameters that apply to `'orthomax'`.
	`'quartimax'`	Special case of the orthomax rotation (default). Use the `'normalize'`, `'reltol'`, and `'maxit'` parameters to control the details of the rotation.

Parameter	Value	
	`'varimax'`	Special case of the orthomax rotation (default). Use the `'normalize'`, `'reltol'`, and `'maxit'` parameters to control the details of the rotation.
	Function	Function handle to rotation function of the form `[B,T] = myrotation(A,...)` where `A` is a `d`-by-`m` matrix of unrotated factor loadings, `B` is a `d`-by-`m` matrix of rotated loadings, and `T` is the corresponding `m`-by-`m` rotation matrix. Use the `factoran` parameter `'userargs'` to pass additional arguments to this rotation function. See "User-Defined Rotation Function" on page 22-1341.
`'coeff'`	Coefficient, often denoted as γ, defining the specific `'orthomax'` criterion. Must be from `0` to `1`. The value `0` corresponds to quartimax, and `1` corresponds to varimax. Default is `1`.	
`'normalize'`	Flag indicating whether the loading matrix should be row-normalized (1) or left unnormalized (0) for `'orthomax'` or `'varimax'` rotation. Default is 1.	
`'reltol'`	Relative convergence tolerance for `'orthomax'` or `'varimax'` rotation. Default is `sqrt(eps)`.	
`'maxit'`	Iteration limit for `'orthomax'` or `'varimax'` rotation. Default is `250`.	
`'target'`	Target factor loading matrix for `'procrustes'` rotation. Required for `'procrustes'` rotation. No default value.	
`'type'`	Type of `'procrustes'` rotation. Can be `'oblique'` (default) or `'orthogonal'`.	
`'power'`	Exponent for creating the target matrix in the `'promax'` rotation. Must be $\geq$ `1`. Default is `4`.	

Parameter	Value
`'userargs'`	Denotes the beginning of additional input values for a user-defined rotation function. `factoran` appends all subsequent values, in order and without processing, to the rotation function argument list, following the unrotated factor loadings matrix `A`. See “User-Defined Rotation Function” on page 22-1341.
`'nobs'`	If `X` is a covariance or correlation matrix, indicates the number of observations that were used in its estimation. This allows calculation of significance for the null hypothesis even when the original data are not available. There is no default. `'nobs'` is ignored if `X` is raw data.
`'delta'`	Lower bound for the specific variances `psi` during the maximum likelihood optimization. Default is `0.005`.
`'optimopts'`	Structure that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. Create this structure with the function `statset`. Enter `statset('factoran')` to see the names and default values of the parameters that `factoran` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Examples

Estimate and Plot Factor Loadings

Load the sample data.

```
load carbig
```

Define the variable matrix.

```
X = [Acceleration Displacement Horsepower MPG Weight];
X = X(all(~isnan(X),2),:);
```

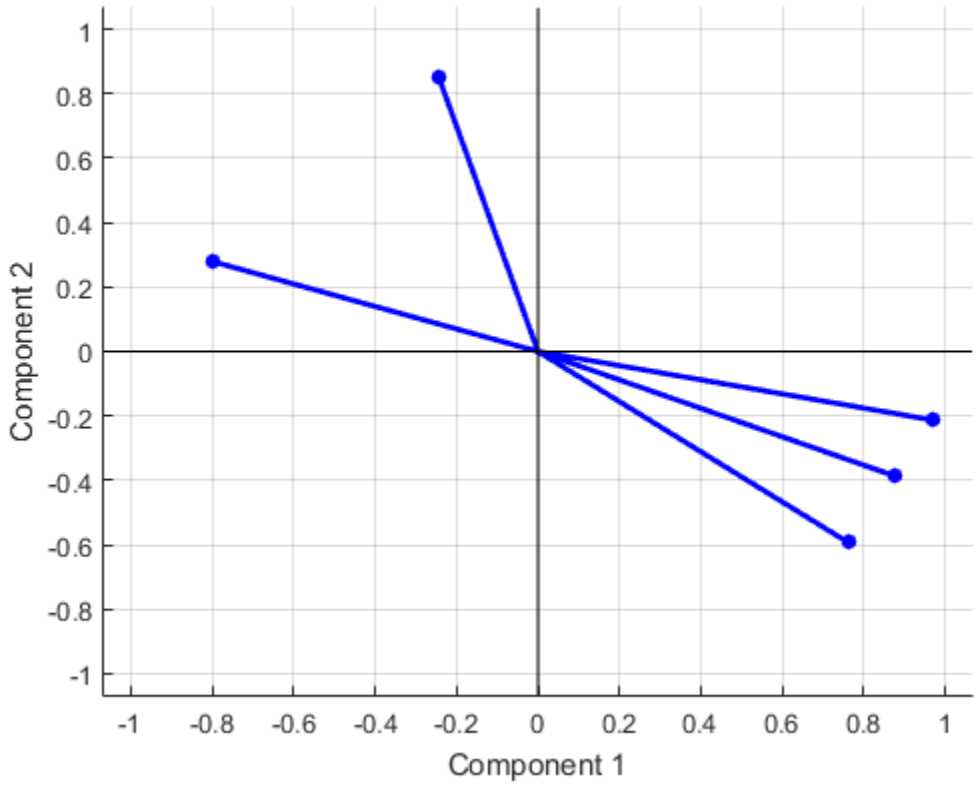
Estimate the factor loadings using a minimum mean squared error prediction for a factor analysis with two common factors.

```
[Lambda,Psi,T,stats,F] = factoran(X,2,'scores','regression');
```

```
inv(T'*T);   % Estimated correlation matrix of F, == eye(2)
Lambda*Lambda' + diag(Psi); % Estimated correlation matrix
Lambda*inv(T);              % Unrotate the loadings
F*T';                       % Unrotate the factor scores
```

Create biplot of two factors.

```
biplot(Lambda,'LineWidth',2,'MarkerSize',20)
```



Estimate the factor loadings using the covariance (or correlation) matrix.

```
[Lambda,Psi,T] = factoran(cov(X),2,'xtype','cov')
% [Lambda,Psi,T] = factoran(corrcoef(X),2,'xtype','cov')
```

```
Lambda =

   -0.2432   -0.8500
    0.8773    0.3871
    0.7618    0.5930
   -0.7978   -0.2786
    0.9692    0.2129


Psi =

    0.2184
    0.0804
    0.0680
    0.2859
    0.0152


T =

    0.9476    0.3195
    0.3195   -0.9476
```

Although the estimates are the same, the use of a covariance matrix rather than raw data doesn't let you request scores or significance level.

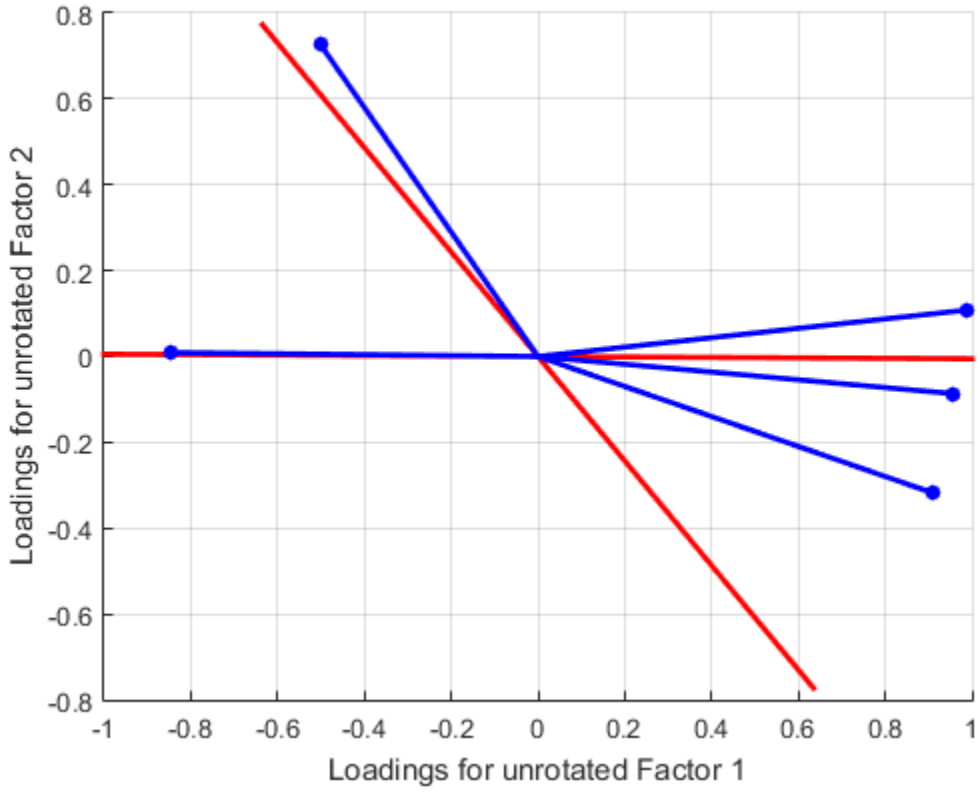
Use promax rotation.

```
[Lambda,Psi,T,stats,F] = factoran(X,2,'rotate','promax',...
                                  'powerpm',4);
inv(T'*T)                              % Estimated correlation of F,
                                       % no longer eye(2)
Lambda*inv(T'*T)*Lambda'+diag(Psi)     % Estimated correlation of X


ans =

    1.0000   -0.6391
   -0.6391    1.0000


ans =
```

```
    1.0000   -0.5424   -0.6893    0.4309   -0.4167
   -0.5424    1.0000    0.8979   -0.8078    0.9328
   -0.6893    0.8979    1.0000   -0.7730    0.8647
    0.4309   -0.8078   -0.7730    1.0000   -0.8326
   -0.4167    0.9328    0.8647   -0.8326    1.0000
```

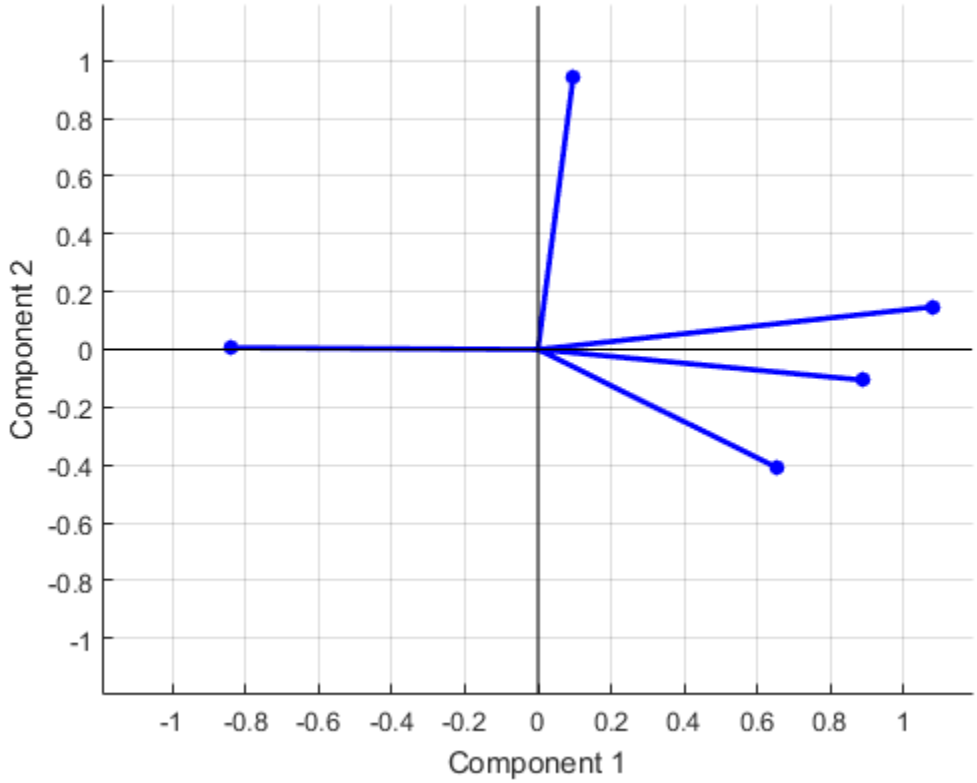
Plot the unrotated variables with oblique axes superimposed.

```
invT = inv(T);
Lambda0 = Lambda*invT;
figure()
line([-invT(1,1) invT(1,1) NaN -invT(2,1) invT(2,1)], ...
     [-invT(1,2) invT(1,2) NaN -invT(2,2) invT(2,2)], ...
     'Color','r','linewidth',2)
grid on
hold on
biplot(Lambda0,'LineWidth',2,'MarkerSize',20)
xlabel('Loadings for unrotated Factor 1')
ylabel('Loadings for unrotated Factor 2')
```



Plot the rotated variables against the oblique axes.

```
figure()
biplot(Lambda,'LineWidth',2,'MarkerSize',20)
```



User-Defined Rotation Function

Syntax for passing additional arguments to a user-defined rotation function:

```
[Lambda,Psi,T] = ...
```

```
factoran(X,2,'rotate',@myrotation,'userargs',1,'two');
```

More About

Tips

Observed Data Variables

The variables in the observed data matrix `X` must be linearly independent, i.e., `cov(X)` must have full rank, for maximum likelihood estimation to succeed. `factoran` reduces both raw data and a covariance matrix to a correlation matrix before performing the fit.

`factoran` standardizes the observed data `X` to zero mean and unit variance before estimating the loadings `lambda`. This does not affect the model fit, because MLEs in this model are invariant to scale. However, `lambda` and `psi` are returned in terms of the standardized variables, i.e., `lambda*lambda'+diag(psi)` is an estimate of the correlation matrix of the original data `X` (although not after an oblique rotation). See "Estimate and Plot Factor Loadings" on page 22-1336 and "User-Defined Rotation Function" on page 22-1341.

Heywood Case

If elements of `psi` are equal to the value of the `'delta'` parameter (i.e., they are essentially zero), the fit is known as a Heywood case, and interpretation of the resulting estimates is problematic. In particular, there can be multiple local maxima of the likelihood, each with different estimates of the loadings and the specific variances. Heywood cases can indicate overfitting (i.e., `m` is too large), but can also be the result of underfitting.

Rotation of Factor Loadings and Scores

Unless you explicitly specify no rotation using the `'rotate'` parameter, `factoran` rotates the estimated factor loadings, `lambda`, and the factor scores, `F`. The output matrix `T` is used to rotate the loadings, i.e., `lambda = lambda0*T`, where `lambda0` is the initial (unrotated) MLE of the loadings. `T` is an orthogonal matrix for orthogonal rotations, and the identity matrix for no rotation. The inverse of `T` is known as the primary axis rotation matrix, while `T` itself is related to the reference axis rotation matrix. For orthogonal rotations, the two are identical.

`factoran` computes factor scores that have been rotated by `inv(T')`, i.e., `F = F0 * inv(T')`, where `F0` contains the unrotated predictions. The estimated covariance of `F` is `inv(T'*T)`, which, for orthogonal or no rotation, is the identity matrix. Rotation of factor loadings and scores is an attempt to create a more easily interpretable structure in the loadings matrix after maximum likelihood estimation.

References

[1] Harman, H. H. *Modern Factor Analysis*. 3rd Ed. Chicago: University of Chicago Press, 1976.

[2] Jöreskog, K. G. "Some Contributions to Maximum Likelihood Factor Analysis." *Psychometrika*. Vol. 32, Issue 4, 1967, pp. 443–482.

[3] Lawley, D. N., and A. E. Maxwell. *Factor Analysis as a Statistical Method*. 2nd Ed. New York: American Elsevier Publishing Co., 1971.

See Also

`biplot` | `pca` | `procrustes` | `statset` | `pcacov` | `rotatefactors`

FBoot property

Class: TreeBagger

Fraction of in-bag observations

Description

The `FBoot` property is the fraction of observations to be randomly selected with replacement for each bootstrap replica. The size of each replica is given by `n*FBoot`, where `n` is the number of observations in the training set. The default value is 1.

fcdf

F cumulative distribution function

Syntax

```
p = fcdf(x,v1,v2)
p = fcdf(x,v1,Vv2,'upper')
```

Description

`p = fcdf(x,v1,v2)` computes the *F* cdf at each of the values in `x` using the corresponding numerator degrees of freedom `v1` and denominator degrees of freedom `v2`. `x`, `v1`, and `v2` can be vectors, matrices, or multidimensional arrays that are all the same size. A scalar input is expanded to a constant matrix with the same dimensions as the other inputs. `v1` and `v2` parameters must contain real positive values.

`p = fcdf(x,v1,Vv2,'upper')` returns the complement of the *F* cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The *F* cdf is

$$p = F(x \mid \nu_1,\nu_2) = \int_0^x \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{t^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)t\right]^{\frac{\nu_1+\nu_2}{2}}}dt$$

The result, *p*, is the probability that a single observation from an *F* distribution with parameters ν_1 and ν_2 will fall in the interval [0 *x*].

Examples

Compute *F* Distribution CDF

The following illustrates a useful mathematical identity for the *F* distribution.

```
nu1 = 1:5;
nu2 = 6:10;
x = 2:6;

F1 = fcdf(x,nu1,nu2)

F1 =
  0.7930  0.8854  0.9481  0.9788  0.9919

F2 = 1 - fcdf(1./x,nu2,nu1)

F2 =
  0.7930  0.8854  0.9481  0.9788  0.9919
```

More About

- “F Distribution” on page B-45

See Also

`cdf` | `fpdf` | `finv` | `fstat` | `frnd`

feval

Class: GeneralizedLinearModel

Evaluate generalized linear regression model prediction

Syntax

```
ypred = feval(mdl,Xnew1,Xnew2,...,Xnewn)
```

Description

`ypred = feval(mdl,Xnew1,Xnew2,...,Xnewn)` returns the predicted response of `mdl` to the input `[Xnew1,Xnew_2,...,Xnewn]`.

Tips

- `feval` allows you to easily evaluate predictions of a model when the model was fitted using a table or dataset array. `predict` requires a table or dataset array with the same predictor names, but you can use simple arrays of scalars with `feval`.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`Xnew1,Xnew2,...,Xnewn`

Predictor components. `Xnewi` can be one of:

- Scalar
- Vector
- Array

Each nonscalar component must have the same size (number of elements in each dimension).

If you pass just one `Xnew` array, `Xnew` can be a table, dataset array, or an array of doubles, where each column of the array represents one predictor.

Output Arguments

`ypred`

Predicted mean values at `Xnew`. `ypred` is the same size as each component of `Xnew`.

For binomial models, `feval` uses `1` as the `BinomialSize` parameter, so `ypred` is predicted probabilities.

For models with an offset, `feval` uses `0` as the offset value.

Examples

Predict Responses Using feval

Generate a generalized linear model, and plot its responses to a range of input data.

Generate artificial data for the model, Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

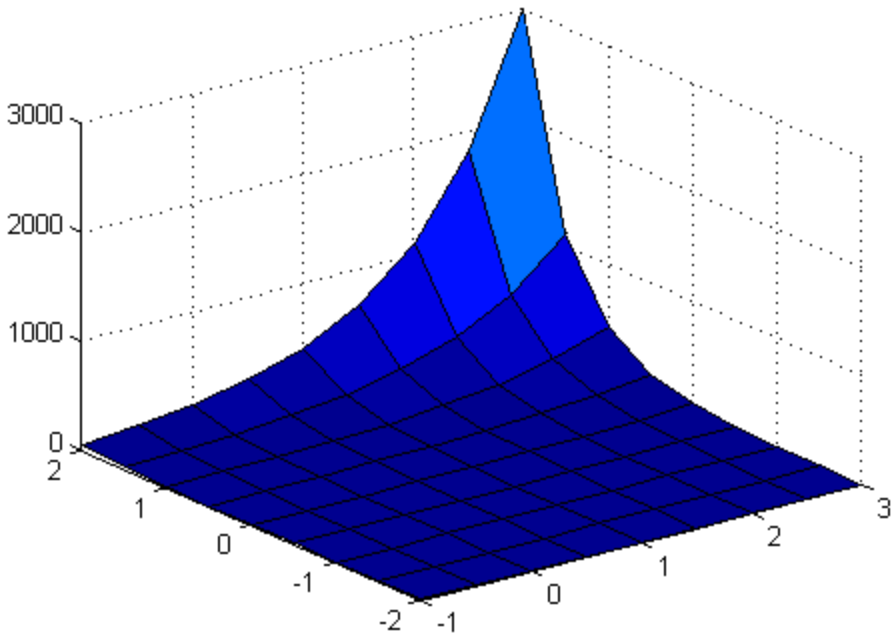
Create a generalized linear regression model of Poisson data.

```
mdl = fitglm(X,y,'y ~ x1 + x2','distr','poisson');
```

Generate a range of values for `X(1)` and `X(2)`, and plot the model predictions at those values.

```
[Xtest1 Xtest2] = meshgrid(-1:.5:3,-2:.5:2);
```

```
Z = feval(mdl,Xtest1,Xtest2);
surf(Xtest1,Xtest2,Z)
```



- “feval” on page 10-35

Alternatives

`predict` gives the same predictions, but uses a single input array with one observation in each row, rather than one component in each input argument.

`random` predicts with added noise.

See Also

`GeneralizedLinearModel` | `predict` | `random`

More About

- “Generalized Linear Models” on page 10-12

feval

Class: LinearModel

Evaluate linear regression model prediction

Syntax

```
ypred = feval(mdl,Xnew1,Xnew2,...,Xnewn)
```

Description

`ypred = feval(mdl,Xnew1,Xnew2,...,Xnewn)` returns the predicted response of `mdl` to the input `[Xnew1,Xnew2,...,Xnewn]`.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`Xnew1,Xnew2,...,Xnewn`

Predictor components. `Xnewi` can be one of:

- Scalar
- Vector
- Array

Each nonscalar component must have the same size (number of elements in each dimension).

If you pass just one `Xnew` array, `Xnew` can be a table, dataset array, or an array of doubles, where each column of the array represents one predictor.

Output Arguments

`ypred`

Predicted mean values at `Xnew`. `ypred` is the same size as each component of `Xnew`.

For models with an offset, `feval` uses `0` as the offset value.

Examples

Plot Different Categorical Levels

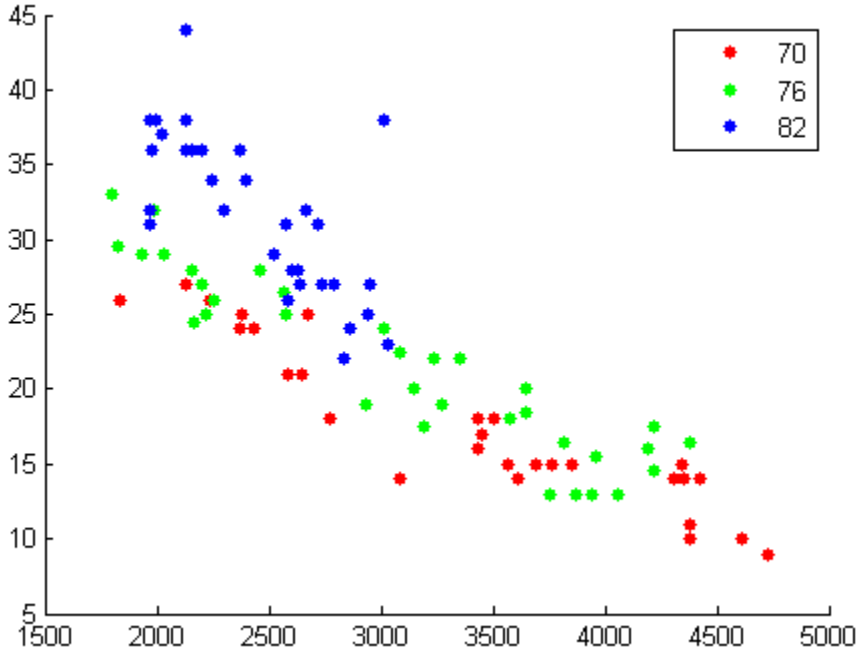
Fit a mileage model to the `smallcar` data, including the `Year` categorical predictor. Superimpose fitted curves on a scatter plot of the data.

Load the data and fit a model.

```
load carsmall
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
mdl = fitlm(tbl,'MPG ~ Year + Weight^2');
```

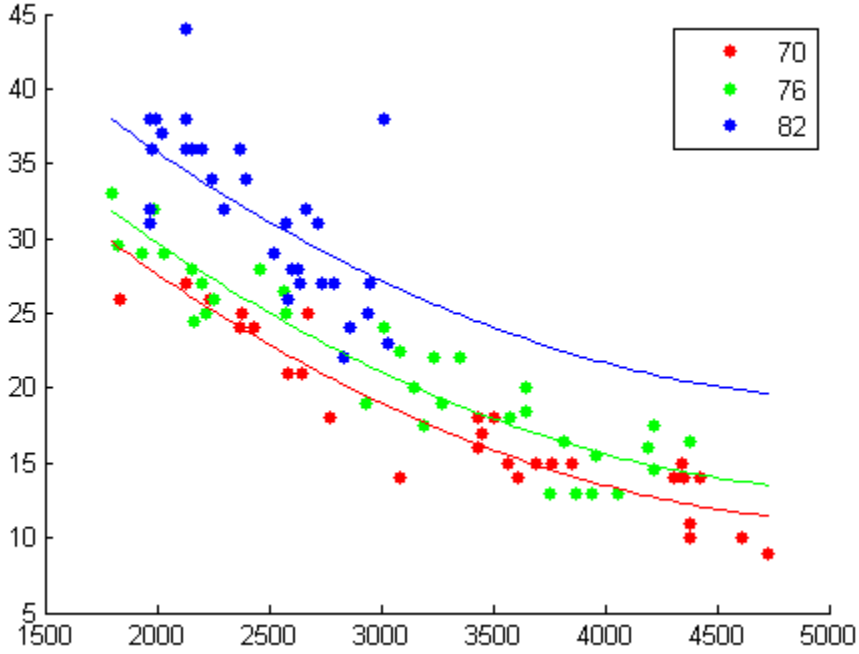
Create a scatter plot of the mileage versus weight.

```
gscatter(tbl.Weight,tbl.MPG,tbl.Year);
```



Use `feval` to plot curves of the model predictions for the various years and weights.

```
w = linspace(min(tbl.Weight),max(tbl.Weight))';
line(w,feval(mdl,w,'70'),'Color','r')
line(w,feval(mdl,w,'76'),'Color','g')
line(w,feval(mdl,w,'82'),'Color','b')
```



- "feval" on page 9-38
- "Linear Regression Workflow" on page 9-41

Alternatives

`predict` gives the same predictions, but uses a single input array with one observation in each row, rather than one component in each input argument. `predict` also gives confidence intervals on its predictions.

`random` predicts with added noise.

See Also

`predict` | `LinearModel` | `random`

How To

- "Linear Regression" on page 9-11

feval

Class: NonLinearModel

Evaluate nonlinear regression model prediction

Syntax

```
ypred = feval(mdl,Xnew1,Xnew2,...,Xnewn)
```

Description

`ypred = feval(mdl,Xnew1,Xnew2,...,Xnewn)` returns the predicted response of `mdl` to the input `[Xnew1,Xnew2,...,Xnewn]`.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

`Xnew1,Xnew2,...,Xnewn`

Predictor components. `Xnewi` can be one of:

- Scalar
- Vector
- Array

Each nonscalar component must have the same size (number of elements in each dimension).

If you pass just one `Xnew` array, `Xnew` can be a table, dataset array, or an array of doubles, where each column of the array represents one predictor.

Output Arguments

`ypred`

Predicted mean values at `Xnew`. `ypred` is the same size as each component of `Xnew`.

Examples

Predict a Nonlinear Model from a Table

Create a nonlinear model for auto mileage based on the `carbig` data. Predict the mileage of an average automobile.

Load the data and create a nonlinear model.

```
load carbig
tbl = table(Horsepower,Weight,MPG);
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
mdl = fitnlm(tbl,modelfun,beta0);
```

Find the predicted mileage of an average auto. The data contain some observations with `NaN`, so compute the mean using `nanmean`.

```
Xnew = nanmean([Horsepower Weight]);
MPGnew = feval(mdl,Xnew)
```

```
MPGnew =

   21.8073
```

- “Predict or Simulate Responses Using a Nonlinear Model” on page 11-10

Alternatives

`predict` gives the same predictions, but uses a single input array with one observation in each row, rather than one component in each input argument. `predict` also gives confidence intervals on its predictions.

`random` predicts with added noise.

See Also

`NonLinearModel` | `predict` | `random`

More About

- "Nonlinear Regression" on page 11-2

ff2n

Two-level full factorial design

Syntax

```
dFF2 = ff2n(n)
```

Description

`dFF2 = ff2n(n)` gives factor settings `dFF2` for a two-level full factorial design with `n` factors. `dFF2` is *m*-by-`n`, where *m* is the number of treatments in the full-factorial design. Each row of `dFF2` corresponds to a single treatment. Each column contains the settings for a single factor, with values of `0` and `1` for the two levels.

Examples

```
dFF2 = ff2n(3)
dFF2 =
   0   0   0
   0   0   1
   0   1   0
   0   1   1
   1   0   0
   1   0   1
   1   1   0
   1   1   1
```

See Also

`fullfact`

fillProximities

Class: TreeBagger

Proximity matrix for training data

Syntax

```
B = fillProximities(B)
B = fillProximities(B,'param1',val1,'param2',val2,...)
```

Description

`B = fillProximities(B)` computes a proximity matrix for the training data and stores it in the Properties field of B.

`B = fillProximities(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Either `'all'` or a vector of indices of the trees in the ensemble to be used in computing the proximity matrix. Default is `'all'`.
`'nprint'`	Number of training cycles (grown trees) after which `TreeBagger` displays a diagnostic message showing training progress. Default is no diagnostic messages.

See Also

`CompactTreeBagger.outlierMeasure` | `CompactTreeBagger.proximity`

findobj

Class: qrandstream

Find objects matching specified conditions

Syntax

```
hm = findobj(h, 'conditions')
```

Description

The `findobj` method of the `handle` class follows the same syntax as the MATLAB `findobj` command, except that the first argument must be an array of handles to objects.

`hm = findobj(h, 'conditions')` searches the handle object array `h` and returns an array of handle objects matching the specified conditions. Only the public members of the objects of `h` are considered when evaluating the conditions.

See Also

`findobj` | `qrandstream`

findprop

Class: qrandstream

Find property of MATLAB handle object

Syntax

```
p = findprop(h,'propname')
```

Description

`p = findprop(h,'propname')` finds and returns the `meta.property` object associated with property name `propname` of scalar handle object `h`. `propname` must be a string. It can be the name of a property defined by the class of `h` or a dynamic property added to scalar object `h`.

If no property named `propname` exists for object `h`, an empty `meta.property` array is returned.

See Also

`dynamicprops` | `findobj` | `meta.property` | `qrandstream`

finv

F inverse cumulative distribution function

Syntax

```
X = finv(P,V1,V2)
```

Description

`X = finv(P,V1,V2)` computes the inverse of the *F* cdf with numerator degrees of freedom `V1` and denominator degrees of freedom `V2` for the corresponding probabilities in `P`. `P`, `V1`, and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

`V1` and `V2` parameters must contain real positive values, and the values in `P` must lie on the interval [0 1].

The *F* inverse function is defined in terms of the *F* cdf as

$$x = F^{-1}\left(p \mid \nu_1,\nu_2\right) = \left\{x : F\left(x \mid \nu_1,\nu_2\right) = p\right\}$$

where

$$p = F(x \mid \nu_1,\nu_2) = \int_0^x \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{t^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)t\right]^{\frac{\nu_1+\nu_2}{2}}}\,dt$$

Examples

Find a value that should exceed 95% of the samples from an *F* distribution with 5 degrees of freedom in the numerator and 10 degrees of freedom in the denominator.

```
x = finv(0.95,5,10)
x =
  3.3258
```

You would observe values greater than 3.3258 only 5% of the time by chance.

More About

- "F Distribution" on page B-45

See Also

`icdf` | `fcdf` | `fpdf` | `fstat` | `frnd`

fishertest

Fisher's exact test

Syntax

```
h = fishertest(x)
[h,p,stats] = fishertest(x)
[ ___ ] = fishertest(x,Name,Value)
```

Description

`h = fishertest(x)` returns a test decision for Fisher's exact test of the null hypothesis that there are no nonrandom associations between the two categorical variables in x, against the alternative that there is a nonrandom association. The result `h` is `1` if the test rejects the null hypothesis at the 5% significance level, or `0` otherwise.

`[h,p,stats] = fishertest(x)` also returns the significance level p of the test and a structure stats containing additional test results, including the odds ratio and its asymptotic confidence interval.

`[ ___ ] = fishertest(x,Name,Value)` returns a test decision using additional options specified by one or more name-value pair arguments. For example, you can change the significance level of the test or conduct a one-sided test.

Examples

Conduct Fisher's Exact Test

In a small survey, a researcher asked 17 individuals if they received a flu shot this year, and whether they caught the flu this winter. The results indicate that, of the nine people who did not receive a flu shot, three got the flu and six did not. Of the eight people who received a flu shot, one got the flu and seven did not.

Create a 2-by-2 contingency table containing the survey data. Row 1 contains data for the individuals who did not receive a flu shot, and row 2 contains data for the individuals

who received a flu shot. Column 1 contains the number of individuals who got the flu, and column 2 contains the number of individuals who did not.

```
x = table([3;1],[6;7],'VariableNames',{'Flu','NoFlu'},'RowNames',{'NoShot','Shot'})
```

```
x =

              Flu    NoFlu
              ___    _____

    NoShot    3      6
    Shot      1      7
```

Use Fisher's exact test to determine if there is a nonrandom association between receiving a flu shot and getting the flu.

```
h = fishertest(x)
```

```
h =

     0
```

The returned test decision `h = 0` indicates that `fishertest` does not reject the null hypothesis of no nonrandom association between the categorical variables at the default 5% significance level. Therefore, based on the test results, individuals who do not get a flu shot do not have different odds of getting the flu than those who got the flu shot.

Conduct a One-Sided Fisher's Exact Test

In a small survey, a researcher asked 17 individuals if they received a flu shot this year, and whether they caught the flu. The results indicate that, of the nine people who did not receive a flu shot, three got the flu and six did not. Of the eight people who received a flu shot, one got the flu and seven did not.

```
x = [3,6;1,7];
```

Use a right-tailed Fisher's exact test to determine if the odds of getting the flu is higher for individuals who did not receive a flu shot than for individuals who did. Conduct the test at the 1% significance level.

```
[h,p,stats] = fishertest(x,'Tail','right','Alpha',0.01)
```

```
h =

     0
```

```
p =

    0.3353


stats =

              OddsRatio: 3.5000
    ConfidenceInterval: [0.1289 95.0408]
```

The returned test decision `h = 0` indicates that `fishertest` does not reject the null hypothesis of no nonrandom association between the categorical variables at the 1% significance level. Since this is a right-tailed hypothesis test, the conclusion is that individuals who do not get a flu shot do not have greater odds of getting the flu than those who got the flu shot.

Generate a Contingency Table Using `crosstab`

Load the hospital data.

```
load hospital
```

The `hospital` dataset array contains data on 100 hospital patients, including last name, gender, age, weight, smoking status, and systolic and diastolic blood pressure measurements.

To determine if smoking status is independent of gender, use `crosstab` to create a 2-by-2 contingency table of smokers and nonsmokers, grouped by gender.

```
[tbl,chi2,p,labels] = crosstab(hospital.Sex,hospital.Smoker)
```

```
tbl =

    40    13
    26    21


chi2 =

    4.5083


p =
```

```
    0.0337


labels =

    'Female'    '0'
    'Male'      '1'
```

The rows of the resulting contingency table `tbl` correspond to the patient's gender, with row 1 containing data for females and row 2 containing data for males. The columns correspond to the patient's smoking status, with column 1 containing data for nonsmokers and column 2 containing data for smokers. The returned result `chi2 = 4.5083` is the value of the chi-squared test statistic for a chi-squared test of independence. The returned value `p = 0.0337` is an approximate *p*-value based on the chi-squared distribution.

Use the contingency table generated by `crosstab` to perform Fisher's exact test on the data.

```
[h,p,stats] = fishertest(tbl)
```

```
h =

     1


p =

    0.0375


stats =

             OddsRatio: 2.4852
    ConfidenceInterval: [1.0624 5.8135]
```

The result `h = 1` indicates that `fishertest` rejects the null hypothesis of nonassociation between smoking status and gender at the 5% significance level. In other words, there is an association between gender and smoking status. The odds ratio indicates that the male patients have about 2.5 times greater odds of being smokers than the female patients.

The returned *p*-value of the test, `p = 0.0375`, is close to, but not exactly the same as, the result obtained by `crosstab`. This is because `fishertest` computes an exact *p*-

value using the sample data, while `crosstab` uses a chi-squared approximation to compute the *p*-value.

Input Arguments

x — Contingency table

2-by-2 matrix of nonnegative integer values | 2-by-2 table of nonnegative integer values

Contingency table, specified as a 2-by-2 matrix or table containing nonnegative integer values. A contingency table contains the frequency distribution of the variables in the sample data. You can use `crosstab` to generate a contingency table from sample data.

Example: `[4,0;0,4]`

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alpha',0.01,'Tail','right'` specifies a right-tailed hypothesis test at the 1% significance level.

'Alpha' — Significance level

0.05 (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

'Tail' — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Two-tailed test. The alternative hypothesis is that there is a nonrandom association between the two variables in x, and the odds ratio is not equal to 1.
`'right'`	Right-tailed test. The alternative hypothesis is that the odds ratio is greater than 1.
`'left'`	Left-tailed test. The alternative hypothesis is that the odds ratio is less than 1.

Example: `'Tail','right'`

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

- If `h` is `1`, then `fishertest` rejects the null hypothesis at the Alpha significance level.
- If `h` is `0`, then `fishertest` fails to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

stats — Test data

structure

Test data, returned as a structure with the following fields:

- `OddsRatio` — A measure of association between the two variables.
- `ConfidenceInterval` — Asymptotic confidence interval for the odds ratio. If any of the cell frequencies in x are 0, then `fishertest` does not compute a confidence interval and instead displays `[-Inf Inf]`.

More About

Fisher's Exact Test

Fisher's exact test is a nonparametric statistical test used to test the null hypothesis that no nonrandom associations exist between two categorical variables, against the alternative that there is a nonrandom association between the variables.

Fisher's exact test provides an alternative to the chi-squared test for small samples, or samples with very uneven marginal distributions. Unlike the chi-squared test, Fisher's exact test does not depend on large-sample distribution assumptions, and instead calculates an exact *p*-value based on the sample data. Although Fisher's exact test is valid for samples of any size, it is not recommended for large samples because it is computationally intensive. If all of the frequency counts in the contingency table are greater than or equal to `1e7`, then `fishertest` errors. For contingency tables that contain large count values or are well-balanced, use `crosstab` or `chi2gof` instead.

`fishertest` accepts a 2-by-2 contingency table as input, and computes the *p*-value of the test as follows:

1. Calculate the sums for each row, column, and total number of observations in the contingency table.
2. Using a multivariate generalization of the hypergeometric probability function, calculate the conditional probability of observing the exact result in the contingency table if the null hypothesis were true, given its row and column sums. The conditional probability is

$$P_{cutoff} = \frac{(R_1!R_2!)(C_1!C_2!)}{N!\prod_{i,j} n_{ij}!},$$

   where R_1 and R_2 are the row sums, C_1 and C_2 are the column sums, N is the total number of observations in the contingency table, and n_{ij} is the value in the ith row and jth column of the table.
3. Find all possible matrices of nonnegative integers consistent with the row and column sums. For each matrix, calculate the associated conditional probability using the equation for P_{cutoff}.
4. Use these values to calculate the *p*-value of the test, based on the alternative hypothesis of interest.

- For a two-sided test, sum all of the conditional probabilities less than or equal to P_{cutoff} for the observed contingency table. This represents the probability of observing a result as extreme as, or more extreme than, the actual outcome if the null hypothesis were true. Small p-values cast doubt on the validity of the null hypothesis, in favor of the alternative hypothesis of association between the variables.
- For a left-sided test, sum the conditional probabilities of all the matrices with a (1,1) cell frequency less than or equal to n_{11}.
- For a right-sided test, sum the conditional probabilities of all the matrices with a (1,1) cell frequency greater than or equal to n_{11} in the observed contingency table.

The odds ratio is

$$OR = \frac{n_{11}n_{22}}{n_{21}n_{12}}.$$

The null hypothesis of conditional independence is equivalent to the hypothesis that the odds ratio equals 1. The left-sided alternative is equivalent to an odds ratio less than 1, and the right-sided alternative is equivalent to an odds ratio greater than 1.

The asymptotic 100(1 – α)% confidence interval for the odds ratio is

$$CI = \left[\exp\left(L - \Phi^{-1}\left(\frac{1-\alpha}{2}\right)SE \right), \exp\left(L + \Phi^{-1}\left(\frac{1-\alpha}{2}\right)SE \right) \right],$$

where L is the log odds ratio, $\Phi^{-1}(\cdot)$ is the inverse of the normal inverse cumulative distribution function, and SE is the standard error for the log odds ratio. If the 100(1 – α)% confidence interval does not contain the value 1, then the association is significant at the α significance level. If any of the four cell frequencies are 0, then `fishertest` does not compute the confidence interval and instead displays `[-Inf Inf]`.

`fishertest` only accepts 2-by-2 contingency tables as input. To test the independence of categorical variables with more than two levels, use the chi-squared test provided by `crosstab`.

See Also

`chi2gof` | `crosstab`

ClassificationDiscriminant.fit

Class: ClassificationDiscriminant

Fit discriminant analysis classifier (to be removed)

Compatibility

`ClassificationDiscriminant.fit` will be removed in a future release. Use `fitcdiscr` instead.

Syntax

```
obj = ClassificationDiscriminant.fit(x,y)
obj = ClassificationDiscriminant.fit(x,y,Name,Value)
```

Description

`obj = ClassificationDiscriminant.fit(x,y)` returns a discriminant analysis classifier based on the input variables (also known as predictors, features, or attributes) x and output (response) y.

`obj = ClassificationDiscriminant.fit(x,y,Name,Value)` fits a classifier with additional options specified by one or more Name,Value pair arguments. If you use one of the following five options, `obj` is of class `ClassificationPartitionedModel`: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. Otherwise, `obj` is of class `ClassificationDiscriminant`.

Input Arguments

x — Predictor values

matrix of numeric values

Predictor values, specified as a matrix of numeric values. Each column of x represents one variable, and each row represents one observation.

`ClassificationDiscriminant.fit` considers `NaN` values in x as missing values. `ClassificationDiscriminant.fit` does not use observations with missing values for x in the fit.

Example:

Data Types: `single` | `double`

y — Classification values

numeric vector | categorical vector | logical vector | character array | cell array of strings

Classification values, specified as a numeric vector, categorical vector (nominal or ordinal), logical vector, character array, or cell array of strings. Each row of y represents the classification of the corresponding row of x.

`ClassificationDiscriminant.fit` considers `NaN` values in y to be missing values. `ClassificationDiscriminant.fit` does not use observations with missing values for y in the fit.

Data Types: `single` | `double` | `logical` | `char` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'ClassNames'` — Class names

array

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and an array. Use the data type that exists in y. The default is the class names that exist in y. Use `ClassNames` to order the classes or to select a subset of classes for training.

Data Types: `single` | `double` | `logical` | `char`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification, specified as the comma-separated pair consisting of `'Cost'` and a square matrix, where `Cost(i,j)` is the cost of classifying a point into class

`j` if its true class is `i`. Alternatively, `Cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Data Types: `single` | `double` | `struct`

`'CrossVal'` — Flag to train cross-validated classifier

`'off'` (default) | `'on'`

Flag to train a cross-validated classifier, specified as the comma-separated pair consisting of `'CrossVal'` and either `'on'` or `'off'`.

If you specify `'on'`, then `ClassificationDiscriminant.fit` creates a cross-validated classifier with 10 folds.

You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments.

You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Alternatively, cross validate obj later using the `crossval` method.

Example: `'CrossVal','on'`

`'CVPartition'` — Cross-validated model partition

`cvpartition` object

Cross-validated model partition, specified as the comma-separated pair consisting of `'CVPartition'` and an object created using `cvpartition`. You can only use one option at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'Delta'` — Linear coefficient threshold

`0` (default) | nonnegative scalar value

Linear coefficient threshold, specified as the comma-separated pair consisting of `'Delta'` and a nonnegative scalar value. If a coefficient of `obj` has magnitude smaller than `Delta`, `obj` sets this coefficient to `0`, and you can eliminate the corresponding predictor from the model. Set `Delta` to a higher value to eliminate more predictors.

`Delta` must be `0` for quadratic discriminant models.

Data Types: `single` | `double`

`'DiscrimType'` — Discriminant type
`'linear'` (default) | `'quadratic'` | `'diagLinear'` | `'diagQuadratic'` | `'pseudoLinear'` | `'pseudoQuadratic'`

Discriminant type, specified as the comma-separated pair consisting of `'DiscrimType'` and one of the following:

- `'linear'`
- `'quadratic'`
- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

Example: `'DiscrimType','quadratic'`

`'FillCoeffs'` — `Coeffs` property flag
`'on'` | `'off'`

`Coeffs` property flag, specified as the comma-separated pair consisting of `'FillCoeffs'` and `'on'` or `'off'`. Setting the flag to `'on'` populates the `Coeffs` property in the classifier object. This can be computationally intensive, especially when cross validating. The default is `'on'`, unless you specify a cross validation name-value pair, in which case the flag is set to `'off'` by default.

Example: `'FillCoeffs','off'`

`'Gamma'` — Regularization parameter
scalar value in the range `[0,1]`

Parameter for regularizing the correlation matrix of predictors, specified as the comma-separated pair consisting of `'Gamma'` and a scalar value in the range `[0,1]`.

- Linear discriminant — Scalar value in the range `[0,1]`.
  - If you pass a value strictly between `0` and `1`, `fitcdiscr` sets the discriminant type to `'Linear'`.

  - If you pass `0` for `Gamma` and `'Linear'` for `DiscrimType`, and if the correlation matrix is singular, `fitcdiscr` sets `Gamma` to the minimal value required for inverting the covariance matrix.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagLinear'`.
- Quadratic discriminant — Either `0` or `1`.
  - If you pass `0` for `Gamma` and `'Quadratic'` for `DiscrimType`, and if one of the classes has a singular covariance matrix, `fitcdiscr` errors.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagQuadratic'`.
  - If you set Gamma to a value between `0` and `1` for a quadratic discriminant, `fitcdiscr` errors.

Example: `'Gamma',1`

Data Types: `single | double`

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). If you specify `'Holdout',p`, then the software:

1. Randomly reserves `p*100`% of the data as validation data, and trains the model using the rest of the data
2. Stores the compact, trained model in CVMdl`.Trained`

If you specify `Holdout`, then you cannot specify any of CVPartition, KFold, or Leaveout.

Example: `'Holdout',0.1`

Data Types: `double | single`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated classifier, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. If you specify `'on'`, then the software implements leave-one-out cross validation.

If you use `'Leaveout'`, you cannot use these `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

Data Types: `char`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

Data Types: `cell`

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- A string:
  - `'empirical'` determines class probabilities from class frequencies in y. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector containing one scalar value for each class.
- A structure S with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as y
  - `S.ClassProbs` containing a vector of corresponding probabilities

Example: `'Prior','uniform'`

Data Types: `single` | `double` | `struct`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable y.

Example: `'ResponseName','Response'`

Data Types: `char`

`'SaveMemory'` — Flag to save covariance matrix

`'off'` (default) | `'on'`

Flag to save covariance matrix, specified as the comma-separated pair consisting of `'SaveMemory'` and either `'on'` or `'off'`. If you specify `'on'`, then `fitcdiscr` does not store the full covariance matrix, but instead stores enough information to compute the matrix. The `predict` method computes the full covariance matrix for prediction, and does not store the matrix. If you specify `'off'`, then `fitcdiscr` computes and stores the full covariance matrix in `obj`.

Specify `SaveMemory` as `'on'` when the input matrix contains thousands of predictors.

Example: `'SaveMemory','on'`

`'ScoreTransform'` — Score transform function

`'none'` (default) | valid score transform string | function handle

Score transform function, specified as the comma-separated pair consisting of `'ScoreTransform'` and one of the following.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to 0.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)

String	Formula
`'sign'`	–1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

Alternatively, you can use your own function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Example: `'ScoreTransform','logit'`

Data Types: `function_handle`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` is the number of rows in x. `fitcdiscr` normalizes the weights to sum to 1.

Data Types: `single` | `double`

Output Arguments

`obj` — Discriminant analysis classifier

classifier object

Discriminant analysis classifier, returned as a classifier object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a tree of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, obj is of class `ClassificationDiscriminant`, and you can use the `predict` method to predict the response of new data.

Definitions

Discriminant Classification

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. That is, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class, only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

For details, see “How the predict Method Classifies” on page 15-6.

Examples

Construct a Discriminant Analysis Classifier

Load the sample data.

```
load fisheriris
```

Construct a discriminant analysis classifier using the sample data.

```
obj = ClassificationDiscriminant.fit(meas,species)
```

```
obj =

  ClassificationDiscriminant
     PredictorNames: {'x1'  'x2'  'x3'  'x4'}
       ResponseName: 'Y'
         ClassNames: {'setosa'  'versicolor'  'virginica'}
     ScoreTransform: 'none'
    NumObservations: 150
        DiscrimType: 'linear'
                 Mu: [3x4 double]
             Coeffs: [3x3 struct]


  Properties, Methods
```

Alternatives

The `classify` function also performs discriminant analysis. `classify` is usually more awkward to use:

- `classify` requires you to fit the classifier every time you make a new prediction.
- `classify` does not perform cross validation.
- `classify` requires you to fit the classifier when changing prior probabilities.

See Also

`fitctree` | `ClassificationDiscriminant`

How To

- “Discriminant Analysis” on page 15-3

ClassificationKNN.fit

Class: ClassificationKNN

Fit *k*-nearest neighbor classifier (to be removed)

Compatibility

`ClassificationKNN.fit` will be removed in a future release. Use `fitcknn` instead.

Syntax

```
mdl = ClassificationKNN.fit(X,y)
mdl = ClassificationKNN.fit(X,y,Name,Value)
```

Description

`mdl = ClassificationKNN.fit(X,y)` returns a classification model based on the input variables (also known as predictors, features, or attributes) X and output (response) y.

`mdl = ClassificationKNN.fit(X,y,Name,Value)` fits a model with additional options specified by one or more Name,Value pair arguments.

If you use one of these options, `mdl` is of class `ClassificationPartitionedModel`: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. Otherwise, `mdl` is of class `ClassificationKNN`.

Input Arguments

X — Predictor values

numeric matrix

Predictor values, specified as a numeric matrix. Each column of X represents one variable, and each row represents one observation.

Data Types: `single` | `double`

y — Classification values

numeric vector | categorical vector | logical vector | character array | cell array of strings

Classification values, specified as a numeric vector, categorical vector, logical vector, character array, or cell array of strings, with the same number of rows as X. Each row of y represents the classification of the corresponding row of X.

Data Types: `single` | `double` | `cell` | `logical` | `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

'BreakTies' — Tie-breaking algorithm

`'smallest'` (default) | `'nearest'` | `'random'`

Tie-breaking algorithm used by the `predict` method if multiple classes have the same smallest cost, specified as the comma-separated pair consisting of `'BreakTies'` and one of the following:

- `'smallest'` — Use the smallest index among tied groups.
- `'nearest'` — Use the class with the nearest neighbor among tied groups.
- `'random'` — Use a random tiebreaker among tied groups.

By default, ties occur when multiple classes have the same number of nearest points among the `K` nearest neighbors.

Example: `'BreakTies','nearest'`

'BucketSize' — Maximum data points in node

50 (default) | positive integer value

Maximum number of data points in the leaf node of the *k*d-tree, specified as the comma-separated pair consisting of `'BucketSize'` and a positive integer value. This argument is meaningful only when `NSMethod` is `'kdtree'`.

Example: `'BucketSize',40`

Data Types: `single` | `double`

`'CategoricalPredictors'` — Categorical predictor flag

`[]` (default) | `'all'`

Categorical predictor flag, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following:

- `'all'` — All predictors are categorical.
- `[]` — No predictors are categorical.

When you set `CategoricalPredictors` to `'all'`, the default `Distance` is `'hamming'`.

Example: `'CategoricalPredictors','all'`

`'ClassNames'` — Class names

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and an array representing the class names. Use the same data type as the values that exist in y.

Use `ClassNames` to order the classes or to select a subset of classes for training. The default is the class names in y.

Data Types: `single` | `double` | `char` | `logical` | `cell`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification of a point, specified as the comma-separated pair consisting of `'Cost'` and one of the following:

- Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.
- Structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Data Types: `single` | `double` | `struct`

`'Cov'` — Covariance matrix

`nancov(X)` (default) | positive definite matrix of scalar values

Covariance matrix, specified as the comma-separated pair consisting of `'Cov'` and a positive definite matrix of scalar values representing the covariance matrix when computing the Mahalanobis distance. This argument is only valid when `'Distance'` is `'mahalanobis'`.

You cannot simultaneously specify `'Standardize'` and either of `'Scale'` or `'Cov'`.

Data Types: `single` | `double`

`'CrossVal'` — Cross-validation flag

`'off'` (default) | `'on'`

Cross-validation flag, specified as the comma-separated pair consisting of `'CrossVal'` and either `'on'` or `'off'`. If `'on'`, `fitcknn` creates a cross-validated model with 10 folds. Use the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` parameters to override this cross-validation setting. You can only use one parameter at a time to create a cross-validated model.

Alternatively, cross validate mdl later using the `crossval` method.

Example: `'Crossval','on'`

`'CVPartition'` — Cross-validated model partition

`cvpartition` object

Cross-validated model partition, specified as the comma-separated pair consisting of `'CVPartition'` and an object created using `cvpartition`. You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'Distance'` — Distance metric

valid distance metric string | function handle

Distance metric, specified as the comma-separated pair consisting of `'Distance'` and a valid distance metric string or function handle. The allowable strings depend on the `NSMethod` parameter, which you set in `fitcknn`, and which exists as a field in

`ModelParameters`. If you specify `CategoricalPredictors` as `'all'`, then the default distance metric is `'hamming'`. Otherwise, the default distance metric is `'euclidean'`.

NSMethod	Distance Metric Names
`exhaustive`	Any distance metric of `ExhaustiveSearcher`
`kdtree`	`'cityblock'`, `'chebychev'`, `'euclidean'`, or `'minkowski'`

For definitions, see “Distance Metrics”.

This table includes valid distance metrics of `ExhaustiveSearcher`.

Value	Description
`'cityblock'`	City block distance.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values).
`'cosine'`	One minus the cosine of the included angle between observations (treated as vectors).
`'euclidean'`	Euclidean distance.
`'hamming'`	Hamming distance, percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of X, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair argument.
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'Exponent'` name-value pair argument.
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between X and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from X, `S = nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair argument.

Value	Description
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@distfun`	Distance function handle. *`distfun`* has the form
	`function D2 = DISTFUN(ZI,ZJ)`
	`% calculation of  distance`
	`...`
	where
	• `ZI` is a `1`-by-`N` vector containing one row of X or y.
	• `ZJ` is an `M2`-by-`N` matrix containing multiple rows of X or y.
	• `D2` is an `M2`-by-`1` vector of distances, and `D2(k)` is the distance between observations `ZI` and `ZJ(J,:)`.

Example: `'Distance','minkowski'`

Data Types: `function_handle`

`'DistanceWeight'` — Distance weighting function

`'equal'` (default) | `'inverse'` | `'squaredinverse'` | function handle

Distance weighting function, specified as the comma-separated pair consisting of `'DistanceWeight'` and either a function handle or one of the following strings specifying the distance weighting function.

DistanceWeight	Meaning
`'equal'`	No weighting
`'inverse'`	Weight is 1/distance
`'squaredinverse'`	Weight is $1/\text{distance}^2$
`@fcn`	*`fcn`* is a function that accepts a matrix of nonnegative distances, and returns a matrix the same size containing nonnegative distance weights. For example, `'squaredinverse'` is equivalent to `@(d)d.^(-2)`.

Example: `'DistanceWeight','inverse'`

Data Types: `function_handle`

`'Exponent'` — Minkowski distance exponent

`2` (default) | positive scalar value

Minkowski distance exponent, specified as the comma-separated pair consisting of `'Exponent'` and a positive scalar value. This argument is only valid when `'Distance'` is `'minkowski'`.

Example: `'Exponent',3`

Data Types: `single` | `double`

`'Holdout'` — Fraction of data for holdout validation

`0` (default) | scalar value in the range `[0,1]`

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the remaining data for training.

If you use `Holdout`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single` | `double`

`'IncludeTies'` — Tie inclusion flag

`false` (default) | `true`

Tie inclusion flag, specified as the comma-separated pair consisting of `'IncludeTies'` and a logical value indicating whether `predict` includes all the neighbors whose distance values are equal to the `K`th smallest distance. If `IncludeTies` is `true`, `predict` includes all these neighbors. Otherwise, `predict` uses exactly `K` neighbors.

Example: `'IncludeTies',true`

Data Types: `logical`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated model, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

If you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. Specify `'on'` to use leave-one-out cross validation.

If you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

`'NSMethod'` — Nearest neighbor search method

`'kdtree'` | `'exhaustive'`

Nearest neighbor search method, specified as the comma-separated pair consisting of `'NSMethod'` and `'kdtree'` or `'exhaustive'`.

- `'kdtree'` — Create and use a *k*d-tree to find nearest neighbors. `'kdtree'` is valid when the distance metric is one of the following:
  - `'euclidean'`
  - `'cityblock'`
  - `'minkowski'`
  - `'chebyshev'`
- `'exhaustive'` — Use the exhaustive search algorithm. The distance values from all points in X to each point in y are computed to find nearest neighbors.

The default is `'kdtree'` when X has `10` or fewer columns, X is not sparse, and the distance metric is a `'kdtree'` type; otherwise, `'exhaustive'`.

Example: `'NSMethod','exhaustive'`

`'NumNeighbors'` — Number of nearest neighbors to find

`1` (default) | positive integer value

Number of nearest neighbors in X to find for classifying each point when predicting, specified as the comma-separated pair consisting of `'NumNeighbors'` and a positive integer value.

Example: `'NumNeighbors',3`

Data Types: `single` | `double`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in X.

Data Types: `cell`

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- A string:
  - `'empirical'` determines class probabilities from class frequencies in y. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class). To specify the class order for the corresponding elements of `Prior`, additionally specify the ClassNames name-value pair argument.
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as y
  - `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `Weights` and `Prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Example: `'Prior','uniform'`

Data Types: `single` | `double` | `struct`

'ResponseName' — Response variable name

'Y' (default) | string

Response variable name, specified as the comma-separated pair consisting of 'ResponseName' and a string containing the name of the response variable y.

Example: 'ResponseName','Response'

Data Types: char

'Scale' — Distance scale

nanstd(X) (default) | vector of nonnegative scalar values

Distance scale, specified as the comma-separated pair consisting of 'Scale' and a vector containing nonnegative scalar values with length equal to the number of columns in X. Each coordinate difference between X and a query point is scaled by the corresponding element of Scale. This argument is only valid when 'Distance' is 'seuclidean'.

You cannot simultaneously specify 'Standardize' and either of 'Scale' or 'Cov'.

Data Types: single | double

'Weights' — Observation weights

ones(size(X,1),1) (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and a vector of scalar values. The length of Weights is the number of rows in X.

The software normalizes the weights in each class to add up to the value of the prior probability of the class.

Data Types: single | double

Output Arguments

mdl — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the 'CrossVal', 'KFold', 'Holdout', 'Leaveout', or 'CVPartition' options results in a model of class

`ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

Definitions

Prediction

`ClassificationKNN` predicts the classification of a point `Xnew` using a procedure equivalent to this:

1. Find the `NumNeighbors` points in the training set `X` that are nearest to `Xnew`.
2. Find the `NumNeighbors` response values `Y` to those nearest points.
3. Assign the classification label `Ynew` that has the largest posterior probability among the values in `Y`.

For details, see “Posterior Probability” on page 22-3654 in the `predict` documentation.

Examples

Train a *k*-Nearest Neighbor Classifier

Construct a *k*-nearest neighbor classifier for Fisher's iris data, where *k*, the number of nearest neighbors in the predictors, is 5.

Load Fisher's iris data.

```
load fisheriris
X = meas;
Y = species;
```

`X` is a numeric matrix that contains four petal measurements for 150 irises. `Y` is a cell array of strings that contains the corresponding iris species.

Train a 5-nearest neighbors classifier. It is good practice to standardize noncategorical predictor data.

```
Mdl = fitcknn(X,Y,'NumNeighbors',5,'Standardize',1)


Mdl =

  ClassificationKNN
     PredictorNames: {'x1'  'x2'  'x3'  'x4'}
       ResponseName: 'Y'
         ClassNames: {'setosa'  'versicolor'  'virginica'}
     ScoreTransform: 'none'
    NumObservations: 150
           Distance: 'euclidean'
       NumNeighbors: 5
```

`Mdl` is a trained `ClassificationKNN` classifier, and some of its properties display in the Command Window.

To access the properties of `Mdl`, use dot notation.

```
Mdl.ClassNames
Mdl.Prior


ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

    0.3333    0.3333    0.3333
```

`Mdl.Prior` contains the class prior probabilities, which are settable using the name-value pair argument `'Prior'` in `fitcknn`. The order of the class prior probabilities corresponds to the order of the classes in `Mdl.ClassNames`. By default, the prior probabilities are the respective relative frequencies of the classes in the data.

You can also reset the prior probabilities after training. For example, set the prior probabilities to 0.5, 0.2, and 0.3 respectively.

```
Mdl.Prior = [0.5 0.2 0.3];
```

You can pass `Mdl` to, for example, predict (ClassificationKNN) to label new measurements, or crossval (ClassificationKNN) to cross validate the classifier.

Train a *k*-Nearest Neighbor Classifier Using the Minkowski Metric

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

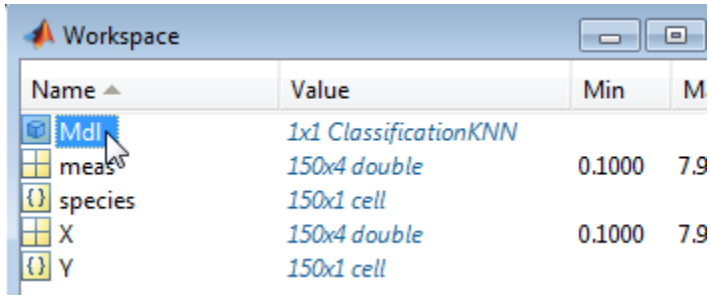
`X` is a numeric matrix that contains four petal measurements for 150 irises. `Y` is a cell array of strings that contains the corresponding iris species.

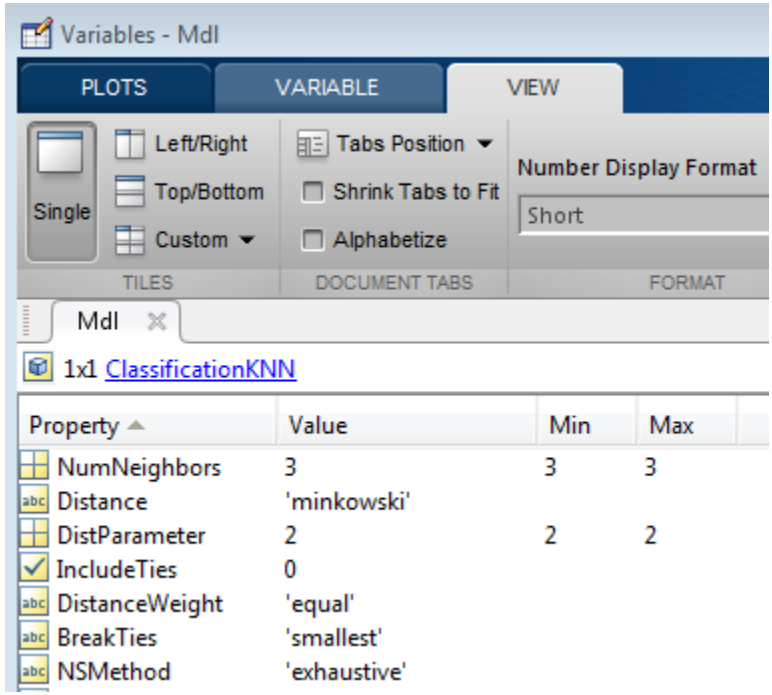
Train a 3-nearest neighbors classifier using the Minkowski metric. To use the Minkowski metric, you must use an exhaustive searcher. It is good practice to standardize noncategorical predictor data.

```
Mdl = fitcknn(X,Y,'NumNeighbors',3,...
    'NSMethod','exhaustive','Distance','minkowski',...
    'Standardize',1);
```

`Mdl` is a `ClassificationKNN` classifier.

You can examine the properties of `Mdl` by double-clicking `Mdl` in the Workspace window. This opens the Variable Editor.





- "Construct a KNN Classifier" on page 16-28
- "Modify a KNN Classifier" on page 16-30

See Also

`ClassificationKNN` | `fitcknn` | `predict`

More About

- "Classification Using Nearest Neighbors" on page 16-8

ClassificationTree.fit

Class: ClassificationTree

Fit classification tree (to be removed)

Compatibility

`ClassificationTree.fit` will be removed in a future release. Use `fitctree` instead.

Syntax

```
tree = ClassificationTree.fit(x,y)
tree = ClassificationTree.fit(x,y,Name,Value)
```

Description

`tree = ClassificationTree.fit(x,y)` returns a classification tree based on the input variables (also known as predictors, features, or attributes) x and output (response) y. tree is a binary tree, where each branching node is split based on the values of a column of x.

`tree = ClassificationTree.fit(x,y,Name,Value)` fits a tree with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a tree of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, `tree` is of class `ClassificationTree`, and you can use the `predict` method to make predictions.

Input Arguments

x — Predictor values

matrix of floating point values

Predictor values, specified as a matrix of floating point values.

`ClassificationTree.fit` considers `NaN` values in x as missing values. `ClassificationTree.fit` does not use observations with all missing values for x in the fit. `ClassificationTree.fit` uses observations with some missing values for x to find splits on variables for which these observations have valid values.

Data Types: `single` | `double`

y — predictor values

numeric vector | categorical vector | logical vector | character array | cell array of strings

Predictor values, specified as a numeric vector, categorical vector, logical vector, character array, or cell array of strings.

Each row of y represents the classification of the corresponding row of x. For numeric y, consider using `fitrtree` instead. `ClassificationTree.fit` considers `NaN` values in y to be missing values.

`ClassificationTree.fit` does not use observations with missing values for y in the fit.

Data Types: `single` | `double` | `char` | `logical` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'AlgorithmForCategorical'` — Algorithm for best split on categorical predictor

`'Exact'` | `'PullLeft'` | `'PCA'` | `'OVAbyClass'`

Algorithm to find the best split on a categorical predictor with L levels for data with $K \geq 3$ classes, specified as the comma-separated pair consisting of `'AlgorithmForCategorical'` and one of the following.

`'Exact'`	Consider all $2^{L-1} - 1$ combinations
`'PullLeft'`	Pull left by purity
`'PCA'`	Principal component-based partition
`'OVAbyClass'`	One versus all by class

`ClassificationTree.fit` selects the optimal subset of algorithms for each split using the known number of classes and levels of a categorical predictor. For $K = 2$ classes, `ClassificationTree.fit` always performs the exact search.

Example: `'AlgorithmForCategorical','PCA'`

`'CategoricalPredictors'` — Categorical predictors list

numeric or logical vector | cell array of strings | character matrix | `'all'`

Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following.

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of x.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of x is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in `PredictorNames` values.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in `PredictorNames` values. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

Example: `'CategoricalPredictors','all'`

Data Types: `single` | `double` | `char`

`'ClassNames'` — Class names

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and an array representing the class names. Use the same data type as the values that exist in y.

Use `ClassNames` to order the classes or to select a subset of classes for training. The default is the class names that exist in y.

Data Types: `single` | `double` | `char` | `logical` | `cell`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification a point, specified as the comma-separated pair consisting of `'Cost'` and one of the following.

- Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`.
- Structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`

Data Types: `single` | `double` | `struct`

`'CrossVal'` — Flag to grow cross-validated tree

`'off'` (default) | `'on'`

Flag to grow a cross-validated decision tree, specified as the comma-separated pair consisting of `'CrossVal'` and either `'on'` or `'off'`.

If `'on'`, `ClassificationTree.fit` grows a cross-validated decision tree with 10 folds. You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments. Note that you can only use one of these four options (`'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`) at a time when creating a cross-validated tree.

Alternatively, cross-validate tree later using the `crossval` method.

Example: `'CrossVal','on'`

`'CVPartition'` — Partition for cross-validation tree

`cvpartition` object

Partition to use in a cross-validated tree, specified as the comma-separated pair consisting of `'CVPartition'` and an object of the `cvpartition` class created using `cvpartition`.

Note that if you use `'CVPartition'`, you cannot use any of the `'KFold'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

`'Holdout'` — Fraction of data for holdout validation

`1` (default) | scalar value in the range (0,1]

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the rest of the data for training.

Note that if you use `'Holdout'`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single` | `double`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated tree, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

Note that if you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross validation flag

`'off'` (default) | `'on'`

Leave-one-out cross validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. Use leave-one-out cross validation by setting to `'on'`.

Note that if you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

`'MaxCat'` — Maximum category levels

`10` (default) | nonnegative scalar value

Maximum category levels, specified as the comma-separated pair consisting of `'MaxCat'` and a nonnegative scalar value. `ClassificationTree.fit` splits a categorical predictor using the exact search algorithm if the predictor has at most `MaxCat` levels in

the split node. Otherwise, `ClassificationTree.fit` finds the best categorical split using one of the inexact algorithms.

Note that passing a small value can lead to loss of accuracy and passing a large value can lead to long computation time and memory overload.

Example: `'MaxCat',8`

`'MergeLeaves'` — Leaf merge flag

`'on'` (default) | `'off'`

Leaf merge flag, specified as the comma-separated pair consisting of `'MergeLeaves'` and either `'on'` or `'off'`. When `'on'`, `ClassificationTree.fit` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `ClassificationTree.fit` does not merge leaves.

Example: `'MergeLeaves','off'`

`'MinLeaf'` — Minimum number of leaf node observations

1 (default) | positive integer value

Minimum number of leaf node observations, specified as the comma-separated pair consisting of `'MinLeaf'` and a positive integer value. Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Example: `'MinLeaf',3`

Data Types: `single` | `double`

`'MinParent'` — Minimum number of branch node observations

10 (default) | positive integer value

Minimum number of branch node observations, specified as the comma-separated pair consisting of `'MinParent'` and a positive integer value. Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Example: `'MinParent',8`

Data Types: `single` | `double`

`'NVarToSample'` — Number of predictors for split

`'all'` | positive integer value

Number of predictors to select at random for each split, specified as the comma-separated pair consisting of `'NVarToSample'` and a positive integer value. You can also specify `'all'` to use all available predictors.

Example: `'NVarToSample',3`

Data Types: `single` | `double`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- A string:
  - `'empirical'` determines class probabilities from class frequencies in y. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class)
- A structure S with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as y
  - `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `weights` and `prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Example: `'Prior','uniform'`

`'Prune'` — Pruning flag

`'on'` (default) | `'off'`

Pruning flag, specified as the comma-separated pair consisting of `'Prune'` and either `'on'` or `'off'`. When `'on'`, `ClassificationTree.fit` grows the classification tree, and computes the optimal sequence of pruned subtrees. When `'off'` `ClassificationTree.fit` grows the classification tree without pruning.

Example: `'Prune','off'`

`'PruneCriterion'` — Pruning criterion
`'error'` (default) | `'impurity'`

Pruning criterion, specified as the comma-separated pair consisting of `'PruneCriterion'` and either `'error'` or `'impurity'`.

Example: `'PruneCriterion','impurity'`

`'ResponseName'` — Response variable name
`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string representing the name of the response variable y.

Example: `'ResponseName','Response'`

`'ScoreTransform'` — Score transform function
`'none'` | `'symmetric'` | `'invlogit'` | `'ismax'` | function handle | ...

Score transform function, specified as the comma-separated pair consisting of `'ScoreTransform'` and a function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Alternatively, you can specify one of the following strings representing a built-in transformation function.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to 0.
`'logit'`	$1/(1 + e^{-x})$

String	Formula
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

Example: `'ScoreTransform','logit'`

`'SplitCriterion'` — Split criterion

`'gdi'` (default) | `'twoing'` | `'deviance'`

Split criterion, specified as the comma-separated pair consisting of `'SplitCriterion'` and `'gdi'` (Gini's diversity index), `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction (also known as cross entropy).

Example: `'SplitCriterion','deviance'`

`'Surrogate'` — Surrogate decision splits flag

`'off'` | `'on'` | `'all'` | positive integer value

Surrogate decision splits flag, specified as the comma-separated pair consisting of `'Surrogate'` and `'on'`, `'off'`, `'all'`, or a positive integer value.

- When set to `'on'`, `ClassificationTree.fit` finds at most 10 surrogate splits at each branch node.
- When set to a positive integer value, `ClassificationTree.fit` finds at most the specified number of surrogate splits at each branch node.
- When set to `'all'`, `ClassificationTree.fit` finds all surrogate splits at each branch node. The `'all'` setting can use much time and memory.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also enables you to compute measures of predictive association between predictors.

Example: `'Surrogate','on'`

'Weights' — Observation weights
ones(size(x,1),1) (default) | vector of scalar values

Vector of observation weights, specified as the comma-separated pair consisting of 'Weights' and a vector of scalar values. The length of Weights is equal to the number of rows in x. ClassificationTree.fit normalizes the weights in each class to add up to the value of the prior probability of the class.

Data Types: single | double

Output Arguments

tree — Classification tree
classification tree object

Classification tree object, returned as a classification tree object.

Note that using the 'CrossVal', 'KFold', 'Holdout', 'Leaveout', or 'CVPartition' options results in a tree of class ClassificationPartitionedModel. You cannot use a partitioned tree for prediction, so this kind of tree does not have a predict method. Instead, use kfoldpredict to predict responses for observations not used for training.

Otherwise, tree is of class ClassificationTree, and you can use the predict method to make predictions.

Definitions

Impurity and Node Error

ClassificationTree splits nodes based on either *impurity* or *node error*.

Impurity means one of several things, depending on your choice of the SplitCriterion name-value pair argument:

- Gini's Diversity Index (gdi) — The Gini index of a node is

$$1 - \sum_i p^2(i),$$

where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined the same as for the Gini index, the deviance of a node is

$$-\sum_i p(i)\log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

$$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

  where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with the largest number of training samples at a node, the node error is $1 - p(j)$.

Examples

Construct a Classification Tree

Construct a classification tree for the data in `ionosphere.mat`.

```
load ionosphere
```

```
tc = ClassificationTree.fit(X,Y)

tc =

  ClassificationTree
            PredictorNames: {1x34 cell}
              ResponseName: 'Y'
                ClassNames: {'b'  'g'}
            ScoreTransform: 'none'
      CategoricalPredictors: []
           NumObservations: 351


  Properties, Methods
```

References

[1] Coppersmith, D., S. J. Hong, and J. R. M. Hosking. “Partitioning Nominal Attributes in Decision Trees.” *Data Mining and Knowledge Discovery*, Vol. 3, 1999, pp. 197–217.

[2] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`kfoldpredict` | `predict` | `ClassificationTree` | `fitctree`

GeneralizedLinearModel.fit

Class: GeneralizedLinearModel

Create generalized linear regression model

Compatibility

`GeneralizedLinearModel.fit` will be removed in a future release. Use `fitglm` instead.

Syntax

```
mdl = GeneralizedLinearModel.fit(tbl)
mdl = GeneralizedLinearModel.fit(X,y)
mdl = GeneralizedLinearModel.fit(...,modelspec)
mdl = GeneralizedLinearModel.fit(...,Name,Value)
mdl = GeneralizedLinearModel.fit(...,modelspec,Name,Value)
```

Description

`mdl = GeneralizedLinearModel.fit(tbl)` creates a generalized linear model of a table or dataset array `tbl`.

`mdl = GeneralizedLinearModel.fit(X,y)` creates a generalized linear model of the responses `y` to a data matrix `X`.

`mdl = GeneralizedLinearModel.fit(...,modelspec)` creates a generalized linear model as specified by `modelspec`.

`mdl = GeneralizedLinearModel.fit(...,Name,Value)` or `mdl = GeneralizedLinearModel.fit(...,modelspec,Name,Value)` creates a generalized linear model with additional options specified by one or more Name,Value pair arguments.

Tips

- The generalized linear model `mdl` is a standard linear model unless you specify otherwise with the `Distribution` name-value pair.
- For other methods such as `devianceTest`, or properties of the `GeneralizedLinearModel` object, see `GeneralizedLinearModel`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables and response variables can be numeric, or any grouping variable type, such as logical or categorical (see "Grouping Variables" on page 2-52).

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

`modelspec` — Model specification

string specifying the model | t-by-(p+1) terms matrix | string of the form `'Y ~ terms'`

Model specification, which is the starting model for `stepwiseglm`, specified as one of the following:

- String specifying the type of model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

- t-by-(p+1) matrix, namely terms matrix, specifying terms to include in model, where t is the number of terms and p is the number of predictor variables, and plus one is for the response variable.
- String representing a formula in the form `'Y ~ terms'`, where the `terms` are in "Wilkinson Notation" on page 22-1421.

Example: `'quadratic'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinomialSize'` — Number of trials for binomial distribution

1 (default) | scalar value | vector

Number of trials for binomial distribution, that is the sample size, specified as the comma-separated pair consisting of a scalar value or a vector of the same length as the response. This is the parameter `n` for the fitted binomial distribution. `BinomialSize` applies only when the `Distribution` parameter is `'binomial'`.

If `BinomialSize` is a scalar value, that means all observations have the same number of trials.

As an alternative to `BinomialSize`, you can specify the response as a two-column vector with counts in column 1 and `BinomialSize` in column 2.

Data Types: `single` | `double`

`'CategoricalVars'` — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of `'CategoricalVars'` and either a cell array of strings of the names of the categorical variables in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array `tbl`, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix `X`, then the default value of this name-value pair argument is an empty matrix `[]`. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: `'CategoricalVars',[2,3]`

Example: `'CategoricalVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

'DispersionFlag' — Indicator to compute dispersion parameter

`false` for `'binomial'` and `'poisson'` distributions (default) | `true`

Indicator to compute dispersion parameter for `'binomial'` and `'poisson'` distributions, specified as the comma-separated pair consisting of `'DispersionFlag'` and one of the following.

`true`	Estimate a dispersion parameter when computing standard errors
`false`	Default. Use the theoretical value when computing standard errors

The fitting function always estimates the dispersion for other distributions.

Example: `'DispersionFlag',true`

'Distribution' — Distribution of the response variable

`'normal'` (default) | `'binomial'` | `'poisson'` | `'gamma'` | `'inverse gaussian'`

Distribution of the response variable, specified as the comma-separated pair consisting of `'Distribution'` and one of the following.

`'normal'`	Normal distribution
`'binomial'`	Binomial distribution
`'poisson'`	Poisson distribution
`'gamma'`	Gamma distribution
`'inverse gaussian'`	Inverse Gaussian distribution

Example: `'Distribution','gamma'`

'Exclude' — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Intercept'` — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

`'Link'` — Link function

The canonical link function (default) | scalar value | structure

Link function to use in place of the canonical link function, specified as the comma-separated pair consisting of `'Link'` and one of the following.

Link Function Name	Link Function	Mean (Inverse) Function
`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'probit'`	$f(\mu) = \Phi^{-1}(\mu)$	$\mu = \Phi(Xb)$
`'comploglog'`	$f(\mu) = \log(-\log(1 - \mu))$	$\mu = 1 - \exp(-\exp(Xb))$
`'reciprocal'`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`p` (a number)	$f(\mu) = \mu^p$	$\mu = Xb^{1/p}$
`S` (a structure) with three fields. Each field holds a function handle that accepts a vector of inputs and returns a vector of the same size: • `S.Link` — The link function • `S.Inverse` — The inverse link function	$f(\mu) =$ `S.Link`(μ)	$\mu =$ `S.Inverse`(Xb)

Link Function Name	Link Function	Mean (Inverse) Function
• `S.Derivative` — The derivative of the link function		

The link function defines the relationship $f(\mu) = X*b$ between the mean response μ and the linear combination of predictors $X*b$.

For more information on the canonical link functions, see `Definitions`.

Example: `'Link','probit'`

`'Offset'` — Offset variable

[ ] (default) | `vector` | string

Offset variable in the fit, specified as the comma-separated pair consisting of `'Offset'` and a vector or name of a variable with the same length as the response.

`fitglm` and `stepwiseglm` use `Offset` as an additional predictor, with a coefficient value fixed at 1.0. In other words, the formula for fitting is

```
μ ~ Offset + (terms involving real predictors)
```

with the `Offset` predictor having coefficient `1`.

For example, consider a Poisson regression model. Suppose the number of counts is known for theoretical reasons to be proportional to a predictor `A`. By using the log link function and by specifying `log(A)` as an offset, you can force the model to satisfy this theoretical constraint.

Data Types: `single` | `double` | `char`

`'PredictorVars'` — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

`'ResponseVar'` — Response variable

last column in `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset array `tbl`, or a logical or numeric index vector indicating which column is the response variable. You typically need to use `'ResponseVar'` when fitting a table or dataset array `tbl`.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

`'VarNames'` — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights

`ones(n,1)` (default) | n-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an n-by-1 vector of nonnegative scalar values, where n is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Generalized linear model

`GeneralizedLinearModel` object

Generalized linear model representing a least-squares fit of the link of the response to the data, returned as a `GeneralizedLinearModel` object.

For properties and methods of the generalized linear model object, `mdl`, see the `GeneralizedLinearModel` class page.

Definitions

Terms Matrix

A terms matrix is a t-by-$(p + 1)$ matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

```
load hospital
ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
```

Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

```
T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     1     0     0     0
     0     0     1     0
     0     0     0     1
```

Redefine the dataset array.

```
ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
```

Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

```
T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]
```

```
T =

     0     0     0
     1     0     0
     0     1     0
     1     1     0
     0     2     0
```

Fit a linear model.

```
mdl = fitlm(X,MPG,T)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1*x2 + x2^2

Estimated Coefficients:
                   Estimate       SE            tStat      pValue
    (Intercept)          48.906        12.589     3.8847    0.00019665
    x1                 0.54418       0.57125    0.95261       0.34337
    x2                -0.012781     0.0060312    -2.1192      0.036857
    x1:x2           -0.00010892    0.00017925    -0.6076         0.545
    x2^2             9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)

1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *Y* is the response name.
- *terms* contains
  - Variable names
  - `+` means include the next variable
  - `-` means do not include the next variable
  - `:` defines an interaction, a product of terms
  - `*` defines an interaction **and all lower-order terms**
  - `^` raises the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
  - `()` groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

For example,
`'Y ~ A + B + C'` means a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example because `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example because `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Canonical Link Function

The default link function for a generalized linear model is the *canonical link function*.

Canonical Link Functions for Generalized Linear Models

Distribution	Link Function Name	Link Function	Mean (Inverse) Function
`'normal'`	`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'binomial'`	`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'poisson'`	`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'gamma'`	`-1`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`'inverse gaussian'`	`-2`	$f(\mu) = 1/\mu^2$	$\mu = (Xb)^{-1/2}$

Examples

Fit a Generalized Linear Model

Make a logistic binomial model of the probability of smoking as a function of age, weight, and sex, using a two-way interactions model.

Load the `hospital` dataset array.

```
load hospital
ds = hospital; % just to use the ds name
```

Specify the model using a formula that allows up to two-way interactions.

```
modelspec = 'Smoker ~ Age*Weight*Sex - Age:Weight:Sex';
```

Create the generalized linear model.

```
mdl = fitglm(ds,modelspec,'Distribution','binomial')
```

```
mdl =


Generalized Linear regression model:
    logit(Smoker) ~ 1 + Sex*Age + Sex*Weight + Age*Weight
    Distribution = Binomial

Estimated Coefficients:
```

```
                    Estimate       SE           tStat       pValue
    (Intercept)          -6.0492       19.749     -0.3063    0.75938
    Sex_Male             -2.2859       12.424    -0.18399    0.85402
    Age                   0.11691      0.50977     0.22934    0.81861
    Weight               0.031109      0.15208     0.20455    0.83792
    Sex_Male:Age         0.020734      0.20681     0.10025    0.92014
    Sex_Male:Weight       0.01216     0.053168     0.22871     0.8191
    Age:Weight         -0.00071959    0.0038964    -0.18468    0.85348


100 observations, 93 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 5.07, p-value = 0.535
```

The large *p*-value indicates the model might not differ statistically from a constant.

- "Generalized Linear Model Workflow" on page 10-39

Alternatives

You can also construct a generalized linear model using `fitglm`.

Use `stepwiseglm` to select a model specification automatically. Use `step`, `addTerms`, or `removeTerms` to adjust a fitted model.

References

[1] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

[2] Dobson, A. J. *An Introduction to Generalized Linear Models*. New York: Chapman & Hall, 1990.

[3] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

See Also

`GeneralizedLinearModel` | `stepwiseglm`

More About

- "Generalized Linear Models" on page 10-12

gmdistribution.fit

Class: gmdistribution

Gaussian mixture parameter estimates

Note: `fit` will be removed in a future release. Use `fitgmdist` instead.

Syntax

```
obj = gmdistribution.fit(X,k)
obj = gmdistribution.fit(...,param1,val1,param2,val2,...)
```

Description

`obj = gmdistribution.fit(X,k)` uses an Expectation Maximization (EM) algorithm to construct an object `obj` of the `gmdistribution` class containing maximum likelihood estimates of the parameters in a Gaussian mixture model with `k` components for data in the n-by-d matrix `X`, where n is the number of observations and d is the dimension of the data.

`gmdistribution` treats `NaN` values as missing data. Rows of `X` with `NaN` values are excluded from the fit.

`obj = gmdistribution.fit(...,param1,val1,param2,val2,...)` provides control over the iterative EM algorithm. Parameters and values are listed below.

Parameter	Value
`'Start'`	Method used to choose initial component parameters. One of the following: • `'randSample'` — To select `k` observations from `X` at random as initial component means. The mixing proportions are uniform.

Parameter	Value
	The initial covariance matrices for all components are diagonal, where the element `j` on the diagonal is the variance of `X(:,j)`. This is the default. • `'plus'` — The software selects `k` observations from `X` using the kmeans++ algorithm. The initial mixing proportions are uniform. The initial covariance matrices for all components are diagonal, where the element `j` on the diagonal is the variance of `X(:,j)`. • `S` — A structure array with fields `mu`, `Sigma`, and `PComponents`. See `gmdistribution` for descriptions of values. • `s` — A vector of length n containing an initial guess of the component index for each point.
`'Replicates'`	A positive integer giving the number of times to repeat the EM algorithm, each time with a new set of parameters. The solution with the largest likelihood is returned. A value larger than 1 requires the `'randSample'` start method. The default is 1.
`'CovType'`	`'diagonal'` if the covariance matrices are restricted to be diagonal; `'full'` otherwise. The default is `'full'`.
`'SharedCov'`	Logical `true` if all the covariance matrices are restricted to be the same (pooled estimate); logical `false` otherwise.
`'Regularize'`	A nonnegative regularization number added to the diagonal of covariance matrices to make them positive-definite. The default is 0.
`'Options'`	Options structure for the iterative EM algorithm, as created by `statset`. `gmdistribution.fit` uses the parameters `'Display'` with a default value of `'off'`, `'MaxIter'` with a default value of `100`, and `'TolFun'` with a default value of `1e-6`.

In some cases, `gmdistribution` may converge to a solution where one or more of the components has an ill-conditioned or singular covariance matrix.

The following issues may result in an ill-conditioned covariance matrix:

- The number of dimension of your data is relatively high and there are not enough observations.
- Some of the features (variables) of your data are highly correlated.
- Some or all the features are discrete.

- You tried to fit the data to too many components.

In general, you can avoid getting ill-conditioned covariance matrices by using one of the following precautions:

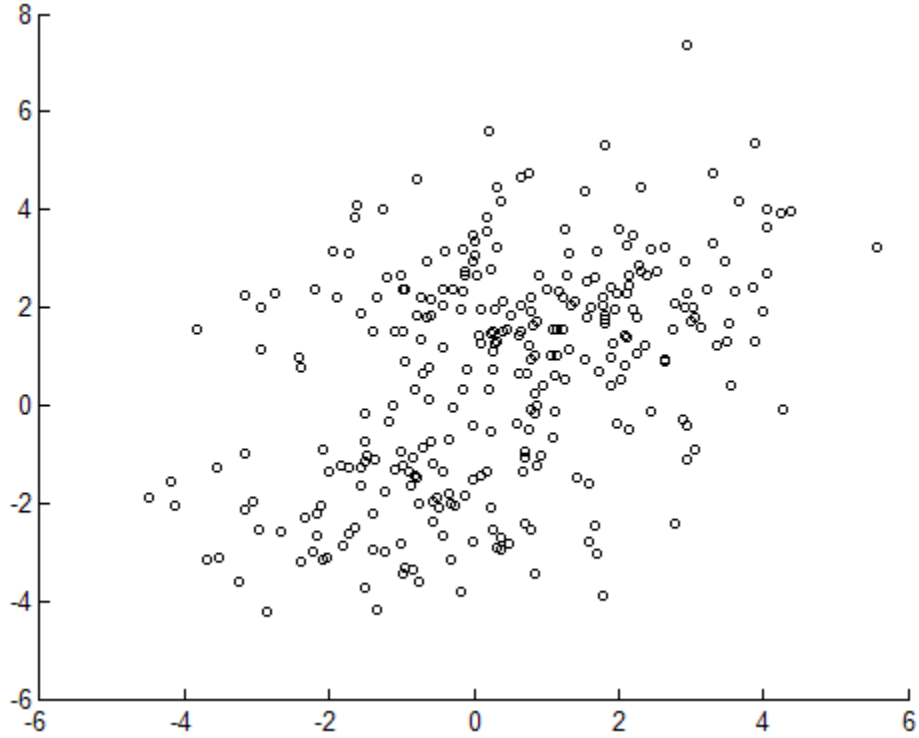
- Pre-process your data to remove correlated features.
- Set `'SharedCov'` to `true` to use an equal covariance matrix for every component.
- Set `'CovType'` to `'diagonal'`.
- Use `'Regularize'` to add a very small positive number to the diagonal of every covariance matrix.
- Try another set of initial values.

In other cases `gmdistribution` may pass through an intermediate step where one or more of the components has an ill-conditioned covariance matrix. Trying another set of initial values may avoid this issue without altering your data or model.

Examples

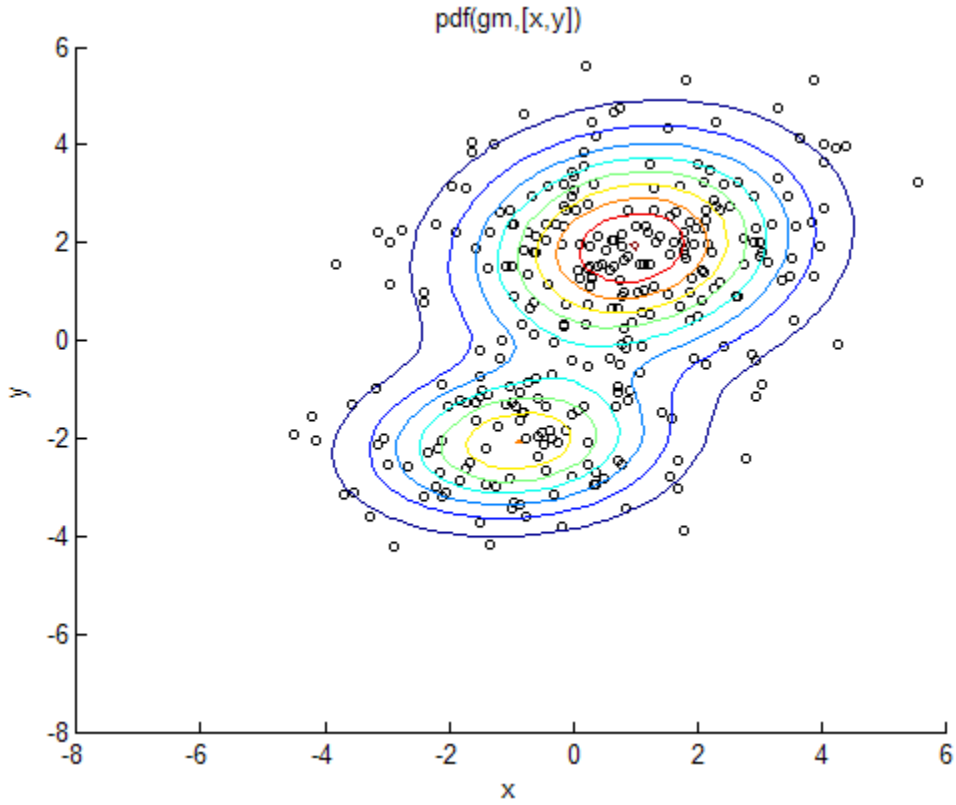
Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function:

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



Next, fit a two-component Gaussian mixture model:

```
options = statset('Display','final');
obj = gmdistribution.fit(X,2,'Options',options);
10 iterations, log-likelihood = -7046.78

h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Among the properties of the fit are the parameter estimates:

```
ComponentMeans = obj.mu
ComponentMeans =
    0.9391    2.0322
   -2.9823   -4.9737

ComponentCovariances = obj.Sigma
ComponentCovariances(:,:,1) =
    1.7786   -0.0528
   -0.0528    0.5312
ComponentCovariances(:,:,2) =
    1.0491   -0.0150
   -0.0150    0.9816
```

```
MixtureProportions = obj.PComponents
MixtureProportions =
    0.5000    0.5000
```

The Akaike information is minimized by the two-component model:

```
AIC = zeros(1,4);
obj = cell(1,4);
for k = 1:4
    obj{k} = gmdistribution.fit(X,k);
    AIC(k)= obj{k}.AIC;
end

[minAIC,numComponents] = min(AIC);
numComponents
numComponents =
     2

model = obj{2}
model =
Gaussian mixture distribution
with 2 components in 2 dimensions
Component 1:
Mixing proportion: 0.500000
Mean:     0.9391    2.0322
Component 2:
Mixing proportion: 0.500000
Mean:    -2.9823   -4.9737
```

Both the Akaike and Bayes information are negative log-likelihoods for the data with penalty terms for the number of estimated parameters. They are often used to determine an appropriate number of components for a model when the number of components is unspecified.

References

[1] McLachlan, G., and D. Peel. *Finite Mixture Models*. Hoboken, NJ: John Wiley & Sons, Inc., 2000.

See Also

`gmdistribution` | `cluster`

LinearModel.fit

Class: LinearModel

Create linear regression model

Compatibility

`LinearModel.fit` will be removed in a future release. Use `fitlm` instead.

Syntax

```
mdl = LinearModel.fit(tbl)
mdl = LinearModel.fit(X,y)
mdl = LinearModel.fit(...,modelspec)
mdl = LinearModel.fit(...,Name,Value)
mdl = LinearModel.fit(...,modelspec,Name,Value)
```

Description

`mdl = LinearModel.fit(tbl)` creates a linear model of a table or dataset array `tbl`.

`mdl = LinearModel.fit(X,y)` creates a linear model of the responses `y` to a data matrix `X`.

`mdl = LinearModel.fit(...,modelspec)` creates a linear model of the specified type.

`mdl = LinearModel.fit(...,Name,Value)` or `mdl = LinearModel.fit(..., modelspec,Name,Value)` creates a linear model with additional options specified by one or more Name,Value pair arguments.

Tips

- Use robust fitting (`RobustOpts` name-value pair) to reduce the effect of outliers automatically.

- Do not use robust fitting when you want to subsequently adjust a model using `step`.
- For other methods or properties of the `LinearModel` object, see `LinearModel`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see "Grouping Variables" on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelspec` — Model specification

string naming the model | t-by-$(p + 1)$ terms matrix | string of the form `'Y ~ terms'`

Model specification, specified as one of the following. The choice is the starting model for `stepwiselm`.

- A string naming the model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

- t-by-$(p + 1)$ matrix, namely terms matrix, specifying terms to include in the model, where t is the number of terms and p is the number of predictor variables, and plus 1 is for the response variable.
- A string representing a formulain the form
  `'Y ~ terms'`,
  where the `terms` are in “Wilkinson Notation” on page 22-1441.

Example: `'quadratic'`

Example: `'y ~ X1 + X2^2 + X1:X2'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CategoricalVars'` — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of `'CategoricalVars'` and either a cell array of strings of the names of the categorical variables in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array `tbl`, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix `X`, then the default value of this name-value pair argument is an empty matrix `[]`. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: `'CategoricalVars',[2,3]`

Example: `'CategoricalVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

'Intercept' — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

'PredictorVars' — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

'ResponseVar' — Response variable

last column in `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset array `tbl`, or a logical or numeric index vector indicating which column is the response variable. You typically need to use `'ResponseVar'` when fitting a table or dataset array `tbl`.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

`'RobustOpts'` — Indicator of robust fitting type

`'off'` (default) | `'on'` | string | structure with string or function handle

Indicator of the robust fitting type to use, specified as the comma-separated pair consisting of `'RobustOpts'` and one of the following.

- `'off'` — No robust fitting. `fitlm` uses ordinary least squares.
- `'on'` — Robust fitting. When you use robust fitting, `'bisquare'` weight function is the default.
- String — Name of the robust fitting weight function from the following table. `fitlm` uses the corresponding default tuning constant in the table.
- Structure with the string `RobustWgtFun` containing the name of the robust fitting weight function from the following table and optional scalar `Tune` fields — `fitlm` uses the `RobustWgtFun` weight function and `Tune` tuning constant from the structure. You can choose the name of the robust fitting weight function from this table. If you do not supply a `Tune` field, the fitting function uses the corresponding default tuning constant.

Weight Function	Equation	Default Tuning Constant
`'andrews'`	`w = (abs(r)<pi) .* sin(r) ./ r`	1.339
`'bisquare'` (default)	`w = (abs(r)<1) .* (1 - r.^2).^2`	4.685
`'cauchy'`	`w = 1 ./ (1 + r.^2)`	2.385
`'fair'`	`w = 1 ./ (1 + abs(r))`	1.400
`'huber'`	`w = 1 ./ max(1, abs(r))`	1.345
`'logistic'`	`w = tanh(r) ./ r`	1.205
`'ols'`	Ordinary least squares (no weighting function)	None
`'talwar'`	`w = 1 * (abs(r)<1)`	2.795

Weight Function	Equation	Default Tuning Constant
'welsch'	w = exp(-(r.^2))	2.985

The value *r* in the weight functions is

```
r = resid/(tune*s*sqrt(1-h)),
```

where `resid` is the vector of residuals from the previous iteration, `h` is the vector of leverage values from a least-squares fit, and `s` is an estimate of the standard deviation of the error term given by

```
s = MAD/0.6745.
```

MAD is the median absolute deviation of the residuals from their median. The constant 0.6745 makes the estimate unbiased for the normal distribution. If there are *p* columns in `X`, the smallest *p* absolute deviations are excluded when computing the median.

Default tuning constants give coefficient estimates that are approximately 95% as statistically efficient as the ordinary least-squares estimates, provided the response has a normal distribution with no outliers. Decreasing the tuning constant increases the downweight assigned to large residuals; increasing the tuning constant decreases the downweight assigned to large residuals.

- Structure with the function handle `RobustWgtFun` and optional scalar `Tune` fields — You can specify a custom weight function. `fitlm` uses the `RobustWgtFun` weight function and `Tune` tuning constant from the structure. Specify `RobustWgtFun` as a function handle that accepts a vector of residuals, and returns a vector of weights the same size. The fitting function scales the residuals, dividing by the tuning constant (default `1`) and by an estimate of the error standard deviation before it calls the weight function.

Example: `'RobustOpts','andrews'`

'VarNames' — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights
`ones(n,1)` (default) | *n*-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an *n*-by-1 vector of nonnegative scalar values, where *n* is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Linear model
`LinearModel` object

Linear model representing a least-squares fit of the response to the data, returned as a `LinearModel` object.

If the value of the `'RobustOpts'` name-value pair is not `[]` or `'ols'`, the model is not a least-squares fit, but uses the robust fitting function.

For properties and methods of the linear model object, `mdl`, see the `LinearModel` class page.

Definitions

Terms Matrix

A terms matrix is a *t*-by-(*p* + 1) matrix specifying terms in a model, where *t* is the number of terms, *p* is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

  ```
  load hospital
  ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
  hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
  ```

  Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

  ```
  T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
  ```

  ```
  T =

       0     0     0     0
       1     0     0     0
       0     0     1     0
       0     0     0     1
  ```

  Redefine the dataset array.

  ```
  ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
  hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
  ```

  Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

  ```
  T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
  ```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

  Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

  ```
  T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]

  T =

       0     0     0
       1     0     0
       0     1     0
       1     1     0
       0     2     0
  ```

  Fit a linear model.

  ```
  mdl = fitlm(X,MPG,T)

  mdl =

  Linear regression model:
      y ~ 1 + x1*x2 + x2^2

  Estimated Coefficients:
                      Estimate       SE            tStat      pValue
      (Intercept)         48.906        12.589     3.8847    0.00019665
      x1                 0.54418       0.57125    0.95261       0.34337
  ```

```
    x2              -0.012781     0.0060312    -2.1192       0.036857
    x1:x2          -0.00010892    0.00017925    -0.6076         0.545
    x2^2            9.7518e-07    7.5389e-07     1.2935        0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)

1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *Y* is the response name.
- *terms* contains
  - Variable names
  - + means include the next variable
  - - means do not include the next variable
  - : defines an interaction, a product of terms
  - * defines an interaction **and all lower-order terms**
  - ^ raises the predictor to a power, exactly as in * repeated, so ^ includes lower order terms as well
  - ( ) groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

For example,
`'Y ~ A + B + C'` means a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example because `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example because `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
1	Constant (intercept) term

Wilkinson Notation	Factors in Standard Notation
`A^k`, where `k` is a positive integer	A, A^2, ..., A^k
`A + B`	A, B
`A*B`	A, B, A*B
`A:B`	A*B only
`-B`	Do not include B
`A*B + C`	A, B, C, A*B
`A + B + C + A:B`	A, B, C, A*B
`A*B*C - A:B:C`	A, B, C, A*B, A*C, B*C
`A*(B + C)`	A, B, C, A*B, A*C

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Examples

Linear Regression Model of Matrix Data

Fit a linear model of the Hald data.

Load the data.

```
load hald
X = ingredients; % Predictor variables
y = heat; % Response
```

Fit a default linear model to the data.

```
mdl = fitlm(X,y)
```

```
mdl =


Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4
```

```
Estimated Coefficients:
                   Estimate      SE        tStat       pValue
                   ________    _______    ________    ________

    (Intercept)      62.405     70.071      0.8906     0.39913
    x1               1.5511    0.74477      2.0827    0.070822
    x2              0.51017    0.72379     0.70486      0.5009
    x3              0.10191    0.75471     0.13503     0.89592
    x4             -0.14406    0.70905    -0.20317     0.84407


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 2.45
R-squared: 0.982,  Adjusted R-Squared 0.974
F-statistic vs. constant model: 111, p-value = 4.76e-07
```

Linear Regression with Categorical Predictor and Nonlinear Model

Fit a model of a table that contains a categorical predictor. Use a nonlinear response formula.

Load the `carsmall` data.

```
load carsmall
```

Construct a table containing continuous predictor variable `Weight`, nominal predictor variable `Year`, and response variable `MPG`.

```
tbl = table(MPG,Weight);
tbl.Year = nominal(Model_Year);
```

Create a fitted model of `MPG` as a function of `Year`, `Weight`, and Weight^2. (You don't have to include `Weight` explicitly in your formula because it is a lower-order term of Weight^2.

```
mdl = fitlm(tbl,'MPG ~ Year + Weight^2')
```

```
mdl =

Linear regression model:
    MPG ~ 1 + Weight + Year + Weight^2

Estimated Coefficients:
                    Estimate      SE           tStat      pValue
    (Intercept)        54.206       4.7117     11.505    2.6648e-19
    Weight          -0.016404    0.0031249    -5.2493    1.0283e-06
    Year_76            2.0887      0.71491     2.9215     0.0044137
    Year_82            8.1864      0.81531     10.041    2.6364e-16
    Weight^2       1.5573e-06    4.9454e-07     3.149     0.0022303
```

```
Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 2.78
R-squared: 0.885,  Adjusted R-Squared 0.88
F-statistic vs. constant model: 172, p-value = 5.52e-41
```

`fitlm` creates two dummy (indicator) variables for the nominal variate, `Year`. The dummy variable `Year_76` takes the value 1 if model year is 1976 and takes the value 0 if it is not. The dummy variable `Year_82` takes the value 1 if model year is 1982 and takes the value 0 if it is not. And the year 1970 is the reference year. The corresponding model is

$$\hat{MPG} = 54.206 - 0.0164(Weight) + 2.0887(Year\_76) + 8.1864(Year\_82) + (1.557e-06)(Weight)^2$$

Simultaneously Specify the Variables and Use Formula

Simultaneously identify response and predictor variables and specify the model using formula in linear regression.

Load sample data.

```
load hospital
```

Fit a linear model with interaction terms to the data.

```
mdl = fitlm(hospital,'Weight~1+Age*Sex*Smoker-Age:Sex:Smoker','ResponseVar','Weight','F
```

```
mdl =


Linear regression model:
    Weight ~ 1 + Sex*Age + Sex*Smoker + Age*Smoker

Estimated Coefficients:
                        Estimate      SE        tStat        pValue
                        ________    _______    ________    __________

    (Intercept)            118.7     7.0718      16.785     6.821e-30
    Sex_Male               68.336    9.7153      7.0339     3.3386e-10
    Age                   0.31068    0.18531     1.6765      0.096991
    Smoker_1               3.0425     10.446    0.29127       0.77149
    Sex_Male:Age          -0.49094    0.24764    -1.9825      0.050377
    Sex_Male:Smoker_1      0.9509     3.8031    0.25003       0.80312
    Age:Smoker_1          -0.07288    0.26275   -0.27737       0.78211
```

```
Number of observations: 100, Error degrees of freedom: 93
Root Mean Squared Error: 8.75
R-squared: 0.898,  Adjusted R-Squared 0.892
F-statistic vs. constant model: 137, p-value = 6.91e-44
```

The weight of the patients do not seem to differ significantly according to age, or the status of smoking, or interaction of these factors with gender at the 5% significance level.

Robust Linear Regression Model

Fit a linear regression model of the Hald data using robust fitting.

Load the data.

```
load hald
X = ingredients; % predictor variables
y = heat; % response
```

Fit a robust linear model to the data.

```
mdl = fitlm(X,y,'linear','RobustOpts','on')
```

```
mdl =

Linear regression model (robust fit):
    y ~ 1 + x1 + x2 + x3 + x4

Estimated Coefficients:
                   Estimate    SE         tStat       pValue
    (Intercept)       60.09     75.818     0.79256      0.4509
    x1               1.5753    0.80585      1.9548    0.086346
    x2               0.5322    0.78315     0.67957     0.51596
    x3              0.13346     0.8166     0.16343     0.87424
    x4             -0.12052     0.7672    -0.15709     0.87906

Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 2.65
R-squared: 0.979,  Adjusted R-Squared 0.969
F-statistic vs. constant model: 94.6, p-value = 9.03e-07
```

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Predict or Simulate Responses to New Data” on page 9-37

- “Linear Regression Workflow” on page 9-41
- “Regression with Categorical Covariates” on page 2-58

Algorithms

The main fitting algorithm is QR decomposition. For robust fitting, the algorithm is `robustfit`.

Alternatives

You can also construct a linear model using `fitlm`.

You can construct a model in a range of possible models using `stepwiselm`. However, you cannot use robust regression and stepwise regression together.

See Also

`predict` | `stepwiselm` | `LinearModel`

How To

- “Linear Regression” on page 9-11

LinearMixedModel.fit

Class: LinearMixedModel

Fit linear mixed-effects model using tables

Compatibility

`LinearMixedModel.fit` will be removed in a future release. Use `fitlme` instead.

Syntax

```
lme = LinearMixedModel.fit(tbl,formula)
lme = LinearMixedModel.fit(tbl,formula,Name,Value)
```

Description

`lme = LinearMixedModel.fit(tbl,formula)` returns a linear mixed-effects model, specified by `formula`, fitted to the variables in the table or dataset array `tbl`.

`lme = LinearMixedModel.fit(tbl,formula,Name,Value)` returns a linear mixed-effects model with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the covariance pattern of the random-effects terms, the method to use in estimating the parameters, or options for the optimization algorithm.

Tips

- If your model is not easily described using a formula, you can create matrices to define the fixed and random effects, and fit the model using `fitlmematrix`.

Input Arguments

`tbl` — Input data

table | `dataset` array

Input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or `dataset` array. The predictor variables can be continuous or grouping variables (see "Grouping Variables" on page 2-52). You must specify the model for the variables using formula.

Data Types: `single | double | char | cell`

`formula` — Formula for model specification
string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`

Formula for model specification, specified as a string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`. For full description, see "Formula" on page 22-1465.

Example: `'y ~ treatment +(1|block)'`

Data Types: `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CovariancePattern'` — Pattern of covariance matrix
`'FullCholesky'` (default) | string | square symmetric logical matrix | cell array of strings or logical matrices

Pattern of the covariance matrix of the random effects, specified as the comma-separated pair consisting of `'CovariancePattern'` and a string, a square symmetric logical matrix, or a cell array of strings or logical matrices.

If there are R random-effects terms, then the value of `'CovariancePattern'` must be a cell array of length R, where each element r of this cell array specifies the pattern of the covariance matrix of the random-effects vector associated with the rth random-effects term. The options for each element follow.

`'FullCholesky'`	Default. Full covariance matrix using the Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.

`'Full'`	Full covariance matrix, using the log-Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.
`'Diagonal'`	Diagonal covariance matrix. That is, off-diagonal elements of the covariance matrix are constrained to be 0. $\begin{pmatrix} \sigma_{b1}^2 & 0 & 0 \\ 0 & \sigma_{b2}^2 & 0 \\ 0 & 0 & \sigma_{b3}^2 \end{pmatrix}$
`'Isotropic'`	Diagonal covariance matrix with equal variances. That is, off-diagonal elements of the covariance matrix are constrained to be 0, and the diagonal elements are constrained to be equal. For example, if there are three random-effects terms with an isotropic covariance structure, this covariance matrix looks like $\begin{pmatrix} \sigma_b^2 & 0 & 0 \\ 0 & \sigma_b^2 & 0 \\ 0 & 0 & \sigma_b^2 \end{pmatrix}$ where σ^2_b is the common variance of the random-effects terms.

`'CompSymm'`	Compound symmetry structure. That is, common variance along diagonals and equal correlation between all random effects. For example, if there are three random-effects terms with a covariance matrix having a compound symmetry structure, this covariance matrix looks like $\begin{pmatrix} \sigma_{b1}^2 & \sigma_{b1,b2} & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1}^2 & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1,b2} & \sigma_{b1}^2 \end{pmatrix}$ where σ^2_{b1} is the common variance of the random-effects terms and $\sigma_{b1,b2}$ is the common covariance between any two random-effects term .
`PAT`	Square symmetric logical matrix. If `'CovariancePattern'` is defined by the matrix `PAT`, and if `PAT(a,b) = false`, then the `(a,b)` element of the corresponding covariance matrix is constrained to be 0.

Example: `'CovariancePattern','Diagonal'`

Example: `'CovariancePattern',{'Full','Diagonal'}`

`'FitMethod'` — Method for estimating parameters

`'ML'` (default) | `'REML'`

Method for estimating parameters of the linear mixed-effects model, specified as the comma-separated pair consisting of `'FitMethod'` and either of the following.

`'ML'`	Default. Maximum likelihood estimation
`'REML'`	Restricted maximum likelihood estimation

Example: `'FitMethod','REML'`

'Weights' — Observation weights

vector of scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and a vector of length n, where n is the number of observations.

Data Types: single | double

'Exclude' — Indices for rows to exclude

use all rows without NaNs (default) | vector of integer or logical values

Indices for rows to exclude from the linear mixed-effects model in the data, specified as the comma-separated pair consisting of 'Exclude' and a vector of integer or logical values.

For example, you can exclude the 13th and 67th rows from the fit as follows.

Example: 'Exclude',[13,67]

Data Types: single | double | logical

'DummyVarCoding' — Coding to use for dummy variables

'reference' (default) | 'effects' | 'full'

Coding to use for dummy variables created from the categorical variables, specified as the comma-separated pair consisting of 'DummyVarCoding' and one of the following.

'reference'	Default. Coefficient for first category set to 0.
'effects'	Coefficients sum to 0.
'full'	One dummy variable for each category.

Example: 'DummyVarCoding','effects'

'Optimizer' — Optimization algorithm

'quasinewton' (default) | 'fminunc'

Optimization algorithm, specified as the comma-separated pair consisting of 'Optimizer' and either of the following.

'quasinewton'	Default. Uses a trust region based quasi-Newton optimizer. Change

	the options of the algorithm using `statset('LinearMixedModel')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `statset('LinearMixedModel')`.
`'fminunc'`	You must have Optimization Toolbox to specify this option. Change the options of the algorithm using `optimoptions('fminunc')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.

Example: `'Optimizer','fminunc'`

`'OptimizerOptions'` — Options for optimization algorithm
structure returned by `statset` | object returned by `optimoptions`

Options for the optimization algorithm, specified as the comma-separated pair consisting of `'OptimizerOptions'` and a structure returned by `statset('LinearMixedModel')` or an object returned by `optimoptions('fminunc')`.

- If `'Optimizer'` is `'fminunc'`, then use `optimoptions('fminunc')` to change the options of the optimization algorithm. See `optimoptions` for the options `'fminunc'` uses. If `'Optimizer'` is `'fminunc'` and you do not supply `'OptimizerOptions'`, then the default for `LinearMixedModel` is the default options created by `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.
- If `'Optimizer'` is `'quasinewton'`, then use `statset('LinearMixedModel')` to change the optimization parameters. If you don't change the optimization parameters, then `LinearMixedModel` uses the default options created by `statset('LinearMixedModel')`:

The `'quasinewton'` optimizer uses the following fields in the structure created by `statset('LinearMixedModel')`.

`'TolFun'` — Relative tolerance on gradient of objective function
`1e-6` (default) | positive scalar value

Relative tolerance on the gradient of the objective function, specified as a positive scalar value.

`'TolX'` — Absolute tolerance on step size
`1e-12` (default) | positive scalar value

Absolute tolerance on the step size, specified as a positive scalar value.

`'MaxIter'` — Maximum number of iterations allowed
`10000` (default) | positive scalar value

Maximum number of iterations allowed, specified as a positive scalar value.

`'Display'` — Level of display
`'off'` (default) | `'iter'` | `'final'`

Level of display, specified as one of `'off'`, `'iter'`, or `'final'`.

`'StartMethod'` — Method to start iterative optimization
`'default'` (default) | `'random'`

Method to start iterative optimization, specified as the comma-separated pair consisting of `'StartMethod'` and either of the following.

`'default'`	Default. An internally defined default value.
`'random'`	A random initial value.

Example: `'StartMethod','random'`

`'Verbose'` — Indicator to display optimization process on screen
`false` (default) | `true`

Indicator to display the optimization process on screen, specified as the comma-separated pair consisting of `'Verbose'` and either `false` or `true`. Default is `false`.

The setting for `'Verbose'` overrides the field `'Display'` in `'OptimizerOptions'`.

Example: `'Verbose',true`

`'CheckHessian'` — Indicator to check positive definiteness of Hessian
`false` (default) | `true`

Indicator to check the positive definiteness of the Hessian of the objective function with respect to unconstrained parameters at convergence, specified as the comma-separated pair consisting of `'CheckHessian'` and either `false` or `true`. Default is `false`.

Specify `'CheckHessian'` as `true` to verify optimality of the solution or to determine if the model is overparameterized in the number of covariance parameters.

Example: `'CheckHessian',true`

Output Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Examples

Random-Intercept Model

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables containing estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the CDC).

To fit a linear-mixed effects model, your data must be in a properly formatted dataset array. To fit a linear mixed-effects model with the influenza rates as the responses, combine the nine columns corresponding to the regions into a tall array. The new dataset array, `flu2`, must have the response variable `FluRate`, the nominal variable `Region` that shows which region each estimate is from, the nationwide estimate `WtdILI`, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Fit a linear mixed-effects model with the nationwide a random intercept that varies by `Date`. The model corresponds to

$$y_{im} = \beta_0 + \beta_1 WtdILI_{im} + b_{0m} + \varepsilon_{im}, \quad i = 1,2,\ldots,468, \quad m = 1,2,\ldots,52,$$

where y_{im} is the observation i for level m of grouping variable `Date`. b_{0m} is the random effect for level m of the grouping variable `Date` and ε_{im} is the observation error for observation i. The random effect has the prior distribution, $b \sim N(0,\sigma^2_b)$ and the error term has the distribution, $\varepsilon \sim N(0,\sigma^2)$.

```
lme = LinearMixedModel.fit(flu2,'FluRate ~ 1 + WtdILI + (1|Date)')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             468
    Fixed effects coefficients           2
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    FluRate ~ 1 + WtdILI + (1 | Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    286.24    302.83    -139.12          278.24

Fixed effects coefficients (95% CIs):
    Name                 Estimate    SE          tStat     DF     pValue         Lower
    '(Intercept)'         0.16385    0.057525    2.8484    466     0.0045885    0.0508
    'WtdILI'               0.7236    0.032219    22.459    466    3.0502e-76     0.660

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1                Name2                Type         Estimate    Lower      Upper
    '(Intercept)'        '(Intercept)'        'std'        0.17146     0.13227    0.222

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.30201     0.28217    0.32324
```

The confidence limits for the standard deviation of the random-effects term, σ^2_b, do not include 0 (0.13227, 0.22226), which indicates that the random-effects term is significant. You can also test the significance of the random-effects terms using the `compare` method.

The estimated value of an observation is the sum of the fixed effects and the random-effect value at the grouping variable level corresponding to that observation. For example, the estimated flu rate for observation 28 is

$$\begin{aligned}\hat{y}_{28} &= \hat{\beta}_0 + \hat{\beta}_1 WtdILI_{28} + \hat{b}_{10/30/2005} \\ &= 0.1639 + 0.7236 * (1.343) + 0.3318 \\ &= 1.46749,\end{aligned}$$

where $\hat{b}$ is the BLUP of the random effects for the intercept. You can compute this value in the following way.

```
beta = fixedEffects(lme);
[~,~,STATS] = randomEffects(lme); % Compute the random-effects statistics (STATS)
STATS.Level = nominal(STATS.Level);
y_hat = beta(1) + beta(2)*flu2.WtdILI(28) + STATS.Estimate(STATS.Level=='10/30/2005')
```

```
y_hat =

    1.4674
```

You can display the fitted value using the `fitted` method.

```
F = fitted(lme);
F(28)
```

```
ans =

    1.4674
```

Randomized-Block Design

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The dataset array shows the absolute deviations from the target quality characteristic measured from the products each of five operators manufacture over three different shifts, morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the absolute deviations of the quality characteristics from the target value. This is simulated data.

Fit a linear mixed-effects model with a random intercept grouped by operator, to assess if there is significant difference in the performance according to the time of the shift. Use the restricted maximum likelihood method and `'effects'` contrasts.

`'effects'` contrasts mean that the coefficients sum to 0, and `LinearMixedModel.fit` creates a matrix called a 'fixed effects design matrix' to describe the effect of Shift. This matrix has two columns, *Shift_Evening* and *Shift_Morning*, where

$$Shift\_Evening = \begin{cases} 0, & if\ Morning \\ 1, & if\ Evening \\ -1, & if\ Night \end{cases} \quad and \quad Shift\_Morning = \begin{cases} 1, & if\ Morning \\ 0, & if\ Evening \\ -1, & if\ Night \end{cases}.$$

The model corresponds to

$$\begin{aligned} &\text{Morning Shift: } QCDev_{im} = \beta_0 + \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \quad m = 1,2,\ldots,5, \\ &\text{Evening Shift: } QCDev_{im} = \beta_0 + \beta_1 Shift\_Evening_i + b_{0m} + \varepsilon_{im}, \\ &\text{Night Shift: } \quad QCDev_{im} = \beta_0 - \beta_1 Shift\_Evening_i - \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \end{aligned}$$

where $b \sim N(0,\sigma^2_b)$ and $\varepsilon \sim N(0,\sigma^2)$.

```
lme = LinearMixedModel.fit(shift,'QCDev ~ Shift + (1|Operator)',...
'FitMethod','REML','DummyVarCoding','effects')
```

```
lme =


Linear mixed-effects model fit by REML

Model information:
    Number of observations             15
    Fixed effects coefficients          3
    Random effects coefficients         5
    Covariance parameters               2

Formula:
```

```
    QCDev ~ 1 + Shift + (1 | Operator)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    58.913    61.337    -24.456          48.913

Fixed effects coefficients (95% CIs):
    Name                  Estimate    SE         tStat      DF    pValue       Lower
    '(Intercept)'           3.6525    0.94109     3.8812    12    0.0021832     1.602
    'Shift_Evening'        -0.53293   0.31206    -1.7078    12      0.11339    -1.212
    'Shift_Morning'        -0.91973   0.31206    -2.9473    12     0.012206    -1.599

Random effects covariance parameters (95% CIs):
Group: Operator (5 Levels)
    Name1               Name2               Type         Estimate    Lower      Upper
    '(Intercept)'       '(Intercept)'       'std'        2.0457      0.98207    4.261

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.85462     0.52357    1.395
```

Compute the best linear unbiased predictor (BLUP) estimates of random effects.

```
B = randomEffects(lme)
```

```
B =

    0.5775
    1.1757
   -2.1715
    2.3655
   -1.9472
```

The estimated absolute deviation from the target quality characteristics for the third operator working in the evening shift is

$$\begin{aligned}\hat{y}_{Evening,Operator3} &= \hat{\beta}_0 + \hat{\beta}_1 Shift\_Evening + \hat{b}_{03} \\ &= 3.6525 - 0.53293 - 2.1715 \\ &= 0.94807.\end{aligned}$$

You can also display this value as follows.

```
F = fitted(lme);
F(shift.Shift=='Evening' & shift.Operator=='3')
```

```
ans =

    0.9481
```

Similarly, you can calculate the estimated absolute deviation from the target quality characteristics for the third operator working in the morning shift is

$$\begin{aligned}\hat{y}_{Morning,Operator3} &= \hat{\beta}_0 + \hat{\beta}_2 Shift\_Morning + \hat{b}_{03} \\ &= 3.6525 - 0.91973 - 2.1715 \\ &= 0.56127.\end{aligned}$$

You can also display this value in the following way.

```
F(shift.Shift=='Morning' & shift.Operator=='3')
```

```
ans =

    0.5613
```

The operator tends to make a smaller magnitude of error in the morning shift.

Split-Plot Experiment

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five types of tomato plants, (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. Then, the tomato plants in the plots are divided into subplots, where each subplot is treated by one of the four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
```

```
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type) and the plots within blocks (tomato types within soil types) independently.

This model corresponds to

$$y_{imjk} = \beta_0 + \sum_{m=2}^{4} \beta_{1m} I[F]_{im} + \sum_{j=2}^{5} \beta_{2j} I[T]_{ij} + \sum_{j=2}^{5}\sum_{m=2}^{4} \beta_{3mj} I[F]_{im}\, I[T]_{ij} + b_{0k} S_k + b_{0jk} (S*T)_{jk} + \varepsilon_{imjk},$$

where $i = 1, 2, ..., 60$, the index m corresponds to the fertilizer types, j corresponds to the tomato types, and $k = 1, 2, 3$ corresponds to the blocks (soil). S_k represents the kth soil type, and $(S*T)_{jk}$ represents the jth tomato type nested in the kth soil type. $I[F]_{im}$ is the dummy variable representing level m of the fertilizer. Similarly, $I[T]_{ij}$ is the dummy variable representing the level j of the tomato type.

The random effects and observation error have the following prior distributions: $b_{0k} \sim N(0,\sigma^2_S)$, $b_{0jk} \sim N(0,\sigma^2_{S*T})$, and $\varepsilon_{imjk} \sim N(0,\sigma^2)$.

```
lme = LinearMixedModel.fit(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             60
    Fixed effects coefficients         20
    Random effects coefficients        18
    Covariance parameters               3

Formula:
    Yield ~ 1 + Tomato*Fertilizer + (1 | Soil) + (1 | Soil:Tomato)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    522.57    570.74    -238.29          476.57

Fixed effects coefficients (95% CIs):
```

```
    Name                                Estimate    SE        tStat       DF    pValu
    '(Intercept)'                            77     8.5836      8.9706    40    4.020
    'Tomato_Grape'                          -16     11.966     -1.3371    40       0
    'Tomato_Heirloom'                    -6.6667    11.966    -0.55714    40       0
    'Tomato_Plum'                         32.333    11.966      2.7022    40     0.0
    'Tomato_Vine'                           -13     11.966     -1.0864    40       0
    'Fertilizer_2'                        34.667     8.572      4.0442    40   0.000
    'Fertilizer_3'                        33.667     8.572      3.9275    40   0.000
    'Fertilizer_4'                        47.667     8.572      5.5607    40   1.956
    'Tomato_Grape:Fertilizer_2'          -2.6667    12.123    -0.21997    40       0
    'Tomato_Heirloom:Fertilizer_2'            -8    12.123    -0.65992    40       0
    'Tomato_Plum:Fertilizer_2'              -15     12.123     -1.2374    40       0
    'Tomato_Vine:Fertilizer_2'              -16     12.123     -1.3198    40       0
    'Tomato_Grape:Fertilizer_3'           16.667    12.123      1.3748    40       0
    'Tomato_Heirloom:Fertilizer_3'        3.3333    12.123     0.27497    40       0
    'Tomato_Plum:Fertilizer_3'            3.6667    12.123     0.30246    40       0
    'Tomato_Vine:Fertilizer_3'                 3    12.123     0.24747    40       0
    'Tomato_Grape:Fertilizer_4'           13.333    12.123      1.0999    40       0
    'Tomato_Heirloom:Fertilizer_4'          -19     12.123     -1.5673    40       0
    'Tomato_Plum:Fertilizer_4'           -2.6667    12.123    -0.21997    40       0
    'Tomato_Vine:Fertilizer_4'            8.6667    12.123     0.71492    40       0

Random effects covariance parameters (95% CIs):
Group: Soil (3 Levels)
    Name1               Name2               Type         Estimate    Lower      Upper
    '(Intercept)'       '(Intercept)'       'std'        2.5028      0.02771    226.0

Group: Soil:Tomato (15 Levels)
    Name1               Name2               Type         Estimate    Lower     Upper
    '(Intercept)'       '(Intercept)'       'std'        10.225      6.1497    17.001

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        10.499      8.5389    12.908
```

The p-values corresponding to the last 12 rows in the fixed-effects coefficients display (0.82701 to 0.47881) indicate that interaction coefficients between the tomato and fertilizer types are not significant. To test for the overall interaction between tomato and fertilizer, use the `anova` method after refitting the model using `'effects'` contrasts.

The confidence interval for the standard deviations of the random-effects terms (σ^2_S), where the intercept is grouped by soil is very large. This term does not appear significant.

Refit the model after removing the interaction term `Tomato:Fertilizer` and the random-effects term `(1 | Soil)`.

```
lme = LinearMixedModel.fit(ds,'Yield ~ Fertilizer + Tomato + (1|Soil:Tomato)')

lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             60
    Fixed effects coefficients          8
    Random effects coefficients        15
    Covariance parameters               2

Formula:
    Yield ~ 1 + Tomato + Fertilizer + (1 | Soil:Tomato)

Model fit statistics:
    AIC       BIC    LogLikelihood    Deviance
    511.06    532    -245.53          491.06

Fixed effects coefficients (95% CIs):
    Name                    Estimate    SE        tStat       DF    pValue        Lowe
    '(Intercept)'            77.733     7.3293      10.606    52    1.3108e-14     63.
    'Tomato_Grape'          -9.1667     9.6045    -0.95441    52       0.34429    -28.
    'Tomato_Heirloom'       -12.583     9.6045     -1.3102    52        0.1959    -31.
    'Tomato_Plum'            28.833     9.6045      3.0021    52     0.0041138     9.5
    'Tomato_Vine'           -14.083     9.6045     -1.4663    52       0.14858    -33.
    'Fertilizer_2'           26.333     4.5004      5.8514    52    3.3024e-07     17.
    'Fertilizer_3'               39     4.5004      8.6659    52    1.1459e-11     29.
    'Fertilizer_4'           47.733     4.5004      10.607    52     1.308e-14     38.

Random effects covariance parameters (95% CIs):
Group: Soil:Tomato (15 Levels)
    Name1               Name2               Type         Estimate    Lower     Upper
    '(Intercept)'       '(Intercept)'       'std'        10.02       6.0812    16.509

Group: Error
    Name            Estimate    Lower     Upper
    'Res Std'       12.325      10.024    15.153
```

You can compare the two models using the `compare` method with the simulated likelihood ratio test since both a fixed-effect and a random-effect term will be tested.

Longitudinal Study with a Covariate

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs (A, B, C, D), and their weight loss is recorded over six two-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

`LinearMixedModel.fit` uses Program A as a reference and creates the necessary dummy variables $I[.]$. Since the model already has an intercept, `LinearMixedModel.fit` only creates dummy variables for program types B, C, D. This is also known as the `'reference'` method of coding dummy variables. This model corresponds to

$$\begin{aligned} y_{im} &= \beta_0 + \beta_1 IW_i + \beta_2 Week_i + \beta_3 I[PB]_i + \beta_4 I[PC]_i + \beta_5 I[PD]_i \\ &\quad + \beta_6 \left(Week_i * I[PB]_i \right) + \beta_7 \left(Week_i * I[PC]_i \right) + \beta_8 \left(Week_i * I[PD]_i \right) \\ &\quad + b_{0m} + b_{1m} Week_{im} + \varepsilon_{im}, \end{aligned}$$

where $i = 1, 2, ..., 120$, and $m = 1, 2, ..., 20$. β_j are the fixed-effects coefficients, $j = 0, 1, ...,8$, and b_{1m} and b_{1m} are random effects. IW stands for initial weight and I[.] is a

dummy variable representing a type of program. For example, $I[PB]_i$ is the dummy variable representing program type B. The random effects and observation error have the following prior distributions: b_{0m}~N(0,σ^2_0), b_{1m}~N(0,σ^2_1), and ε_{im} ~ N(0,σ^2).

```
lme = LinearMixedModel.fit(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           9
    Random effects coefficients         40
    Covariance parameters                4

Formula:
    Linear Mixed Formula with 4 predictors.

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -22.981    13.257    24.49            -48.981

Fixed effects coefficients (95% CIs):
    Name                    Estimate     SE           tStat
    '(Intercept)'             0.66105      0.25892      2.5531
    'InitialWeight'         0.0031879    0.0013814      2.3078
    'Program_B'               0.36079      0.13139       2.746
    'Program_C'             -0.033263      0.13117    -0.25358
    'Program_D'               0.11317      0.13132     0.86175
    'Week'                     0.1732     0.067454      2.5677
    'Program_B:Week'         0.038771     0.095394     0.40644
    'Program_C:Week'         0.030543     0.095394     0.32018
    'Program_D:Week'         0.033114     0.095394     0.34713


    DF     pValue       Lower         Upper
    111     0.012034       0.14798       1.1741
    111     0.022863    0.00045067    0.0059252
    111    0.0070394       0.10044      0.62113
    111      0.80029      -0.29319      0.22666
    111      0.39068      -0.14706       0.3734
    111     0.011567      0.039536      0.30686
```

```
    111      0.68521      -0.15026       0.2278
    111      0.74944      -0.15849      0.21957
    111      0.72915      -0.15592      0.22214

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1               Name2               Type
    '(Intercept)'       '(Intercept)'       'std'
    'Week'              '(Intercept)'       'corr'
    'Week'              'Week'              'std'


    Estimate    Lower      Upper
    0.18407     0.12281    0.27587
    0.66841     0.21076    0.88573
    0.15033     0.11004    0.20537

Group: Error
    Name            Estimate    Lower       Upper
    'Res Std'       0.10261     0.087882    0.11981
```

The p-values 0.022863 and 0.011567 indicate significant effects of subject initial weights and time in the amount of weight lost. The weight loss of subjects who are in Program B is significantly different relative to the weight loss of subjects who are in Program A. The lower and upper limits of the covariance parameters for the random effects do not include 0, thus they are significant. You can also test the significance of the random effects using the `compare` method.

Definitions

Formula

In general, a formula for model specification is a string of the form `'y ~ terms'`. For the linear mixed-effects models, this formula is in the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` and `random` contain the fixed-effects and the random-effects terms.

Suppose a table `tbl` contains the following:

- A response variable, `y`
- Predictor variables, X_j, which can be continuous or grouping variables

- Grouping variables, g_1, g_2, ..., g_R,

where the grouping variables in X_j and g_r can be categorical, logical, character arrays, or cell arrays of strings.

Then, in a formula of the form, `'y ~ fixed + (random`$_1$`|g`$_1$`) + ... + (random`$_R$`|g`$_R$`)'`, the term `fixed` corresponds to a specification of the fixed-effects design matrix `X`, `random`$_1$ is a specification of the random-effects design matrix Z_1 corresponding to grouping variable g_1, and similarly `random`$_R$ is a specification of the random-effects design matrix Z_R corresponding to grouping variable g_R. You can express the `fixed` and `random` terms using Wilkinson notation.

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1.*X2 (elementwise multiplication of X1 and X2)`
`X1:X2`	`X1.*X2` only
`- X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`. Here are some examples for linear mixed-effects model specification.

Examples:

Formula	Description
`'y ~ X1 + X2'`	Fixed effects for the intercept, `X1` and `X2`. This is equivalent to `'y ~ 1 + X1 + X2'`.

Formula	Description
`'y ~ -1 + X1 + X2'`	No intercept and fixed effects for `X1` and `X2`. The implicit intercept term is suppressed by including `-1`.
`'y ~ 1 + (1 | g1)'`	Fixed effects for the intercept plus random effect for the intercept for each level of the grouping variable `g1`.
`'y ~ X1 + (1 | g1)'`	Random intercept model with a fixed slope.
`'y ~ X1 + (X1 | g1)'`	Random intercept and slope, with possible correlation between them. This is equivalent to `'y ~ 1 + X1 + (1 + X1| g1)'`.
`'y ~ X1 + (1 | g1) + (-1 + X1 | g1)'`	Independent random effects terms for intercept and slope.
`'y ~ 1 + (1 | g1) + (1 | g2) + (1 | g1:g2)'`	Random intercept model with independent main effects for `g1` and `g2`, plus an independent interaction effect.

Cholesky Parameterization

One of the assumptions of linear mixed-effects models is that the random effects have the following prior distribution.

$$b \sim N\left(0,\sigma^2 D(\theta)\right),$$

where D is a q-by-q symmetric and positive semidefinite matrix, parameterized by a variance component vector θ, q is the number of variables in the random-effects term, and σ^2 is the observation error variance. Since the covariance matrix of the random effects, D, is symmetric, it has $q(q+1)/2$ free parameters. Suppose L is the lower triangular Cholesky factor of $D(\theta)$ such that

$$D(\theta) = L(\theta)L(\theta)^T,$$

then the $q*(q+1)/2$-by-1 unconstrained parameter vector θ is formed from elements in the lower triangular part of L.

For example, if

$$L = \begin{bmatrix} L_{11} & 0 & 0 \\ L_{21} & L_{22} & 0 \\ L_{31} & L_{32} & L_{33} \end{bmatrix},$$

then

$$\theta = \begin{bmatrix} L_{11} \\ L_{21} \\ L_{31} \\ L_{22} \\ L_{32} \\ L_{33} \end{bmatrix}.$$

Log-Cholesky Parameterization

When the diagonal elements of L in Cholesky parameterization are constrained to be positive, then the solution for L is unique. Log-Cholesky parameterization is the same as Cholesky parameterization except that the logarithm of the diagonal elements of L are used to guarantee unique parameterization.

For example, for the 3-by-3 example in Cholesky parameterization, enforcing $L_{ii} \geq 0$,

$$\theta = \begin{bmatrix} \log(L_{11}) \\ L_{21} \\ L_{31} \\ \log(L_{22}) \\ L_{32} \\ \log(L_{33}) \end{bmatrix}.$$

Alternatives

You can also construct a linear mixed-effects model using `fitlme`. If your data is in matrix format, then use `fitlmematrix`.

See Also

`LinearMixedModel` | `anova` | `compare` | `fitlme` | `fitlmematrix`

fit

Class: NaiveBayes

Create Naive Bayes classifier object by fitting training data

Syntax

```
nb = NaiveBayes.fit(training, class)
nb = NaiveBayes.fit(..., 'param1',val1, 'param2',val2, ...)
```

Note: `fit` will be removed in a future release. Use `fitNaiveBayes` instead.

Description

`nb = NaiveBayes.fit(training, class)` builds a `NaiveBayes` classifier object `nb`. `training` is an `N`-by-`D` numeric matrix of training data. Rows of `training` correspond to observations; columns correspond to features. `class` is a classing variable for `training` taking `K` distinct levels. Each element of `class` defines which class the corresponding row of `training` belongs to. `training` and `class` must have the same number of rows.

`nb = NaiveBayes.fit(..., 'param1',val1, 'param2',val2, ...)` specifies one or more of the following name/value pairs:

- `'Distribution'` – a string or a 1-by-`D` cell vector of strings, specifying which distributions `fit` uses to model the data. If the value is a string, `fit` models all the features using one type of distribution. `fit` can also model different features using different types of distributions. If the value is a cell vector, its `j`th element specifies the distribution `fit` uses for the `j`th feature. The available types of distributions are:

`'normal'` (default)	Normal (Gaussian) distribution.
`'kernel'`	Kernel smoothing density estimate.
`'mvmn'`	Multivariate multinomial distribution for discrete data. `fit` assumes each individual feature follows a multinomial model within a class. The parameters for a feature include

	the probabilities of all possible values that the corresponding feature can take.
`'mn'`	Multinomial distribution for classifying the count-based data such as the bag-of-tokens model. In the bag-of-tokens model, the value of the `j`th feature is the number of occurrences of the `j`th token in this observation, so it must be a nonnegative integer. When `'mn'` is used, `fit` considers each observation as multiple trials of a multinomial distribution, and considers each occurrence of a token as one trial. The number of categories (bins) in this multinomial model is the number of distinct tokens, i.e., the number of columns of `training`. If you specify `mn`, then all features are components of a multinomial distribution. Therefore, you cannot include `'mn'` as an element of a cell array of strings.

- `'Prior'` – The prior probabilities for the classes, specified as one of the following:

`'empirical'` (default)	`fit` estimates the prior probabilities from the relative frequencies of the classes in `training`.
`'uniform'`	The prior probabilities are equal for all classes.
vector	A numeric vector of length `K` specifying the prior probabilities in the class order of `class`.
structure	A structure `S` containing class levels and their prior probabilities. `S` must have two fields: • `S.prob`: A numeric vector of prior probabilities. • S.class: A vector of the same type as `class`, containing unique class levels indicating the class for the corresponding element of prob. `S.class` must contain all the `K` levels in `class`. It can also contain classes that do not appear in `class`. This can be useful if `training` is a subset of a larger training set. `fit` ignores any classes that appear in `S.class` but not in `class`.

  If the prior probabilities don't sum to one, `fit` will normalize them.

- `'KSWidth'` – The bandwidth of the kernel smoothing window. The default is to select a default bandwidth automatically for each combination of feature and class, using a

value that is optimal for a Gaussian distribution. You can specify the value as one of the following:

scalar	Width for all features in all classes.
row vector	1-by-`D` vector where the `j`th element is the bandwidth for the `j`th feature in all classes.
column vector	`K`-by-1 vector where the `i`th element specifies the bandwidth for all features in the `i`th class. `K` represents the number of class levels.
matrix	`K`-by-`D` matrix `M` where `M(i,j)` specifies the bandwidth for the `j`th feature in the `i`th class.
structure	A structure `S` containing class levels and their bandwidths. `S` must have two fields: • `S.width` – A numeric array of bandwidths specified as a row vector, or a matrix with `D` columns. • `S.class` – A vector of the same type as `class`, containing unique class levels indicating the class for the corresponding row of width.

- `'KSSupport'` – The regions where the density can be applied. It can be a string, a two-element vector as shown below, or a 1-by-`D` cell array of these values:

`'unbounded'` (default)	The density can extend over the whole real line.
`'positive'`	The density is restricted to positive values.
`[L,U]`	A two-element vector specifying the finite lower bound `L` and upper bound `U` for the support of the density.

- `'KSType'` – The type of kernel smoother to use. It can be a string or a 1-by-`D` cell array of strings. Each string can be `'normal'` (default), `'box'`, `'triangle'`, or `'epanechnikov'`.

How To

- “Naive Bayes Classification” on page 15-31
- “Grouping Variables” on page 2-52

NonLinearModel.fit

Class: NonLinearModel

Fit nonlinear regression model

Compatibility

`NonLinearModel.fit` will be removed in a future release. Use `fitnlm` instead.

Syntax

```
mdl = NonLinearModel.fit(tbl,modelfun,beta0)
mdl = NonLinearModel.fit(X,y,modelfun,beta0)
mdl = NonLinearModel.fit(...,modelfun,beta0,Name,Value)
```

Description

`mdl = NonLinearModel.fit(tbl,modelfun,beta0)` fits the model specified by `modelfun` to variables in the table or dataset array `tbl`, and returns the nonlinear model `mdl`. `NonLinearModel.fit` estimates model coefficients using an iterative procedure starting from the initial values in `beta0`.

`mdl = NonLinearModel.fit(X,y,modelfun,beta0)` fits a nonlinear regression model using the column vector `y` as a response variable and the columns of the matrix `X` as predictor variables.

`mdl = NonLinearModel.fit(...,modelfun,beta0,Name,Value)` fits a nonlinear regression model with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. If you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables and response variable must be numeric.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single | double | logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single | double | logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single | double`

`modelfun` — Functional form of the model

function handle | string of the form `'y ~ f(b1,b2,...,bj,x1,x2,...,xk)'`

Functional form of the model, specified as either of the following.

- Function handle `@modelfun` or `@(b,x)modelfun`, where
  - `b` is a coefficient vector with the same number of elements as `beta0`.
  - `x` is a matrix with the same number of columns as `X` or the number of predictor variable columns of `tbl`.

modelfun(b,x) returns a column vector that contains the same number of rows as x. Each row of the vector is the result of evaluating *modelfun* on the corresponding row of x. In other words, *modelfun* is a vectorized function, one that operates on all data rows and returns all evaluations in one function call. *modelfun* should return real numbers to obtain meaningful coefficients.

- String of the form '*y* ~ *f*(b1,b2,...,bj,x1,x2,...,xk)', where *f* represents a scalar function of the scalar coefficient variables b1,...,bj and the scalar data variables x1,...,xk.

beta0 — Coefficients

numeric vector

Coefficients for the nonlinear model, specified as a numeric vector. NonLinearModel starts its search for optimal coefficients from beta0.

Data Types: single | double

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. Name is the argument name and Value is the corresponding value. Name must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as Name1,Value1,...,NameN,ValueN.

'CoefficientNames' — Names of the model coefficients

{'b1','b2',...,'b*k*'} (default) | cell array of strings

Names of the model coefficients, specified as a cell array of strings.

Data Types: char

'ErrorModel' — Form of the error variance model

'constant' (default) | 'proportional' | 'combined'

Form of the error variance model, specified as one of the following. Each model defines the error using a standard mean-zero and unit-variance variable e in combination with independent components: the function value f, and one or two parameters a and b

'constant' (default) $y = f + ae$

`'proportional'`	$y = f + bfe$
`'combined'`	$y = f + \left(a + b\left\|f\right\|\right)e$

The only allowed error model when using Weights is `'constant'`.

Note: `options.RobustWgtFun` must have value `[]` when using an error model other than `'constant'`.

Example: `'ErrorModel','proportional'`

`'ErrorParameters'` — Initial estimates of the error model parameters

numeric array

Initial estimates of the error model parameters for the chosen ErrorModel, specified as a numeric array.

Error Model	Parameters	Default Values
`'constant'`	a	1
`'proportional'`	b	1
`'combined'`	a, b	`[1,1]`

You can only use the `'constant'` error model when using Weights.

Note: `options.RobustWgtFun` must have value `[]` when using an error model other than `'constant'`.

For example, if `'ErrorModel'` has the value `'combined'`, you can specify the starting value 1 for a and the starting value 2 for b as follows.

Example: `'ErrorParameters',[1,2]`

Data Types: `char`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Options'` — Options for controlling the iterative fitting procedure

[ ] (default) | structure

Options for controlling the iterative fitting procedure, specified as a structure created by `statset`. The relevant fields are the nonempty fields in the structure returned by the call `statset('nlinfit')`.

Option	Meaning	Default
`DerivStep`	Relative difference used in finite difference derivative calculations. A positive scalar, or a vector of positive scalars the same size as the vector of parameters estimated by the Statistics and Machine Learning Toolbox function using the options structure.	`eps^(1/3)`
`Display`	Amount of information displayed by the fitting algorithm. • `'off'` — Displays no information. • `'final'` — Displays the final output. • `'iter'` — Displays iterative output to the Command Window.	`'off'`
`FunValCheck`	String indicating to check for invalid values, such as `NaN` or `Inf`, from the model function.	`'on'`
`MaxIter`	Maximum number of iterations allowed. Positive integer.	`200`
`RobustWgtFun`	Weight function for robust fitting. Can also be a function handle that accepts a normalized residual	`[]`

Option	Meaning	Default
	as input and returns the robust weights as output. If you use a function handle, give a `Tune` constant. See "Robust Options" on page 22-1820	
`Tune`	Tuning constant used in robust fitting to normalize the residuals before applying the weight function. A positive scalar. Required if the weight function is specified as a function handle.	See "Robust Options" on page 22-1820 for the default, which depends on `RobustWgtFun`.
`TolFun`	Termination tolerance for the objective function value. Positive scalar.	`1e-8`
`TolX`	Termination tolerance for the parameters. Positive scalar.	`1e-8`

Data Types: `struct`

`'PredictorVars'` — Predictor variables
cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

`'ResponseVar'` — Response variable
last column in `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset array `tbl`, or a logical or numeric index vector indicating which column is the response variable. You typically need to use `'ResponseVar'` when fitting a table or dataset array `tbl`.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

`'VarNames'` — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights

`ones(n,1)` (default) | vector of nonnegative scalar values | function handle

Observation weights, specified as a vector of nonnegative scalar values or function handle.

- If you specify a vector, then it must have n elements, where n is the number of rows in `tbl` or `y`.
- If you specify a function handle, then the function must accept a vector of predicted response values as input, and return a vector of real positive weights as output.

Given weights, `W`, `NonLinearModel` estimates the error variance at observation `i` by `MSE*(1/W(i))`, where MSE is the mean squared error.

Data Types: `single` | `double` | `function_handle`

Output Arguments

`mdl` — Nonlinear model

`NonLinearModel` object

Nonlinear model representing a least-squares fit of the response to the data, returned as a `NonLinearModel` object.

If the `Options` structure contains a nonempty `RobustWgtFun` field, the model is not a least-squares fit, but uses the `RobustWgtFun` robust fitting function.

For properties and methods of the nonlinear model object, `mdl`, see the `NonLinearModel` class page.

Definitions

Robust Options

Weight Function	Equation	Default Tuning Constant
`'andrews'`	`w = (abs(r)<pi) .* sin(r) ./ r`	1.339
`'bisquare'` (default)	`w = (abs(r)<1) .* (1 - r.^2).^2`	4.685
`'cauchy'`	`w = 1 ./ (1 + r.^2)`	2.385
`'fair'`	`w = 1 ./ (1 + abs(r))`	1.400
`'huber'`	`w = 1 ./ max(1, abs(r))`	1.345
`'logistic'`	`w = tanh(r) ./ r`	1.205
`'talwar'`	`w = 1 * (abs(r)<1)`	2.795
`'welsch'`	`w = exp(-(r.^2))`	2.985
`[]`	No robust fitting	—

Examples

Nonlinear Model from a Table

Create a nonlinear model for auto mileage based on the `carbig` data.

Load the data and create a nonlinear model.

```
load carbig
tbl = table(Horsepower,Weight,MPG);
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
mdl = NonLinearModel.fit(tbl,modelfun,beta0)
```

```
mdl =


Nonlinear regression model:
    MPG ~ b1 + b2*Horsepower^b3 + b4*Weight^b5

Estimated Coefficients:
          Estimate      SE        tStat       pValue
          ________    _______    ________    ________

    b1      -49.383     119.97    -0.41164     0.68083
    b2       376.43     567.05     0.66384     0.50719
    b3     -0.78193    0.47168     -1.6578    0.098177
    b4       422.37     776.02     0.54428     0.58656
    b5     -0.24127    0.48325    -0.49926     0.61788


Number of observations: 392, Error degrees of freedom: 387
Root Mean Squared Error: 3.96
R-Squared: 0.745,  Adjusted R-Squared 0.743
F-statistic vs. constant model: 283, p-value = 1.79e-113
```

Nonlinear Model from Matrix Data

Create a nonlinear model for auto mileage based on the `carbig` data.

Load the data and create a nonlinear model.

```
load carbig
X = [Horsepower,Weight];
```

```
y = MPG;
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
mdl = NonLinearModel.fit(X,y,modelfun,beta0)

mdl =


Nonlinear regression model:
    y ~ b1 + b2*x1^b3 + b4*x2^b5

Estimated Coefficients:
          Estimate    SE         tStat       pValue
    b1     -49.383     119.97    -0.41164     0.68083
    b2      376.43     567.05     0.66384     0.50719
    b3    -0.78193    0.47168     -1.6578    0.098177
    b4      422.37     776.02     0.54428     0.58656
    b5    -0.24127    0.48325    -0.49926     0.61788


Number of observations: 392, Error degrees of freedom: 387
Root Mean Squared Error: 3.96
R-Squared: 0.745,  Adjusted R-Squared 0.743
F-statistic vs. constant model: 283, p-value = 1.79e-113
```

Adjust Fitting Options in the Nonlinear Model

Create a nonlinear model for auto mileage based on the `carbig` data. Strive for more accuracy by lowering the `TolFun` option, and observe the iterations by setting the `Display` option.

Load the data and create a nonlinear model.

```
load carbig
X = [Horsepower,Weight];
y = MPG;
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
```

Create options to lower `TolFun` and to report iterative display, and create a model using the options.

```
opts = statset('Display','iter','TolFun',1e-10);
```

```
mdl = NonLinearModel.fit(X,y,modelfun,beta0,'Options',opts);
```

```
                                  Norm of         Norm of
   Iteration            SSE       Gradient           Step
  -----------------------------------------------------------
           0     1.82248e+06
           1          678600          788810         1691.07
           2          616716     6.12739e+06         45.4738

%%%     Many iterations deleted   %%%

         122         6068.48         1.56393        0.629325
         123         6068.48         1.13809        0.432543
         124         6068.48        0.295962        0.297511
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
```

Specify Nonlinear Regression Using Model String Syntax

Specify a nonlinear regression model for estimation using a function handle or model string syntax.

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Use a function handle to specify the Hougen-Watson model for the rate data.

```
mdl = NonLinearModel.fit(X,y,@hougen,beta0)
```

```
mdl =


Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1      1.2526     0.86701    1.4447    0.18654
    b2    0.062776    0.043561    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075157    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.193
```

```
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 3.91e+03, p-value = 2.54e-13
```

Alternatively, you can use a string expression to specify the Hougen-Watson model for the rate data.

```
myfun = 'y~(b1*x2-x3/b5)/(1+b2*x1+b3*x2+b4*x3)';
mdl2 = NonLinearModel.fit(X,y,myfun,beta0)
```

```
mdl2 =


Nonlinear regression model:
    y ~ (b1*x2 - x3/b5)/(1 + b2*x1 + b3*x2 + b4*x3)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1      1.2526     0.86701    1.4447    0.18654
    b2    0.062776    0.043561    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075157    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.193
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 3.91e+03, p-value = 2.54e-13
```

Estimate Nonlinear Regression Using Robust Fitting Options

Generate sample data from the nonlinear regression model

$$y = b_1 + b_2 \exp\{-b_3 x\} + \varepsilon,$$

where b_1, b_2, and b_3 are coefficients, and the error term is normally distributed with mean 0 and standard deviation 0.5.

```
modelfun = @(b,x)(b(1)+b(2)*exp(-b(3)*x));

rng('default') % for reproducibility
b = [1;3;2];
x = exprnd(2,100,1);
y = modelfun(b,x) + normrnd(0,0.5,100,1);
```

Set robust fitting options.

```
opts = statset('nlinfit');
opts.RobustWgtFun = 'bisquare';
```

Fit the nonlinear model using the robust fitting options. Here, use a string expression to specify the model.

```
b0 = [2;2;2];
modelstr = 'y ~ b1 + b2*exp(-b3*x)';

mdl = NonLinearModel.fit(x,y,modelstr,b0,'Options',opts)
```

```
mdl =


Nonlinear regression model (robust fit):
    y ~ b1 + b2*exp( - b3*x)

Estimated Coefficients:
          Estimate    SE         tStat     pValue
    b1    1.0218      0.07202    14.188    2.1344e-25
    b2    3.6619      0.25429    14.401     7.974e-26
    b3    2.9732      0.38496    7.7232    1.0346e-11


Number of observations: 100, Error degrees of freedom: 97
Root Mean Squared Error: 0.501
R-Squared: 0.807,  Adjusted R-Squared 0.803
F-statistic vs. constant model: 203, p-value = 2.34e-35
```

Fit Nonlinear Regression Model Using Weights Function Handle

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Specify a function handle for observation weights. The function accepts the model fitted values as input, and returns a vector of weights.

```
a = 1; b = 1;
weights = @(yhat) 1./((a + b*abs(yhat)).^2);
```

Fit the Hougen-Watson model to the rate data using the specified observation weights function.

```
mdl = NonLinearModel.fit(X,y,@hougen,beta0,'Weights',weights)
```

```
mdl =


Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1     0.83085     0.58224     1.427    0.19142
    b2     0.04095    0.029663    1.3805    0.20477
    b3    0.025063    0.019673     1.274    0.23842
    b4    0.080053    0.057812    1.3847    0.20353
    b5      1.8261       1.281    1.4256    0.19183


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.037
R-Squared: 0.998,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 1.14e+03, p-value = 3.49e-11
```

Nonlinear Regression Model Using Nonconstant Error Model

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Fit the Hougen-Watson model to the rate data using the combined error variance model.

```
mdl = NonLinearModel.fit(X,y,@hougen,beta0,'ErrorModel','combined')
```

```
mdl =


Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
```

```
        Estimate    SE          tStat     pValue
    b1      1.2526     0.86702    1.4447    0.18654
    b2    0.062776    0.043561    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075158    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 1.27
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 3.91e+03, p-value = 2.54e-13
```

- "Examine Quality and Adjust the Fitted Nonlinear Model" on page 11-7
- "Predict or Simulate Responses Using a Nonlinear Model" on page 11-10
- "Nonlinear Regression Workflow" on page 11-14

Algorithms

`NonLinearModel.fit` uses the same fitting algorithm as `nlinfit`.

Alternatives

You can also construct a nonlinear model using `fitnlm`.

References

[1] Seber, G. A. F., and C. J. Wild. *Nonlinear Regression*. Hoboken, NJ: Wiley-Interscience, 2003.

[2] DuMouchel, W. H., and F. L. O'Brien. "Integrating a Robust Option into a Multiple Regression Computing Environment." *Computer Science and Statistics: Proceedings of the 21st Symposium on the Interface*. Alexandria, VA: American Statistical Association, 1989.

[3] Holland, P. W., and R. E. Welsch. "Robust Regression Using Iteratively Reweighted Least-Squares." *Communications in Statistics: Theory and Methods*, *A6*, 1977, pp. 813–827.

See Also

`nlinfit` | `NonLinearModel`

More About

- “Nonlinear Regression” on page 11-2

RegressionTree.fit

Class: RegressionTree

Binary decision tree for regression (to be removed)

Compatibility

`RegressionTree.fit` will be removed in a future release. Use `fitrtree` instead.

Syntax

```
tree = RegressionTree.fit(x,y)
tree = RegressionTree.fit(x,y,Name,Value)
```

Description

`tree = RegressionTree.fit(x,y)` returns a regression tree based on the input variables (also known as predictors, features, or attributes) x and output (response) y. `tree` is a binary tree where each branching node is split based on the values of a column of x.

`tree = RegressionTree.fit(x,y,Name,Value)` fits a tree with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a tree of class `RegressionPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, `tree` is of class `RegressionTree`, and you can use the `predict` method to make predictions.

Input Arguments

x — Predictor values
matrix of scalar values

Predictor values, specified as a matrix of scalar values. Each column of x represents one variable, and each row represents one observation.

`RegressionTree.fit` considers `NaN` values in x as missing values.
`RegressionTree.fit` does not use observations with all missing values for x the fit.
`RegressionTree.fit` uses observations with some missing values for x to find splits on variables for which these observations have valid values.

Data Types: `single` | `double`

y — Response values
vector of scalar values

Response values, specified as a vector of scalar values with the same number of rows as x. Each entry in y is the response to the data in the corresponding row of x.

`RegressionTree.fit` considers `NaN` values in y to be missing values.
`RegressionTree.fit` does not use observations with missing values for y in the fit.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

'CategoricalPredictors' — Categorical predictors list
numeric or logical vector | cell array of strings | character matrix | `'all'`

Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following.

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of x.

- A logical vector of length `p`, where a `true` entry means that the corresponding column of x is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in the `PredictorNames` property.
- A character matrix, where each row of the matrix is a name of a predictor variable. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

Example:

Data Types: `single` | `double` | `logical` | `char` | `struct` | `cell`

`'CrossVal'` — Cross-validation flag

`'off'` (default) | `'on'`

Cross-validation flag, specified as the comma-separated pair consisting of `'CrossVal'` and either `'on'` or `'off'`.

If `'on'`, `RegressionTree.fit` grows a cross-validated decision tree with 10 folds. You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments. Note that you can only use one of these four options (`'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`) at a time when creating a cross-validated tree.

Alternatively, cross-validate tree later using the `crossval` method.

Example: `'CrossVal','on'`

`'CVPartition'` — Partition for cross-validation tree

`cvpartition` object

Partition for cross-validated tree, specified as the comma-separated pair consisting of `'CVPartition'` and an object of the `cvpartition` class created using `cvpartition`.

Note that if you use `'CVPartition'`, you cannot use any of the `'KFold'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example:

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range `[0,1]`

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the rest of the data for training.

Note that if you use `'Holdout'`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single | double`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated tree, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

Note that if you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single | double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off`. Use leave-one-out cross validation by setting to `'on'`.

Note that if you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

`'MergeLeaves'` — Leaf merge flag

`'on'` (default) | `'off'`

Leaf merge flag, specified as the comma-separated pair consisting of `'MergeLeaves'` and either `'on'` or `'off'`. When `'on'`, `RegressionTree.fit` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `RegressionTree.fit` does not merge leaves.

Example: `'MergeLeaves','off'`

`'MinLeaf'` — Minimum number of leaf node observations

`1` (default) | positive integer value

Minimum number of leaf node observations, specified as the comma-separated pair consisting of `'MinLeaf'` and a positive integer value. Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `RegressionTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Example: `'MinLeaf',3`

Data Types: `single` | `double`

`'MinParent'` — Minimum number of branch node observations

`10` (default) | positive integer value

Minimum number of branch node observations, specified as the comma-separated pair consisting of `'MinParent'` and a positive integer value. Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `RegressionTree.fit` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Example: `'MinParent',8`

Data Types: `single` | `double`

`'NVarToSample'` — Number of predictors for split

`'all'` (default) | positive integer value

Number of predictors to select at random for each split, specified as the comma-separated pair consisting of `'NVarToSample'` and a positive integer value. You can also specify `'all'`to use all available predictors.

Example: `'NVarToSample',3`

Data Types: `single` | `double`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

Example:

Data Types: `cell`

`'Prune'` — Pruning flag

`'on'` (default) | `'off'`

Pruning flag, specified as the comma-separated pair consisting of `'Prune'` and either `'on'` or `'off'`. When `'on'`, `RegressionTree.fit` computes the full tree and the optimal sequence of pruned subtrees. When `'off'`, `RegressionTree.fit` computes the full tree without pruning.

Example: `'Prune','off'`

`'PruneCriterion'` — Pruning criterion

`'mse'` (default)

Pruning criterion, specified as the comma-separated pair consisting of `'PruneCriterion'` and `'mse'`.

Example: `'PruneCriterion','mse'`

`'QEToler'` — Quadratic error tolerance

`1e-6` (default) | positive scalar value

Quadratic error tolerance per node, specified as the comma-separated pair consisting of `'QEToler'` and a positive scalar value. Splitting nodes stops when quadratic error per node drops below `QEToler*QED`, where `QED` is the quadratic error for the entire data computed before the decision tree is grown.

Example: `'QEToler',1e4`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable in y.

Example: `'ResponseName','Response'`

Data Types: `char`

`'ResponseTransform'` — Response transform function

`'none'` (default) | function handle

Response transform function for transforming the raw response values, specified as the comma-separated pair consisting of `'ResponseTransform'` and either a function handle or `'none'`. The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function using dot notation:

```
tree.ResponseTransform = @function
```

Example:

Data Types: `function_handle`

`'SplitCriterion'` — Split criterion

`'MSE'` (default)

Split criterion, specified as the comma-separated pair consisting of `'SplitCriterion'` and `'MSE'`, meaning mean squared error.

Example: `'SplitCriterion','MSE'`

`'Surrogate'` — Surrogate decision splits flag

`'off'` | `'on'` | `'all'` | positive integer value

Surrogate decision splits flag, specified as the comma-separated pair consisting of `'Surrogate'` and `'on'`, `'off'`, `'all'`, or a positive integer value.

- When `'on'`, `RegressionTree.fit` finds at most 10 surrogate splits at each branch node.
- When set to a positive integer value, `RegressionTree.fit` finds at most the specified number of surrogate splits at each branch node.
- When set to `'all'`, `RegressionTree.fit` finds all surrogate splits at each branch node. The `'all'` setting can use much time and memory.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also enables you to compute measures of predictive association between predictors.

Example: `'Surrogate','on'`

Data Types: `single` | `double`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` is the number of rows in x.

Example:

Data Types: `single` | `double`

Output Arguments

`tree` — Regression tree

regression tree object

Regression tree, returned as a regression tree object. Note that using the `'Crossval'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a tree of class `RegressionPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, `tree` is of class `RegressionTree`, and you can use the `predict` method to make predictions.

Examples

Predict Values Using a Regression Tree

Load the sample data.

```
load carsmall
```

Construct a regression tree to predict the mileage of cars based on their weights and numbers of cylinders.

```
tree = RegressionTree.fit([Weight, Cylinders],MPG,...
                'MinParent',20,...
                'PredictorNames',{'W','C'})
```

```
tree =

  RegressionTree
           PredictorNames: {'W'  'C'}
             ResponseName: 'Y'
        ResponseTransform: 'none'
```

```
    CategoricalPredictors: []
          NumObservations: 94
```

Predict the mileage of a car that weighs 2200 lbs and has four cylinders.

```
predict(tree,[2200,4])
```

```
ans =
   29.6111
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`predict` | `view` | `fitrtree`

How To

- “Splitting Categorical Predictors” on page 16-65

fitcdiscr

Fit discriminant analysis classifier

Syntax

```
obj = fitcdiscr(x,y)
obj = fitcdiscr(x,y,Name,Value)
```

Description

`obj = fitcdiscr(x,y)` returns a discriminant analysis classifier based on the input variables (also known as predictors, features, or attributes) x and output (response) y.

`obj = fitcdiscr(x,y,Name,Value)` fits a classifier with additional options specified by one or more name-value pair arguments. For example, you can specify the cost of misclassification, prior probabilities for each class, or observation weights.

Examples

Construct a Discriminant Analysis Classifier

Construct a discriminant analysis classifier for the Fisher iris data.

```
load fisheriris
obj = fitcdiscr(meas,species)
```

```
obj =

  ClassificationDiscriminant
     PredictorNames: {'x1'  'x2'  'x3'  'x4'}
       ResponseName: 'Y'
         ClassNames: {'setosa'  'versicolor'  'virginica'}
     ScoreTransform: 'none'
    NumObservations: 150
        DiscrimType: 'linear'
                 Mu: [3x4 double]
```

```
            Coeffs: [3x3 struct]

  Properties, Methods
```

Input Arguments

x — Predictor values

matrix of numeric values

Predictor values, specified as a matrix of numeric values. Each column of x represents one variable, and each row represents one observation.

`fitcdiscr` considers `NaN` values in x as missing values. `fitcdiscr` does not use observations with missing values for x in the fit.

Data Types: `single` | `double`

y — Classification values

numeric vector | categorical vector | logical vector | character array | cell array of strings

Classification values, specified as a categorical or character array, logical or numeric vector, or cell array of strings. Each row of y represents the classification of the corresponding row of x.

`fitcdiscr` considers `NaN` values in y to be missing values. `fitcdiscr` does not use observations with missing values for y in the fit.

Data Types: `single` | `double` | `logical` | `char` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'DiscrimType','quadratic','SaveMemory','on'` specifies a quadratic discriminant classifier and does not store the covariance matrix in the output object.

'ClassNames' — Class names

array

Class names, specified as the comma-separated pair consisting of 'ClassNames' and an array. Use the data type that exists in y. The default is the class names that exist in y. Use ClassNames to order the classes or to select a subset of classes for training.

Data Types: single | double | logical | char

'Cost' — Cost of misclassification

square matrix | structure

Cost of misclassification of a point, specified as the comma-separated pair consisting of 'Cost' and one of the following:

- Square matrix, where Cost(i,j) is the cost of classifying a point into class j if its true class is i (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding rows and columns of Cost, additionally specify the ClassNames name-value pair argument.
- Structure S having two fields: S.ClassNames containing the group names as a variable of the same type as y, and S.ClassificationCosts containing the cost matrix.

The default is Cost(i,j)=1 if i~=j, and Cost(i,j)=0 if i=j.

Data Types: single | double | struct

'CrossVal' — Flag to train cross-validated classifier

'off' (default) | 'on'

Flag to train a cross-validated classifier, specified as the comma-separated pair consisting of 'CrossVal' and either 'on' or 'off'.

If you specify 'on', then fitcdiscr creates a cross-validated classifier with 10 folds.

You can override this cross-validation setting using one of the 'KFold', 'Holdout', 'Leaveout', or 'CVPartition' name-value pair arguments.

You can only use one of these four options at a time to create a cross-validated model: 'KFold', 'Holdout', 'Leaveout', or 'CVPartition'.

Alternatively, cross validate obj later using the crossval method.

Example: `'CrossVal','on'`

`'CVPartition'` — Cross-validated model partition
`cvpartition` object

Cross-validated model partition, specified as the comma-separated pair consisting of `'CVPartition'` and an object created using `cvpartition`. You can only use one option at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'Delta'` — Linear coefficient threshold
`0` (default) | nonnegative scalar value

Linear coefficient threshold, specified as the comma-separated pair consisting of `'Delta'` and a nonnegative scalar value. If a coefficient of `obj` has magnitude smaller than `Delta`, `obj` sets this coefficient to `0`, and you can eliminate the corresponding predictor from the model. Set `Delta` to a higher value to eliminate more predictors.

`Delta` must be `0` for quadratic discriminant models.

Data Types: `single` | `double`

`'DiscrimType'` — Discriminant type
`'linear'` (default) | `'quadratic'` | `'diagLinear'` | `'diagQuadratic'` | `'pseudoLinear'` | `'pseudoQuadratic'`

Discriminant type, specified as the comma-separated pair consisting of `'DiscrimType'` and one of the following:

- `'linear'`
- `'quadratic'`
- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

Example: `'DiscrimType','quadratic'`

`'FillCoeffs'` — `Coeffs` property flag
`'on'` | `'off'`

`Coeffs` property flag, specified as the comma-separated pair consisting of `'FillCoeffs'` and `'on'` or `'off'`. Setting the flag to `'on'` populates the `Coeffs` property in the classifier object. This can be computationally intensive, especially when cross validating. The default is `'on'`, unless you specify a cross validation name-value pair, in which case the flag is set to `'off'` by default.

Example: `'FillCoeffs','off'`

`'Gamma'` — Regularization parameter

scalar value in the range `[0,1]`

Parameter for regularizing the correlation matrix of predictors, specified as the comma-separated pair consisting of `'Gamma'` and a scalar value in the range `[0,1]`.

- Linear discriminant — Scalar value in the range `[0,1]`.
  - If you pass a value strictly between `0` and `1`, `fitcdiscr` sets the discriminant type to `'Linear'`.
  - If you pass `0` for `Gamma` and `'Linear'` for `DiscrimType`, and if the correlation matrix is singular, `fitcdiscr` sets `Gamma` to the minimal value required for inverting the covariance matrix.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagLinear'`.
- Quadratic discriminant — Either `0` or `1`.
  - If you pass `0` for `Gamma` and `'Quadratic'` for `DiscrimType`, and if one of the classes has a singular covariance matrix, `fitcdiscr` errors.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagQuadratic'`.
  - If you set Gamma to a value between `0` and `1` for a quadratic discriminant, `fitcdiscr` errors.

Example: `'Gamma',1`

Data Types: `single | double`

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). If you specify `'Holdout',`*p*, then the software:

1. Randomly reserves `p*100`% of the data as validation data, and trains the model using the rest of the data
2. Stores the compact, trained model in CVMdl`.Trained`

If you specify `Holdout`, then you cannot specify any of CVPartition, KFold, or Leaveout.

Example: `'Holdout',0.1`

Data Types: `double | single`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated classifier, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'KFold',8`

Data Types: `single | double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. If you specify `'on'`, then the software implements leave-one-out cross validation.

If you use `'Leaveout'`, you cannot use these `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

Data Types: `char`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

Data Types: `cell`

'Prior' — Prior probabilities

'empirical' (default) | 'uniform' | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of 'Prior' and one of the following.

- A string:
  - 'empirical' determines class probabilities from class frequencies in y. If you pass observation weights, they are used to compute the class probabilities.
  - 'uniform' sets all class probabilities equal.
- A vector (one scalar value for each class). To specify the class order for the corresponding elements of Prior, additionally specify the ClassNames name-value pair argument.
- A structure S with two fields:
  - S.ClassNames containing the class names as a variable of the same type as y
  - S.ClassProbs containing a vector of corresponding probabilities

If you set values for both Weights and Prior, the weights are renormalized to add up to the value of the prior probability in the respective class.

Example: 'Prior','uniform'

Data Types: single | double | struct

'ResponseName' — Response variable name

'Y' (default) | string

Response variable name, specified as the comma-separated pair consisting of 'ResponseName' and a string containing the name of the response variable y.

Example: 'ResponseName','Response'

Data Types: char

'SaveMemory' — Flag to save covariance matrix

'off' (default) | 'on'

Flag to save covariance matrix, specified as the comma-separated pair consisting of 'SaveMemory' and either 'on' or 'off'. If you specify 'on', then fitcdiscr does not store the full covariance matrix, but instead stores enough information to compute the matrix. The predict method computes the full covariance matrix for prediction, and

does not store the matrix. If you specify `'off'`, then `fitcdiscr` computes and stores the full covariance matrix in `obj`.

Specify `SaveMemory` as `'on'` when the input matrix contains thousands of predictors.

Example: `'SaveMemory','on'`

`'ScoreTransform'` — Score transform function

`'none'` (default) | valid score transform string | function handle

Score transform function, specified as the comma-separated pair consisting of `'ScoreTransform'` and one of the following.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to 0.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to -1.

Alternatively, you can use your own function handle for transforming scores. Your function should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Example: `'ScoreTransform','logit'`

Data Types: `function_handle`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` is the number of rows in x. `fitcdiscr` normalizes the weights to sum to 1.

Data Types: `single | double`

Output Arguments

`obj` — Discriminant analysis classifier

classifier object

Discriminant analysis classifier, returned as a classifier object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a tree of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, obj is of class `ClassificationDiscriminant`, and you can use the `predict` method to predict the response of new data.

Alternative Functionality

Functions

The `classify` function also performs discriminant analysis. `classify` is usually more awkward to use.

- `classify` requires you to fit the classifier every time you make a new prediction.
- `classify` does not perform cross validation.
- `classify` requires you to fit the classifier when changing prior probabilities.

More About

Discriminant Classification

The model for discriminant analysis is:

- Each class (`Y`) generates data (`X`) using a multivariate normal distribution. That is, the model assumes `X` has a Gaussian mixture distribution (`gmdistribution`).
  - For linear discriminant analysis, the model has the same covariance matrix for each class, only the means vary.
  - For quadratic discriminant analysis, both means and covariances of each class vary.

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

For details, see "How the predict Method Classifies" on page 15-6.

- "Discriminant Analysis" on page 15-3

See Also

`ClassificationDiscriminant` | `ClassificationPartitionedModel` | `classify` | `crossval` | `predict`

fitcecoc

Fit multiclass models for support vector machines or other classifiers

Syntax

```
Mdl = fitcecoc(X,Y)
Mdl = fitcecoc(X,Y,Name,Value)
```

Description

`Mdl = fitcecoc(X,Y)` returns a full, trained error-correcting output codes (ECOC) multiclass model using the predictors `X` and the class labels `Y`. By default, `fitcecoc` uses $K(K-1)/2$ binary support vector machine (SVM) models using the one-versus-one coding design, where K is the number of unique class labels (levels). `Mdl` is a `ClassificationECOC` model.

`Mdl = fitcecoc(X,Y,Name,Value)` returns an ECOC model with additional options specified by one or more `Name,Value` pair arguments.

For example, specify different binary learners, a different coding design, or to cross validate. It is good practice to cross validate using the `Kfold` `Name,Value` pair argument. The cross-validation results determine how well the ECOC classifier generalizes.

Examples

Train a Multiclass Model Using SVM Learners

Train an error-correcting output codes (ECOC) multiclass model using support vector machine (SVM) binary learners.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

Train an ECOC multiclass model using the default options.

```
Mdl = fitcecoc(X,Y)
```

```
Mdl =

  ClassificationECOC
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
    BinaryLearners: {3x1 cell}
        CodingName: 'onevsone'
```

`Mdl` is a `ClassificationECOC` model. By default, `fitcecoc` uses SVM binary learners, and uses a one-versus-one coding design. You can access `Mdl` properties using dot notation.

Display the coding design matrix.

```
Mdl.ClassNames
CodingMat = Mdl.CodingMatrix
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


CodingMat =

     1     1     0
    -1     0     1
     0    -1    -1
```

A one-versus-one coding design on three classes yields three binary learners. Columns of `CodingMat` correspond to learners and rows correspond to classes. The class order corresponds to the order in `Mdl.ClassNames`. For example, `CodingMat(:,1)` is `[1; -1; 0]`, and indicates that the software trains the first SVM binary learner using all

observations classified as `'setosa'` and `'versicolor'`. Since `'setosa'` corresponds to `1`, it is the positive class, and since `'versicolor'` corresponds to `-1`, it is the negative class.

You can access each binary learner using cell indexing and dot notation.

```
Mdl.BinaryLearners{1}                % The first binary learner
Mdl.BinaryLearners{1}.SupportVectors % Support vector indices
```

```
ans =

  classreg.learning.classif.CompactClassificationSVM
      PredictorNames: {'x1'  'x2'  'x3'  'x4'}
        ResponseName: 'Y'
          ClassNames: [-1 1]
      ScoreTransform: 'none'
                Beta: [4x1 double]
                Bias: 1.4505
    KernelParameters: [1x1 struct]



ans =

     []
```

Compute the in-sample classification error.

```
isLoss = resubLoss(Mdl)
```

```
isLoss =

    0.0067
```

The classification error is small, but the classifier might have been overfit. You can cross validate the classifier using `crossval`.

Cross Validate an ECOC Classifier

Train a one-versus-one ECOC classifier using binary SVM learners.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
rng(1); % For reproducibility
```

Create an SVM template. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1)
```

```
t =

Fit template for classification SVM.

                     Alpha: [0x1 double]
           BoxConstraint: []
               CacheSize: []
           CachingMethod: ''
    DeltaGradientTolerance: []
            GapTolerance: []
            KKTTolerance: []
          IterationLimit: []
          KernelFunction: ''
             KernelScale: []
            KernelOffset: []
     KernelPolynomialOrder: []
                 NumPrint: []
                       Nu: []
          OutlierFraction: []
          ShrinkagePeriod: []
                   Solver: ''
          StandardizeData: 1
       SaveSupportVectors: []
           VerbosityLevel: []
                   Method: 'SVM'
                     Type: 'classification'
```

`t` is an SVM template. All of its properties are empty, except for `StandardizeData`, `Method`, and `Type`. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier. It is good practice to specify the class order.

```
Mdl = fitcecoc(X,Y,'Learners',t,...
```

```
    'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationECOC` classifier. You can access its properties using dot notation.

Cross validate `Mdl` using 10-fold cross validation.

```
CVMdl = crossval(Mdl);
```

`CVMdl` is a `ClassificationPartitionedECOC` cross-validated ECOC classifier.

Estimate the generalization error.

```
oosLoss = kfoldLoss(CVMdl)
```

```
oosLoss =

    0.0400
```

The out-of-sample classification error is 4%, which indicates that the ECOC classifier generalizes fairly well.

Estimate Posterior Probabilities Using ECOC Classifiers

Load Fisher's iris data set. Train the classifier using the petal dimensions as predictors.

```
load fisheriris
X = meas(:,3:4);
Y = species;
rng(1); % For reproducibility
```

Create an SVM template, and specify the Gaussian kernel. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1,'KernelFunction','gaussian');
```

`t` is an SVM template. Most of its properties are empty. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier using the SVM template. Transform classification scores to class posterior probabilities (which are returned by `predict` or `resubPredict`) using the `'FitPosterior'` name-value pair argument. Display diagnostic messages during the training using the `'Verbose'` name-value pair argument. It is good practice to specify the class order.

```
Mdl = fitcecoc(X,Y,'Learners',t,'FitPosterior',1,...
    'ClassNames',{'setosa','versicolor','virginica'},...
    'Verbose',2);

Training binary learner 1 (SVM) out of 3 with 50 negative and 50 positive observations.
Negative class indices: 2
Positive class indices: 1

Fitting posterior probabilities for learner 1 (SVM).
Training binary learner 2 (SVM) out of 3 with 50 negative and 50 positive observations.
Negative class indices: 3
Positive class indices: 1

Fitting posterior probabilities for learner 2 (SVM).
Training binary learner 3 (SVM) out of 3 with 50 negative and 50 positive observations.
Negative class indices: 3
Positive class indices: 2

Fitting posterior probabilities for learner 3 (SVM).
```

`Mdl` is a `ClassificationECOC` model. The same SVM template applies to each binary learner, but you can adjust options for each binary learner by passing in a cell vector of templates.

Predict the in-sample labels and class posterior probabilities. Display diagnostic messages during the computation of labels and class posterior probabilities using the `'Verbose'` name-value pair argument.

```
[label,~,~,Posterior] = resubPredict(Mdl,'Verbose',1);
Mdl.BinaryLoss

Predictions from all learners have been computed.
Loss for all observations has been computed.
Computing posterior probabilities...

ans =

quadratic
```

The software assigns an observation to the class that yields the smallest average binary loss. Since all binary learners are computing posterior probabilities, the binary loss function is `quadratic`.

Display a random set of results.

```
idx = randsample(size(X,1),10,1);
Mdl.ClassNames
table(Y(idx),label(idx),Posterior(idx,:),...
    'VariableNames',{'TrueLabel','PredLabel','Posterior'})
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'
```

```
ans =

     TrueLabel       PredLabel                  Posterior
    ____________    ____________    ____________________________________

    'virginica'     'virginica'      0.0039321     0.0039869       0.99208
    'virginica'     'virginica'       0.017067      0.018263       0.96467
    'virginica'     'virginica'       0.014948      0.015856        0.9692
    'versicolor'    'versicolor'    2.2197e-14       0.87317       0.12683
    'setosa'        'setosa'             0.999    0.00025091    0.00074639
    'versicolor'    'virginica'     2.2195e-14      0.059429       0.94057
    'versicolor'    'versicolor'    2.2194e-14       0.97001      0.029986
    'setosa'        'setosa'             0.999     0.0002499    0.00074741
    'versicolor'    'versicolor'     0.0085646       0.98259      0.008849
    'setosa'        'setosa'             0.999    0.00025013    0.00074718
```

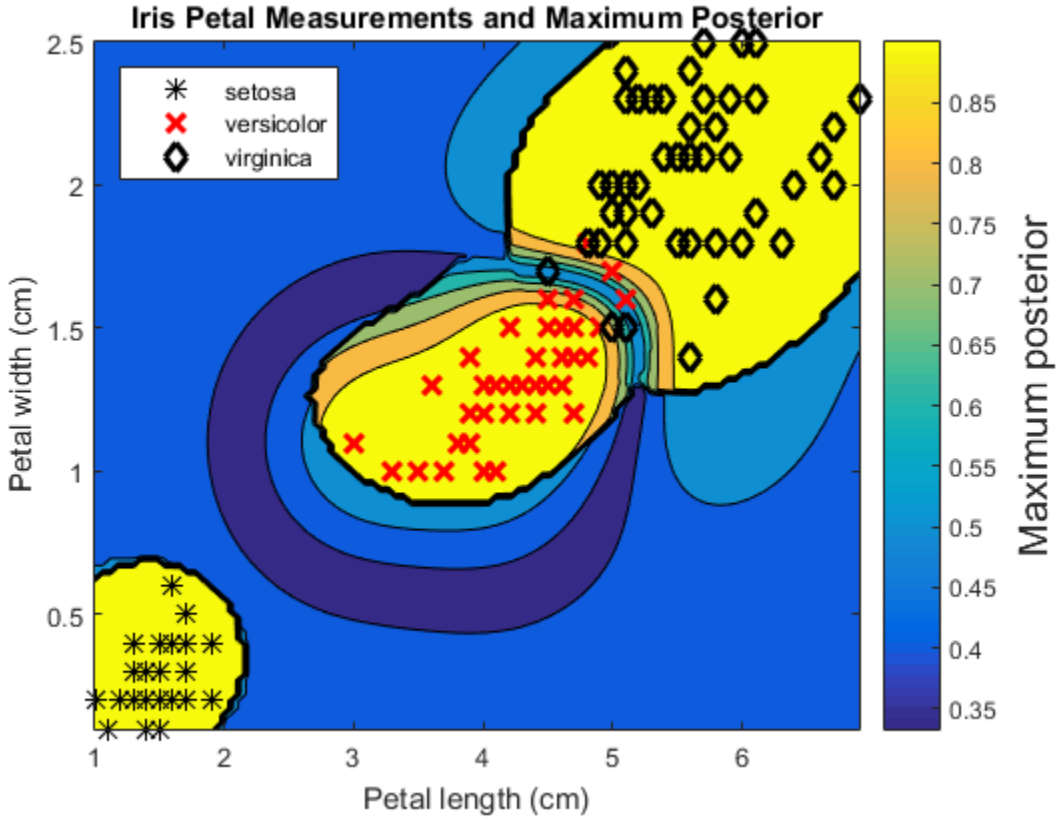
The columns of `Posterior` correspond to the class order of `Mdl.ClassNames`.

Define a grid of values in the observed predictor space. Predict the posterior probabilities for each instance in the grid.

```
xMax = max(X);
xMin = min(X);

x1Pts = linspace(xMin(1),xMax(1));
x2Pts = linspace(xMin(2),xMax(2));
[x1Grid,x2Grid] = meshgrid(x1Pts,x2Pts);

[~,~,~,PosteriorRegion] = predict(Mdl,[x1Grid(:),x2Grid(:)]);
```

For each coordinate on the grid, plot the maximum class posterior probability among all classes.

```
figure;
contourf(x1Grid,x2Grid,...
        reshape(max(PosteriorRegion,[],2),size(x1Grid,1),size(x1Grid,2)));
h = colorbar;
h.YLabel.String = 'Maximum posterior';
h.YLabel.FontSize = 15;
hold on
gh = gscatter(X(:,1),X(:,2),Y,'krk','*xd',8);
gh(2).LineWidth = 2;
gh(3).LineWidth = 2;

title 'Iris Petal Measurements and Maximum Posterior';
xlabel 'Petal length (cm)';
ylabel 'Petal width (cm)';
axis tight
legend(gh,'Location','NorthWest')
hold off
```



Train ECOC Classifiers Using Ensembles and Parallel Computing

Train a one-versus-all ECOC classifier using a GentleBoost ensemble of decision trees with surrogate splits. Estimate the classification error using 10-fold cross validation.

Load and inspect the `arrhythmia` data set.

```
load arrhythmia
[n,p] = size(X)
isLabels = unique(Y);
nLabels = numel(isLabels)
tabulate(categorical(Y))
```

```
n =
```

```
   452

p =

   279

nLabels =

    13

    Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

There are 279 predictors, and a relatively small sample size of 452. There are 16 distinct labels, but only 13 are represented in the response (Y), and each label describes various degrees of arrhythmia. 54.20% of the observations are in class 1.

Create an ensemble template. You must specify at least three arguments: a method, a number of learners, and the type of learner. For this example, specify `'GentleBoost'` for the method, 100 for the number of learners, and a decision tree template that uses surrogate splits since there are missing observations.

```
tTree = templateTree('surrogate','on');
tEnsemble = templateEnsemble('GentleBoost',100,tTree);
```

`tEnsemble` is a template object. Most of its properties are empty, but the software fills them with their default values during training.

Train a one-versus-all ECOC classifier using the ensembles of decision trees as binary learners. If you have a Parallel Computing Toolbox license, then you can speed up the

computation by specifying to use parallel computing. This sends each binary learner to a worker in the pool (the number of workers depends on your system configuration). Also, specify that the prior probabilities are $1/K$, where $K = 13$, which is the number of distinct classes.

```
pool = parpool; % Invoke workers
options = statset('UseParallel',1);
Mdl = fitcecoc(X,Y,'Coding','onevsall','Learners',tEnsemble,...
               'Prior','uniform','Options',options);
```

```
Starting parallel pool (parpool) using the 'local' profile ... connected to 2 workers.
```

`Mdl` is a `ClassificationECOC` model.

Cross validate the ECOC classifier using 10-fold cross validation.

```
CVMdl = crossval(Mdl,'Options',options);
```

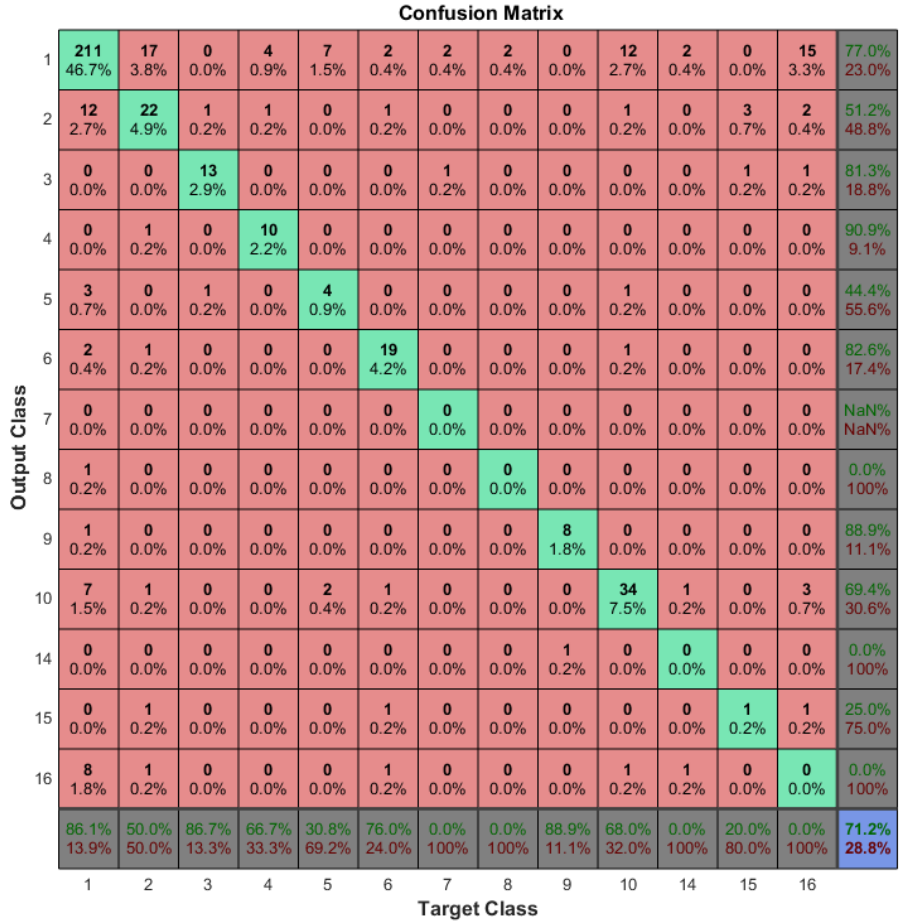
```
Warning: One or more folds do not contain points from all the groups.
```

`CVMdl` is a `ClassificationPartitionedECOC` model. The warning indicates that some classes are not represented while the software trains at least one fold. Therefore, those folds cannot predict labels for the missing classes. You can inspect the results of a fold using cell indexing and dot notation, e.g., access the results of the first fold by entering `CVMdl.Trained{1}`. Your results might vary.

Use the cross-validated ECOC classifier to predict out-of-fold labels. You can compute the confusion matrix using `confusionmat`. However, if you have a Neural Network Toolbox license, you can plot the confusion matrix using `plotconfusion`. The input arguments of `plotconfusion` are not vectors of the true and predicted labels like `confusionmat`, but indicator matrices of the true and predicted labels. Both start as K-by-n matrices of 0s. If observation j has label index k (or has predicted label k), then element (k,j) of the true label indicator matrix (or predicted label indicator matrix) is `1`. You can convert label indices returned by `predict`, `resubPredict`, or `kfoldPredict` to label indicator matrices using linear indexing. For details on linear indexing, see `sub2ind` and `ind2sub`.

```
oofLabel = kfoldPredict(CVMdl,'Options',options);
ConfMat = confusionmat(Y,oofLabel);

% Convert the integer label vector to a class-identifier matrix.
[~,grp] = ismember(oofLabel,isLabels);
oofLabelMat = zeros(nLabels,n);
idxLinear = sub2ind([nLabels n],grp,(1:n)');
```

```
oofLabelMat(idxLinear) = 1; % Flags the row corresponding to the class
YMat = zeros(nLabels,n);
idxLinearY = sub2ind([nLabels n],grp,(1:n)');
YMat(idxLinearY) = 1;

figure;
plotconfusion(YMat,oofLabelMat);
h = gca;
h.XTickLabel = [num2cell(isLabels); {''}];
h.YTickLabel = [num2cell(isLabels); {''}];
```



- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

Input Arguments

X — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature).

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to standardize the continuous predictor variables. For *k*NN and SVM binary classifiers, set `'Standardize',1` in the template functions `templateKNN` or `templateSVM`, respectively.

Data Types: `double` | `single`

Y — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels to which the ECOC model is trained, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to specify the class order using the `ClassNames` name-value pair argument.

Note: The software treats `NaN`, empty string (`''`), and `<undefined>` elements as missing data. The software removes rows of `X` corresponding to missing values in `Y`. However, the treatment of missing values in `X` varies among binary learners. For details, see the training functions for your binary learners: `fitcdiscr`, `fitcknn`, `fitcnb`, `fitcsvm`, `fitctree`, or `fitensemble`. Removing observations decreases the effective training or cross-validation sample size.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Learners','tree','Coding','onevsone','CrossVal','on'` specifies to use decision trees for all binary learners, a one-versus-one coding design, and to implement 10-fold cross validation.

ECOC Classifier Options

`'Coding'` — Coding design
`'onevsall'` (default) | `'allpairs'` | `'binarycomplete'` | `'denserandom'` | `'onevsone'` | `'ordinal'` | `'sparserandom'` | `'ternarycomplete'` | numeric matrix

Coding design name, specified as the comma-separated pair consisting of `'Coding'` and a numeric matrix or string.

This table summarizes the available, built-in coding designs.

Value	Number of Binary Learners	Description
`'allpairs'` and `'onevsone'`	$K(K-1)/2$	For each binary learner, one class is positive, another is negative, and the software ignores the rest. This design exhausts all combinations of class pair assignments.
`'binarycomplete'`	$2^{(K-1)}-1$	This design partitions the classes into all binary combinations, and does not ignore any classes. For each binary learner, all class assignments are `-1` and `1` with at least one positive and negative class in the assignment.

Value	Number of Binary Learners	Description
`'denserandom'`	Random, but approximately $10 \log_2 K$	For each binary learner, the software randomly assigns classes into positive or negative classes, with at least one of each type. For more details, see "Random Coding Design Matrices" on page 22-1542.
`'onevsall'`	K	For each binary learner, one class is positive and the rest are negative. This design exhausts all combinations of positive class assignments.
`'ordinal'`	$K - 1$	For the first binary learner, the first class is negative, and the rest positive. For the second binary learner, the first two classes are negative, the rest positive, and so on.
`'sparserandom'`	Random, but approximately $15 \log_2 K$	For each binary learner, the software randomly assigns classes as positive or negative with probability 0.25 for each, and ignores classes with probability 0.5. For more details, see "Random Coding Design Matrices" on page 22-1542.
`'ternarycomplete'`	$\left(3^K - 2^{(K+1)} + 1\right)/2$	This design partitions the classes into all ternary combinations. All class assignments are `0`, `-1`, and `1` with at least one positive and one negative class in the assignment.

You can also specify a coding design using a custom coding matrix. The custom coding matrix is a *K*-by-*L* matrix. Each row corresponds to a class and each column corresponds to a binary learner. The class order (rows) corresponds to the order in `ClassNames`. Compose the matrix by following these guidelines:

- Every element of the custom coding matrix must be `-1`, `0`, or `1`, and the value must correspond to a dichotomous class assignment. This table describes the meaning of `Coding(i,j)`, that is, the class that learner `j` assigns to observations in class `i`.

Value	Dichotomous Class Assignment
`-1`	Negative class
`0`	Before training, learner `j` removes observations in class `i` from the data set.
`1`	Positive class

- Every column must contain at least one `-1` or `1`.
- For all column indices `i`,`j` such that `i` ≠ `j`, `Coding(:,i)` cannot equal `Coding(:,j)` and `Coding(:,i)` cannot equal `-Coding(:,j)`.
- All rows of the custom coding matrix must be different.

For more details on the form of custom coding design matrices, see "Custom Coding Design Matrices" on page 22-1540.

Example: `'Coding','ternarycomplete'`

Data Types: `char` | `double` | `single` | `int16` | `int32` | `int64` | `int8`

`'FitPosterior'` — Flag indicating whether to transform scores to posterior probabilities
`false` or `0` (default) | `true` or `1`

Flag indicating whether to transform scores to posterior probabilities, specified as the comma-separated pair consisting of `'FitPosterior'` and a `true` (`1`) or `false` (`0`).

If `FitPosterior` is `true`, then the software transforms binary-learner classification scores to posterior probabilities. You can obtain posterior probabilities by using `kfoldPredict`, `predict`, or `resubPredict`.

Ensemble methods that do not fit posterior probabilities are `AdaBoostM2`, `LPBoost`, `RUSBoost`, `RobustBoost`, and `TotalBoost`. Therefore, if any binary learner is an ensemble that uses any of these methods, then the software generates an error.

Example: `'FitPosterior',true`

Data Types: `logical`

`'Learners'` — Binary learner templates

`'svm'` (default) | `'discriminant'` | `'knn'` | `'tree'` | template object | cell vector of template objects

Binary learner templates, specified as the comma-separated pair consisting of `'Learners'` and a string, template object, or cell vector of template objects. Specifically, you can specify binary classifiers such as SVM, and the ensembles that use `GentleBoost`, `LogitBoost`, and `RobustBoost`, to solve multiclass problems. However, `fitcecoc` also supports multiclass models as binary classifiers.

- If `Learners` is a string, then the software trains each binary learner using the default values of the algorithm corresponding to the string. This table summarizes the available strings.

Value	Description
`'discriminant'`	Discriminant analysis. For default options, see `templateDiscriminant`.
`'knn'`	*k*-nearest neighbors. For default options, see `templateKNN`.
`'naivebayes'`	Naive Bayes. For default options, see `templateNaiveBayes`.
`'svm'`	SVM. For default options, see `templateSVM`.
`'tree'`	Classification trees. For default options, see `templateTree`.

- If `Learners` is a template object, then each binary learner trains according to the stored options. You can create a template object using:
  - `templateDiscriminant`, for discriminant analysis.
  - `templateEnsemble`, for ensemble learning. You must at least specify the learning method (`Method`), the number of learners (`NLearn`), and the type of learner (`Learners`). You cannot use the `AdaBoostM2` ensemble method for binary learning.
  - `templateKNN`, for *k*-nearest neighbors.

  - `templateNaiveBayes`, for naive Bayes.
  - `templateSVM`, for SVM.
  - `templateTree`, for classification trees.
- If `Learners` is cell vector of template objects, then:
  - Cell *j* corresponds to binary learner *j* (in other words, column *j* of the coding design matrix), and the cell vector must have length *L*. *L* is the number of columns in the coding design matrix. For details, see Coding.
  - To use one of the built-in loss functions for prediction, then all binary learners must return a score in the same range. For example, you cannot include default SVM binary learners with default naive Bayes binary learners. The former returns a score in the range (-∞,∞), and the latter returns a posterior probability as a score. Otherwise, you must provide a custom loss as a function handle to functions such as `predict` and `loss`.

By default, the software trains learners using default SVM templates.

Example: `'Learners','tree'`

Cross-Validation Options

`'CrossVal'` — Flag to train cross-validated classifier

`'off'` (default) | `'on'`

Flag to train a cross-validated classifier, specified as the comma-separated pair consisting of `'Crossval'` and `'on'` or `'off'`.

If you specify `'on'`, then the software trains a cross-validated classifier with 10 folds.

You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments.

You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Alternatively, cross-validate Mdl later by passing it to `crossval`.

Example: `'Crossval','on'`

Data Types: `char`

`'CVPartition'` — Cross-validation partition

`[]` (default) | `cvpartition` partition object

Cross-validation partition, specified as the comma-separated pair consisting of `'CVPartition'` and a `cvpartition` partition object as created by `cvpartition`. The partition object specifies the type of cross-validation, and also the indexing for training and validation sets.

If you specify `CVPartition`, then you cannot specify any of Holdout, KFold, or Leaveout.

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). If you specify `'Holdout',`*p*, then the software:

1. Randomly reserves *p*`*100`% of the data as validation data, and trains the model using the rest of the data
2. Stores the compact, trained model in CVMdl`.Trained`

If you specify `Holdout`, then you cannot specify any of CVPartition, KFold, or Leaveout.

Example: `'Holdout',0.1`

Data Types: `double` | `single`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated classifier, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. If you specify `'on'`, then the software implements leave-one-out cross validation.

If you use `'Leaveout'`, you cannot use these `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

Data Types: `char`

Other Classification Options

`'CategoricalPredictors'` — Categorical predictors list

character array | logical vector | numeric vector | cell array of strings | `'all'`

Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following:

- A numeric vector with indices from `1` through `p`, where `p` is the number of columns of X.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of X is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match the entries in `PredictorNames`.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match the entries in `PredictorNames`. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

Specification of `CategoricalPredictors` is appropriate if:

- At least one predictor is categorical and all binary learners are classification trees, naive Bayes learners, or ensembles of classification trees.
- All predictors are categorical and at least one binary learner is *k*NN.

If you specify `CategoricalPredictors` for any other case, then the software warns that it cannot train that binary learner. For example, the software cannot train SVM learners using categorical predictors.

The default is `[]`, which indicates that there are no categorical predictors.

Example: `'CategoricalPredictors','all'`

Data Types: `single` | `double` | `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

The default is the distinct class names in `Y`.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for training.

Example: `'ClassNames',{'setosa','virginica','versicolor'}`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure. If you specify:

- The square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.
- The structure `S`, then it must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y
  - `S.ClassificationCosts`, which contains the cost matrix with rows and columns ordered as in `S.ClassNames`

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double` | `single` | `struct`

`'Options'` — Parallel computing options

`[ ]` (default) | structure array returned by `statset`

Parallel computing options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`. These options require Parallel Computing Toolbox. `fitcecoc` uses `'Streams'`, `'UseParallel'`, and `'UseSubtreams'` fields.

This table summarizes the available options.

Option	Description
`'Streams'`	A `RandStream` object or cell array of such objects. If you do not specify `Streams`, the software uses the default stream or streams. If you specify `Streams`, use a single object except when the following are true: • You have an open parallel pool. • `UseParallel` is `true`. • `UseSubstreams` is `false`. In that case, use a cell array of the same size as the parallel pool. If a parallel pool is not open, then the software tries to open one (depending on your preferences), and `Streams` must supply a single random number stream.
`'UseParallel'`	If you have Parallel Computing Toolbox, then you can invoke a pool of workers by setting `'UseParallel',1`.
`'UseSubstreams'`	Set to `true` to compute in parallel using the stream specified by `'Streams'`. Default is `false`. For example, set `Streams` to a type allowing substreams, such as `'mlfg6331_64'` or `'mrg32k3a'`.

A best practice to ensure more predictable results is to use `parpool` and explicitly create a parallel pool before you invoke parallel computing using `fitcecoc`.

Example: `'Options',statset('UseParallel',1)`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in X.

Example: `'PredictorNames',{'PedalWidth','PedalLength'}`

Data Types: `cell`

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | numeric vector | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and a string, numeric vector, or a structure.

This table summarizes the available options for setting prior probabilities.

Value	Description
`'empirical'`	The class prior probabilities are the class relative frequencies in Y.
`'uniform'`	All class prior probabilities are equal to $1/K$, where K is the number of classes.
numeric vector	Each element is a class prior probability. Order the elements according to Mdl`.ClassNames` or specify the order using the ClassNames name-value pair argument. The software normalizes the elements such that they sum to `1`.
structure	A structure `S` with two fields: • `S.ClassNames` contains the class names as a variable of the same type as Y. • `S.ClassProbs` contains a vector of corresponding prior probabilities. The software normalizes the elements such that they sum to `1`.

For more details on how the software incorporates class prior probabilities, see “Prior Probabilities and Cost” on page 22-1541.

Example: `'Prior',struct('ClassNames',{{'setosa','versicolor'}},'ClassProbs',[1,2])`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable Y.

Example: `'ResponseName','IrisType'`

Data Types: `char`

`'Verbose'` — Verbosity level

`0` (default) | `1` | `2`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0`, `1`, or `2`. `Verbose` controls the amount of diagnostic information per binary learner that the software displays in the Command Window.

This table summarizes the available verbosity level options.

Value	Description
0	The software does not display diagnostic information.
1	The software displays diagnostic messages every time it trains a new binary learner.
2	The software displays extra diagnostic messages every time it trains a new binary learner.

Example: `'Verbose',1`

Data Types: `double` | `single`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector.

The size of `Weights` must equal the number of rows of X. The software weighs the observations in each row of `X` with the corresponding weight in `Weights`.

The software normalizes `Weights` to sum up to the value of the prior probability in the respective class.

Data Types: `double | single`

Output Arguments

`Mdl` — Trained ECOC model

`ClassificationECOC` model | `ClassificationPartitionedECOC` cross-validated model

Trained ECOC classifier, returned as a `ClassificationECOC` model or `ClassificationPartitionedECOC` cross-validated model.

If you set any of the name-value pair arguments KFold, Holdout, Leaveout, CrossVal, or CVPartition, then `Mdl` is a `ClassificationPartitionedECOC` cross-validated model. Otherwise, `Mdl` is a `ClassificationECOC` model.

To reference properties of `Mdl`, use dot notation. For example, enter `Mdl.BinaryLearners` in the Command Window to display a cell vector of trained binary learner models.

More About

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left|m_{kj}\right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Coding Design

A *coding design* is a matrix where elements direct which classes are trained by each binary learner, that is, how the multiclass problem is reduced to a series of binary problems.

Each row of the coding design corresponds to a distinct class, and each column corresponds to a binary learner. In a ternary coding design (adopted by the software), for a particular column (or binary learner):

- Rows containing a 1 indicate to the binary learner to group all observations in the corresponding classes into a positive class.
- Rows containing a -1 indicate to the binary learner to group all observations in the corresponding classes into a negative class.
- Rows containing a 0 indicate to the binary learner to ignore all observations in the corresponding classes.

Coding matrices with large, minimal, pair-wise row distances based on the Hamming measure are desirable. For details on the pair-wise row distance measure, see "Random Coding Design Matrices" on page 22-1542 and [4].

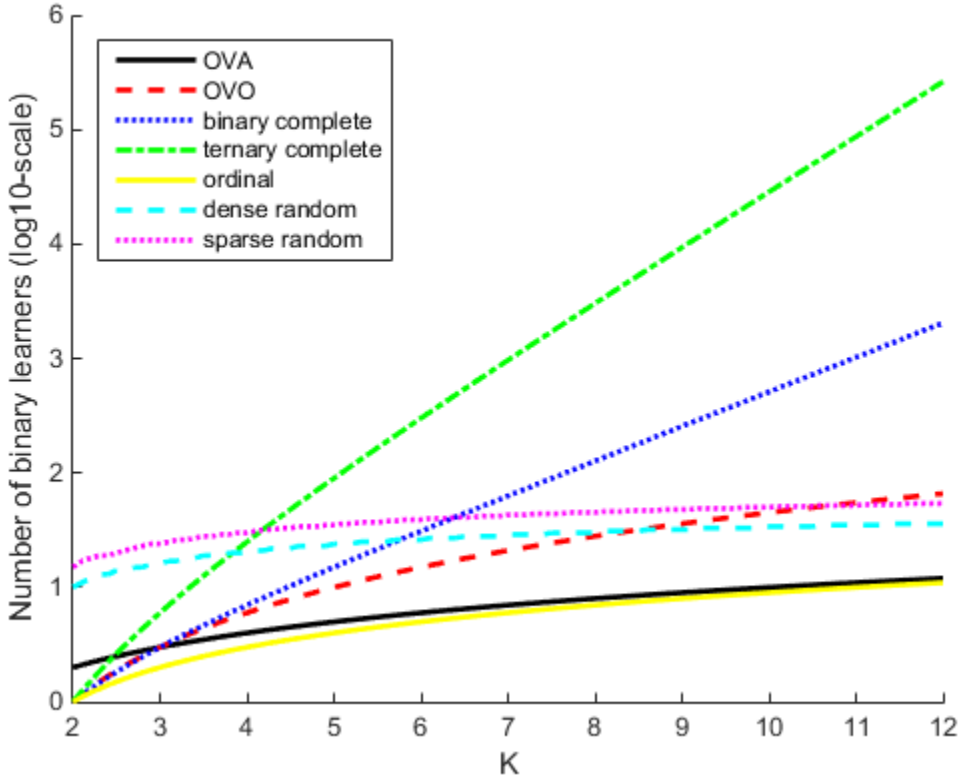
This table describes popular coding designs. For the example, suppose K (the number of distinct classes) is 3.

Coding Design	Description	Number of Learners	Minimal Pair-Wise Row Distance
one-versus-all (OVA)	For each binary learner, one class is positive and the rest are negative. This design exhausts all combinations of positive class assignments.	K	2
one-versus-one (OVO)	For each binary learner, one class is positive, another is negative, and the rest are ignored. This design exhausts	$K(K-1)/2$	1

Coding Design	Description	Number of Learners	Minimal Pair-Wise Row Distance
	all combinations of class pair assignments.		
binary complete	This design partitions the classes into all binary combinations, and does not ignore any classes. That is, all class assignments are `-1` and `1` with at least one positive and negative class in the assignment for each binary learner.	$2^{K-1}-1$	2^{K-2}
ternary complete	This design partitions the classes into all ternary combinations. That is, all class assignments are `0`, `-1`, and `1` with at least one positive and negative class in the assignment for each binary learner.	$(3^K-2^{K+1}+1)/2$	3^{K-2}
ordinal	For the first binary learner, the first class is negative, and the rest positive. For the second binary learner, the first two classes are negative, and the rest positive, and so on.	$K-1$	1

Coding Design	Description	Number of Learners	Minimal Pair-Wise Row Distance
dense random	For each binary learner, the software randomly assigns classes into positive or negative classes, with at least one of each type. For more details, see "Random Coding Design Matrices" on page 22-1542.	Random, but approximately 10 $\log_2 K$	Variable
sparse random	For each binary learner, the software randomly assigns classes as positive or negative with probability 0.25 for each, and ignores classes with probability 0.5. For more details, see "Random Coding Design Matrices" on page 22-1542.	Random, but approximately 15 $\log_2 K$	Variable

This plot compares the number of binary learners for the coding designs with increasing K.



Error-Correcting Output Code Multiclass Model

An *error-correcting output code multiclass model* (ECOC) reduces the problem of classification with three or more classes to a set of binary classifiers.

ECOC classification requires a coding design, which determines the classes that the binary learners train on, and a decoding scheme, which determines how the results (predictions) of the binary classifiers are aggregated. Suppose that there are three classes, the coding design is one-versus-one, the decoding scheme uses loss g, and the learners are SVMs. To build this classification model, ECOC follows these steps.

1

A one-versus-one coding design is

	Learner 1	Learner 2	Learner 3
Class 1	1	1	0
Class 2	–1	0	1
Class 3	0	–1	–1

Learner 1 trains on observations having Class 1 and Class 2, and treats Class 1 as the positive class and Class 2 as the negative class. The other learners are trained similarly. Let M be the coding design matrix with elements m_{kl}, and s_l be the predicted classification score for the positive class of learner l.

2 A new observation is assigned to the class ($\hat{k}$) that minimizes the aggregation of the losses for the L binary learners. That is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{l=1}^{L} |m_{kl}| g(m_{kl}, s_l)}{\sum_{l=1}^{L} |m_{kl}|}.$$

ECOC models can improve classification accuracy, even compared to other multiclass models [2].

Tips

- The number of binary learners grows with the number of classes. For a problem with many classes, the `binarycomplete` and `ternarycomplete` coding designs are not efficient. However:
  - If $K \leq 4$, then use `ternarycomplete` coding design rather than `sparserandom`.
  - If $K \leq 5$, then use `binarycomplete` coding design rather than `denserandom`.

  You can display the coding design matrix of a trained ECOC classifier by entering `Mdl.CodingMatrix` into the Command Window.
- You should form a coding matrix using intimate knowledge of the application, and taking into account computational constraints. If you have sufficient computational power and time, then try several coding matrices and choose the one with the best performance (e.g., check the confusion matrices for each model using `confusionmat`).

Algorithms

Custom Coding Design Matrices

Custom coding matrices must have a certain form. The software validates custom coding matrices by ensuring:

- Every element is -1, 0, or 1.
- Every column contains as least one -1 and one 1.
- For all distinct column vectors u and v, $u \neq v$ and $u \neq -v$.
- All rows vectors are unique.
- The matrix can separate any two classes. That is, you can travel from any row to any other row following these rules:
  - You can move vertically from 1 to -1 or -1 to 1.
  - You can move horizontally from a nonzero element to another nonzero element.
  - You can use a column of the matrix for a vertical move only once.

  If it is not possible to move from row i to row j using these rules, then classes i and j cannot be separated by the design. For example, in the coding design

$$\begin{bmatrix} 1 & 0 \\ -1 & 0 \\ 0 & 1 \\ 0 & -1 \end{bmatrix}$$

  classes 1 and 2 cannot be separated from classes 3 and 4 (that is, you cannot move horizontally from the -1 in row 2 to column 2 since there is a 0 in that position). Therefore, the software rejects this coding design.

Parallel Computing

If you use parallel computing (see Options), then `fitcecoc` trains binary learners in parallel.

Prior Probabilities and Cost

- Prior probabilities — The software normalizes the specified class prior probabilities (Prior) for each binary learner. Let M be the coding design matrix and $I(A,c)$ be an indicator matrix. The indicator matrix has the same dimensions as A, and has elements equaling one if the corresponding element of A is c, and zero otherwise. Let M_{+1} and M_{-1} be K-by-L matrices such that:

  - $M_{+1} = M \circ I(M,1)$, where $\circ$ is element-wise multiplication (that is, `Mplus = M.*(M == 1)`). Also, let $m_l^{(+1)}$ be column vector l of M_{+1}.
  - $M_{-1} = -M \circ I(M,-1)$ (that is, `Mminus = -M.*(M == -1)`). Also, let $m_l^{(-1)}$ be column vector l of M_{-1}.

  Let $\pi_l^{+1} = m_l^{(+1)} \circ \pi$ and $\pi_l^{-1} = m_l^{(-1)} \circ \pi$, where π is the vector of specified, class prior probabilities (Prior).

  Then, the positive and negative, scalar class prior probabilities for binary learner l are

  $$\hat{\pi}_l^{(j)} = \frac{\left\| \pi_l^{(j)} \right\|_1}{\left\| \pi_l^{(+1)} \right\|_1 + \left\| \pi_l^{(-1)} \right\|_1},$$

  where $j = \{-1,1\}$ and $\|\alpha\|_1$ is the one-norm of α.

- Cost — The software normalizes the K-by-K cost matrix C (Cost) for each binary learner. For binary learner l, the cost of classifying a negative-class observation into the positive class is

  $$c_l^{-+} = \left(\pi_l^{(-1)}\right)' C \pi_l^{(+1)}.$$

  Similarly, the cost of classifying a positive-class observation into the negative class is

  $$c_l^{+-} = \left(\pi_l^{(+1)}\right)' C \pi_l^{(-1)}.$$

The cost matrix for binary learner l is

$$C_l = \begin{bmatrix} 0 & c_l^{-+} \\ c_l^{+-} & 0 \end{bmatrix}.$$

ECOC models accommodate misclassification costs by incorporating them with class prior probabilities. If you specify `Prior` and `Cost`, then the software adjusts the class prior probabilities as follows:

$$\bar{\pi}_l^{-1} = \frac{c_l^{-+}\hat{\pi}_l^{-1}}{c_l^{-+}\hat{\pi}_l^{-1} + c^{+-}\hat{\pi}_l^{+1}}$$

$$\bar{\pi}_l^{+1} = \frac{c_l^{+-}\hat{\pi}_l^{+1}}{c_l^{-+}\hat{\pi}_l^{-1} + c^{+-}\hat{\pi}_l^{+1}}.$$

Random Coding Design Matrices

For a given number of classes, e.g., K, the software generates random coding design matrices as follows.

1. The software generates one of the following:
   a. Dense random — The software sets each element of the K-by-L_d coding design matrix with a 1 or a -1 with equal probability, where $L_d \approx \lceil 10 \log_2 K \rceil$.
   b. Sparse random — The software sets each element of the K-by-L_s coding design matrix with a 1, with probability 0.25, a -1 with probability 0.25, and a 0 with probability 0.5, where $L_s \approx \lceil 15 \log_2 K \rceil$.
2. If a column does not contain at least one 1 and at least one -1, then the software removes that column.
3. For distinct columns u and v, if $u = v$ or $u \neq -v$, then the software removes v from the coding design matrix.

The software randomly generates 10,000 matrices by default, and retains the matrix with the largest, minimal pair-wise row distance based on the Hamming measure ([4]) given by

$$\Delta(k_1,k_2)=0.5\sum_{l=1}^{L}\left|m_{k_1 l}\right|\left|m_{k_2 l}\right|\left|m_{k_1 l}-m_{k_2 l}\right|,$$

where m_{kjl} is an element of coding design matrix j.

Support Vector Storage

For linear, SVM binary learners, and for efficiency, `fitcecoc` empties the properties `Alpha`, `SupportVectorLabels`, and `SupportVectors`. `fitcecoc` lists `Beta`, rather than `Alpha`, in the model display.

To store `Alpha`, `SupportVectorLabels`, and `SupportVectors`, pass a linear, SVM template that specifies storing support vectors to `fitcecoc`. For example, enter:

```
t = templateSVM('SaveSupportVectors','on')
Mdl = fitcecoc(X,Y,'Learners',t);
```

You can subsequently remove the support vectors and related values by passing the resulting `ClassificationECOC` model to `discardSupportVectors`.

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Fürnkranz, Johannes, "Round Robin Classification." *J. Mach. Learn. Res.*, Vol. 2, 2002, pp. 721–747.

[3] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[4] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recog. Lett.*, Vol. 30, Issue 3, 2009, pp. 285–297.

See Also

`ClassificationECOC` | `ClassificationPartitionedECOC` | `CompactClassificationECOC` | `designecoc` | `loss` | `predict` | `statset` | `templateDiscriminant` | `templateEnsemble` | `templateKNN` | `templateSVM` | `templateTree`

Introduced in R2014b

fitcknn

Fit *k*-nearest neighbor classifier

Syntax

```
mdl = fitcknn(X,y)
mdl = fitcknn(X,y,Name,Value)
```

Description

`mdl = fitcknn(X,y)` returns a classification model based on the input variables (also known as predictors, features, or attributes) X and output (response) y.

`mdl = fitcknn(X,y,Name,Value)` fits a model with additional options specified by one or more name-value pair arguments. For example, you can specify the tie-breaking algorithm, distance metric, or observation weights.

Examples

Train a *k*-Nearest Neighbor Classifier

Construct a *k*-nearest neighbor classifier for Fisher's iris data, where *k*, the number of nearest neighbors in the predictors, is 5.

Load Fisher's iris data.

```
load fisheriris
X = meas;
Y = species;
```

`X` is a numeric matrix that contains four petal measurements for 150 irises. `Y` is a cell array of strings that contains the corresponding iris species.

Train a 5-nearest neighbors classifier. It is good practice to standardize noncategorical predictor data.

```
Mdl = fitcknn(X,Y,'NumNeighbors',5,'Standardize',1)
```

```
Mdl =

  ClassificationKNN
     PredictorNames: {'x1'  'x2'  'x3'  'x4'}
       ResponseName: 'Y'
         ClassNames: {'setosa'  'versicolor'  'virginica'}
     ScoreTransform: 'none'
    NumObservations: 150
           Distance: 'euclidean'
       NumNeighbors: 5
```

`Mdl` is a trained `ClassificationKNN` classifier, and some of its properties display in the Command Window.

To access the properties of `Mdl`, use dot notation.

```
Mdl.ClassNames
Mdl.Prior
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

    0.3333    0.3333    0.3333
```

`Mdl.Prior` contains the class prior probabilities, which are settable using the name-value pair argument `'Prior'` in `fitcknn`. The order of the class prior probabilities corresponds to the order of the classes in `Mdl.ClassNames`. By default, the prior probabilities are the respective relative frequencies of the classes in the data.

You can also reset the prior probabilities after training. For example, set the prior probabilities to 0.5, 0.2, and 0.3 respectively.

```
Mdl.Prior = [0.5 0.2 0.3];
```

You can pass `Mdl` to, for example, predict (ClassificationKNN) to label new measurements, or crossval (ClassificationKNN) to cross validate the classifier.

Train a *k*-Nearest Neighbor Classifier Using the Minkowski Metric

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

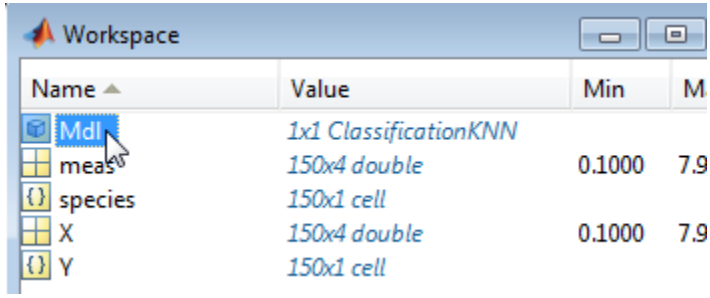
`X` is a numeric matrix that contains four petal measurements for 150 irises. `Y` is a cell array of strings that contains the corresponding iris species.

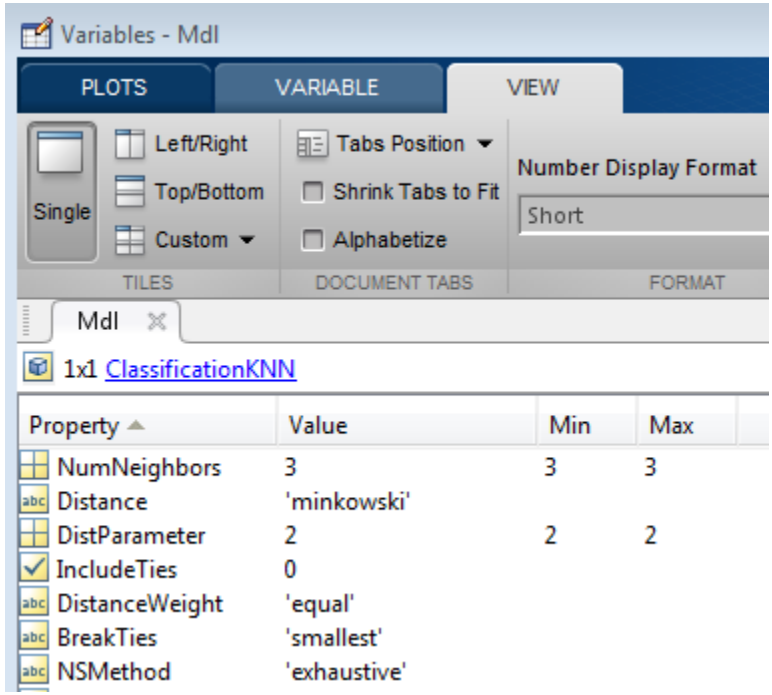
Train a 3-nearest neighbors classifier using the Minkowski metric. To use the Minkowski metric, you must use an exhaustive searcher. It is good practice to standardize noncategorical predictor data.

```
Mdl = fitcknn(X,Y,'NumNeighbors',3,...
    'NSMethod','exhaustive','Distance','minkowski',...
    'Standardize',1);
```

`Mdl` is a `ClassificationKNN` classifier.

You can examine the properties of `Mdl` by double-clicking `Mdl` in the Workspace window. This opens the Variable Editor.





Train a *k*-Nearest Neighbor Classifier Using a Custom Distance Metric

Train a *k*-nearest neighbor classifier using the chi-square distance.

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
```

The chi-square distance between *j*-dimensional points *x* and *z* is

$$\chi(x,z) = \sqrt{\sum_{j=1}^{J} w_j (x_j - z_j)^2},$$

where w_j is a weight associated with dimension *j*.

Specify the chi-square distance function. The distance function must:

- Take one row of `X`, e.g., `x`, and the matrix `Z`.
- Compare `x` to each row of `Z`.
- Return a vector `D` of length n_z, where n_z is the number of rows of `Z`. Each element of `D` is the distance between the observation corresponding to `x` and the observations corresponding to each row of `Z`.

```
chiSqrDist = @(x,Z,wt)sqrt((bsxfun(@minus,x,Z).^2)*wt);
```

This example uses arbitrtary weights for illustration.

Train a 3-nearest neighbor classifier. It is good practoce to standardize noncategorical predictor data.

```
k = 3;
w = [0.3; 0.3; 0.2; 0.2];
KNNMdl = fitcknn(X,Y,'Distance',@(x,Z)chiSqrDist(x,Z,w),...
    'NumNeighbors',k,'Standardize',1);
```

`KNNMdl` is a ClassificationKNN class classifier.

Cross validate the KNN classifier using the default 10-fold cross validation. Examine the classification error.

```
rng(1); % For reproducibility
CVKNNMdl = crossval(KNNMdl);
classError = kfoldLoss(CVKNNMdl)
```

```
classError =

    0.0600
```

`CVKNNMdl` is a ClassificationPartitionedModel class classifier. The 10-fold classification error is 4%.

Compare the classifier with one that uses a different weighting scheme.

```
w2 = [0.2; 0.2; 0.3; 0.3];
CVKNNMdl2 = fitcknn(X,Y,'Distance',@(x,Z)chiSqrDist(x,Z,w2),...
    'NumNeighbors',k,'KFold',10,'Standardize',1);
classError2 = kfoldLoss(CVKNNMdl2)
```

```
classError2 =
```

```
    0.0400
```

The second weighting scheme yields a classifier that has better out-of-sample performance.

- "Construct a KNN Classifier" on page 16-28
- "Modify a KNN Classifier" on page 16-30

Input Arguments

X — Predictor values

numeric matrix

Predictor values, specified as a numeric matrix. Each column of X represents one variable, and each row represents one observation.

Data Types: `single` | `double`

y — Classification values

numeric vector | categorical vector | logical vector | character array | cell array of strings

Classification values, specified as a numeric vector, categorical vector, logical vector, character array, or cell array of strings, with the same number of rows as X. Each row of y represents the classification of the corresponding row of X.

Data Types: `single` | `double` | `cell` | `logical` | `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'NumNeighbors',3,'NSMethod','exhaustive','Distance','minkowski'` specifies a classifier for three-nearest neighbors using the nearest neighbor search method and the Minkowski metric.

`'BreakTies'` — Tie-breaking algorithm

`'smallest'` (default) | `'nearest'` | `'random'`

Tie-breaking algorithm used by the `predict` method if multiple classes have the same smallest cost, specified as the comma-separated pair consisting of `'BreakTies'` and one of the following:

- `'smallest'` — Use the smallest index among tied groups.
- `'nearest'` — Use the class with the nearest neighbor among tied groups.
- `'random'` — Use a random tiebreaker among tied groups.

By default, ties occur when multiple classes have the same number of nearest points among the `K` nearest neighbors.

Example: `'BreakTies','nearest'`

`'BucketSize'` — Maximum data points in node

`50` (default) | positive integer value

Maximum number of data points in the leaf node of the *k*d-tree, specified as the comma-separated pair consisting of `'BucketSize'` and a positive integer value. This argument is meaningful only when `NSMethod` is `'kdtree'`.

Example: `'BucketSize',40`

Data Types: `single` | `double`

`'CategoricalPredictors'` — Categorical predictor flag

`[]` (default) | `'all'`

Categorical predictor flag, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following:

- `'all'` — All predictors are categorical.
- `[]` — No predictors are categorical.

When you set `CategoricalPredictors` to `'all'`, the default `Distance` is `'hamming'`.

Example: `'CategoricalPredictors','all'`

`'ClassNames'` — Class names

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and an array representing the class names. Use the same data type as the values that exist in y.

Use `ClassNames` to order the classes or to select a subset of classes for training. The default is the class names in y.

Data Types: `single` | `double` | `char` | `logical` | `cell`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification of a point, specified as the comma-separated pair consisting of `'Cost'` and one of the following:

- Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.
- Structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Data Types: `single` | `double` | `struct`

`'Cov'` — Covariance matrix

`nancov(X)` (default) | positive definite matrix of scalar values

Covariance matrix, specified as the comma-separated pair consisting of `'Cov'` and a positive definite matrix of scalar values representing the covariance matrix when computing the Mahalanobis distance. This argument is only valid when `'Distance'` is `'mahalanobis'`.

You cannot simultaneously specify `'Standardize'` and either of `'Scale'` or `'Cov'`.

Data Types: `single` | `double`

`'CrossVal'` — Cross-validation flag

`'off'` (default) | `'on'`

Cross-validation flag, specified as the comma-separated pair consisting of `'CrossVal'` and either `'on'` or `'off'`. If `'on'`, `fitcknn` creates a cross-validated model with 10

folds. Use the 'KFold', 'Holdout', 'Leaveout', or 'CVPartition' parameters to override this cross-validation setting. You can only use one parameter at a time to create a cross-validated model.

Alternatively, cross validate mdl later using the crossval method.

Example: 'Crossval','on'

'CVPartition' — Cross-validated model partition

cvpartition object

Cross-validated model partition, specified as the comma-separated pair consisting of 'CVPartition' and an object created using cvpartition. You can only use one of these four options at a time to create a cross-validated model: 'KFold', 'Holdout', 'Leaveout', or 'CVPartition'.

'Distance' — Distance metric

valid distance metric string | function handle

Distance metric, specified as the comma-separated pair consisting of 'Distance' and a valid distance metric string or function handle. The allowable strings depend on the NSMethod parameter, which you set in fitcknn, and which exists as a field in ModelParameters. If you specify CategoricalPredictors as 'all', then the default distance metric is 'hamming'. Otherwise, the default distance metric is 'euclidean'.

NSMethod	Distance Metric Names
exhaustive	Any distance metric of ExhaustiveSearcher
kdtree	'cityblock', 'chebychev', 'euclidean', or 'minkowski'

For definitions, see “Distance Metrics”.

This table includes valid distance metrics of ExhaustiveSearcher.

Value	Description
'cityblock'	City block distance.
'chebychev'	Chebychev distance (maximum coordinate difference).
'correlation'	One minus the sample linear correlation between observations (treated as sequences of values).
'cosine'	One minus the cosine of the included angle between observations (treated as vectors).

Value	Description
`'euclidean'`	Euclidean distance.
`'hamming'`	Hamming distance, percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of X, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair argument.
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'Exponent'` name-value pair argument.
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between X and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from X, `S = nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair argument.
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@`*`distfun`*	Distance function handle. *`distfun`* has the form
	`function D2 = DISTFUN(ZI,ZJ)`
	`% calculation of  distance`
	`...`
	where
	• `ZI` is a `1`-by-`N` vector containing one row of X or y.
	• `ZJ` is an `M2`-by-`N` matrix containing multiple rows of X or y.
	• `D2` is an `M2`-by-`1` vector of distances, and `D2(k)` is the distance between observations `ZI` and `ZJ(J,:)`.

Example: `'Distance','minkowski'`

Data Types: `function_handle`

`'DistanceWeight'` — Distance weighting function

`'equal'` (default) | `'inverse'` | `'squaredinverse'` | function handle

Distance weighting function, specified as the comma-separated pair consisting of `'DistanceWeight'` and either a function handle or one of the following strings specifying the distance weighting function.

DistanceWeight	Meaning
`'equal'`	No weighting
`'inverse'`	Weight is 1/distance
`'squaredinverse'`	Weight is $1/\text{distance}^2$
`@fcn`	*`fcn`* is a function that accepts a matrix of nonnegative distances, and returns a matrix the same size containing nonnegative distance weights. For example, `'squaredinverse'` is equivalent to `@(d)d.^(-2)`.

Example: `'DistanceWeight','inverse'`

Data Types: `function_handle`

`'Exponent'` — Minkowski distance exponent

`2` (default) | positive scalar value

Minkowski distance exponent, specified as the comma-separated pair consisting of `'Exponent'` and a positive scalar value. This argument is only valid when `'Distance'` is `'minkowski'`.

Example: `'Exponent',3`

Data Types: `single` | `double`

`'Holdout'` — Fraction of data for holdout validation

`0` (default) | scalar value in the range `[0,1]`

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the remaining data for training.

If you use `Holdout`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single` | `double`

`'IncludeTies'` — Tie inclusion flag

`false` (default) | `true`

Tie inclusion flag, specified as the comma-separated pair consisting of `'IncludeTies'` and a logical value indicating whether `predict` includes all the neighbors whose distance values are equal to the `K`th smallest distance. If `IncludeTies` is `true`, `predict` includes all these neighbors. Otherwise, `predict` uses exactly `K` neighbors.

Example: `'IncludeTies',true`

Data Types: `logical`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated model, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

If you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. Specify `'on'` to use leave-one-out cross validation.

If you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

`'NSMethod'` — Nearest neighbor search method

`'kdtree'` | `'exhaustive'`

Nearest neighbor search method, specified as the comma-separated pair consisting of `'NSMethod'` and `'kdtree'` or `'exhaustive'`.

- `'kdtree'` — Create and use a *k*d-tree to find nearest neighbors. `'kdtree'` is valid when the distance metric is one of the following:
  - `'euclidean'`
  - `'cityblock'`
  - `'minkowski'`
  - `'chebyshev'`
- `'exhaustive'` — Use the exhaustive search algorithm. The distance values from all points in X to each point in y are computed to find nearest neighbors.

The default is `'kdtree'` when X has `10` or fewer columns, X is not sparse, and the distance metric is a `'kdtree'` type; otherwise, `'exhaustive'`.

Example: `'NSMethod','exhaustive'`

`'NumNeighbors'` — Number of nearest neighbors to find

`1` (default) | positive integer value

Number of nearest neighbors in X to find for classifying each point when predicting, specified as the comma-separated pair consisting of `'NumNeighbors'` and a positive integer value.

Example: `'NumNeighbors',3`

Data Types: `single` | `double`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in X.

Data Types: `cell`

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- A string:

  - `'empirical'` determines class probabilities from class frequencies in y. If you pass observation weights, they are used to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class). To specify the class order for the corresponding elements of `Prior`, additionally specify the ClassNames name-value pair argument.
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as y
  - `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `Weights` and `Prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Example: `'Prior','uniform'`

Data Types: `single` | `double` | `struct`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable y.

Example: `'ResponseName','Response'`

Data Types: `char`

`'Scale'` — Distance scale

`nanstd(X)` (default) | vector of nonnegative scalar values

Distance scale, specified as the comma-separated pair consisting of `'Scale'` and a vector containing nonnegative scalar values with length equal to the number of columns in X. Each coordinate difference between X and a query point is scaled by the corresponding element of `Scale`. This argument is only valid when `'Distance'` is `'seuclidean'`.

You cannot simultaneously specify `'Standardize'` and either of `'Scale'` or `'Cov'`.

Data Types: `single` | `double`

`'ScoreTransform'` — Score transform function

`'none'` (default) | `'doublelogit'` | `'invlogit'` | `'ismax'` | `'logit'` | `'sign'` | `'symmetric'` | `'symmetriclogit'` | `'symmetricismax'` | function handle

Score transform function, specified as the comma-separated pair consisting of `'ScoreTransform'` and a string or function handle.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the available, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `0`.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to `1`, and scores for all other classes to `-1`.

- For a MATLAB function, or a function that you define, enter its function handle.

  ```
  Mdl.ScoreTransform = @function;
  ```

  `function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Example: `'ScoreTransform','sign'`

Data Types: `char | function_handle`

`'Standardize'` — Flag to standardize predictors

`false` (default) | `true`

Flag to standardize the predictors, specified as the comma-separated pair consisting of `'Standardize'` and `true` (`1`) or `false (0)`.

If you set `'Standardize',true`, then the software centers and scales each column of the predictor data (X) by the column mean and standard deviation, respectively.

The software does not standardize categorical predictors, and throws an error if all predictors are categorical.

You cannot simultaneously specify `'Standardize',1` and either of `'Scale'` or `'Cov'`.

It is good practice to standardize the predictor data.

Example: `'Standardize',true`

Data Types: `logical`

`'Weights'` — Observation weights
`ones(size(X,1),1)` (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` is the number of rows in X.

The software normalizes the weights in each class to add up to the value of the prior probability of the class.

Data Types: `single` | `double`

Output Arguments

`mdl` — Classifier model
classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

Alternatives

Although `fitcknn` can train a multiclass KNN classifier, you can reduce a multiclass learning problem to a series of KNN binary learners using `fitcecoc`.

More About

Prediction

`ClassificationKNN` predicts the classification of a point `Xnew` using a procedure equivalent to this:

1. Find the `NumNeighbors` points in the training set `X` that are nearest to `Xnew`.
2. Find the `NumNeighbors` response values `Y` to those nearest points.
3. Assign the classification label `Ynew` that has the largest posterior probability among the values in `Y`.

For details, see "Posterior Probability" on page 22-3654 in the `predict` documentation.

Algorithms

- `NaN`s or `<undefined>`s indicate missing observations. The following describes the behavior of `fitcknn` when the data set or weights contain missing observations.
  - If any value of y or any weight is missing, then `fitcknn` removes those values from `y`, the weights, and the corresponding rows of X from the data. The software renormalizes the weights to sum to `1`.
  - If you specify to standardize predictors (`'Standardize',1`) or the standardized Euclidean distance (`'Distance','seuclidean'`) without a scale, then `fitcknn` removes missing observations from individual predictors before computing the mean and standard deviation. In other words, the software implements `nanmean` and `nanstd` on each predictor.
  - If you specify the Mahalanobis distance (`'Distance','mahalanbois'`) without its covariance matrix, then `fitcknn` removes rows of `X` that contain at least one missing value. In other words, the software implements `nancov` on the predictor matrix `X`.
- Suppose that you set `'Standardize',1`.

- If you also specify Prior or Weights, then the software takes the observation weights into account. Specifically, the weighted mean of predictor j is

$$\bar{x}_j = \sum_{B_j} w_k x_{jk}$$

and the weighted standard deviation is

$$s_j = \sum_{Bj} w_k (x_{jk} - \bar{x}_j),$$

where B_j is the set of indices k for which x_{jk} and w_k are not missing.

- If you also set `'Distance','mahalanobis'` or `'Distance','seuclidean'`, then you cannot specify Scale or Cov. Instead, the software:

  1. Computes the means and standard deviations of each predictor
  2. Standardizes the data using the results of step 1
  3. Computes the distance parameter values using their respective default.

- If you specify `Scale` and either of `Prior` or `Weights`, then the software scales observed distances by the weighted standard deviations.
- If you specify `Cov` and either of `Prior` or `Weights`, then the software applies the weighted covariance matrix to the distances. In other words,

$$\texttt{Cov} = \frac{\sum_B w_j}{\left(\sum_B w_j\right)^2 - \sum_B w_j^2} \sum_B w_j \left(x_j - \bar{x}\right)' \left(x_j - \bar{x}\right),$$

where B is the set of indices j for which the observation x_j does not have any missing values and w_j is not missing.

- "Classification Using Nearest Neighbors" on page 16-8

See Also

`ClassificationKNN` | `ClassificationPartitionedModel` | `fitcecoc` | `fitensemble` | `predict` | `templateKNN`

fitcnb

Train multiclass naive Bayes model

Syntax

```
Mdl = fitcnb(X,Y)
Mdl = fitcnb(X,Y,Name,Value)
```

Description

`Mdl = fitcnb(X,Y)` returns a multiclass naive Bayes model (Mdl), trained by predictors X and class labels Y.

Predict labels for new data by passing the data and `Mdl` to `predict`.

`Mdl = fitcnb(X,Y,Name,Value)` returns a naive Bayes classifier with additional options specified by one or more Name,Value pair arguments.

For example, you can specify a distribution to model the data, prior probabilities for the classes, or the kernel smoothing window bandwidth.

Examples

Train a Naive Bayes Classifier

Load Fisher's iris data set.

```
load fisheriris
X = meas(:,3:4);
Y = species;
tabulate(Y)
```

```
       Value    Count   Percent
      setosa       50     33.33%
  versicolor       50     33.33%
   virginica       50     33.33%
```

The software can classify data with more than two classes using naive Bayes methods.

Train a naive Bayes classifier. It is good practice to specify the class order.

```
Mdl = fitcnb(X,Y,...
    'ClassNames',{'setosa','versicolor','virginica'})
```

```
Mdl =

  ClassificationNaiveBayes
           PredictorNames: {'x1'  'x2'}
             ResponseName: 'Y'
                ClassNames: {'setosa'  'versicolor'  'virginica'}
           ScoreTransform: 'none'
          NumObservations: 150
        DistributionNames: {'normal'  'normal'}
    DistributionParameters: {3x2 cell}
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier.

By default, the software models the predictor distribution within each class using a Gaussian distribution having some mean and standard deviation. Use dot notation to display the parameters of a particular Gaussian fit, e.g., display the fit for the first feature within `setosa`.

```
setosaIndex = strcmp(Mdl.ClassNames,'setosa');
estimates = Mdl.DistributionParameters{setosaIndex,1}
```

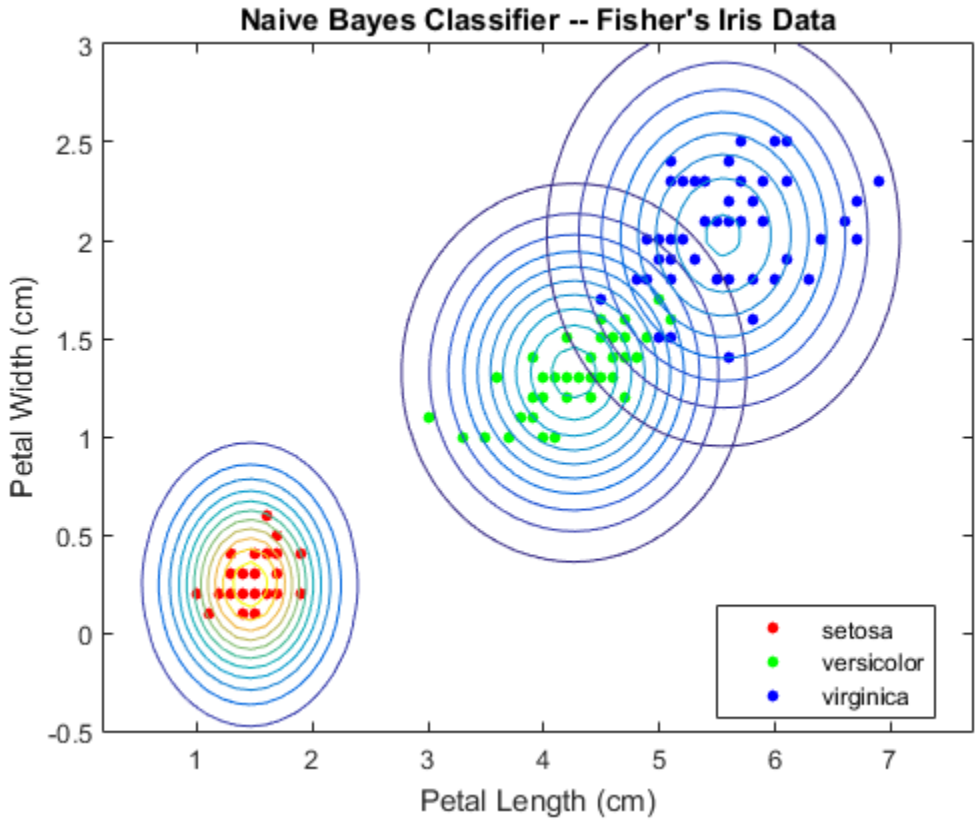
```
estimates =

    1.4620
    0.1737
```

The mean is `1.4620` and the standard deviation is `0.1737`.

Plot the Gaussian contours.

```
figure
gscatter(X(:,1),X(:,2),Y);
h = gca;
xylim = [h.XLim h.YLim]; % Get current axis limits
```

```
hold on
Params = cell2mat(Mdl.DistributionParameters);
Mu = Params(2*(1:3)-1,1:2); % Extract the means
Sigma = zeros(2,2,3);
for j = 1:3
    Sigma(:,:,j) = diag(Params(2*j,:)); % Extract the standard deviations
    ezcontour(@(x1,x2)mvnpdf([x1,x2],Mu(j,:),Sigma(:,:,j)),...
        xylim+0.5*[-1,1,-1,1]) ...
        % Draw contours for the multivariate normal distributions
end
title('Naive Bayes Classifier -- Fisher''s Iris Data')
xlabel('Petal Length (cm)')
ylabel('Petal Width (cm)')
hold off
```



You can change the default distribution using the name-value pair argument `'DistributionNames'`. For example, if some predictors are categorical, then you can specify that they are multivariate, multinomial random variables using `'DistributionNames','mvmn'`.

Specify Prior Probabilites When Training Naive Bayes Classifiers

Construct a naive Bayes classifier for Fisher's iris data set. Also, specify prior probabilities during training.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
classNames = {'setosa','versicolor','virginica'}; % Class order
```

`X` is a numeric matrix that contains four petal measurements for 150 irises. `Y` is a cell array of strings that contains the corresponding iris species.

By default, the prior class probability distribution is the relative frequency distribution of the classes in the data set, which in this case is 33% for each species. However, suppose you know that in the population 50% of the irises are setosa, 20% are versicolor, and 30% are virginica. You can incorporate this information by specifying this distribution as a prior probability during training.

Train a naive Bayes classifier. Specify the class order and prior class probability distribution.

```
prior = [0.5 0.2 0.3];
Mdl = fitcnb(X,Y,'ClassNames',classNames,'Prior',prior)
```

```
Mdl =

  ClassificationNaiveBayes
             PredictorNames: {'x1'  'x2'  'x3'  'x4'}
               ResponseName: 'Y'
                 ClassNames: {'setosa'  'versicolor'  'virginica'}
             ScoreTransform: 'none'
            NumObservations: 150
          DistributionNames: {'normal'  'normal'  'normal'  'normal'}
    DistributionParameters: {3x4 cell}
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier, and some of its properties appear in the Command Window. The software treats the predictors as independent given a class, and, by default, fits them using normal distributions.

The naive Bayes algorithm does not use the prior class probabilities during training. Therefore, you can specify prior class probabilities after training using dot notation. For example, suppose that you want to see the difference in performance between a model that uses the default prior class probabilities and a model that uses `prior`.

Create a new naive Bayes model based on `Mdl`, and specify that the prior class probability distribution is an empirical class distribution.

```
defaultPriorMdl = Mdl;
FreqDist = cell2table(tabulate(Y));
defaultPriorMdl.Prior = FreqDist{:,3};
```

The software normalizes the prior class probabilities to sum to `1`.

Estimate the cross-validation error for both models using 10-fold cross validation.

```
rng(1); % For reproducibility
defaultCVMdl = crossval(defaultPriorMdl);
defaultLoss = kfoldLoss(defaultCVMdl)
CVMdl = crossval(Mdl);
Loss = kfoldLoss(CVMdl)
```

```
defaultLoss =

    0.0533


Loss =

    0.0340
```

`Mdl` performs better than `defaultPriorMdl`.

Specify Predictor Distributions for Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;
```

```
Y = species;
```

Train a naive Bayes classifier using every predictor. It is good practice to specify the class order.

```
Mdl1 = fitcnb(X,Y,...
    'ClassNames',{'setosa','versicolor','virginica'})
Mdl1.DistributionParameters
Mdl1.DistributionParameters{1,2}
```

```
Mdl1 =

  ClassificationNaiveBayes
           PredictorNames: {'x1'  'x2'  'x3'  'x4'}
             ResponseName: 'Y'
                ClassNames: {'setosa'  'versicolor'  'virginica'}
           ScoreTransform: 'none'
          NumObservations: 150
        DistributionNames: {'normal'  'normal'  'normal'  'normal'}
    DistributionParameters: {3x4 cell}



ans =

    [2x1 double]    [2x1 double]    [2x1 double]    [2x1 double]
    [2x1 double]    [2x1 double]    [2x1 double]    [2x1 double]
    [2x1 double]    [2x1 double]    [2x1 double]    [2x1 double]


ans =

    3.4280
    0.3791
```

By default, the software models the predictor distribution within each class as a Gaussian with some mean and standard deviation. There are four predictors and three class levels. Each cell in `Mdl1.DistributionParameters` corresponds to a numeric vector containing the mean and standard deviation of each distribution, e.g., the mean and standard deviation for setosa iris sepal widths are `3.4280` and `0.3791`, respectively.

Estimate the confusion matrix for `Mdl1`.

```
isLabels1 = resubPredict(Mdl1);
ConfusionMat1 = confusionmat(Y,isLabels1)
```

```
ConfusionMat1 =

    50     0     0
     0    47     3
     0     3    47
```

Element (*j*, *k*) of `ConfusionMat1` represents the number of observations that the software classifies as *k*, but are truly in class *j* according to the data.

Retrain the classifier using the Gaussian distribution for predictors 1 and 2 (the sepal lengths and widths), and the default normal kernel density for predictors 3 and 4 (the petal lengths and widths).

```
Mdl2 = fitcnb(X,Y,...
    'Distribution',{'normal','normal','kernel','kernel'},...
    'ClassNames',{'setosa','versicolor','virginica'});
Mdl2.DistributionParameters{1,2}
```

```
ans =

    3.4280
    0.3791
```

The software does not train parameters to the kernel density. Rather, the software chooses an optimal width. However, you can specify a width using the `'Width'` name-value pair argument.

Estimate the confusion matrix for `Mdl2`.

```
isLabels2 = resubPredict(Mdl2);
ConfusionMat2 = confusionmat(Y,isLabels2)
```

```
ConfusionMat2 =

    50     0     0
     0    47     3
     0     3    47
```

Based on the confusion matrices, the two classifiers perform similarly in the training sample.

Compare Classifiers Using Cross Validation

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
rng(1); % For reproducibility
```

Train and cross validate a naive Bayes classifier using the default options and *k*-fold cross validation. It is good practice to specify the class order.

```
CVMdl1 = fitcnb(X,Y,...
    'ClassNames',{'setosa','versicolor','virginica'},...
    'CrossVal','on');
```

By default, the software models the predictor distribution within each class as a Gaussian with some mean and standard deviation. `CVMdl1` is a `ClassificationPartitionedModel` model.

Create a default naive Bayes binary classifier template, and train an error-correcting, output codes multiclass model.

```
t = templateNaiveBayes();
CVMdl2 = fitcecoc(X,Y,'CrossVal','on','Learners',t);
```

`CVMdl2` is a `ClassificationPartitionedECOC` model. You can specify options for the naive Bayes binary learners using the same name-value pair arguments as for `fitcnb`.

Compare the out-of-sample *k*-fold classification error (proportion of misclassified observartions).

```
classErr1 = kfoldLoss(CVMdl1,'LossFun','ClassifErr')
classErr2 = kfoldLoss(CVMdl2,'LossFun','ClassifErr')
```

```
classErr1 =

    0.0533


classErr2 =
```

```
    0.0467
```

`Mdl2` has a lower generalization error.

Train Naive Bayes Classifiers Using Multinomial Predictors

Some spam filters classify an incoming email as spam based on how many times a word or punctuation (called tokens) occurs in an email. The predictors are the frequencies of particular words or punctuations in an email. Therefore, the predictors compose multinomial random variables.

This example illustrates classification using naive Bayes and multinomial predictors.

Create Training Data

Suppose you observed 1000 emails and classified them as spam or not spam. Do this by randomly assigning -1 or 1 to `y` for each email.

```
n = 1000;                          % Sample size
rng(1);                            % For reproducibility
Y = randsample([-1 1],n,true);  % Random labels
```

To build the predictor data, suppose that there are five tokens in the vocabulary, and 20 observed tokens per email. Generate predictor data from the five tokens by drawing random, multinomial deviates. The relative frequencies for tokens corresponding to spam emails should differ from emails that are not spam.

```
tokenProbs = [0.2 0.3 0.1 0.15 0.25;...
    0.4 0.1 0.3 0.05 0.15];             % Token relative frequencies
tokensPerEmail = 20;                    % Fixed for convenience
X = zeros(n,5);
X(Y == 1,:) = mnrnd(tokensPerEmail,tokenProbs(1,:),sum(Y == 1));
X(Y == -1,:) = mnrnd(tokensPerEmail,tokenProbs(2,:),sum(Y == -1));
```

Train the Classifier

Train a naive Bayes classifier. Specify that the predictors are multinomial.

```
Mdl = fitcnb(X,Y,'Distribution','mn');
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier.

Assess the in-sample performance of `Mdl` by estimating the misclassification error.

```
isGenRate = resubLoss(Mdl,'LossFun','ClassifErr')
```

```
isGenRate =

    0.0200
```

The in-sample misclassification rate is 2%.

Create New Data

Randomly generate deviates that represent a new batch of emails.

```
newN = 500;
newY = randsample([-1 1],newN,true);
newX = zeros(newN,5);
newX(newY == 1,:) = mnrnd(tokensPerEmail,tokenProbs(1,:),...
    sum(newY == 1));
newX(newY == -1,:) = mnrnd(tokensPerEmail,tokenProbs(2,:),...
    sum(newY == -1));
```

Assess Classifier Performance

Classify the new emails using the trained naive Bayes classifier `Mdl`, and determine whether the algorithm generalizes.

```
oosGenRate = loss(Mdl,newX,newY)
```

```
oosGenRate =

    0.0261
```

The out-of-sample misclassification rate is 2.6% indicating that the classifier generalizes fairly well.

Input Arguments

X — Predictor data

matrix of numeric values

Predictor data to which the naive Bayes classifier is trained, specified as a matrix of numeric values.

Each row of X corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature).

The length of Y and the number of rows of X must be equivalent.

Data Types: double

Y — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels to which the naive Bayes classifier is trained, specified as a categorical or character array, logical or numeric vector, or cell array of strings. Each element of Y defines the class membership of the corresponding row of X. Y supports K class levels.

If Y is a character array, then each row must correspond to one class label.

The length of Y and the number of rows of X must be equivalent.

Data Types: cell | char | double | logical

Note: The software treats NaN, empty string (''), and <undefined> elements as missing values.

- If Y contains missing values, then the software removes them and the corresponding rows of X.
- If X contains any rows composed entirely of missing values, then the software removes those rows and the corresponding elements of Y.
- If X contains missing values and you set 'Distribution','mn', then the software removes those rows of X and the corresponding elements of Y.
- If a predictor is not represented in a class, that is, if all of its values are NaN within a class, then the software returns an error.

Removing rows of X and corresponding elements of Y decreases the effective training or cross-validation sample size.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. Name is the argument name and Value is the corresponding value. Name must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Distribution','mn','Prior','uniform','KSWidth',0.5` specifies that the data distribution is multinomial, the prior probabilities for all classes are equal, and the kernel smoothing window bandwidth for all classes is `0.5` units.

Naive Bayes Options

`'DistributionNames'` — Data distributions

`'kernel'` | `'mn'` | `'mvmn'` | `'normal'` | cell array of strings

Data distributions `fitcnb` uses to model the data, specified as the comma-separated pair consisting of `'DistributionNames'` and a string or cell array of strings.

This table summarizes the available distributions.

Value	Description
`'kernel'`	Kernel smoothing density estimate.
`'mn'`	Multinomial distribution. If you specify `mn`, then all features are components of a multinomial distribution. Therefore, you cannot include `'mn'` as an element of a cell array of strings. For details, see "Algorithms".
`'mvmn'`	Multivariate multinomial distribution. For details, see "Algorithms".
`'normal'`	Normal (Gaussian) distribution.

If you specify a string, then the software models all the features using that distribution. If you specify a 1-by-P cell array of strings, then the software models feature j using the distribution in element j of the cell array.

By default, the software sets all predictors specified as categorical predictors (using the CategoricalPredictors name-value pair argument) to `'mvmn'`. Otherwise, the default distribution is `'normal'`.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'Distribution','mn'`

Data Types: `cell` | `char`

`'Kernel'` — Kernel smoother type

`'normal'` (default) | `'box'` | `'epanechnikov'` | `'triangle'` | cell array of strings

Kernel smoother type, specified as the comma-separated pair consisting of `'Kernel'` and a string or cell array of strings.

This table summarizes the available options for setting the kernel smoothing density region. Let $I\{u\}$ denote the indictor function.

Value	Kernel	Formula
`'box'`	Box (uniform)	$f(x) = 0.5I\{\lvert x\rvert \le 1\}$
`'epanechni`	Epanechnikov	$f(x) = 0.75\left(1 - x^2\right)I\{\lvert x\rvert \le 1\}$
`'normal'`	Gaussian	$f(x) = \frac{1}{\sqrt{2\pi}}\exp\left(-0.5x^2\right)$
`'triangle'`	Triangular	$f(x) = \left(1 - \lvert x\rvert\right)I\{\lvert x\rvert \le 1\}$

If you specify a 1-by-P cell array, with each cell containing any value in the table, then the software trains the classifier using the kernel smoother type in cell j for feature j in X. The software ignores cells of `Kernel` not corresponding to a predictor whose distribution is `'kernel'`.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'Kernel',{'epanechnikov','normal'}`

Data Types: `cell` | `char`

`'Support'` — Kernel smoothing density support

`'unbounded'` (default) | `'positive'` | cell array | numeric row vector

Kernel smoothing density support, specified as the comma-separated pair consisting of `'Support'` and `'positive'`, `'unbounded'`, a cell array, or a numeric row vector. The software applies the kernel smoothing density to the specified region.

This table summarizes the available options for setting the kernel smoothing density region.

Value	Description
1-by-2 numeric row vector	For example, `[L,U]`, where `L` and `U` are the finite lower and upper bounds, respectively, for the density support.
`'positive'`	The density support is all positive real values.
`'unbounded'`	The density support is all real values.

If you specify a 1-by-*P* cell array, with each cell containing any value in the table, then the software trains the classifier using the kernel support in cell *j* for feature *j* in X. The software ignores cells of `Kernel` not corresponding to a predictor whose distribution is `'kernel'`.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'KSSupport',{[-10,20],'unbounded'}`

Data Types: `cell` | `char` | `double`

`'Width'` — Kernel smoothing window width

matrix of numeric values | numeric column vector | numeric row vector | scalar

Kernel smoothing window width, specified as the comma-separated pair consisting of `'Width'` and a matrix of numeric values, numeric column vector, numeric row vector, or scalar.

Suppose there are *K* class levels and *P* predictors. This table summarizes the available options for setting the kernel smoothing window width.

Value	Description
K-by-*P* matrix of numeric values	Element (*k*,*j*) specifies the width for predictor *j* in class *k*.
K-by-1 numeric column vector	Element *k* specifies the width for all predictors in class *k*.
1-by-*P* numeric row vector	Element *j* specifies the width in all class levels for predictor *j*.

Value	Description
scalar	Specifies the bandwidth for all features in all classes.

By default, the software selects a default width automatically for each combination of predictor and class by using a value that is optimal for a Gaussian distribution. If you specify `Width` and it contains `NaN`s, then the software selects widths for the elements containing `NaN`s.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'Width',[NaN NaN]`

Data Types: `double | struct`

Cross-Validation Options

`'CrossVal'` — Cross-validation flag

`'off'` (default) | `'on'`

Cross-validation flag, specified as the comma-separated pair consisting of `'CrossVal'` and either `'on'` or `'off'`. If `'on'`, `fitcknn` creates a cross-validated model with 10 folds. Use the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` parameters to override this cross-validation setting. You can only use one parameter at a time to create a cross-validated model.

Alternatively, cross validate Mdl after training using the `crossval` method.

Example: `'Crossval','on'`

`'CVPartition'` — Cross-validated model partition

`cvpartition` object

Cross-validated model partition, specified as the comma-separated pair consisting of `'CVPartition'` and an object created using `cvpartition`. You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'Holdout'` — Fraction of data for holdout validation

`0` (default) | scalar value in the range `[0,1]`

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the remaining data for training.

If you use `Holdout`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single` | `double`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated model, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

If you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. Specify `'on'` to use leave-one-out cross validation.

If you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

Other Classification Options

`'CategoricalPredictors'` — Categorical predictors list

`[]` (default) | `'all'` | cell array of strings | character array | logical vector | numeric vector

Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following:

- A numeric vector with indices from `1` through `p`, where `p` is the number of columns of X.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of X is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in `PredictorNames` values.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in `PredictorNames` values. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

By default, no predictors are categorical.

Example: `'CategoricalPredictors','all'`

Data Types: `single` | `double` | `char` | `cell`

`'ClassNames'` — Class names

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and an array representing the class names. Use the same data type as the values that exist in Y.

Use `ClassNames` to order the classes or to select a subset of classes for training.

The default is the class names in Y.

Example: `'ClassNames',{'b','g'}`

Data Types: `single` | `double` | `char` | `logical` | `cell`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification of a point, specified as the comma-separated pair consisting of `'Cost'` and one of the following:

- Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- Structure S having two fields: `S.ClassNames` containing the group names as a variable of the same type as Y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Example: `'Cost',struct('ClassNames',{{'b','g'}},'ClassificationCosts',[0 0.5; 1 0])`

Data Types: `single` | `double` | `struct`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in X.

Data Types: `cell`

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- A string:
  - `'empirical'` determines class probabilities from class frequencies in Y.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class). To specify the class order for the corresponding elements of `Prior`, additionally specify the ClassNames name-value pair argument.
- A structure S with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as Y
  - `S.ClassProbs` containing a vector of corresponding probabilities

The software normalizes the values of `Prior` so that they sum to `1`. If you set values for both `Weights` and `Prior`, the weights are renormalized to sum to the value of the prior probability in their respective class.

Example: `'Prior','uniform'`

Data Types: `single` | `double` | `struct`

`'ResponseName'` — Response variable name
`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable Y.

Example: `'ResponseName','Response'`

Data Types: `char`

`'ScoreTransform'` — Score transform function
`'none'` (default) | `'doublelogit'` | `'invlogit'` | `'ismax'` | `'logit'` | `'sign'` | `'symmetric'` | `'symmetriclogit'` | `'symmetricismax'` | function handle

Score transform function, specified as the comma-separated pair consisting of `'ScoreTransform'` and a string or function handle.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the available, built-in functions.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to 0.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to -1.

- For a MATLAB function, or a function that you define, enter its function handle.

```
Mdl.ScoreTransform = @function;
```

`function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Example: `'ScoreTransform','sign'`

Data Types: `char` | `function_handle`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` is the number of rows in X.

The software normalizes the weights in each class to add up to the value of the prior probability of the class.

Data Types: `single` | `double`

Output Arguments

`Mdl` — Trained naive Bayes classifier

`ClassificationNaiveBayes` classifier

Trained naive Bayes classifier, returned as a `ClassificationNaiveBayes` classifier.

More About

Bag-of-Tokens Model

In the bag-of-tokens model, the value of predictor *j* is the nonnegative number of occurrences of token *j* in this observation. The number of categories (bins) in this multinomial model is the number of distinct tokens, that is, the number of predictors.

Naive Bayes

Naive Bayes is a classification algorithm that applies density estimation to the data.

The algorithm leverages Bayes theorem, and (naively) assumes that the predictors are conditionally independent, given the class. Though the assumption is usually violated

in practice, naive Bayes classifiers tend to yield posterior distributions that are robust to biased class density estimates, particularly where the posterior is 0.5 (the decision boundary) [1].

Naive Bayes classifiers assign observations to the most probable class (in other words, the *maximum a posteriori* decision rule). Explicitly, the algorithm:

1. Estimates the densities of the predictors within each class.
2. Models posterior probabilities according to Bayes rule. That is, for all $k = 1,...,K$,

$$\hat{P}(Y = k \mid X_1,..,X_P) = \frac{\pi(Y = k)\prod_{j=1}^{P} P(X_j \mid Y = k)}{\sum_{k=1}^{K}\pi(Y = k)\prod_{j=1}^{P} P(X_j \mid Y = k)},$$

   where:

   - Y is the random variable corresponding to the class index of an observation.
   - $X_1,...,X_P$ are the random predictors of an observation.
   - $\pi(Y = k)$ is the prior probability that a class index is k.
3. Classifies an observation by estimating the posterior probability for each class, and then assigns the observation to the class yielding the maximum posterior probability.

If the predictors compose a multinomial distribution, then the posterior probability $\hat{P}(Y = k \mid X_1,..,X_P) \propto \pi(Y = k)P_{mn}(X_1,...,X_P \mid Y = k)$, where $P_{mn}(X_1,...,X_P \mid Y = k)$ is the probability mass function of a multinomial distribution.

Tips

For classifying count-based data, such as the bag-of-tokens model, use the multinomial distribution (e.g., set `'Distribution','mn'`).

Algorithms

- If you specify `'Distribution','mn'` when training Mdl using `fitcnb`, then the software fits a multinomial distribution using the bag-of-tokens model. The

software stores the probability that token j appears in class k in the property `DistributionParameters{`k`,`j`}`. Using additive smoothing [2], the estimated probability is

$$P(\text{token } j \mid \text{class } k) = \frac{1 + c_{j|k}}{P + c_k},$$

where:

- $c_{j|k} = n_k \dfrac{\sum_{i:y_i \in \text{class } k} x_{ij} w_i}{\sum_{i:y_i \in \text{class } k} w_i}$; which is the weighted number of occurrences of token j in class k.
- n_k is the number of observations in class k.
- w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.
- $c_k = \sum_{j=1}^{P} c_{j|k}$; which is the total weighted number of occurrences of all tokens in class k.

- If you specify `'Distribution','mvmn'` when training Mdl using `fitcnb`, then:

  1. For each predictor, the software collects a list of the unique levels, stores the sorted list in `CategoricalLevels`, and considers each level a bin. Each predictor/class combination is a separate, independent multinomial random variable.
  2. For predictor j in class k, the software counts instances of each categorical level using the list stored in `CategoricalLevels{`j`}`.
  3. The software stores the probability that predictor j, in class k, has level L in the property `DistributionParameters{`k`,`j`}`, for all levels in `CategoricalLevels{`j`}`. Using additive smoothing [2], the estimated probability is

$$P(\text{predictor } j = L \mid \text{class } k) = \frac{1 + m_{j|k}(L)}{m_j + m_k},$$

where:

- $m_{j|k}(L) = n_k \dfrac{\sum_{i:y_i \in \text{ class } k} I\{x_{ij} = L\} w_i}{\sum_{i:y_i \in \text{ class } k} w_i}$; which is the weighted number of observations for which predictor j equals L in class k.
- n_k is the number of observations in class k.
- $I\{x_{ij} = L\} = 1$ if $x_{ij} = L$, 0 otherwise.
- w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.
- m_j is the number of distinct levels in predictor j.
- m_k is the weighted number of observations in class k.

- "Naive Bayes Classification" on page 15-31
- "Grouping Variables" on page 2-52

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[2] Manning, C. D., P. Raghavan, and M. Schütze. *Introduction to Information Retrieval*, NY: Cambridge University Press, 2008.

See Also

`ClassificationNaiveBayes` | `ClassificationPartitionedModel` | `predict` | `templateNaiveBayes`

fitcsvm

Train binary support vector machine classifier

Syntax

```
SVMModel = fitcsvm(X,Y)
SVMModel = fitcsvm(X,Y,Name,Value)
```

Description

`SVMModel = fitcsvm(X,Y)` returns a support vector machine classifier SVMModel, trained by predictors X and class labels Y for one- or two-class classification.

`SVMModel = fitcsvm(X,Y,Name,Value)` returns a support vector machine classifier with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the type of cross validation, the cost for misclassification, or the type of score transformation function.

Examples

Train a Support Vector Machine Classifier

Load Fisher's iris data set. Remove the sepal lengths and widths, and all observed setosa irises.

```
load fisheriris
inds = ~strcmp(species,'setosa');
X = meas(inds,3:4);
y = species(inds);
```

Train an SVM classifier using the processed data set.

```
SVMModel = fitcsvm(X,y)
```

```
SVMModel =

  ClassificationSVM
      PredictorNames: {'x1'  'x2'}
        ResponseName: 'Y'
          ClassNames: {'versicolor'  'virginica'}
      ScoreTransform: 'none'
     NumObservations: 100
               Alpha: [24x1 double]
                Bias: -14.4149
    KernelParameters: [1x1 struct]
      BoxConstraints: [100x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [100x1 logical]
              Solver: 'SMO'
```

The Command Window shows that `SVMModel` is a trained `ClassificationSVM` classifier and a property list. Display the properties of `SVMModel`, for example, to determine the class order, by using dot notation.

```
classOrder = SVMModel.ClassNames
```

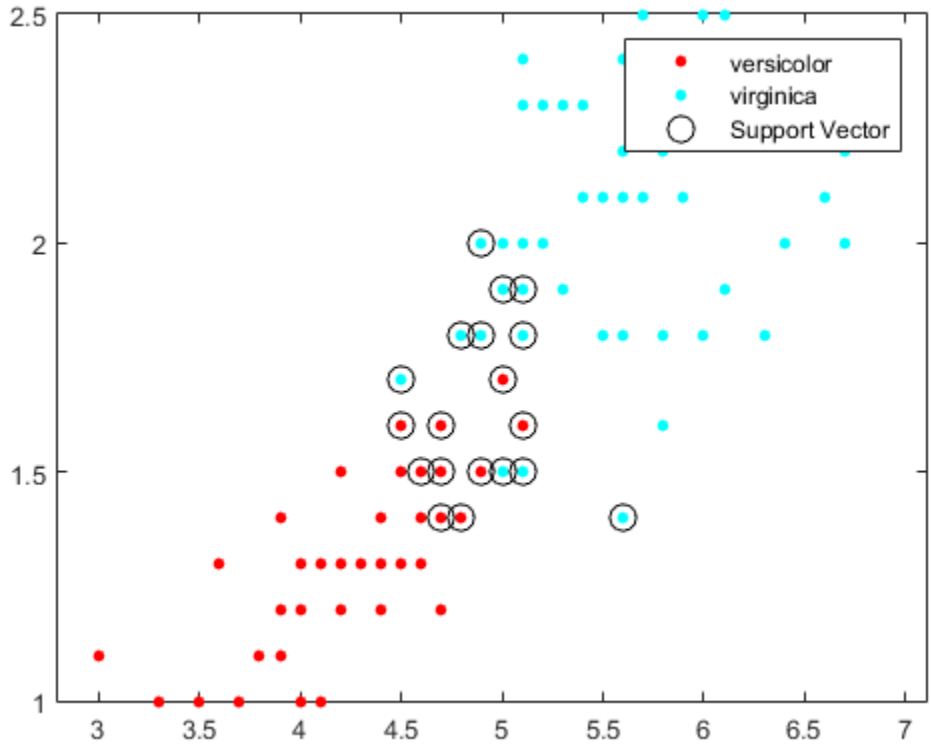
```
classOrder =

    'versicolor'
    'virginica'
```

The first class (`'versicolor'`) is the negative class, and the second (`'virginica'`) is the positive class. You can change the class order during training by using the `'ClassNames'` name-value pair argument.

Plot a scatter diagram of the data and circle the support vectors.

```
sv = SVMModel.SupportVectors;
figure
gscatter(X(:,1),X(:,2),y)
hold on
plot(sv(:,1),sv(:,2),'ko','MarkerSize',10)
legend('versicolor','virginica','Support Vector')
```

```
hold off
```



The support vectors are observations that occur on or beyond their estimated class boundaries.

You can adjust the boundaries (and therefore the number of support vectors) by setting a box constraint during training using the `'BoxConstraint'` name-value pair argument.

Train and Cross Validate an SVM Classifier

Load the `ionosphere` data set.

```
load ionosphere
```

```
rng(1); % For reproducibility
```

Train an SVM classifier using the radial basis kernel. Let the software find a scale value for the kernel function. It is good practice to standardize the predictors.

```
SVMModel = fitcsvm(X,Y,'Standardize',true,'KernelFunction','RBF',...
    'KernelScale','auto');
```

`SVMModel` is a trained `ClassificationSVM` classifier.

Cross validate the SVM classifier. By default, the software uses 10-fold cross validation.

```
CVSVMModel = crossval(SVMModel);
```

`CVSVMModel` is a `ClassificationPartitionedModel` cross-validated classifier.

Estimate the out-of-sample misclassification rate.

```
classLoss = kfoldLoss(CVSVMModel)
```

```
classLoss =

    0.0484
```

The generalization rate is approximately 5%.

Detect Outliers Using SVM and One-Class Learning

Load Fisher's iris data set. Remove the petal lengths and widths. Treat all irises as coming from the same class.

```
load fisheriris
X = meas(:,1:2);
y = ones(size(X,1),1);
```

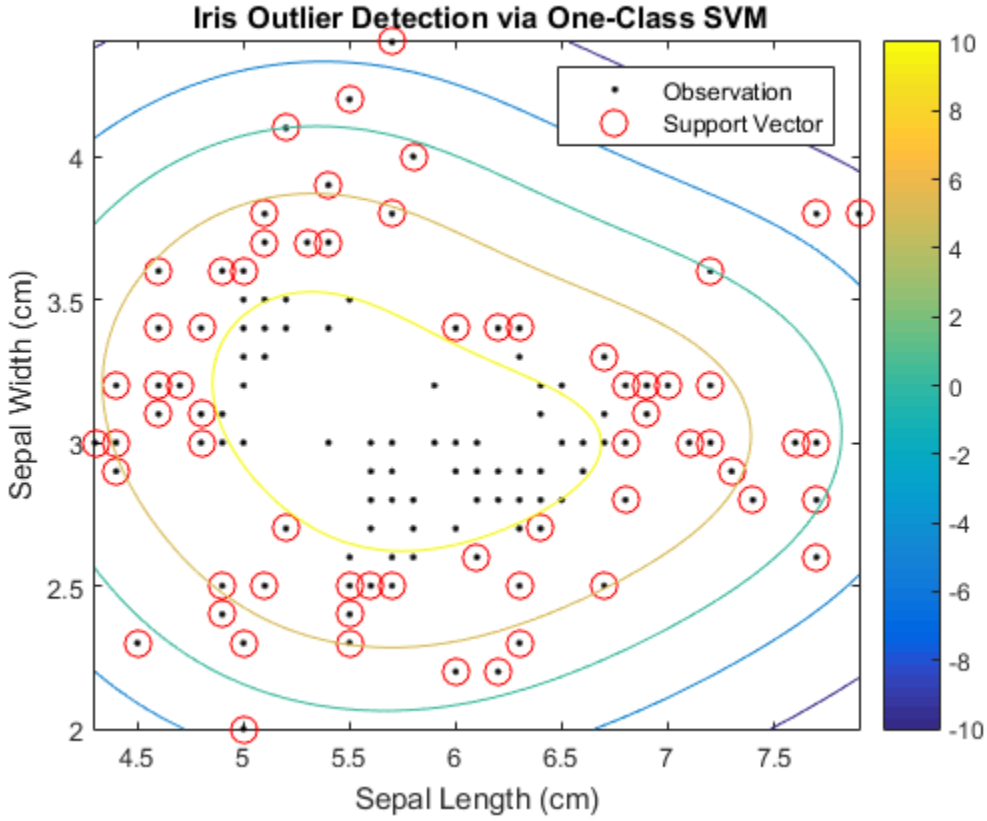
Train an SVM classifier using the processed data set. Assume that 5% of the observations are outliers. It is good practice to standardize the predictors.

```
rng(1);
SVMModel = fitcsvm(X,y,'KernelScale','auto','Standardize',true,...
    'OutlierFraction',0.05);
```

`SVMModel` is a trained `ClassificationSVM` classifier. By default, the software uses the Gaussian kernel for one-class learning.

Plot the observations and the decision boundary. Flag the support vectors and potential outliers.

```
svInd = SVMModel.IsSupportVector;
h = 0.02; % Mesh grid step size
[X1,X2] = meshgrid(min(X(:,1)):h:max(X(:,1)),...
    min(X(:,2)):h:max(X(:,2)));
[~,score] = predict(SVMModel,[X1(:),X2(:)]);
scoreGrid = reshape(score,size(X1,1),size(X2,2));

figure
plot(X(:,1),X(:,2),'k.')
hold on
plot(X(svInd,1),X(svInd,2),'ro','MarkerSize',10)
contour(X1,X2,scoreGrid)
colorbar;
title('{\bf Iris Outlier Detection via One-Class SVM}')
xlabel('Sepal Length (cm)')
ylabel('Sepal Width (cm)')
legend('Observation','Support Vector')
hold off
```



The boundary separating the outliers from the rest of the data occurs where the contour value is 0.

Verify that the fraction of observations with negative scores in the cross-validated data is close to 5%.

```
CVSVMModel = crossval(SVMModel);
[~,scorePred] = kfoldPredict(CVSVMModel);
outlierRate = mean(scorePred<0)
```

```
outlierRate =

    0.0467
```

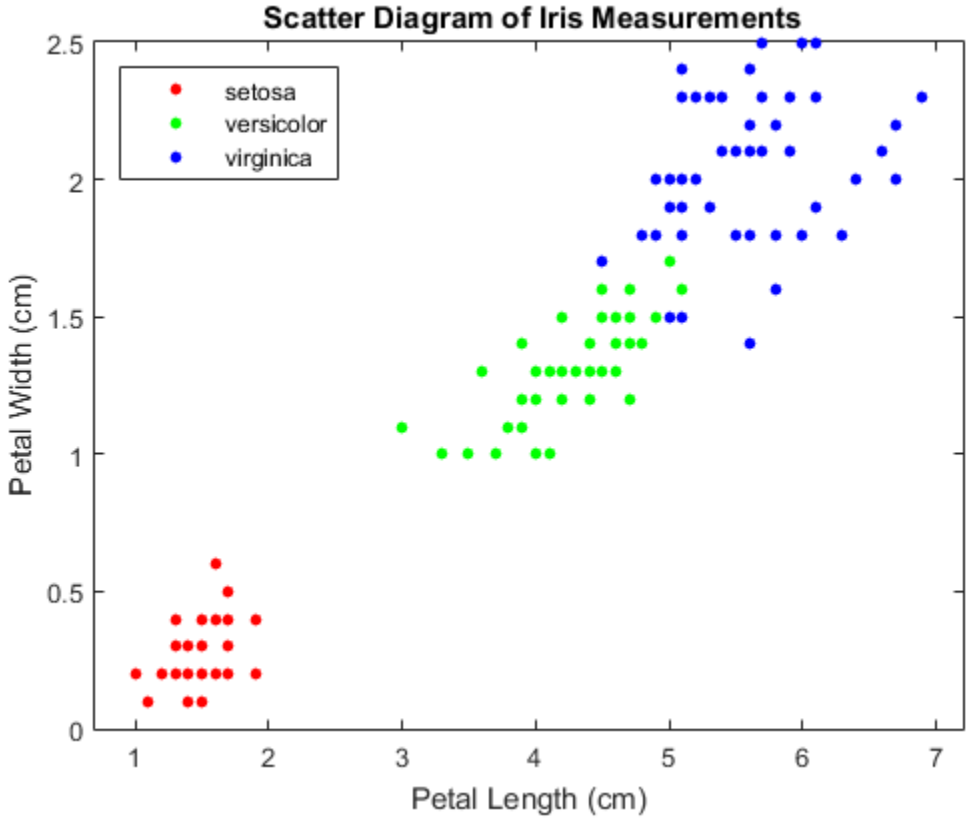
Find Multiple Class Boundaries Using Binary SVM

Load Fisher's iris data set. Use the petal lengths and widths.

```
load fisheriris
X = meas(:,3:4);
Y = species;
```

Examine a scatter plot of the data.

```
figure
gscatter(X(:,1),X(:,2),Y);
h = gca;
lims = [h.XLim h.YLim]; % Extract the x and y axis limits
title('{\bf Scatter Diagram of Iris Measurements}');
xlabel('Petal Length (cm)');
ylabel('Petal Width (cm)');
legend('Location','Northwest');
```



There are three classes, one of which is linearly separable from the others.

For each class:

1. Create a logical vector (`indx`) indicating whether an observation is a member of the class.
2. Train an SVM classifier using the predictor data and `indx`.
3. Store the classifier in a cell of a cell array.

```
% It is good practice to define the class order and standardize the
% predictors.
SVMModels = cell(3,1);
classes = unique(Y);
```

```
rng(1); % For reproducibility

for j = 1:numel(classes);
    indx = strcmp(Y,classes(j)); % Create binary classes for each classifier
    SVMModels{j} = fitcsvm(X,indx,'ClassNames',[false true],'Standardize',true,...
        'KernelFunction','rbf','BoxConstraint',1);
end
```

`SVMModels` is a 3-by-1 cell array, with each cell containing a `ClassificationSVM` classifier. For each cell, the positive class is setosa, versicolor, and virginica, respectively.

Define a fine grid within the plot, and treat the coordinates as new observations from the distribution of the training data. Estimate the score of the new observations using each classifier.

```
d = 0.02;
[x1Grid,x2Grid] = meshgrid(min(X(:,1)):d:max(X(:,1)),...
    min(X(:,2)):d:max(X(:,2)));
xGrid = [x1Grid(:),x2Grid(:)];
N = size(xGrid,1);
Scores = zeros(N,numel(classes));

for j = 1:numel(classes);
    [~,score] = predict(SVMModels{j},xGrid);
    Scores(:,j) = score(:,2); % Second column contains positive-class scores
end
```

Each row of `Scores` contains three scores. The index of the element with the largest score is the index of the class to which the new class observation most likely belongs.

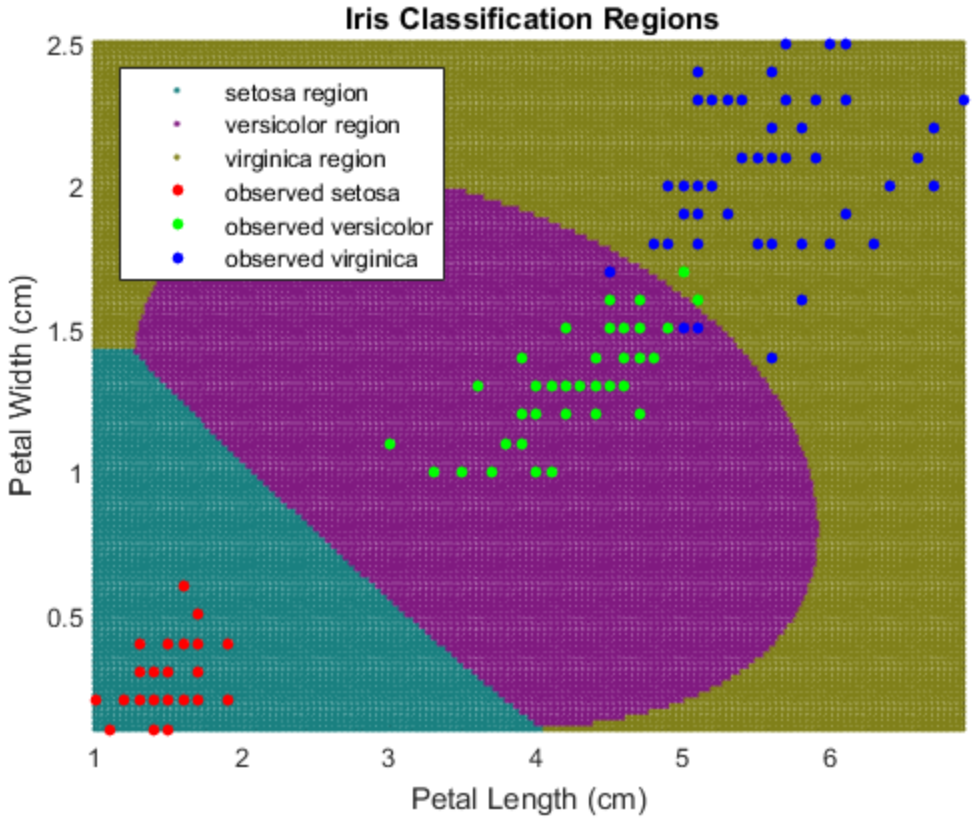
Associate each new observation with the classifier that gives it the maximum score.

```
[~,maxScore] = max(Scores,[],2);
```

Color in the regions of the plot based on which class the corresponding new observation belongs.

```
figure
h(1:3) = gscatter(xGrid(:,1),xGrid(:,2),maxScore,...
    [0.1 0.5 0.5; 0.5 0.1 0.5; 0.5 0.5 0.1]);
hold on
h(4:6) = gscatter(X(:,1),X(:,2),Y);
title('{\bf Iris Classification Regions}');
```

```
xlabel('Petal Length (cm)');
ylabel('Petal Width (cm)');
legend(h,{'setosa region','versicolor region','virginica region',...
    'observed setosa','observed versicolor','observed virginica'},...
    'Location','Northwest');
axis tight
hold off
```



- "Train SVM Classifiers Using a Gaussian Kernel" on page 16-178
- "Train SVM Classifiers Using a Custom Kernel" on page 16-183
- "Train and Cross Validate SVM Classifiers" on page 16-189

Input Arguments

`X` — Predictor data

matrix of numeric values

Predictor data to which the SVM classifier is trained, specified as a matrix of numeric values.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one predictor.

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to:

- Cross validate using the `KFold` name-value pair argument. The cross-validation results determine how well the SVM classifier generalizes.
- Standardize the predictor variables using the `Standardize` name-value pair argument.

To specify the names of the predictors in the order of their appearance in `X`, use the `PredictorNames` name-value pair argument.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels to which the SVM classifier is trained, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The length of `Y` and the number of rows of `X` must be equal.

It is good practice to specify the order of the classes using the `ClassNames` name-value pair argument.

To specify the response variable name, use the `ResponseName` name-value pair argument.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'KFold',10,'Cost',[0 2;1 0],'ScoreTransform','sign'` specifies to perform 10-fold cross validation, apply double the penalty to false positives compared to false negatives, and transform the scores using the sign function.

`'Alpha'` — Initial estimates of alpha coefficients

vector of nonnegative real values

Initial estimates of alpha coefficients, specified as the comma-separated pair consisting of `'Alpha'` and a vector of nonnegative real values. The length of `Alpha` must be equal to the number of rows of `X`.

- Each element of `Alpha` corresponds to an observation in `X`.
- `Alpha` cannot contain any `NaN`s.
- If you specify `Alpha` and any of the cross-validation name-value pair arguments (`'CrossVal'`, `'CVPartition'`, `'Holdout'`, `'KFold'`, or `'Leaveout'`), then the software returns an error.

The defaults are:

- `0.5*ones(size(X,1),1)` for one-class learning
- `zeros(size(X,1),1)` for two-class learning

Example: `'Alpha',0.1*ones(size(X,1),1)`

Data Types: `double | single`

`'BoxConstraint'` — Box constraint

1 (default) | positive scalar

Box constraint, specified as the comma-separated pair consisting of `'BoxConstraint'` and a positive scalar.

For one-class learning, the software always sets the box constraint to `1`.

Example: `'BoxConstraint',100`

Data Types: `double` | `single`

`'CacheSize'` — Cache size

`1000` (default) | `'maximal'` | positive scalar

Cache size, specified as the comma-separated pair consisting of `'CacheSize'` and `'maximal'` or a positive scalar.

If `CacheSize` is `'maximal'`, then the software reserves enough disk space to hold the entire n-by-n Gram matrix.

If `CacheSize` is a positive scalar, then the software reserves `CacheSize` megabytes of disk space for training the classifier.

Example: `'CacheSize','maximal'`

Data Types: `double` | `char` | `single`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of `Y`.

The default is the distinct class names of `Y`.

If `Y` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for training.

Example: `'ClassNames',logical([0,1])`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure. If you specify:

- The square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding

rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- The structure `S`, then it must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y
  - `S.ClassificationCosts`, which contains the cost matrix with rows and columns ordered as in `S.ClassNames`

For two-class learning, if you specify a cost matrix, then the software updates the prior probabilities by incorporating the penalties described in the cost matrix. Subsequently, the cost matrix resets to the default. For more details, see "Algorithms" on page 22-1616.

The defaults are:

- For one-class learning, `Cost = 0`.
- For two-class learning, `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0,1;2,0]`

Data Types: `double | single | struct`

`'CrossVal'` — Flag to train cross-validated classifier

`'off'` (default) | `'on'`

Flag to train a cross-validated classifier, specified as the comma-separated pair consisting of `'Crossval'` and a string.

If you specify `'on'`, then the software trains a cross-validated classifier with 10 folds.

You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments.

You can only use one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Alternatively, cross-validate SVMModel later by passing it to `crossval`.

Example: `'Crossval','on'`

Data Types: `char`

`'CVPartition'` — Cross-validation partition

`[]` (default) | `cvpartition` partition object

Cross-validation partition, specified as the comma-separated pair consisting of `'CVPartition'` and a `cvpartition` partition object as created by `cvpartition`. The partition object specifies the type of cross-validation, and also the indexing for training and validation sets.

If you specify `CVPartition`, then you cannot specify any of Holdout, KFold, or Leaveout.

`'DeltaGradientTolerance'` — Tolerance for gradient difference

nonnegative scalar

Tolerance for the gradient difference between upper and lower violators obtained by Sequential Minimal Optimization (SMO) or Iterative Single Data Algorithm (ISDA), specified as the comma-separated pair consisting of `'DeltaGradientTolerance'` and a nonnegative scalar.

If `DeltaGradientTolerance` is `0`, then the software does not use the tolerance for the gradient difference to check for optimization convergence.

The defaults are:

- `1e-3` if the solver is SMO (for example, you set `'Solver','SMO'`)
- `0` if the solver is ISDA (for example, you set `'Solver','ISDA'`)

Example: `'DeltaGapTolerance',1e-2`

Data Types: `double` | `single`

`'GapTolerance'` — Feasibility gap tolerance

`0` (default) | nonnegative scalar

Feasibility gap tolerance obtained by SMO or ISDA, specified as the comma-separated pair consisting of `'GapTolerance'` and a nonnegative scalar.

If `GapTolerance` is `0`, then the software does not use the feasibility gap tolerance to check for optimization convergence.

Example: `'GapTolerance',1e-2`

Data Types: `double` | `single`

'Holdout' — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of 'Holdout' and a scalar value in the range (0,1). If you specify 'Holdout',*p*, then the software:

1. Randomly reserves *p**100% of the data as validation data, and trains the model using the rest of the data
2. Stores the compact, trained model in CVMdl.Trained

If you specify Holdout, then you cannot specify any of CVPartition, KFold, or Leaveout.

Example: 'Holdout',0.1

Data Types: double | single

'IterationLimit' — Maximal number of numerical optimization iterations

1e6 (default) | positive integer

Maximal number of numerical optimization iterations, specified as the comma-separated pair consisting of 'IterationLimit' and a positive integer.

The software returns a trained classifier regardless of whether the optimization routine successfully converges.

Example: 'IterationLimit',1e8

Data Types: double | single

'KernelFunction' — Kernel function

string

Kernel function used to compute the Gram matrix, specified as the comma-separated pair consisting of 'KernelFunction' and a string.

This table summarizes the available options for setting a kernel function.

Value	Description	Formula
'gaussian' or 'rbf'	Gaussian or Radial Basis Function (RBF) kernel, default for one-class learning	$G(x_1,x_2) = \exp\left(-\|x_1 - x_2\|^2\right)$

Value	Description	Formula
`'linear'`	Linear kernel, default for two-class learning	$G(x_1,x_2) = x_1'x_2$
`'polynomial'`	Polynomial kernel. Use `'PolynomialOrder',polyO` to specify a polynomial kernel of order `polyOrder`.	$G(x_1,x_2) = (1 + x_1'x_2)^p$

You can set your own kernel function, for example, `kernel`, by setting `'KernelFunction','kernel'`. `kernel` must have the following form:

```
function G = kernel(U,V)
```

where:

- `U` is an m-by-p matrix.
- `V` is an n-by-p matrix.
- `G` is an m-by-n Gram matrix of the rows of `U` and `V`.

And `kernel.m` must be on the MATLAB path.

It is good practice to avoid using generic names for kernel functions. For example, call a sigmoid kernel function `'mysigmoid'` rather than `'sigmoid'`.

Example: `'KernelFunction','gaussian'`

Data Types: `char`

`'KernelOffset'` — Kernel offset parameter

nonnegative scalar

Kernel offset parameter, specified as the comma-separated pair consisting of `'KernelOffset'` and a nonnegative scalar.

The software adds `KernelOffset` to each element of the Gram matrix.

The defaults are:

- `0` if the solver is SMO (for example, you set `'Solver','SMO'`)
- `0.1` if the solver is ISDA (for example, you set `'Solver','ISDA'`)

Example: `'KernelOffset',0`

Data Types: `double` | `single`

`'KernelScale'` — Kernel scale parameter

`1` (default) | `'auto'` | positive scalar

Kernel scale parameter, specified as the comma-separated pair consisting of `'KernelScale'` and `'auto'` or a positive scalar.

- If `KernelFunction` is `'gaussian'` (`'rbf'`), `'linear'`, or `'polymonial'`, then the software divides all elements of the predictor matrix X by the value of `KernelScale`. Then, the software applies the appropriate kernel norm to compute the Gram matrix.
- If you specify `'auto'`, then the software uses a heuristic procedure to select the scale value. The heuristic procedure uses subsampling. Therefore, to reproduce results, set a random number seed using `rng` before training the classifier.
- If you specify `KernelScale` and your own kernel function, for example, `kernel`, using `'KernelFunction','kernel'`, then the software displays an error. You must apply scaling within `kernel`.

Example: `'KernelScale',''auto'`

Data Types: `double` | `single` | `char`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated classifier, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

You can only use one of these four options at a time to create a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'KFold',8`

Data Types: `single` | `double`

`'KKTTolerance'` — Karush-Kuhn-Tucker complementarity conditions violation tolerance

nonnegative scalar

Karush-Kuhn-Tucker (KKT) complementarity conditions violation tolerance, specified as the comma-separated pair consisting of `'KKTTolerance'` and a nonnegative scalar.

If `KKTTolerance` is `0`, then the software does not use the KKT complementarity conditions violation tolerance to check for optimization convergence.

The defaults are:

- `0` if the solver is SMO (for example, you set `'Solver','SMO'`)
- `1e-3` if the solver is ISDA (for example, you set `'Solver','ISDA'`)

Example: `'KKTTolerance',1e-2`

Data Types: `double | single`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off'`. If you specify `'on'`, then the software implements leave-one-out cross validation.

If you use `'Leaveout'`, you cannot use these `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

Data Types: `char`

`'Nu'` — ν parameter for one-class learning

`0.5` (default) | positive scalar

ν parameter for one-class learning, specified as the comma-separated pair consisting of `'Nu'` and a positive scalar. `Nu` must be greater than `0` and at most `1`.

Set `Nu` to control the tradeoff between ensuring most training examples are in the positive class and minimizing the weights in the score function.

Example: `'Nu',0.25`

Data Types: `double | single`

`'NumPrint'` — Number of iterations between optimization diagnostic message output

`1000` (default) | nonnegative integer

Number of iterations between optimization diagnostic message output, specified as the comma-separated pair consisting of `'NumPrint'` and a nonnegative integer.

If you use `'Verbose',1` and `'NumPrint',numprint`, then the software displays all optimization diagnostic messages from SMO and ISDA every `numprint` iterations in the Command Window.

Example: `'NumPrint',500`

Data Types: `double` | `single`

`'OutlierFraction'` — Expected proportion of outliers in training data

`0` (default) | nonnegative scalar

Expected proportion of outliers in the training data, specified as the comma-separated pair consisting of `'OutlierFraction'` and a nonnegative scalar. `OutlierFraction` must be at least `0` and less than `1`.

If you set `'OutlierFraction',outlierfraction`, where `outlierfraction` is a value greater than 0, then:

- For two-class learning, the software implements *robust learning*. In other words, the software attempts to remove 100*`outlierfraction`% of the observations when the optimization algorithm converges. The removed observations correspond to gradients that are large in magnitude.
- For one-class learning, the software finds an appropriate bias term such that `outlierfraction` of the observations in the training set have negative scores.

Example: `'OutlierFraction',0.01`

Data Types: `double` | `single`

`'PolynomialOrder'` — Polynomial kernel function order

`3` (default) | positive integer

Polynomial kernel function order, specified as the comma-separated pair consisting of `'PolynomialOrder'` and a positive integer.

If you set `'PolynomialOrder'` and `KernelFunction` is not `'polynomial'`, then the software displays an error.

Example: `'PolynomialOrder',2`

Data Types: `double` | `single`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in X.

Example: `'PredictorNames',{'PedalWidth','PedalLength'}`

Data Types: `cell`

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | numeric vector | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and a string, numeric vector, or a structure.

This table summarizes the available options for setting prior probabilities.

Value	Description
`'empirical'`	The class prior probabilities are the class relative frequencies in Y.
`'uniform'`	All class prior probabilities are equal to $1/K$, where K is the number of classes.
numeric vector	Each element is a class prior probability. Order the elements according to `SVMModel.ClassNames` or specify the order using the ClassNames name-value pair argument. The software normalizes the elements such that they sum to `1`.
structure	A structure `S` with two fields: • `S.ClassNames` contains the class names as a variable of the same type as Y. • `S.ClassProbs` contains a vector of corresponding prior probabilities. The software normalizes the elements such that they sum to `1`.

For two-class learning, if you specify a cost matrix, then the software updates the prior probabilities by incorporating the penalties described in the cost matrix. For more details, see “Algorithms” on page 22-1616.

Example: `struct('ClassNames',{{'setosa','versicolor'}},'ClassProbs',[1,2])`

Data Types: `char` | `double` | `single` | `struct`

'ResponseName' — Response variable name
'Y' (default) | string

Response variable name, specified as the comma-separated pair consisting of 'ResponseName' and a string containing the name of the response variable Y.

Example: 'ResponseName','IrisType'

Data Types: char

'ScoreTransform' — Score transform function
'none' (default) | 'doublelogit' | 'invlogit' | 'ismax' | 'logit' | 'sign' | 'symmetric' | 'symmetriclogit' | 'symmetricismax' | function handle

Score transform function, specified as the comma-separated pair consisting of 'ScoreTransform' and a string or function handle.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the available, built-in functions.

String	Formula
'doublelogit'	$1/(1 + e^{-2x})$
'invlogit'	$\log(x / (1-x))$
'ismax'	Set the score for the class with the largest score to 1, and scores for all other classes to 0.
'logit'	$1/(1 + e^{-x})$
'none'	x (no transformation)
'sign'	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
'symmetric'	$2x - 1$
'symmetriclogit'	$2/(1 + e^{-x}) - 1$
'symmetricismax'	Set the score for the class with the largest score to 1, and scores for all other classes to -1.

- For a MATLAB function, or a function that you define, enter its function handle.

```
SVMModel.ScoreTransform = @function;
```

`function` should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Example: `'ScoreTransform','sign'`

Data Types: `char` | `function_handle`

`'ShrinkagePeriod'` — Number of iterations between movement of observations from active to inactive set

0 (default) | nonnegative integer

Number of iterations between the movement of observations from the active to inactive set, specified as the comma-separated pair consisting of `'ShrinkagePeriod'` and a nonnegative integer.

If you set `'ShrinkagePeriod',0`, then the software does not shrink the active set.

Example: `'ShrinkagePeriod',1000`

Data Types: `double` | `single`

`'Solver'` — Optimization routine

`'ISDA'` | `'L1QP'` | `'SMO'`

Optimization routine, specified as a string.

This table summarizes the available optimization routine options.

Value	Description
`'ISDA'`	Iterative Single Data Algorithm (see [4])
`'L1QP'`	Uses `quadprog` to implement $L1$ soft-margin minimization by quadratic programming. This option requires an Optimization Toolbox license. For more details, see "Quadratic Programming Definition".
`'SMO'`	Sequential Minimal Optimization (see [2])

The defaults are:

- `'ISDA'` if you set `'OutlierFraction'` to a positive value and for two-class learning

- `'SMO'` otherwise

Example: `'Solver','ISDA'`

Data Types: `char`

`'Standardize'` — Flag to standardize predictors

`false` (default) | `true`

Flag to standardize the predictors, specified as the comma-separated pair consisting of `'Standardize'` and `true` (`1`) or `false` (`0`).

If you set `'Standardize',true`, then the software centers and scales each column of the predictor data (X) by the column mean and standard deviation, respectively. It is good practice to standardize the predictor data.

Example: `'Standardize',true`

Data Types: `logical`

`'Verbose'` — Verbosity level

`0` (default) | `1` | `2`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and either `0`, `1`, or `2`. `Verbose` controls the amount of optimization information that the software displays in the Command Window and saves as a structure to `SVMModel.ConvergenceInfo.History`.

This table summarizes the available verbosity level options.

Value	Description
0	The software does not display or save convergence information.
1	The software displays diagnostic messages and saves convergence criteria every `numprint` iterations, where `numprint` is the value of the name-value pair argument `'NumPrint'`.
2	The software displays diagnostic messages and saves convergence criteria at every iteration.

Example: `'Verbose',1`

Data Types: `double` | `single`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector.

The size of `Weights` must equal the number of rows of X. The software weighs the observations in each row of `X` with the corresponding weight in `Weights`.

The software normalizes `Weights` to sum up to the value of the prior probability in the respective class.

Data Types: `double` | `single`

Output Arguments

`SVMModel` — Trained SVM classifier

`ClassificationSVM` classifier | `ClassificationPartitionedModel` cross-validated classifier

Trained SVM classifier, returned as a `ClassificationSVM` classifier or `ClassificationPartitionedModel` cross-validated classifier.

If you set any of the name-value pair arguments KFold, Holdout, Leaveout, CrossVal, or CVPartition, then `SVMModel` is a `ClassificationPartitionedModel` cross-validated classifier. Otherwise, `SVMModel` is a `ClassificationSVM` classifier.

To reference properties of `SVMModel`, use dot notation. For example, enter `SVMModel.Alpha` in the Command Window to display the trained Lagrange multipliers.

Limitations

- `fitcsvm` trains SVM classifiers for one- or two-class learning applications. To train SVM classifiers using data with more than two classes, use `fitcecoc`.

More About

Box Constraint

A parameter that controls the maximum penalty imposed on margin-violating observations, and aids in preventing overfitting (regularization).

If you increase the box constraint, then the SVM classifier assigns fewer support vectors. However, increasing the box constraint can lead to longer training times.

Gram Matrix

The Gram matrix of a set of n vectors $\{x_1,..,x_n; x_j \in R^p\}$ is an n-by-n matrix with element (j,k) defined as $G(x_j,x_k) = <\phi(x_j),\phi(x_k)>$, an inner product of the transformed predictors using the kernel function ϕ.

For nonlinear SVM, the algorithm forms a Gram matrix using the predictor matrix columns. The dual formalization replaces the inner product of the predictors with corresponding elements of the resulting Gram matrix (called the "kernel trick"). Subsequently, nonlinear SVM operates in the transformed predictor space to find a separating hyperplane.

Karush-Kuhn-Tucker Complementarity Conditions

KKT complementarity conditions are optimization constraints required for optimal nonlinear programming solutions.

In SVM, the KKT complementarity conditions are

$$\begin{cases} \alpha_j \left[y_j \left(w'\phi\left(x_j\right) + b \right) - 1 + \xi_j \right] = 0 \\ \xi_j \left(C - \alpha_j \right) = 0 \end{cases}$$

for all $j = 1,...,n$, where w_j is a weight, ϕ is a kernel function (see Gram matrix), and ξ_j is a slack variable. If the classes are perfectly separable, then $\xi_j = 0$ for all $j = 1,...,n$.

One-Class Learning

One-class learning, or unsupervised SVM, aims at separating data from the origin in the high-dimensional, predictor space (not the original predictor space), and is an algorithm used for outlier detection.

The algorithm resembles that of SVM for binary classification. The objective is to minimize dual expression

$$0.5\sum_{jk}\alpha_j\alpha_k G(x_j,x_k)$$

with respect to $\alpha_1,...,\alpha_n$, subject to

$$\sum\alpha_j = n\nu$$

and $0 \le \alpha_j \le 1$ for all $j = 1,...,n$. $G(x_j,x_k,)$ is element (j,k) of the Gram matrix.

A small value of ν leads to fewer support vectors, and, therefore, a smooth, crude decision boundary. A large value of ν leads to more support vectors, and therefore, a curvy, flexible decision boundary. The optimal value of ν should be large enough to capture the data complexity and small enough to avoid overtraining. Also, $0 < \nu \le 1$.

For more details, see [5].

Support Vector

Support vectors are observations corresponding to strictly positive estimates of $\alpha_1,...,\alpha_n$.

SVM classifiers that yield fewer support vectors for a given training set are more desirable.

Support Vector Machines for Binary Classification

The SVM binary classification algorithm searches for an optimal hyperplane that separates the data into two classes. For separable classes, the optimal hyperplane maximizes a *margin* (space that does not contain any observations) surrounding itself, which creates boundaries for the positive and negative classes. For inseparable classes, the objective is the same, but the algorithm imposes a penalty on the length of the margin for every observation that is on the wrong side of its class boundary.

The linear SVM score function is

$$f(x) = x'\beta + \beta_0,$$

where:

- x is an observation (corresponding to a row of `X`).
- The vector β contains the coefficients that define an orthogonal vector to the hyperplane (corresponding to `SVMModel.Beta`). For separable data, the optimal margin length is $2/\|\beta\|$.
- β_0 is the bias term (corresponding to `SVMModel.Bias`).

The root of $f(x)$ for particular coefficients defines a hyperplane. For a particular hyperplane, $f(z)$ is the distance from point z to the hyperplane.

An SVM classifier searches for the maximum margin length, while keeping observations in the positive ($y = 1$) and negative ($y = –1$) classes separate. Therefore:

- For separable classes, the objective is to minimize $\|\beta\|$ with respect to the β and β_0 subject to $y_j f(x_j) \geq 1$, for all $j = 1,..,n$. This is the *primal* formalization for separable classes.
- For inseparable classes, SVM uses slack variables (ξ_j) to penalize the objective function for observations that cross the margin boundary for their class. $\xi_j = 0$ for observations that do not cross the margin boundary for their class, otherwise $\xi_j \geq 0$.

  The objective is to minimize $0.5\|\beta\|^2 + C\sum \xi_j$ with respect to the β, β_0, and ξ_j subject to $y_j f(x_j) \geq 1 - \xi_j$ and $\xi_j \geq 0$ for all $j = 1,..,n$, and for a positive scalar box constraint C. This is the primal formalization for inseparable classes.

SVM uses the Lagrange multipliers method to optimize the objective. This introduces n coefficients $\alpha_1,...,\alpha_n$ (corresponding to `SVMModel.Alpha`). The dual formalizations for linear SVM are:

- For separable classes, minimize

  $$0.5\sum_{j=1}^{n}\sum_{k=1}^{n}\alpha_j\alpha_k y_j y_k x_j' x_k - \sum_{j=1}^{n}\alpha_j$$

  with respect to $\alpha_1,...,\alpha_n$, subject to $\sum \alpha_j y_j = 0$, $\alpha_j \geq 0$ for all $j = 1,...,n$, and Karush-Kuhn-Tucker (KKT) complementarity conditions.

- For inseparable classes, the objective is the same as for separable classes, except for the additional condition $0 \le \alpha_j \le C$ for all $j = 1,..,n$.

The resulting score function is

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j x' x_j + b.$$

The score function is free of the estimate of β as a result of the primal formalization.

In some cases, there is a nonlinear boundary separating the classes. *Nonlinear SVM* works in a transformed predictor space to find an optimal, separating hyperplane.

The dual formalization for nonlinear SVM is

$$0.5 \sum_{j=1}^{n} \sum_{k=1}^{n} \alpha_j \alpha_k y_j y_k G(x_j, x_k) - \sum_{j=1}^{n} \alpha_j$$

with respect to $\alpha_1,...,\alpha_n$, subject to $\sum \alpha_j y_j = 0$, $0 \le \alpha_j \le C$ for all $j = 1,..,n$, and the KKT complementarity conditions.$G(x_k,x_j)$ are elements of the Gram matrix. The resulting score function is

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x, x_j) + b.$$

For more details, see Understanding Support Vector Machines, [1], and [3].

Tips

- For one-class learning:
  - The default setting for the name-value pair argument `'Alpha'` can lead to long training times. To speed up training, set `Alpha` to a vector mostly composed of `0`s.
  - Set the name-value pair argument `Nu` to a value closer to `0` to yield fewer support vectors, and, therefore, a smoother, but crude decision boundary

- Sparsity in support vectors is a desirable property of an SVM classifier. To decrease the number of support vectors, set `BoxConstraint` to a large value. This also increases the training time.
- For large data sets, try optimizing the cache size. This can have a significant impact on the training speed.
- If the support vector set is much less than the number of observations in the training set, then you might significantly speed up convergence by shrinking the active-set using the name-value pair argument `'ShrinkagePeriod'`. It is good practice to use `'ShrinkagePeriod',1000`.

Algorithms

- All solvers implement $L1$ soft-margin minimization.
- `fitcsvm` and `svmtrain` use, among other algorithms, SMO for optimization. The software implements SMO differently between the two functions, but numerical studies show that there is sensible agreement in the results.
- For one-class learning, the software estimates the Lagrange multipliers, $\alpha_1,...,\alpha_n$, such that

$$\sum_{j=1}^{n}\alpha_j = n\nu.$$

- For two-class learning, if you specify a cost matrix C, then the software updates the class prior probabilities (p) to p_c by incorporating the penalties described in C. The formula for the updated prior probability vector is

$$p_c = \frac{p'C}{\sum p'C}.$$

  Subsequently, the software resets the cost matrix to the default:

$$C = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}.$$

- If you set `'Standardize',true` when you train the SVM classifier using `fitcsvm`, then the software trains the classifier using the standardized predictor matrix, but stores the unstandardized data in the classifier property `X`. However, if you standardize the data, then the data size in memory doubles until optimization ends.

- If you set `'Standardize',true` and any of `'Cost'`, `'Prior'`, or `'Weights'`, then the software standardizes the predictors using their corresponding weighted means and weighted standard deviations.
- Let `p` be the proportion of outliers you expect in the training data. If you use `'OutlierFraction',p` when you train the SVM classifier using `fitcsvm`, then:
  - For one-class learning, the software trains the bias term such that 100`p`% of the observations in the training data have negative scores.
  - The software implements *robust learning* for two-class learning. In other words, the software attempts to remove 100`p`% of the observations when the optimization algorithm converges. The removed observations correspond to gradients that are large in magnitude.
- "Understanding Support Vector Machines" on page 16-170

References

[1] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[2] Fan, R.-E., P.-H. Chen, and C.-J. Lin. "Working set selection using second order information for training support vector machines." *Journal of Machine Learning Research*, Vol 6, 2005, pp. 1889–1918.

[3] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[4] Kecman V., T. -M. Huang, and M. Vogt. "Iterative Single Data Algorithm for Training Kernel Machines from Huge Data Sets: Theory and Performance." In *Support Vector Machines: Theory and Applications*. Edited by Lipo Wang, 255–274. Berlin: Springer-Verlag, 2005.

[5] Scholkopf, B., J. C. Platt, J. C. Shawe-Taylor, A. J. Smola, and R. C. Williamson. "Estimating the Support of a High-Dimensional Distribution." *Neural Comput*., Vol. 13, Number 7, 2001, pp. 1443–1471.

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See Also

`ClassificationPartitionedModel` | `ClassificationSVM` | `CompactClassificationSVM` | `fitcecoc` | `fitSVMPosterior` | `predict` | `quadprog` | `rng`

fitctree

Fit classification tree

Syntax

```
tree = fitctree(X,Y)
tree = fitctree(X,Y,Name,Value)
```

Description

`tree = fitctree(X,Y)` returns a classification tree based on the input variables (also known as predictors, features, or attributes) X and output (response or labels) Y. The returned tree is a binary tree, where each branching node is split based on the values of a column of X.

`tree = fitctree(X,Y,Name,Value)` fits a tree with additional options specified by one or more name-value pair arguments. For example, you can specify the algorithm used to find the best split on a categorical predictor, grow a cross-validated tree, or hold out a fraction of the input data for validation.

Examples

Grow a Classification Tree

Grow a classification tree using the `ionosphere` data set.

```
load ionosphere
tc = fitctree(X,Y)
```

```
tc =

  ClassificationTree
            PredictorNames: {1x34 cell}
              ResponseName: 'Y'
```

```
               ClassNames: {'b'   'g'}
           ScoreTransform: 'none'
    CategoricalPredictors: []
          NumObservations: 351
```

Control Tree Depth

You can control the depth of the trees using the `MaxNumSplits`, `MinLeafSize`, or `MinParentSize` name-value pair parameters. `fitctree` grows deep decision trees by default. You can grow shallower trees to reduce model complexity or computation time.

Load the `ionosphere` data set.

```
load ionosphere
```

The default values of the tree depth controllers for growing classification trees are:

- `n - 1` for `MaxNumSplits`. `n` is the training sample size.
- `1` for `MinLeafSize`.
- `10` for `MinParentSize`.

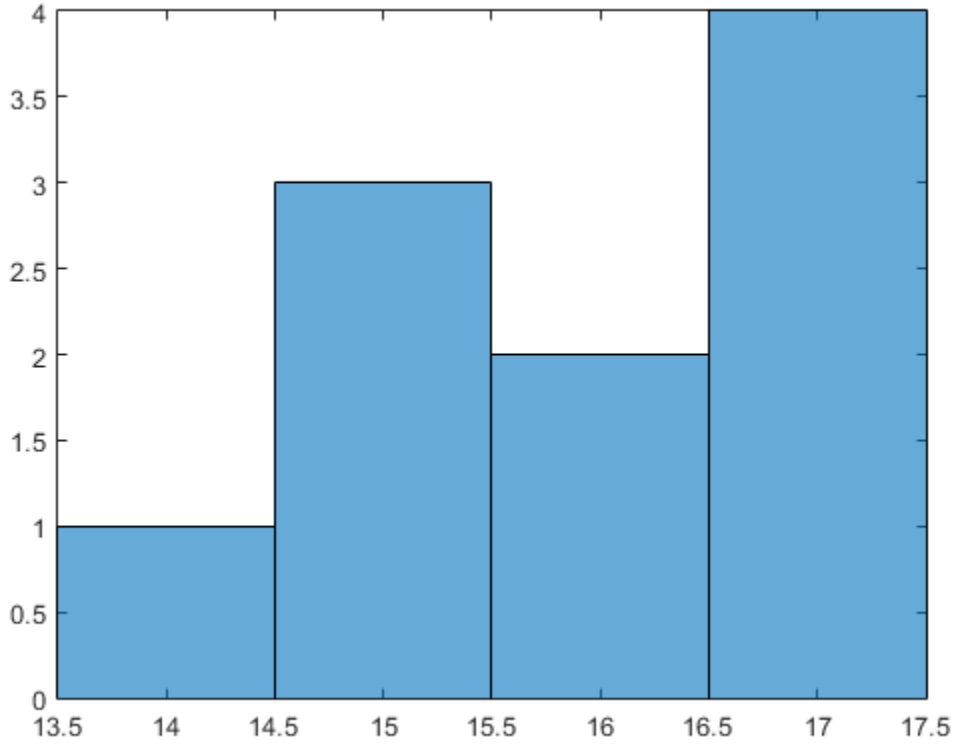
These default values tend to grow deep trees for large training sample sizes.

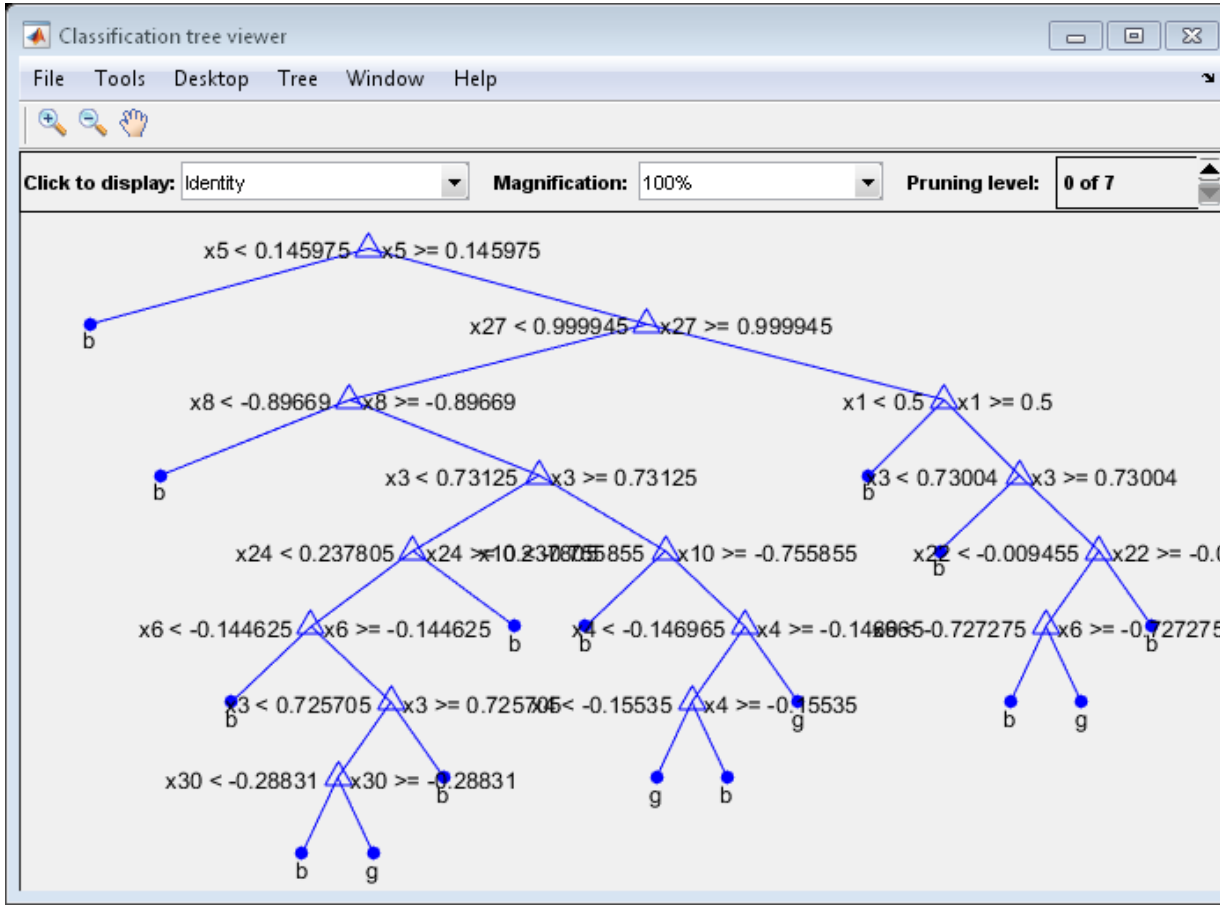
Train a classification tree using the default values for tree depth control. Cross validate the model using 10-fold cross validation.

```
rng(1); % For reproducibility
MdlDefault = fitctree(X,Y,'CrossVal','on');
```

Draw a histogram of the number of imposed on the trees. Also, view one of the trees.

```
numBranches = @(x)sum(x.IsBranch);
mdlDefaultNumSplits = cellfun(numBranches, MdlDefault.Trained);

figure;
histogram(mdlDefaultNumSplits)

view(MdlDefault.Trained{1},'Mode','graph')
```

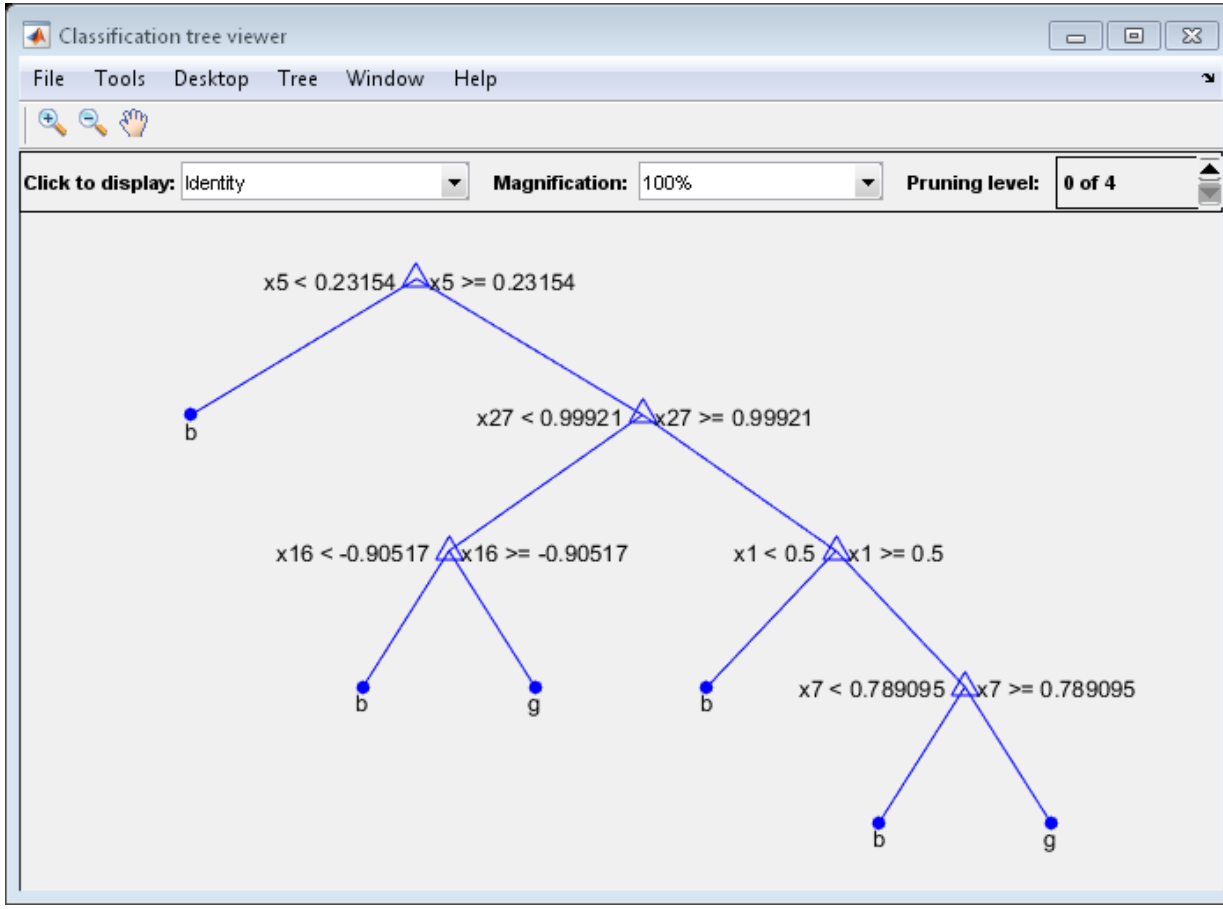

4
3.5
3
2.5
2
1.5
1
0.5
0
13.5
14
14.5
15
15.5
16
16.5
17
17.5



The average number of splits is around 15.

Suppose that you want a classification tree that is not as complex (deep) as the ones trained using the default number of splits. Train another classification tree, but set the maximum number of splits at 7, which is about half the mean number of splits from the default classification tree. Cross validate the model using 10-fold cross validation.

```
Mdl7 = fitctree(X,Y,'MaxNumSplits',7,'CrossVal','on');
view(Mdl7.Trained{1},'Mode','graph')
```



Compare the cross validation classification errors of the models.

```
classErrorDefault = kfoldLoss(MdlDefault)
classError7 = kfoldLoss(Mdl7)
```

```
classErrorDefault =

    0.1140


classError7 =
```

```
    0.1254
```

`Mdl7` is much less complex and performs only slightly worse than `MdlDefault`.

Input Arguments

`X` — Predictor values

matrix of floating-point values

Predictor values, specified as a matrix of floating-point values.

`fitctree` considers `NaN` values in X as missing values. `fitctree` does not use observations with all missing values for X in the fit. `fitctree` uses observations with some missing values for X to find splits on variables for which these observations have valid values.

Data Types: `single` | `double`

`Y` — Class labels

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class labels, specified as a numeric vector, categorical vector, logical vector, character array, or cell array of strings.

Each row of X represents the classification of the corresponding row of X. For numeric Y, consider using `fitrtree` instead. `fitctree` considers `NaN`, `''` (empty string), and `<undefined>` values in Y to be missing values.

`fitctree` does not use observations with missing values for Y in the fit.

Data Types: `single` | `double` | `char` | `logical` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'CrossVal','on','MinLeafSize',40` specifies a cross-validated classification tree with a minimum of 40 observations per leaf.

`'AlgorithmForCategorical'` — Algorithm for best categorical predictor split

`'Exact' | 'PullLeft' | 'PCA' | 'OVAbyClass'`

Algorithm to find the best split on a categorical predictor with C categories for data and $K \geq 3$ classes, specified as the comma-separated pair consisting of `'AlgorithmForCategorical'` and one of the following.

`'Exact'`	Consider all $2^{C-1} - 1$ combinations.
`'PullLeft'`	Start with all C categories on the right branch. Consider moving each category to the left branch as it achieves the minimum impurity for the K classes among the remaining categories. From this sequence, choose the split that has the lowest impurity.
`'PCA'`	Compute a score for each category using the inner product between the first principal component of a weighted covariance matrix (of the centered class probability matrix) and the vector of class probabilities for that category. Sort the scores in ascending order, and consider all $C - 1$ splits.
`'OVAbyClass'`	Start with all C categories on the right branch. For each class, order the categories based on their probability for that class. For the first class, consider moving each category to the left branch in order, recording the impurity criterion at each move. Repeat for the remaining classes. From this sequence, choose the split that has the minimum impurity.

`fitctree` automatically selects the optimal subset of algorithms for each split using the known number of classes and levels of a categorical predictor. For $K = 2$ classes, `fitctree` always performs the exact search. Use the `'AlgorithmForCategorical'` name-value pair argument to specify a particular algorithm.

Example: `'AlgorithmForCategorical','PCA'`

`'CategoricalPredictors'` — Categorical predictors list

numeric or logical vector | cell array of strings | character matrix | `'all'`

Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following:

- A numeric vector with indices from `1` through `p`, where `p` is the number of columns of X.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of X is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in `PredictorNames` values.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in `PredictorNames` values. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

Example: `'CategoricalPredictors','all'`

Data Types: `single` | `double` | `char`

`'ClassNames'` — Class names

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and an array representing the class names. Use the same data type as the values that exist in Y.

Use `ClassNames` to order the classes or to select a subset of classes for training. The default is the class names that exist in Y.

Data Types: `single` | `double` | `char` | `logical` | `cell`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification of a point, specified as the comma-separated pair consisting of `'Cost'` and one of the following:

- Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond

to the predicted class). To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

- Structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same data type as Y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Data Types: `single` | `double` | `struct`

`'CrossVal'` — Flag to grow cross-validated decision tree

`'off'` (default) | `'on'`

Flag to grow a cross-validated decision tree, specified as the comma-separated pair consisting of `'CrossVal'` and `'on'` or `'off'`.

If `'on'`, `fitctree` grows a cross-validated decision tree with 10 folds. You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments. Note that you can only use one of these four arguments at a time when creating a cross-validated tree.

Alternatively, cross validate tree later using the `crossval` method.

Example: `'CrossVal','on'`

`'CVPartition'` — Partition for cross-validated tree

`cvpartition` object

Partition to use in a cross-validated tree, specified as the comma-separated pair consisting of `'CVPartition'` and an object created using `cvpartition`.

If you use `'CVPartition'`, you cannot use any of the `'KFold'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

`'Holdout'` — Fraction of data for holdout validation

`0` (default) | scalar value in the range `[0,1]`

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the rest of the data for training.

If you use `'Holdout'`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single` | `double`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use in a cross-validated tree, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

If you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and `'on'` or `'off'`. Specify `'on'` to use leave-one-out cross-validation.

If you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

`'MaxNumCategories'` — Maximum category levels

`10` (default) | nonnegative scalar value

Maximum category levels, specified as the comma-separated pair consisting of `'MaxNumCategories'` and a nonnegative scalar value. `fitctree` splits a categorical predictor using the exact search algorithm if the predictor has at most `MaxNumCategories` levels in the split node. Otherwise, `fitctree` finds the best categorical split using one of the inexact algorithms.

Passing a small value can lead to loss of accuracy and passing a large value can increase computation time and memory overload.

Example: `'MaxNumCategories',8`

`'MaxNumSplits'` — Maximal number of decision splits

`size(X,1) - 1` (default) | positive integer

Maximal number of decision splits (or branch nodes), specified as the comma-separated pair consisting of `'MaxNumSplits'` and a positive integer. `fitctree` splits `MaxNumSplits` or fewer branch nodes. For more details on splitting behavior, see Algorithms.

Example: `'MaxNumSplits',5`

Data Types: `single | double`

`'MergeLeaves'` — Leaf merge flag

`'on'` (default) | `'off'`

Leaf merge flag, specified as the comma-separated pair consisting of `'MergeLeaves'` and `'on'` or `'off'`.

If `MergeLeaves` is `'on'`, then `fitctree`:

- Merges leaves that originate from the same parent node, and that yields a sum of risk values greater or equal to the risk associated with the parent node
- Estimates the optimal sequence of pruned subtrees, but does not prune the classification tree

Otherwise, `fitctree` does not merge leaves.

Example: `'MergeLeaves','off'`

`'MinLeafSize'` — Minimum number of leaf node observations

1 (default) | positive integer value

Minimum number of leaf node observations, specified as the comma-separated pair consisting of `'MinLeafSize'` and a positive integer value. Each leaf has at least `MinLeafSize` observations per tree leaf. If you supply both `MinParentSize` and `MinLeafSize`, `fitctree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinLeafSize',3`

Data Types: `single | double`

`'MinParentSize'` — Minimum number of branch node observations

10 (default) | positive integer value

Minimum number of branch node observations, specified as the comma-separated pair consisting of `'MinParentSize'` and a positive integer value. Each branch node in the

tree has at least `MinParentSize` observations. If you supply both `MinParentSize` and `MinLeafSize`, `fitctree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinParentSize',8`

Data Types: `single` | `double`

`'NumVariablesToSample'` — Number of predictors to select at random for each split
`'all'` | positive integer value

Number of predictors to select at random for each split, specified as the comma-separated pair consisting of `'NumVariablesToSample'` and a positive integer value. You can also specify `'all'` to use all available predictors.

Example: `'NumVariablesToSample',3`

Data Types: `single` | `double`

`'PredictorNames'` — Predictor variable names
`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in X.

`'Prior'` — Prior probabilities
`'empirical'` (default) | `'uniform'` | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- A string:
  - `'empirical'` determines class probabilities from class frequencies in Y. If you pass observation weights, `fitctree` uses the weights to compute the class probabilities.
  - `'uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class). To specify the class order for the corresponding elements of `Prior`, additionally specify the ClassNames name-value pair argument.
- A structure S with two fields:

- `S.ClassNames` containing the class names as a variable of the same type as Y
- `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `weights` and `prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

Example: `'Prior','uniform'`

`'Prune'` — Flag to estimate optimal sequence of pruned subtrees

`'on'` (default) | `'off'`

Flag to estimate the optimal sequence of pruned subtrees, specified as the comma-separated pair consisting of `'Prune'` and `'on'` or `'off'`.

If `Prune` is `'on'`, then `fitctree` grows the classification tree without pruning it, but estimates the optimal sequence of pruned subtrees. Otherwise, `fitctree` grows the classification tree without estimating the optimal sequence of pruned subtrees.

To prune a trained `ClassificationTree` model, pass it to `prune`.

Example: `'Prune','off'`

`'PruneCriterion'` — Pruning criterion

`'error'` (default) | `'impurity'`

Pruning criterion, specified as the comma-separated pair consisting of `'PruneCriterion'` and `'error'` or `'impurity'`.

Example: `'PruneCriterion','impurity'`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string representing the name of the response variable Y.

Example: `'ResponseName','Response'`

`'ScoreTransform'` — Score transform function

`'none'` | `'symmetric'` | `'invlogit'` | `'ismax'` | function handle | ...

Score transform function, specified as the comma-separated pair consisting of `'ScoreTransform'` and a function handle for transforming scores. Your function

should accept a matrix (the original scores) and return a matrix of the same size (the transformed scores).

Alternatively, you can specify one of the following strings representing a built-in transformation function.

String	Formula
`'doublelogit'`	$1/(1 + e^{-2x})$
`'invlogit'`	$\log(x / (1-x))$
`'ismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to 0.
`'logit'`	$1/(1 + e^{-x})$
`'none'`	x (no transformation)
`'sign'`	-1 for $x < 0$ 0 for $x = 0$ 1 for $x > 0$
`'symmetric'`	$2x - 1$
`'symmetriclogit'`	$2/(1 + e^{-x}) - 1$
`'symmetricismax'`	Set the score for the class with the largest score to 1, and scores for all other classes to -1.

Example: `'ScoreTransform','logit'`

`'SplitCriterion'` — Split criterion

`'gdi'` (default) | `'twoing'` | `'deviance'`

Split criterion, specified as the comma-separated pair consisting of `'SplitCriterion'` and `'gdi'` (Gini's diversity index), `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction (also known as cross entropy).

Example: `'SplitCriterion','deviance'`

`'Surrogate'` — Surrogate decision splits flag

`'off'` | `'on'` | `'all'` | positive integer value

Surrogate decision splits flag, specified as the comma-separated pair consisting of `'Surrogate'` and `'on'`, `'off'`, `'all'`, or a positive integer value.

- When set to `'on'`, `fitctree` finds at most 10 surrogate splits at each branch node.

- When set to `'all'`, `fitctree` finds all surrogate splits at each branch node. The `'all'` setting can use considerable time and memory.
- When set to a positive integer value, `fitctree` finds at most the specified number of surrogate splits at each branch node.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also lets you compute measures of predictive association between predictors.

Example: `'Surrogate','on'`

`'Weights'` — Observation weights

`ones(size(x,1),1)` (default) | vector of scalar values

Vector of observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` equals the number of rows in `X`. `fitctree` normalizes the weights in each class to add up to the value of the prior probability of the class.

Data Types: `single` | `double`

Output Arguments

`tree` — Classification tree

classification tree object

Classification tree, returned as a classification tree object.

Using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a tree of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method. Instead, use `kfoldpredict` to predict responses for observations not used for training.

Otherwise, `tree` is of class `ClassificationTree`, and you can use the `predict` method to make predictions.

More About

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*.

Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair argument:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

  $$1-\sum_i p^2(i),$$

  where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.
- Deviance (`'deviance'`) — With $p(i)$ defined the same as for the Gini index, the deviance of a node is

  $$-\sum_i p(i)\log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.
- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

  $$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

  where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.
- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with the largest number of training samples at a node, the node error is $1-p(j)$.

Tips

By default, Prune is `'on'`. However, this specification does not prune the classification tree. To prune a trained classification tree, pass the classification tree to `prune`.

Algorithms

- If MergeLeaves is `'on'` and PruneCriterion is `'error'` (which are the default values for these name-value pair arguments), then the software applies pruning only to the leaves and by using classification error. This specification amounts to merging leaves that share the most popular class per leaf.
- To accommodate `MaxNumSplits`, `fitctree` splits all nodes in the current *layer*, and then counts the number of branch nodes. A layer is the set of nodes that are equidistant from the root node. If the number of branch nodes exceeds `MaxNumSplits`, `fitctree` follows this procedure:

  1. Determine how many branch nodes in the current layer must be unsplit so that there are at most `MaxNumSplits` branch nodes.
  2. Sort the branch nodes by their impurity gains.
  3. Unsplit the number of least successful branches.
  4. Return the decision tree grown so far.

  This procedure produces maximally balanced trees.
- The software splits branch nodes layer by layer until at least one of these events occurs:

  - There are MaxNumSplits branch nodes.
  - A proposed split causes the number of observations in at least one branch node to be fewer than MinParentSize.
  - A proposed split causes the number of observations in at least one leaf node to be fewer than MinLeafSize.
  - The algorithm cannot find a good split within a layer (i.e., the pruning criterion (see PruneCriterion), does not improve for all proposed splits in a layer). A special case is when all nodes are pure (i.e., all observations in the node have the same class).

  `MaxNumSplits` and `MinLeafSize` do not affect splitting at their default values. Therefore, if you set `'MaxNumSplits'`, splitting might stop due to the value of `MinParentSize`, before `MaxNumSplits` splits occur.

- For dual-core systems and above, `fitctree` parallelizes training decision trees using Intel Threading Building Blocks (TBB). For details on Intel TBB, see https://software.intel.com/en-us/intel-tbb.

- "Splitting Categorical Predictors" on page 16-65

References

[1] Coppersmith, D., S. J. Hong, and J. R. M. Hosking. "Partitioning Nominal Attributes in Decision Trees." *Data Mining and Knowledge Discovery*, Vol. 3, 1999, pp. 197–217.

[2] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`ClassificationPartitionedModel` | `ClassificationTree` | `kfoldpredict` | `predict` | `prune`

fitglm

Create generalized linear regression model

Syntax

```
mdl = fitglm(tbl)
mdl = fitglm(X,y)
mdl = fitglm(___,modelspec)
mdl = fitglm(___,Name,Value)
```

Description

`mdl = fitglm(tbl)` returns a generalized linear model fit to variables in the table or dataset array `tbl`. By default, `fitglm` takes the last variable as the response variable.

`mdl = fitglm(X,y)` returns a generalized linear model of the responses `y`, fit to the data matrix `X`.

`mdl = fitglm(___,modelspec)` returns a generalized linear model of the type you specify in `modelspec`.

`mdl = fitglm(___,Name,Value)` returns a generalized linear model with additional options specified by one or more Name,Value pair arguments.

For example, you can specify which variables are categorical, the distribution of the response variable, and the link function to use.

Examples

Fit a Logistic Regression Model

Make a logistic binomial model of the probability of smoking as a function of age, weight, and sex, using a two-way interactions model.

Load the `hospital` dataset array.

```
load hospital
```

```
ds = hospital; % just to use the ds name
```

Specify the model using a formula that allows up to two-way interactions between the variables age, weight, and sex. Smoker is the response variable.

```
modelspec = 'Smoker ~ Age*Weight*Sex - Age:Weight:Sex';
```

Fit a logistic binomial model.

```
mdl = fitglm(ds,modelspec,'Distribution','binomial')
```

```
mdl =


Generalized Linear regression model:
    logit(Smoker) ~ 1 + Sex*Age + Sex*Weight + Age*Weight
    Distribution = Binomial

Estimated Coefficients:
                       Estimate       SE           tStat       pValue
    (Intercept)            -6.0492       19.749     -0.3063    0.75938
    Sex_Male               -2.2859       12.424     -0.18399    0.85402
    Age                    0.11691      0.50977     0.22934    0.81861
    Weight                0.031109      0.15208     0.20455    0.83792
    Sex_Male:Age          0.020734      0.20681     0.10025    0.92014
    Sex_Male:Weight        0.01216     0.053168     0.22871     0.8191
    Age:Weight         -0.00071959    0.0038964    -0.18468    0.85348


100 observations, 93 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 5.07, p-value = 0.535
```

All of the p-values (under pValue) are large. This means none of the coefficients are significant. The large *p*-value for the test of the model, 0.535, indicates that this model might not differ statistically from a constant model.

GLM for Poisson Response

Create sample data with 20 predictors, and Poisson response using just three of the predictors, plus a constant.

```
rng('default') % for reproducibility
X = randn(100,7);
mu = exp(X(:,[1 3 6])*[.4;.2;.3] + 1);
y = poissrnd(mu);
```

Fit a generalized linear model using the Poisson distribution.

```
mdl =  fitglm(X,y,'linear','Distribution','poisson')
```

```
mdl =
```

```
Generalized Linear regression model:
    log(y) ~ 1 + x1 + x2 + x3 + x4 + x5 + x6 + x7
    Distribution = Poisson

Estimated Coefficients:
                   Estimate     SE          tStat       pValue
    (Intercept)      0.88723    0.070969      12.502    7.3149e-36
    x1               0.44413    0.052337      8.4858    2.1416e-17
    x2             0.0083388    0.056527     0.14752       0.88272
    x3               0.21518    0.063416      3.3932    0.00069087
    x4              -0.058386   0.065503     -0.89135       0.37274
    x5              -0.060824   0.073441      -0.8282       0.40756
    x6               0.34267    0.056778      6.0352    1.5878e-09
    x7               0.04316     0.06146     0.70225       0.48252


100 observations, 92 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 119, p-value = 1.55e-22
```

The *p*-values of 2.14e-17, 0.00069, and 1.58e-09 indicate that the coefficients of the variables *x*1, *x*3, and *x*6 are statistically significant.

- "Generalized Linear Model Workflow" on page 10-39

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables and response variables can be numeric, or any grouping variable type, such as logical or categorical (see "Grouping Variables" on page 2-52).

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

`modelspec` — Model specification

string specifying the model | t-by-(p+1) terms matrix | string of the form `'Y ~ terms'`

Model specification, which is the starting model for `stepwiseglm`, specified as one of the following:

- String specifying the type of model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

- *t*-by-(*p*+1) matrix, namely "Terms Matrix" on page 22-1647, specifying terms to include in model, where *t* is the number of terms and *p* is the number of predictor variables, and plus one is for the response variable.
- String representing a "Formula" on page 22-1650 in the form
  `'Y ~ terms'`,
  where the `terms` are in "Wilkinson Notation" on page 22-1651.

Example: `'quadratic'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Distribution','normal','link','probit','Exclude',[23,59]` specifies that the distribution of the response is normal, and instructs `fitglm` to use the probit link function and exclude the 23rd and 59th observations from the fit.

`'BinomialSize'` — Number of trials for binomial distribution

1 (default) | scalar value | vector

Number of trials for binomial distribution, that is the sample size, specified as the comma-separated pair consisting of a scalar value or a vector of the same length as the response. This is the parameter `n` for the fitted binomial distribution. `BinomialSize` applies only when the `Distribution` parameter is `'binomial'`.

If `BinomialSize` is a scalar value, that means all observations have the same number of trials.

As an alternative to `BinomialSize`, you can specify the response as a two-column vector with counts in column 1 and `BinomialSize` in column 2.

Data Types: `single` | `double`

`'CategoricalVars'` — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of `'CategoricalVars'` and either a cell array of strings of the names of the categorical

variables in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array `tbl`, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix `X`, then the default value of this name-value pair argument is an empty matrix `[]`. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: `'CategoricalVars',[2,3]`

Example: `'CategoricalVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'DispersionFlag'` — Indicator to compute dispersion parameter

`false` for `'binomial'` and `'poisson'` distributions (default) | `true`

Indicator to compute dispersion parameter for `'binomial'` and `'poisson'` distributions, specified as the comma-separated pair consisting of `'DispersionFlag'` and one of the following.

`true`	Estimate a dispersion parameter when computing standard errors
`false`	Default. Use the theoretical value when computing standard errors

The fitting function always estimates the dispersion for other distributions.

Example: `'DispersionFlag',true`

`'Distribution'` — Distribution of the response variable

`'normal'` (default) | `'binomial'` | `'poisson'` | `'gamma'` | `'inverse gaussian'`

Distribution of the response variable, specified as the comma-separated pair consisting of `'Distribution'` and one of the following.

`'normal'`	Normal distribution
`'binomial'`	Binomial distribution

`'poisson'`	Poisson distribution
`'gamma'`	Gamma distribution
`'inverse gaussian'`	Inverse Gaussian distribution

Example: `'Distribution','gamma'`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Intercept'` — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

`'Link'` — Link function

The canonical link function (default) | scalar value | structure

Link function to use in place of the canonical link function, specified as the comma-separated pair consisting of `'Link'` and one of the following.

Link Function Name	Link Function	Mean (Inverse) Function
`'identity'`	$f(\mu) = \mu$	$\mu = Xb$

Link Function Name	Link Function	Mean (Inverse) Function
`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'probit'`	$f(\mu) = \Phi^{-1}(\mu)$	$\mu = \Phi(Xb)$
`'comploglog'`	$f(\mu) = \log(-\log(1 - \mu))$	$\mu = 1 - \exp(-\exp(Xb))$
`'reciprocal'`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`p` (a number)	$f(\mu) = \mu^p$	$\mu = Xb^{1/p}$
`S` (a structure) with three fields. Each field holds a function handle that accepts a vector of inputs and returns a vector of the same size: • `S.Link` — The link function • `S.Inverse` — The inverse link function • `S.Derivative` — The derivative of the link function	$f(\mu)$ = `S.Link`(μ)	μ = `S.Inverse`(Xb)

The link function defines the relationship $f(\mu) = X*b$ between the mean response μ and the linear combination of predictors $X*b$.

For more information on the canonical link functions, see `Definitions`.

Example: `'Link','probit'`

`'Offset'` — Offset variable

[ ] (default) | `vector` | string

Offset variable in the fit, specified as the comma-separated pair consisting of `'Offset'` and a vector or name of a variable with the same length as the response.

`fitglm` and `stepwiseglm` use `Offset` as an additional predictor, with a coefficient value fixed at 1.0. In other words, the formula for fitting is
`μ ~ Offset + (terms involving real predictors)`

with the `Offset` predictor having coefficient `1`.

For example, consider a Poisson regression model. Suppose the number of counts is known for theoretical reasons to be proportional to a predictor `A`. By using the log link function and by specifying `log(A)` as an offset, you can force the model to satisfy this theoretical constraint.

Data Types: `single` | `double` | `char`

`'PredictorVars'` — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

`'ResponseVar'` — Response variable

last column in `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset array `tbl`, or a logical or numeric index vector indicating which column is the response variable. You typically need to use `'ResponseVar'` when fitting a table or dataset array `tbl`.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

`'VarNames'` — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights

`ones(n,1)` (default) | *n*-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an *n*-by-1 vector of nonnegative scalar values, where *n* is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Generalized linear model

`GeneralizedLinearModel` object

Generalized linear model representing a least-squares fit of the link of the response to the data, returned as a `GeneralizedLinearModel` object.

For properties and methods of the generalized linear model object, `mdl`, see the `GeneralizedLinearModel` class page.

Alternative Functionality

Use `stepwiseglm` to select a model specification automatically. Use `step`, `addTerms`, or `removeTerms` to adjust a fitted model.

More About

Terms Matrix

A terms matrix is a t-by-(p + 1) matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

  ```
  load hospital
  ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
  hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
  ```

  Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

  ```
  T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]

  T =
  ```

```
     0     0     0     0
     1     0     0     0
     0     0     1     0
     0     0     0     1
```

Redefine the dataset array.

```
ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
```

Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

```
T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

  Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

  ```
  T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]
  ```

  ```
  T =

       0     0     0
       1     0     0
       0     1     0
       1     1     0
  ```

```
     0     2     0
```

Fit a linear model.

```
mdl = fitlm(X,MPG,T)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1*x2 + x2^2

Estimated Coefficients:
                   Estimate       SE            tStat      pValue
    (Intercept)         48.906        12.589     3.8847    0.00019665
    x1                0.54418       0.57125    0.95261       0.34337
    x2               -0.012781     0.0060312    -2.1192      0.036857
    x1:x2          -0.00010892    0.00017925    -0.6076         0.545
    x2^2            9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)
```

```
1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2              -0.0086119    0.0005348    -16.103    1.6434e-28
```

```
Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *`Y`* is the response name.
- *`terms`* contains
  - Variable names
  - `+` means include the next variable
  - `-` means do not include the next variable
  - `:` defines an interaction, a product of terms
  - `*` defines an interaction **and all lower-order terms**
  - `^` raises the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
  - `()` groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

For example,
`'Y ~ A + B + C'` means a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example because `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example because `A*B = A + B + A:B`.

`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Canonical Link Function

The default link function for a generalized linear model is the *canonical link function*.

Canonical Link Functions for Generalized Linear Models

Distribution	Link Function Name	Link Function	Mean (Inverse) Function
`'normal'`	`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'binomial'`	`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'poisson'`	`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'gamma'`	`-1`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$

Distribution	Link Function Name	Link Function	Mean (Inverse) Function
`'inverse gaussian'`	`-2`	$f(\mu) = 1/\mu^2$	$\mu = (Xb)^{-1/2}$

Tips

- The generalized linear model `mdl` is a standard linear model unless you specify otherwise with the `Distribution` name-value pair.
- For methods such as `plotResiduals` or `devianceTest`, or properties of the `GeneralizedLinearModel` object, see `GeneralizedLinearModel`.
- "Generalized Linear Models" on page 10-12

References

[1] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

[2] Dobson, A. J. *An Introduction to Generalized Linear Models*. New York: Chapman & Hall, 1990.

[3] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

See Also

`GeneralizedLinearModel` | `stepwiseglm`

fitglme

Fit generalized linear mixed-effects model

Syntax

```
glme = fitglme(tbl,formula)
glme = fitglme(tbl,formula,Name,Value)
```

Description

`glme = fitglme(tbl,formula)` returns a generalized linear mixed-effects model, glme. The model is specified by formula and fitted to the predictor variables in the table or dataset array, tbl.

`glme = fitglme(tbl,formula,Name,Value)` returns a generalized linear mixed-effects model using additional options specified by one or more Name,Value pair arguments. For example, you can specify the distribution of the response, the link function, or the covariance pattern of the random-effects terms.

Examples

Fit a Generalized Linear Mixed-Effects Model

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the

20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where $i = 1, 2, ..., 20$) during batch j (where $j = 1, 2, ..., 5$).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.

- *supplier_*C_{ij} and *supplier_*B_{ij} are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Display the model.

```
disp(glme)
```

```
glme =


Generalized linear mixed-effects model fit by ML

Model information:
    Number of observations             100
    Fixed effects coefficients           6
    Random effects coefficients         20
    Covariance parameters                1
    Distribution                   Poisson
    Link                           Log
    FitMethod                      Laplace

Formula:
    defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1 | factory)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    416.35    434.58    -201.17          402.35

Fixed effects coefficients (95% CIs):
    Name                Estimate     SE          tStat       DF    pValue
    '(Intercept)'          1.4689     0.15988      9.1875     94    9.8194e-15
    'newprocess'          -0.36766    0.17755     -2.0708     94      0.041122
    'time_dev'            -0.094521   0.82849     -0.11409    94      0.90941
    'temp_dev'            -0.28317    0.9617      -0.29444    94      0.76907
    'supplier_C'          -0.071868   0.078024    -0.9211     94      0.35936
    'supplier_B'           0.071072   0.07739      0.91836    94      0.36078


    Lower        Upper
```

```
       1.1515       1.7864
      -0.72019    -0.015134
       -1.7395       1.5505
       -2.1926       1.6263
      -0.22679     0.083051
     -0.082588      0.22473

Random effects covariance parameters:
Group: factory (20 Levels)
    Name1                Name2                Type         Estimate
    '(Intercept)'        '(Intercept)'        'std'        0.31381

Group: Error
    Name                      Estimate
    'sqrt(Dispersion)'        1
```

The `Model information` table displays the total number of observations in the sample data (100), the number of fixed- and random-effects coefficients (6 and 20, respectively), and the number of covariance parameters (1). It also indicates that the response variable has a `Poisson` distribution, the link function is `Log`, and the fit method is `Laplace`.

`Formula` indicates the model specification using Wilkinson's notation.

The `Model fit statistics` table displays statistics used to assess the goodness of fit of the model. This includes the Akaike information criterion (`AIC`), Bayesian information criterion (`BIC`) values, log likelihood (`LogLikelihood`), and deviance (`Deviance`) values.

The `Fixed effects coefficients` table indicates that `fitglme` returned 95% confidence intervals. It contains one row for each fixed-effects predictor, and each column contains statistics corresponding to that predictor. Column 1 (`Name`) contains the name of each fixed-effects coefficient, column 2 (`Estimate`) contains its estimated value, and column 3 (`SE`) contains the standard error of the coefficient. Column 4 (`tStat`) contains the *t*-statistic for a hypothesis test that the coefficient is equal to 0. Column 5 (`DF`) and column 6 (`pValue`) contain the degrees of freedom and *p*-value that correspond to the *t*-statistic, respectively. The last two columns (`Lower` and `Upper`) display the lower and upper limits, respectively, of the 95% confidence interval for each fixed-effects coefficient.

`Random effects covariance parameters` displays a table for each grouping variable (here, only `factory`), including its total number of levels (20), and the type and estimate of the covariance parameter. Here, `std` indicates that `fitglme` returns the standard deviation of the random effect associated with the factory predictor, which has an estimated value of 0.31381. It also displays a table containing the error parameter type (here, the square root of the dispersion parameter), and its estimated value of 1.

The standard display generated by `fitglme` does not provide confidence intervals for the random-effects parameters. To compute and display these values, use `covarianceParameters`.

- "Fit a Generalized Linear Mixed-Effects Model" on page 10-79

Input Arguments

`tbl` — Input data

table | dataset array

Input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or dataset array. The predictor variables can be continuous or grouping variables (see "Grouping Variables" on page 2-52). You must specify the model for the variables using formula.

Data Types: `single` | `double` | `char` | `cell`

`formula` — Formula for model specification

string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`

Formula for model specification, specified as a string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`. The string is case sensitive. For a full description, see "Formula" on page 22-1669.

Example: `'y ~ treatment + (1|block)'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example:
`'Distribution','Poisson','Link','log','FitMethod','Laplace','DummyVarCoding','`
specifies the response variable distribution as Poisson, the link function as log, the fit method as Laplace, and dummy variable coding where the coefficients sum to 0.

`'BinomialSize'` — Number of trials for binomial distribution

1 (default) | scalar value | vector | variable name

Number of trials for binomial distribution, that is the sample size, specified as the comma-separated pair consisting of a scalar value, a vector of the same length as the response, or the name of a variable in the input table. If you specify the name of a variable, then the variable must be of the same length as the response. `BinomialSize` applies only when the `Distribution` parameter is `'binomial'`.

If `BinomialSize` is a scalar value, that means all observations have the same number of trials.

Data Types: `single | double`

`'CheckHessian'` — Indicator to check positive definiteness of Hessian
`false` (default) | `true`

Indicator to check the positive definiteness of the Hessian of the objective function with respect to unconstrained parameters at convergence, specified as the comma-separated pair consisting of `'CheckHessian'` and either `false` or `true`. Default is `false`.

Specify `'CheckHessian'` as `true` to verify optimality of the solution or to determine if the model is overparameterized in the number of covariance parameters.

If you specify `'FitMethod'` as `'MPL'` or `'REMPL'`, then the covariance of the fixed effects and the covariance parameters is based on the fitted linear mixed-effects model from the final pseudo likelihood iteration.

Example: `'CheckHessian',true`

`'CovarianceMethod'` — Method to compute covariance of estimated parameters
`'conditional'` (default) | `'JointHessian'`

Method to compute covariance of estimated parameters, specified as the comma-separated pair consisting of `'CovarianceMethod'` and either `'conditional'` or `'JointHessian'`. If you specify `'conditional'`, then `fitglme` computes a fast approximation to the covariance of fixed effects given the estimated covariance parameters. It does not compute the covariance of covariance parameters. If you specify `'JointHessian'`, then `fitglme` computes the joint covariance of fixed effects and covariance parameters via the observed information matrix using the Laplacian loglikelihood.

If you specify `'FitMethod'` as `'MPL'` or `'REMPL'`, then the covariance of the fixed effects and the covariance parameters is based on the fitted linear mixed-effects model from the final pseudo likelihood iteration.

Example: `'CovarianceMethod','JointHessian'`

`'CovariancePattern'` — Pattern of covariance matrix

`'FullCholesky'` | `'Isotropic'` | `'Full'` | `'Diagonal'` | `'CompSymm'` | square symmetric logical matrix | cell array of strings or logical matrices

Pattern of the covariance matrix of the random effects, specified as the comma-separated pair consisting of `'CovariancePattern'` and a string, a square symmetric logical matrix, or a cell array containing strings or logical matrices.

If there are R random-effects terms, then the value of `'CovariancePattern'` must be a cell array of length R, where each element r of this cell array specifies the pattern of the covariance matrix of the random-effects vector associated with the rth random-effects term. The options for each element follow.

`'FullCholesky'`	Full covariance matrix using the Cholesky parameterization. `fitglme` estimates all elements of the covariance matrix.
`'Isotropic'`	Diagonal covariance matrix with equal variances. That is, off-diagonal elements of the covariance matrix are constrained to be 0, and the diagonal elements are constrained to be equal. For example, if there are three random-effects terms with an isotropic covariance structure, this covariance matrix looks like $\begin{pmatrix} \sigma_b^2 & 0 & 0 \\ 0 & \sigma_b^2 & 0 \\ 0 & 0 & \sigma_b^2 \end{pmatrix}$ where σ^2_1 is the common variance of the random-effects terms.
`'Full'`	Full covariance matrix, using the log-Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.
`'Diagonal'`	Diagonal covariance matrix. That is, off-diagonal elements of the covariance matrix are constrained to be 0.

$$\begin{pmatrix} \sigma_{b1}^2 & 0 & 0 \\ 0 & \sigma_{b2}^2 & 0 \\ 0 & 0 & \sigma_{b3}^2 \end{pmatrix}$$

`'CompSymm'`	Compound symmetry structure. That is, common variance along diagonals and equal correlation between all random effects. For example, if there are three random-effects terms with a covariance matrix having a compound symmetry structure, this covariance matrix looks like

$$\begin{pmatrix} \sigma_{b1}^2 & \sigma_{b1,b2} & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1}^2 & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1,b2} & \sigma_{b1}^2 \end{pmatrix}$$

where σ^2_{b1} is the common variance of the random-effects terms and $\sigma_{b1,b2}$ is the common covariance between any two random-effects term .

`PAT`	Square symmetric logical matrix. If `'CovariancePattern'` is defined by the matrix `PAT`, and if `PAT(a,b) = false`, then the `(a,b)` element of the corresponding covariance matrix is constrained to be 0.

For scalar random-effects terms, the default is `'Isotropic'`. Otherwise, the default is `'FullCholesky'`.

Example: `'CovariancePattern','Diagonal'`

Example: `'CovariancePattern',{'Full','Diagonal'}`

`'DispersionFlag'` — Indicator to compute dispersion parameter
`false` for `'binomial'` and `'poisson'` distributions (default) | `true`

Indicator to compute dispersion parameter for `'binomial'` and `'poisson'` distributions, specified as the comma-separated pair consisting of `'DispersionFlag'` and one of the following.

`true`	Estimate a dispersion parameter when computing standard errors
`false`	Use the theoretical value of `1.0` when computing standard errors

`'DispersionFlag'` only applies if `'FitMethod'` is `'MPL'` or `'REMPL'`.

The fitting function always estimates the dispersion for other distributions.

Example: `'DispersionFlag',true`

`'Distribution'` — Distribution of the response variable

`'Normal'` (default) | `'Binomial'` | `'Poisson'` | `'Gamma'` | `'InverseGaussian'`

Distribution of the response variable, specified as the comma-separated pair consisting of `'Distribution'` and one of the following.

`'Normal'`	Normal distribution
`'Binomial'`	Binomial distribution
`'Poisson'`	Poisson distribution
`'Gamma'`	Gamma distribution
`'InverseGaussian'`	Inverse Gaussian distribution

Example: `'Distribution','Binomial'`

`'DummyVarCoding'` — Coding to use for dummy variables

`'reference'` (default) | `'effects'` | `'full'`

Coding to use for dummy variables created from the categorical variables, specified as the comma-separated pair consisting of `'DummyVarCoding'` and one of the following.

`'reference'`	Default. Coefficient for first category set to 0.
`'effects'`	Coefficients sum to 0.

`'full'`	One dummy variable for each category.

Example: `'DummyVarCoding','effects'`

`'EBMethod'` — Method used to approximate empirical Bayes estimates of random effects

`'Auto'` (default) | `'LineSearchNewton'` | `'TrustRegion2D'` | `'fsolve'`

Method used to approximate empirical Bayes estimates of random effects, specified as the comma-separated pair consisting of `'EBMethod'` and one of the following.

- `'Auto'`
- `'LineSearchNewton'`
- `'TrustRegion2D'`
- `'fsolve'`

`'Auto'` is similar to `'LineSearchNewton'` but uses a different convergence criterion and does not display iterative progress. `'Auto'` and `'LineSearchNewton'` may fail for non-canonical link functions. For non-canonical link functions, `'TrustRegion2D'` or `'fsolve'` are recommended. You must have Optimization Toolbox to use `'fsolve'`.

Example: `'EBMethod','LineSearchNewton'`

`'EBOptions'` — Options for empirical Bayes optimization

structure

Options for empirical Bayes optimization, specified as the comma-separated pair consisting of `'EBOptions'` and a structure containing the following.

`'TolFun'`	Relative tolerance on the gradient norm. Default is 1e-6.
`'TolX'`	Absolute tolerance on the step size. Default is 1e-8.
`'MaxIter'`	Maximum number of iterations. Default is 100.
`'Display'`	`'off'`, `'iter'`, or `'final'`. Default is `'off'`.

If `EBMethod` is `'Auto'` and `'FitMethod'` is `'Laplace'`, `TolFun` is the relative tolerance on the linear predictor of the model, and the `'Display'` option does not apply.

If `'EBMethod'` is `'fsolve'`, then `'EBOptions'` must be specified as an object created by `optimoptions('fsolve')`.

Data Types: `struct`

`'Exclude'` — Indices for rows to exclude

use all rows without `NaNs` (default) | vector of integer or logical values

Indices for rows to exclude from the generalized linear mixed-effects model in the data, specified as the comma-separated pair consisting of `'Exclude'` and a vector of integer or logical values.

For example, you can exclude the 13th and 67th rows from the fit as follows.

Example: `'Exclude',[13,67]`

Data Types: `single` | `double` | `logical`

`'FitMethod'` — Method for estimating model parameters

`'MPL'` (default) | `'REMPL'` | `'Laplace'` | `'ApproximateLaplace`

Method for estimating model parameters, specified as the comma-separated pair consisting of `'FitMethod'` and one of the following.

- `'MPL'` — Maximum pseudo likelihood
- `'REMPL'` — Restricted maximum pseudo likelihood
- `'Laplace'` — Maximum likelihood using Laplace approximation
- `'ApproximateLaplace'` — Maximum likelihood using approximate Laplace approximation with fixed effects profiled out

Example: `'FitMethod','REMPL'`

`'InitPLIterations'` — Initial number of pseudo likelihood iterations

10 (default) | integer value in the range [1,∞)

Initial number of pseudo likelihood iterations used to initialize parameters for `ApproximateLaplace` and `Laplace` fit methods, specified as the comma-separated pair consisting of `'InitPLIterations'` and an integer value greater than or equal to 1.

Data Types: `single` | `double`

`'Link'` — Link function

`'identity'` | `'log'` | `'logit'` | `'probit'` | `'comploglog'` | `'reciprocal'` | scalar value | structure

Link function, specified as the comma-separated pair consisting of `'Link'` and one of the following.

`'identity'`	`g(mu) = mu` This is the default for the normal distribution.
`'log'`	`g(mu) = log(mu)` This is the default for the Poisson distribution.
`'logit'`	`g(mu) = log(mu/(1-mu))` This is the default for the binomial distribution.
`'loglog'`	`g(mu) = log(-log(mu))`
`'probit'`	`g(mu) = norminv(mu)`
`'comploglog'`	`g(mu) = log(-log(1-mu))`
`'reciprocal'`	`g(mu) = mu.^(-1)`
Scalar value `P`	`g(mu) = mu.^P`
Structure `S`	A structure containing four fields whose values are function handles with the following names: • `S.Link` — Link function • `S.Derivative` — Derivative • `S.SecondDerivative` — Second derivative • `S.Inverse` — Inverse of link Specification of `S.SecondDerivative` can be omitted if `FitMethod` is `MPL` or `REMPL`, or if `S` is the canonical link for the specified distribution.

The default link function used by `fitglme` is the canonical link that depends on the distribution of the response.

`'Normal'`	`'identity'`
`'Binomial'`	`'logit'`
`'Poisson'`	`'log'`
`'Gamma'`	`-1`
`'InverseGaussian'`	`-2`

Example: `'Link','log'`

Data Types: `single` | `double` | `struct`

`'MuStart'` — Starting value for conditional mean

scalar value

Starting value for conditional mean, specified as the comma-separated pair consisting of `'MuStart'` and a scalar value. Valid values are as follows.

Distribution	Values
`'Normal'`	`(-Inf,Inf)`
`'Binomial'`	`(0,1)`
`'Poisson'`	`(0,Inf)`
`'Gamma'`	`(0,Inf)`
`'InverseGaussian'`	`(0,Inf)`

Data Types: `single` | `double`

`'Offset'` — Offset

`zeros(n,1)` (default) | *n*-by-1 vector of scalar values

Offset, specified as the comma-separated pair consisting of `'Offset'` and an *n*-by-1 vector of scalar values, where *n* is the length of the response vector. You can also specify the variable name of an *n*-by-1 vector of scalar values. `'Offset'` is used as an additional predictor that has a coefficient value fixed at `1.0`.

Data Types: `single` | `double`

`'Optimizer'` — Optimization algorithm

`'quasinewton'` (default) | `'fminsearch'` | `'fminunc'`

Optimization algorithm, specified as the comma-separated pair consisting of `'Optimizer'` and either of the following.

`'quasinewton'`	Uses a trust region based quasi-Newton optimizer. You can change the options of the algorithm using `statset('fitglme')`. If you do not specify the options, then `fitglme` uses the default options of `statset('fitglme')`.
`'fminsearch'`	Uses a derivative-free Nelder-Mead method. You can change the options of the algorithm using `optimset('fminsearch')`. If you do not specify the options, then `fitglme` uses the default options of `optimset('fminsearch')`.
`'fminunc'`	Uses a line search-based quasi-Newton method. You must have Optimization Toolbox to specify this option. You can change the options of the algorithm using `optimoptions('fminunc')`. If you do not specify the options, then `fitglme` uses the default options of `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.

Example: `'Optimizer','fminsearch'`

`'OptimizerOptions'` — Options for optimization algorithm

structure returned by `statset` | structure returned by `optimset` | object returned by `optimoptions`

Options for the optimization algorithm, specified as the comma-separated pair consisting of `'OptimizerOptions'` and a structure returned by `statset('fitglme')`, a structure created by `optimset('fminsearch')`, or an object returned by `optimoptions('fminunc')`.

- If `'Optimizer'` is `'fminsearch'`, then use `optimset('fminsearch')` to change the options of the algorithm. If `'Optimizer'` is `'fminsearch'` and you do not supply `'OptimizerOptions'`, then the defaults used in `fitglme` are the default options created by `optimset('fminsearch')`.
- If `'Optimizer'` is `'fminunc'`, then use `optimoptions('fminunc')` to change the options of the optimization algorithm. See `optimoptions` for the

options `'fminunc'` uses. If `'Optimizer'` is `'fminunc'` and you do not supply `'OptimizerOptions'`, then the defaults used in `fitglme` are the default options created by `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.

- If `'Optimizer'` is `'quasinewton'`, then use `statset('fitglme')` to change the optimization parameters. If `'Optimizer'` is `'quasinewton'` and you do not change the optimization parameters using `statset`, then `fitglme` uses the default options created by `statset('fitglme')`.

The `'quasinewton'` optimizer uses the following fields in the structure created by `statset('fitglme')`.

`'TolFun'` — Relative tolerance on gradient of objective function
`1e-6` (default) | positive scalar value

Relative tolerance on the gradient of the objective function, specified as a positive scalar value.

`'TolX'` — Absolute tolerance on step size
`1e-12` (default) | positive scalar value

Absolute tolerance on the step size, specified as a positive scalar value.

`'MaxIter'` — Maximum number of iterations allowed
`10000` (default) | positive scalar value

Maximum number of iterations allowed, specified as a positive scalar value.

`'Display'` — Level of display
`'off'` (default) | `'iter'` | `'final'`

Level of display, specified as one of `'off'`, `'iter'`, or `'final'`.

`'PLIterations'` — Maximum number of pseudo likelihood iterations
`100` (default) | positive integer value

Maximum number of pseudo likelihood (PL) iterations, specified as the comma-separated pair consisting of `'PLIterations'` and a positive integer value. PL is used for fitting the model if `'FitMethod'` is `'MPL'` or `'REMPL'`. For other `'FitMethod'` values, PL iterations are used to initialize parameters for subsequent optimization.

Example: `'PLIterations',200`

Data Types: `single` | `double`

`'PLTolerance'` — Relative tolerance factor for pseudo likelihood iterations
`1e–08` (default) | positive scalar value

Relative tolerance factor for pseudo likelihood iterations, specified as the comma-separated pair consisting of `'PLTolerance'` and a positive scalar value.

Example: `'PLTolerance',1e-06`

Data Types: `single` | `double`

`'StartMethod'` — Method to start iterative optimization
`'default'` (default) | `'random'`

Method to start iterative optimization, specified as the comma-separated pair consisting of `'StartMethod'` and either of the following.

`'default'`	Default. An internally defined default value.
`'random'`	A random initial value.

Example: `'StartMethod','random'`

`'UseSequentialFitting'` — Initial fitting type
`false` (default) | `true`

, specified as the comma-separated pair consisting of `'UseSequentialFitting'` and either `false` or `true`. If `'UseSequentialFitting'` is `false`, all maximum likelihood methods are initialized using one or more pseudo likelihood iterations. If `'UseSequentialFitting'` is `true`, the initial values from pseudo likelihood iterations are refined using `'ApproximateLaplace'` for `'Laplace'` fitting.

Example: `'UseSequentialFitting',true`

`'Verbose'` — Indicator to display optimization process on screen
`0` (default) | `1` | `2`

Indicator to display the optimization process on screen, specified as the comma-separated pair consisting of `'Verbose'` and `0`, `1`, or `2`. If `'Verbose'` is specified as `1` or `2`, then `fitglme` displays the progress of the iterative model-fitting process. Specifying `'Verbose'` as `2` displays iterative optimization information from the individual pseudo likelihood iterations. Specifying `'Verbose'` as `1` omits this display.

The setting for `'Verbose'` overrides the field `'Display'` in `'OptimizerOptions'`.

Example: `'Verbose',true`

`'Weights'` — Observation weights

vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an n-by-1 vector of nonnegative scalar values, where n is the number of observations. If the response distribution is binomial or Poisson, then `'Weights'` must be a vector of positive integers.

Data Types: `single | double`

Output Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

More About

Formula

In general, a formula for model specification is a string of the form `'y ~ terms'`. For the generalized linear mixed-effects models, this formula is in the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` and `random` contain the fixed-effects and the random-effects terms.

Suppose a table `tbl` contains the following:

- A response variable, `y`
- Predictor variables, X_j, which can be continuous or grouping variables
- Grouping variables, g_1, g_2, ..., g_R,

where the grouping variables in X_j and g_r can be categorical, logical, character arrays, or cell arrays of strings.

Then, in a formula of the form, `'y ~ fixed + (random1|g1) + ... + (randomR|gR)'`, the term `fixed` corresponds to a specification of the fixed-effects design matrix `X`, $\texttt{random}_1$ is a specification of the random-effects design matrix Z_1 corresponding to grouping variable g_1, and similarly $\texttt{random}_R$ is a specification of the random-effects design matrix Z_R corresponding to grouping variable g_R. You can express the `fixed` and `random` terms using Wilkinson notation.

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1.*X2 (elementwise multiplication of X1 and X2)`
`X1:X2`	`X1.*X2` only
`- X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`. Here are some examples for generalized linear mixed-effects model specification.

Examples:

Formula	Description
`'y ~ X1 + X2'`	Fixed effects for the intercept, `X1` and `X2`. This is equivalent to `'y ~ 1 + X1 + X2'`.
`'y ~ -1 + X1 + X2'`	No intercept and fixed effects for `X1` and `X2`. The implicit intercept term is suppressed by including `-1`.

Formula	Description
`'y ~ 1 + (1 | g1)'`	Fixed effects for the intercept plus random effect for the intercept for each level of the grouping variable `g1`.
`'y ~ X1 + (1 | g1)'`	Random intercept model with a fixed slope.
`'y ~ X1 + (X1 | g1)'`	Random intercept and slope, with possible correlation between them. This is equivalent to `'y ~ 1 + X1 + (1 + X1| g1)'`.
`'y ~ X1 + (1 | g1) + (-1 + X1 | g1)'`	Independent random effects terms for intercept and slope.
`'y ~ 1 + (1 | g1) + (1 | g2) + (1 | g1:g2)'`	Random intercept model with independent main effects for `g1` and `g2`, plus an independent interaction effect.

- “Generalized Linear Mixed-Effects Models” on page 10-64

See Also

`GeneralizedLinearMixedModel`

fitgmdist

Fit Gaussian mixture distribution to data

Syntax

```
GMModel = fitgmdist(X,k)
GMModel = fitgmdist(X,k,Name,Value)
```

Description

`GMModel = fitgmdist(X,k)` returns a Gaussian mixture distribution model (`GMModel`) with `k` components fitted to data (`X`).

`GMModel = fitgmdist(X,k,Name,Value)` returns a Gaussian mixture distribution model with additional options specified by one or more Name,Value pair arguments.

For example, you can specify a regularization value or the covariance type.

Examples

Cluster Data Using a Gaussian Mixture Model

Generate data from a mixture of two bivariate Gaussian distributions.

```
mu1 = [1 2];
Sigma1 = [2 0; 0 0.5];
mu2 = [-3 -5];
Sigma2 = [1 0;0 1];
rng(1); % For reproducibility
X = [mvnrnd(mu1,Sigma1,1000);mvnrnd(mu2,Sigma2,1000)];
```

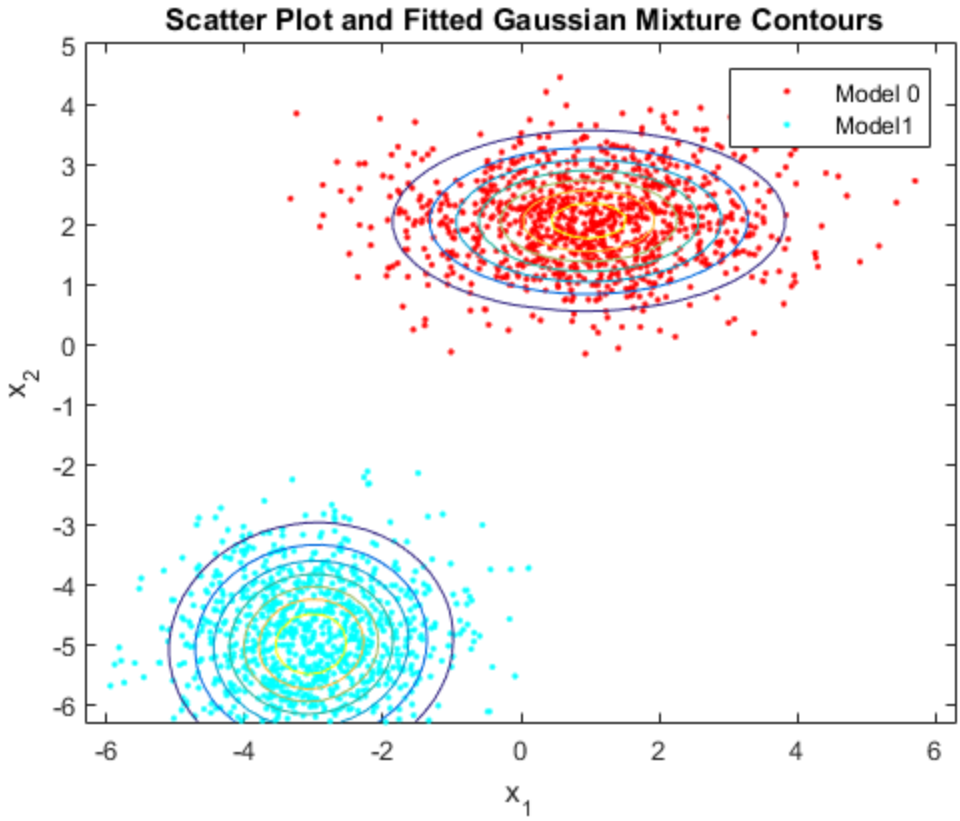
Fit a Gaussian mixture model. Specify that there are two components.

```
GMModel = fitgmdist(X,2);
```

Plot the data over the fitted Gaussian mixture model contours.

```
figure
y = [zeros(1000,1);ones(1000,1)];
```

```
h = gscatter(X(:,1),X(:,2),y);
hold on
ezcontour(@(x1,x2)pdf(GMModel,[x1 x2]),get(gca,{'XLim','YLim'}))
title('{\bf Scatter Plot and Fitted Gaussian Mixture Contours}')
legend(h,'Model 0','Model1')
hold off
```



Regularize Gaussian Mixture Model Estimation

Generate data from a mixture of two bivariate Gaussian distributions. Create a third predictor that is the sum of the first and second predictors.

```
mu1 = [1 2];
Sigma1 = [1 0; 0 1];
mu2 = [3 4];
```

```
Sigma2 = [0.5 0; 0 0.5];
rng(1); % For reproducibility
X1 = [mvnrnd(mu1,Sigma1,100);mvnrnd(mu2,Sigma2,100)];
X = [X1,X1(:,1)+X1(:,2)];
```

The columns of `X` are linearly dependent. This can cause ill-conditioned covariance estimates.

Fit a Gaussian mixture model to the data. You can use `try` / `catch` statements to help manage error messages.

```
rng(1); % Reset seed for common start values
try
    GMModel = fitgmdist(X,2)
catch exception
    disp('There was an error fitting the Gaussian mixture model')
    error = exception.message
end
```

```
There was an error fitting the Gaussian mixture model

error =

Ill-conditioned covariance created at iteration 2.
```

The covariance estimates are ill-conditioned. Subsequently, optimization stops and an error appears.

Fit a Gaussian mixture model again, but use regularization.

```
rng(1); % Reset seed for common start values
GMModel = fitgmdist(X,2,'RegularizationValue',0.1)
```

```
GMModel =

Gaussian mixture distribution with 2 components in 3 dimensions
Component 1:
Mixing proportion: 0.507057
Mean:    0.9767    2.0130    2.9897

Component 2:
Mixing proportion: 0.492943
Mean:    3.1030    3.9544    7.0574
```

In this case, the algorithm converges to a solution due to regularization.

Select the Number of Gaussian Mixture Model Components Using PCA

Gaussian mixture models require that you specify a number of components before being fit to data. For many applications, it might be diffcult to know the appropriate number of components. This example shows how to explore the data, and try to get an initial guess at the number of components using principal component analysis.

Load Fisher's iris data set.

```
load fisheriris
classes = unique(species)
```

```
classes =

    'setosa'
    'versicolor'
    'virginica'
```

The data set contains three classes of iris species. The analysis proceeds as if this is unknown.

Use principal component analysis to reduce the dimension of the data to two dimensions for visualization.

```
[~,score] = pca(meas,'NumComponents',2);
```

Fit three Gaussian mixture models to the data by specifying 1, 2, and 3 components. Increase the number of optimization iterations to 1000. Use dot notation to store the final parameter estimates. By default, the software fits full and different covariances for each component.

```
GMModels = cell(3,1); % Preallocation
options = statset('MaxIter',1000);
rng(1); % For reproducibility

for j = 1:3
    GMModels{j} = fitgmdist(score,j,'Options',options);
    fprintf('\n GM Mean for %i Component(s)\n',j)
```

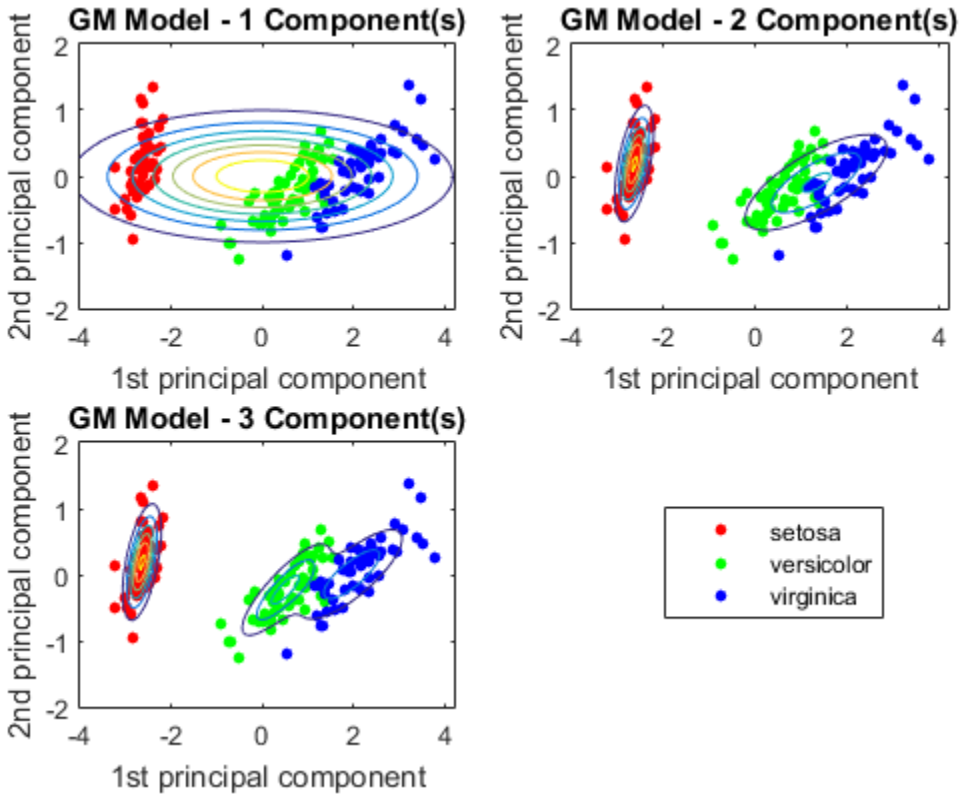
```
    Mu = GMModels{j}.mu
end


 GM Mean for 1 Component(s)

Mu =

   1.0e-14 *

   -0.2805   -0.0931


 GM Mean for 2 Component(s)

Mu =

    1.3212   -0.0954
   -2.6424    0.1909


 GM Mean for 3 Component(s)

Mu =

    1.9642    0.0062
   -2.6424    0.1909
    0.4750   -0.2292
```

`GMModels` is a cell array containing three, fitted `gmdistribution` models. The means in the three component models are different, suggesting that the model distinguishes among the three iris species.

Plot the scores over the fitted Gaussian mixture model contours. Since the data set includes labels, use `gscatter` to distinguish between the true number of components.

```
figure
for j = 1:3
    subplot(2,2,j)
    gscatter(score(:,1),score(:,2),species)
    h = gca;
    hold on
    ezcontour(@(x1,x2)pdf(GMModels{j},[x1 x2]),...
        [h.XLim h.YLim],100)
```

```
    title(sprintf('GM Model - %i Component(s)',j));
    xlabel('1st principal component');
    ylabel('2nd principal component');
    if(j ~= 3)
        legend off;
    end
    hold off
end
g = legend;
g.Position = [0.7 0.25 0.1 0.1];
%set(g,'Position',[0.7,0.25,0.1,0.1])
```



The three-component Gaussian mixture model, in conjunction with PCA, looks like it distinguishes between the three iris species.

There are other options you can use to help select the appropriate number of components for a Gaussian mixture model. For example,

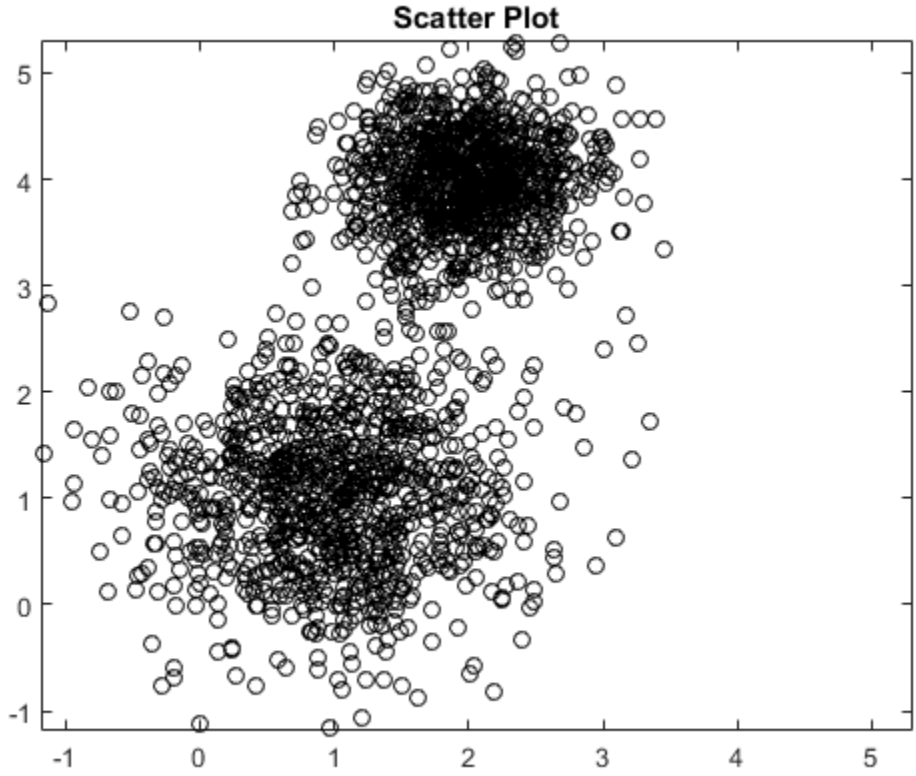
- Compare multiple models with varying numbers of components using information criteria, e.g., AIC or BIC.
- Estimate the number of clusters using `evalclusters`, which supports, the Calinski-Harabasz criterion and the gap statistic, or other criteria.

Determine the Best Gaussian Mixture Fit Using AIC

Gaussian mixture models require that you specify a number of components before being fit to data. For many applications, it might be diffcult to know the appropriate number of components. This example uses the AIC fit statistic to help you choose the best fitting Gaussian mixture model over varying numbers of components.

Generate data from a mixture of two bivariate Gaussian distributions.

```
mu1 = [1 1];
Sigma1 = [0.5 0; 0 0.5];
mu2 = [2 4];
Sigma2 = [0.2 0; 0 0.2];
rng(1);
X = [mvnrnd(mu1,Sigma1,1000);mvnrnd(mu2,Sigma2,1000)];

plot(X(:,1),X(:,2),'ko')
title('Scatter Plot')
xlim([min(X(:)) max(X(:))]) % Make axes have the same scale
ylim([min(X(:)) max(X(:))])
```



Supposing that you do not know the underlying parameter values, the scatter plots suggests:

- There are two components.
- The variances between the clusters are different.
- The variance within the clusters is the same.
- There is no covariance within the clusters.

Fit a two-component Gaussian mixture model. Based on the scatter plot inspection, specify that the covariance matrices are diagonal. Print the final iteration and loglikelihood statistic to the Command Window by passing a `statset` structure as the value of the `Options` name-value pair argument.

```
options = statset('Display','final');
GMModel = fitgmdist(X,2,'CovarianceType','diagonal','Options',options);

10 iterations, log-likelihood = -4787.38
```

`GMModel` is a fitted `gmdistribution` model.

Examine the AIC over varying numbers of components.

```
AIC = zeros(1,4);
GMModels = cell(1,4);
options = statset('MaxIter',500);
for k = 1:4
    GMModels{k} = fitgmdist(X,k,'Options',options,'CovarianceType','diagonal');
    AIC(k)= GMModels{k}.AIC;
end

[minAIC,numComponents] = min(AIC);
numComponents

BestModel = GMModels{numComponents}


numComponents =

     2


BestModel =

Gaussian mixture distribution with 2 components in 2 dimensions
Component 1:
Mixing proportion: 0.501736
Mean:    1.9824    4.0013

Component 2:
Mixing proportion: 0.498264
Mean:    0.9879    1.0511
```

The smallest AIC occurs when the software fits the two-component Gaussian mixture model.

Set Initial Values When Fitting Gaussian Mixture Models

Gaussian mixture model parameter estimates might vary with different initial values. This example shows how to control initial values when you fit Gaussian mixture models using `fitgmdist`.

Load Fisher's iris data set. Use the petal lengths and widths as predictors.

```
load fisheriris
X = meas(:,3:4);
```

Fit a Gaussian mixture model to the data using default initial values. There are three iris species, so specify $k = 3$ components.

```
rng(10); % For reproducibility
GMModel1 = fitgmdist(X,3);
```

By default, the software:

1. Randomly chooses $k = 3$ data points
2. Treats the chosen data points as initial means for each component
3. Sets the initial covariance matrices as diagonal, where element (`j`, `j`) is the variance of `X(:,j)`
4. Treats the initial mixing proportions as uniform

Fit a Gaussian mixture model by connecting each observation to its label.

```
y = ones(size(X,1),1);
y(strcmp(species,'setosa')) = 2;
y(strcmp(species,'virginica')) = 3;

GMModel2 = fitgmdist(X,3,'Start',y);
```

Fit a Gaussian mixture model by explicitly specifying the initial means, covariance matrices, and mixing proportions.

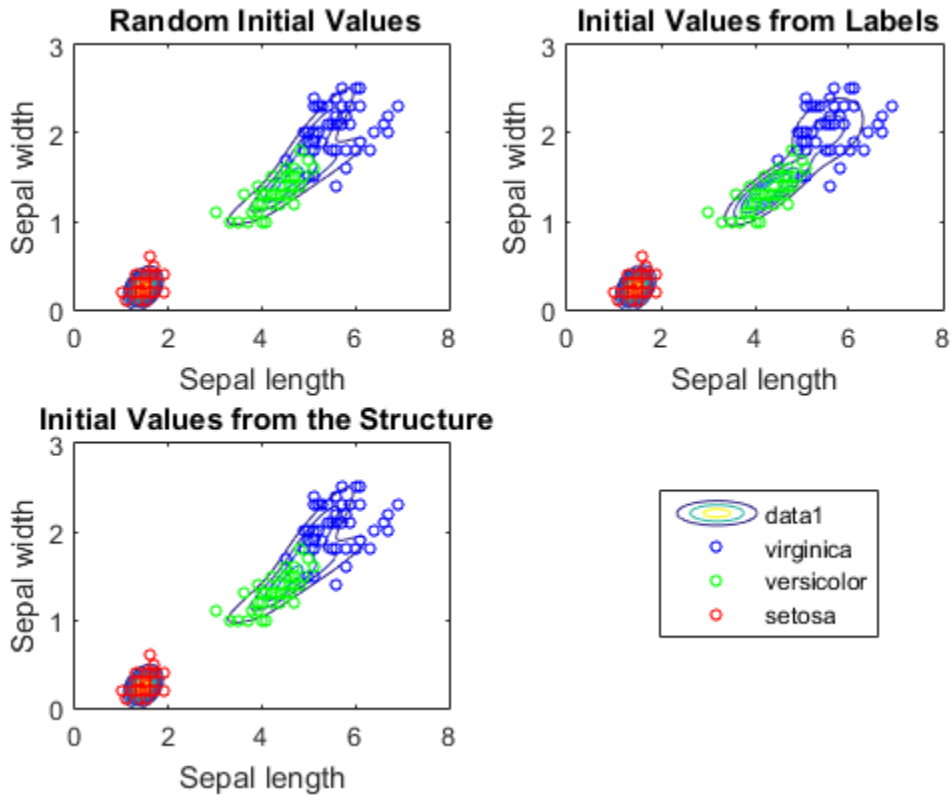
```
Mu = [1 1; 2 2; 3 3];
Sigma(:,:,1) = [1 1; 1 2];
Sigma(:,:,2) = 2*[1 1; 1 2];
```

```
Sigma(:,:,3) = 3*[1 1; 1 2];
PComponents = [1/2,1/4,1/4];
S = struct('mu',Mu,'Sigma',Sigma,'ComponentProportion',PComponents);

GMModel3 = fitgmdist(X,3,'Start',S);
```

Use `gscatter` to plot a scatter diagram that distinguishes between the iris species. For each model, plot the fitted Gaussian mixture model contours.

```
figure
subplot(2,2,1)
h = gscatter(X(:,1),X(:,2),species,[],'o',4);
haxis = gca;
xlim = haxis.XLim;
ylim = haxis.YLim;
d = (max([xlim ylim])-min([xlim ylim]))/1000;
[X1Grid,X2Grid] = meshgrid(xlim(1):d:xlim(2),ylim(1):d:ylim(2));
hold on
contour(X1Grid,X2Grid,reshape(pdf(GMModel1,[X1Grid(:) X2Grid(:)]),...
    size(X1Grid,1),size(X1Grid,2)),20)
uistack(h,'top')
title('{\bf Random Initial Values}');
xlabel('Sepal length');
ylabel('Sepal width');
legend off;
hold off
subplot(2,2,2)
h = gscatter(X(:,1),X(:,2),species,[],'o',4);
hold on
contour(X1Grid,X2Grid,reshape(pdf(GMModel2,[X1Grid(:) X2Grid(:)]),...
    size(X1Grid,1),size(X1Grid,2)),20)
uistack(h,'top')
title('{\bf Initial Values from Labels}');
xlabel('Sepal length');
ylabel('Sepal width');
legend off
hold off
subplot(2,2,3)
h = gscatter(X(:,1),X(:,2),species,[],'o',4);
hold on
contour(X1Grid,X2Grid,reshape(pdf(GMModel3,[X1Grid(:) X2Grid(:)]),...
    size(X1Grid,1),size(X1Grid,2)),20)
uistack(h,'top')
title('{\bf Initial Values from the Structure}');
xlabel('Sepal length');
```

```
ylabel('Sepal width');
legend('Location',[0.7,0.25,0.1,0.1]);
hold off
```



According to the countors, `GMModel2` seems to suggest a slight trimodality, while the others suggest bimodel distributions.

Display the estimated component means.

```
table(GMModel1.mu,GMModel2.mu,GMModel3.mu,'VariableNames',...
    {'Model1','Model2','Model3'})
```

```
ans =
```

```
      Model1                Model2                Model3
_________________     _________________     _________________

5.0241     1.8658     4.2857     1.3339     1.4604     0.2429
4.7471     1.4616      1.462      0.246     4.7509     1.4629
1.4605    0.24306     5.5507     2.0316     5.0158     1.8592
```

`GMModel2` seems to distinguish between the iris species the best.

- "Clustering Using Gaussian Mixture Models" on page 14-29

Input Arguments

`X` — Data

numeric matrix

Data to which the Gaussian mixture model is fit, specified as a numeric matrix.

The rows of `X` correspond to observations, and columns correspond to variables.

`NaN`s indicate missing values. The software removes rows of `X` containing at least one `NaN` before fitting, which decreases the effective sample size.

Data Types: `double`

`k` — Number of components

positive integer

Number of components to use when fitting Gaussian mixture model, specified as a positive integer. For example, if you specify `k = 3`, then the software fits a Gaussian mixture model with three distinct means, covariances matrices, and component proportions to the data (`X`).

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'RegularizationValue',0.1,'CovarianceType','diagonal'` specifies a regularization parameter value of 0.1 and to fit diagonal covariance matrices.

`'CovarianceType'` — Type of covariance matrix

`'full'` (default) | `'diagonal'`

Type of covariance matrix to fit to the data, specified as the comma-separated pair consisting of `'CovarianceType'` and either `'diagonal'` or `'full'`.

If you set `'diagonal'`, then the software fits diagonal covariance matrices. In this case, the software estimates `k*d` covariance parameters, where `d` is the number of columns in X (i.e., `d = size(X,2)`).

Otherwise, the software fits full covariance matrices. In this case, the software estimates `k*d*(d+1)/2` covariance parameters.

Example: `'CovarianceType','diagonal'`

Data Types: `char`

`'Options'` — Iterative EM algorithm optimization options

`statset` options structure

Iterative EM algorithm optimization options, specified as the comma-separated pair consisting of `'Options'` and a `statset` options structure.

This table describes the available name-value pair arguments.

Name	Value
`'Display'`	`'final'`: Display the final output. `'iter'`: Display iterative output to the Command Window for some functions; otherwise display the final output. `'off'`: Do not display optimization information.
`'MaxIter'`	Positive integer indicating the maximum number of iterations allowed. The default is `100`

Name	Value
'TolFun'	Positive scalar indicating the termination tolerance for the loglikelihood function value. The default is 1e-6.

Example:
'Options',statset('Display','final','MaxIter',1500,'TolFun',1e-5)

'RegularizationValue' — Regularization parameter value
0 (default) | nonnegative scalar

Regularization parameter value, specified as the comma-separated pair consisting of 'RegularizationValue' and a nonnegative scalar.

Set RegularizationValue to a small positive scalar to ensure that the estimated covariance matrices are positive definite.

Example: 'RegularizationValue',0.01

Data Types: double

'Replicates' — Number of times to repeat EM algorithm
1 (default) | positive integer

Number of times to repeat the EM algorithm using a new set of initial values, specified as the comma-separated pair consisting of 'Replicates' and a positive integer.

If Replicates is greater than 1, then:

- The name-value pair argument Start must be randSample (which is the default value) or plus.
- GMModel is the fit with the largest loglikelihood.

Example: 'Replicates',10

Data Types: double

'SharedCovariance' — Flag indicating whether all covariance matrices are identical
logical false (default) | logical true

Flag indicating whether all covariance matrices are identical (i.e., fit a pooled estimate), specified as the comma-separated pair consisting of 'SharedCovariance' and either logical value false or true.

If `SharedCovariance` is `true`, then all `k` covariance matrices are equal, and the number of covariance parameters is scaled down by a factor of `k`.

`'Start'` — Initial value setting method

`'randSample'` (default) | `'plus'` | vector of integers | structure array

Initial value setting method, specified as the comma-separated pair consisting of `'Start'` and `'randSample'`, `'plus'`, a vector of integers, or a structure array.

The value of `Start` determines the initial values required by the optimization routine for each Gaussian component parameter — mean, covariance, and mixing proportion. This table summarizes the available options.

Value	Description
`'randSample`	The software selects `k` observations from `X` at random as initial component means. The mixing proportions are uniform. The initial covariance matrices for all components are diagonal, where the element `j` on the diagonal is the variance of `X(:,j)`.
`'plus'`	The software selects `k` observations from `X` using the kmeans++ algorithm. The initial mixing proportions are uniform. The initial covariance matrices for all components are diagonal, where the element `j` on the diagonal is the variance of `X(:,j)`.
Vector of integers	A vector of length n (the number of observations) containing an initial guess of the component index for each point. That is, each element is an integer from 1 to `k`, which corresponds to a component. The software collects all observations corresponding to the same component, computes means, covariances, and mixing proportions for each, and sets the initial values to these statistics.

Structure array	Suppose that there are `d` variables (i.e., `d = size(X,2)`). The structure array, e.g., `S`, must have three fields:
	• `S.mu`: A `k`-by-`d` matrix specifying the initial mean of each component
	• `S.Sigma`: A numeric array specifying the covariance matrix of each component. `Sigma` is one of the following:
	  • A `d`-by-`d`-by-`k` array. `Sigma(:,:,j)` is the initial covariance matrix of component `j`.
	  • A `1`-by-`d`-by-`k` array. `diag(Sigma(:,:,j))` is the initial covariance matrix of component `j`.

Value	Description
	• A `d`-by-`d` matrix. `Sigma` is the initial covariance matrix for all components. • A `1`-by-`d` vector. `diag(Sigma)` is the initial covariance matrix for all components. • `S.ComponentProportion`: A `1`-by-`k` vector of scalars specifying the initial mixing proportions of each component. The default is uniform.

Example: `'Start',ones(n,1)`

Data Types: `char | double | struct`

Output Arguments

`GMModel` — Fitted Gaussian mixture model

`gmdistribution` model

Fitted Gaussian mixture model, returned as a `gmdistribution` model.

Access properties of `GMModel` using dot notation. For example, display the AIC by entering `GMModel.AIC`.

More About

Tips

`gmdistribution` might:

- Converge to a solution where one or more of the components has an ill-conditioned or singular covariance matrix.

  The following issues might result in an ill-conditioned covariance matrix:

  - The number of dimensions of your data is relatively high and there are not enough observations.
  - Some of the predictors (variables) of your data are highly correlated.

- Some or all the features are discrete.
- You tried to fit the data to too many components.

In general, you can avoid getting ill-conditioned covariance matrices by using one of the following precautions:

- Preprocess your data to remove correlated features.
- Set `'SharedCovariance'` to `true` to use an equal covariance matrix for every component.
- Set `'CovarianceType'` to `'diagonal'`.
- Use `'RegularizationValue'` to add a very small positive number to the diagonal of every covariance matrix.
- Try another set of initial values.

- Pass through an intermediate step where one or more of the components has an ill-conditioned covariance matrix. Try another set of initial values to avoid this issue without altering your data or model.

Algorithms

Gaussian Mixture Model Likelihood Optimization

The software optimizes the Gaussian mixture model likelihood using the iterative Expectation-Maximization (EM) algorithm.

k-means++ Algorithm for Initialization

The *k*-means++ algorithm uses an heuristic to find centroid seeds for *k*-means clustering. `fitgmdist` can apply the same principle to initialize the EM algorithm by using the k-means++ algorithm to select the initial parameter values for a fitted Gaussian mixture model.

The *k*-means++ algorithm assumes the number of clusters is *k* and chooses the initial parameter values as follows.

1. Select the component mixture probability to be the uniform probability $p_i = \frac{1}{k}$, where $i = 1, ..., k$.

2. Select the covariance matrices to be diagonal and identical, where $\sigma_i = diag(a_1, a_2, \ldots, a_k)$ and $a_j = \mathrm{var}(X_j)$.
3. Select the first initial component center μ_1 uniformly from all data points in X.
4. To choose center j:
   a. Compute the Mahalanobis distances from each observation to each centroid, and assign each observation to its closest centroid.
   b. For $m = 1,\ldots,n$ and $p = 1,\ldots,j-1$, select centroid j at random from X with probability

$$\frac{d^2(x_m, \mu_p)}{\sum_{h; x_h \in M_p} d^2(x_h, \mu_p)}$$

      where $d(x_m, \mu_p)$ is the distance between observation m and μ_p, and M_p is the set of all observations closest to centroid μ_p and x_m belongs to M_p.

      That is, select each subsequent center with a probability proportional to the distance from itself to the closest center that you already chose.
5. Repeat step 4 until k centroids are chosen.

- "Gaussian Mixture Models" on page 5-150

References

[1] McLachlan, G., and D. Peel. *Finite Mixture Models*. Hoboken, NJ: John Wiley & Sons, Inc., 2000.

See Also

`cluster` | `gmdistribution`

fitlm

Create linear regression model

`fitlm` creates a `LinearModel` object. Once you create the object, you can see it in the workspace. You can see all the properties the object contains by clicking on it. You can create plots and do further diagnostic analysis by using methods such as `plot`, `plotResiduals`, and `plotDiagnostics`. For a full list of methods for `LinearModel`, see methods.

Syntax

```
mdl = fitlm(tbl)
mdl = fitlm(tbl,modelspec)

mdl = fitlm(X,y)
mdl = fitlm(X,y,modelspec)

mdl = fitlm(___,Name,Value)
```

Description

`mdl = fitlm(tbl)` returns a linear model fit to variables in the table or dataset array `tbl`. By default, `fitlm` takes the last variable as the response variable.

`mdl = fitlm(tbl,modelspec)` returns a linear model of the type you specify in `modelspec` fit to variables in the table or dataset array `tbl`.

`mdl = fitlm(X,y)` returns a linear model of the responses `y`, fit to the data matrix `X`.

`mdl = fitlm(X,y,modelspec)` returns a linear model of the type you specify in `modelspec` for the responses `y`, fit to the data matrix `X`.

`mdl = fitlm(___,Name,Value)` returns a linear model with additional options specified by one or more Name,Value pair arguments.

For example, you can specify which variables are categorical, perform robust regression, or use observation weights.

Examples

Fit Linear Regression Using Data in Table

Load the sample data.

```
load carsmall
```

Store the variables in a table.

```
tbl = table(Weight,Acceleration,MPG,'VariableNames',{'Weight','Acceleration','MPG'});
```

Display the first five rows of the table.

```
tbl(1:5,:)
```

```
ans =

    Weight    Acceleration    MPG
    ______    ____________    ___

    3504        12            18
    3693      11.5            15
    3436        11            18
    3433        12            16
    3449      10.5            17
```

Fit a linear regression model for miles per gallon (MPG).

```
lm = fitlm(tbl,'MPG~Weight+Acceleration')
```

```
lm =


Linear regression model:
    MPG ~ 1 + Weight + Acceleration

Estimated Coefficients:
                    Estimate         SE         tStat       pValue
                   __________    __________    _______    __________

    (Intercept)        45.155        3.4659     13.028    1.6266e-22
    Weight          -0.0082475    0.00059836    -13.783    5.3165e-24
```

```
    Acceleration       0.19694       0.14743     1.3359       0.18493


Number of observations: 94, Error degrees of freedom: 91
Root Mean Squared Error: 4.12
R-squared: 0.743,  Adjusted R-Squared 0.738
F-statistic vs. constant model: 132, p-value = 1.38e-27
```

This syntax uses formula to specify the modelspec.

The model `'MPG~Weight+Acceleration'` in this example is equivalent to fitting the model using the string `'linear'` as modelspec. For example,

```
lm2 = fitlm(tbl,'linear');
```

When you use a string as modelspec and do not specify the response variable, `fitlm` by default accepts the last variable in tbl as the response variable and the other variables as the predictor variables. If you there are any categorical variables and you use `'linear'` as the modelspec, then you must explicitly specify those variables as categorical variables using the CategoricalVars name-value pair argument.

Fit Linear Regression Using Formula (Wilkinson's Notation)

Load the sample data.

```
load carsmall
```

Store the variables in a table.

```
tbl = table(Weight,Acceleration,Model_Year,MPG,'VariableNames',{'Weight','Acceleration
```

Fit a linear regression model for miles per gallon (MPG) with weight and acceleration as the predictor variables.

```
lm = fitlm(tbl,'MPG~Weight+Acceleration')
```

```
lm =


Linear regression model:
    MPG ~ 1 + Weight + Acceleration

Estimated Coefficients:
```

```
                    Estimate         SE         tStat       pValue
                   ___________    __________    _______    __________

    (Intercept)         45.155        3.4659     13.028    1.6266e-22
    Weight           -0.0082475    0.00059836    -13.783    5.3165e-24
    Acceleration        0.19694       0.14743     1.3359       0.18493


Number of observations: 94, Error degrees of freedom: 91
Root Mean Squared Error: 4.12
R-squared: 0.743,  Adjusted R-Squared 0.738
F-statistic vs. constant model: 132, p-value = 1.38e-27
```

The *p*-value of 0.18493 indicates that `Acceleration` does not have a significant impact on `MPG`.

Remove `Acceleration` from the model, and try improving the model by adding the predictor variable `Model_Year`. First define `Model_Year` as a nominal variable.

```
tbl.Model_Year = nominal(tbl.Model_Year)
lm = fitlm(tbl,'MPG~Weight+Model_Year')

lm =


Linear regression model:
    MPG ~ 1 + Weight + Acceleration

Estimated Coefficients:
                    Estimate         SE         tStat       pValue
                   ___________    __________    _______    __________

    (Intercept)         45.155        3.4659     13.028    1.6266e-22
    Weight           -0.0082475    0.00059836    -13.783    5.3165e-24
    Acceleration        0.19694       0.14743     1.3359       0.18493


Number of observations: 94, Error degrees of freedom: 91
Root Mean Squared Error: 4.12
R-squared: 0.743,  Adjusted R-Squared 0.738
F-statistic vs. constant model: 132, p-value = 1.38e-27
```

Specifying modelspec using formula enables you to update the model without having to change the design matrix. `fitlm` uses only the variables that are specified in the

formula. It also creates the necessary two "Dummy Indicator Variables" on page 2-55 for the categorical variable `Model_Year`.

Linear Regression with Categorical Predictor and Quadratic Term

Fit a quadratic linear regression model to variables in a table. The data includes continuous and categorical predictor variables.

Load the sample data.

```
load carsmall
```

Construct a table containing continuous predictor variable `Weight` and response variable `MPG`. Add the nominal predictor variable `Year`.

```
tbl = table(MPG,Weight);
tbl.Year = nominal(Model_Year);
```

Create a fitted model of `MPG` as a function of `Year`, `Weight`, and $\texttt{Weight}^2$. You don't have to include `Weight` explicitly in your formula because it is a lower-order term of $\texttt{Weight}^2$. For details, see "Formula" on page 22-1707.

```
mdl = fitlm(tbl,'MPG ~ Year + Weight^2')
```

```
mdl =


Linear regression model:
    MPG ~ 1 + Weight + Year + Weight^2

Estimated Coefficients:
                    Estimate         SE         tStat
                    ________    __________    _______

    (Intercept)        54.206       4.7117     11.505
    Weight          -0.016404    0.0031249    -5.2493
    Year_76            2.0887      0.71491     2.9215
    Year_82            8.1864      0.81531     10.041
    Weight^2       1.5573e-06    4.9454e-07      3.149


                      pValue
                    _________

    (Intercept)    2.6648e-19
    Weight         1.0283e-06
    Year_76         0.0044137
    Year_82        2.6364e-16
    Weight^2        0.0022303


Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 2.78
```

```
R-squared: 0.885,  Adjusted R-Squared 0.88
F-statistic vs. constant model: 172, p-value = 5.52e-41
```

When you use formula to specify modelspec, you do not have to explicitly specify the categorical variables. `fitlm` creates two dummy (indicator) variables for the nominal variable, `Year`. The dummy variable `Year_76` takes the value 1 if the model year is 1976 and takes the value 0 if it is not. The dummy variable `Year_82` takes the value 1 if model year is 1982 and takes the value 0 if it is not. 1970 is the reference year (for details on dummy variables, see "Dummy Indicator Variables" on page 2-55). The fitted model is

$$\hat{MPG} = 54.206 - 0.0164(Weight) + 2.0887(Year\_76) + 8.1864(Year\_82) + (1.557e-06)(Weight)^2$$

Simultaneously Specify the Variables and Use Formula

Simultaneously identify response and predictor variables and specify the model using a formula in linear regression.

Load sample data.

```
load hospital
```

Fit a linear model with interaction terms to the data. Indicate which variable is the response variable and identify the continuous and categorical predictors using name-value pair arguments.

```
mdl = fitlm(hospital,'Weight~1+Age*Sex*Smoker-Age:Sex:Smoker','ResponseVar','Weight','F
```

```
mdl =

Linear regression model:
    Weight ~ 1 + Sex*Age + Sex*Smoker + Age*Smoker

Estimated Coefficients:
                       Estimate    SE         tStat       pValue
    (Intercept)           118.7     7.0718      16.785     6.821e-30
    Sex_Male              68.336    9.7153      7.0339     3.3386e-10
    Age                  0.31068    0.18531     1.6765       0.096991
    Smoker_1              3.0425     10.446     0.29127       0.77149
    Sex_Male:Age         -0.49094    0.24764    -1.9825       0.050377
    Sex_Male:Smoker_1     0.9509     3.8031     0.25003       0.80312
    Age:Smoker_1         -0.07288    0.26275    -0.27737       0.78211


Number of observations: 100, Error degrees of freedom: 93
```

```
Root Mean Squared Error: 8.75
R-squared: 0.898,  Adjusted R-Squared 0.892
F-statistic vs. constant model: 137, p-value = 6.91e-44
```

The *t*-statistics in `tStat` and corresponding *p*-values in `pValue` indicate that patient weights do not seem to differ significantly according to age, or the status of smoking, or the interaction of these factors with gender at the 5% significance level.

Robust Linear Regression Model

Fit a linear regression model of the Hald data using robust fitting.

Load the data.

```
load hald
X = ingredients; % Predictor variables
y = heat; % Response
```

Fit a robust linear model to the data.

```
mdl = fitlm(X,y,'linear','RobustOpts','on')
```

```
mdl =

Linear regression model (robust fit):
    y ~ 1 + x1 + x2 + x3 + x4

Estimated Coefficients:
                   Estimate    SE         tStat       pValue
    (Intercept)       60.09     75.818     0.79256      0.4509
    x1               1.5753    0.80585      1.9548    0.086346
    x2               0.5322    0.78315     0.67957     0.51596
    x3              0.13346     0.8166     0.16343     0.87424
    x4             -0.12052     0.7672    -0.15709     0.87906

Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 2.65
R-squared: 0.979,  Adjusted R-Squared 0.969
F-statistic vs. constant model: 94.6, p-value = 9.03e-07
```

- “Examine Quality and Adjust the Fitted Model” on page 9-20
- “Predict or Simulate Responses to New Data” on page 9-37
- “Linear Regression Workflow” on page 9-41
- “Regression with Categorical Covariates” on page 2-58

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see "Grouping Variables" on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelspec` — Model specification

`'linear'` (default) | string naming the model | t-by-$(p + 1)$ terms matrix | string of the form `'Y ~ terms'`

Model specification, specified as one of the following. The choice is the starting model for `stepwiselm`. Default is `'linear'`.

- A string naming the model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

- *t*-by-(*p* + 1) matrix, namely terms matrix, specifying terms to include in the model, where *t* is the number of terms and *p* is the number of predictor variables, and plus 1 is for the response variable.
- A string representing a formula in the form
  `'Y ~ terms'`,
  where the `terms` are in Wilkinson Notation.

Example: `'quadratic'`

Example: `'y ~ X1 + X2^2 + X1:X2'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Intercept',false,'PredictorVars',[1,3],'ResponseVar',5,'RobustOpts','logistic'` specifies a robust regression model with no constant term, where the algorithm uses the logistic weighting function with the default tuning constant, first and third variables are the predictor variables, and fifth variable is the response variable.

`'CategoricalVars'` — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of `'CategoricalVars'` and either a cell array of strings of the names of the categorical variables in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array `tbl`, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix `X`, then the default value of this name-value pair argument is an empty matrix `[]`. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: `'CategoricalVars',[2,3]`

Example: `'CategoricalVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Intercept'` — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

`'PredictorVars'` — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

`'ResponseVar'` — Response variable

last column in `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset array `tbl`, or a logical or numeric index vector indicating which column is the response variable. You typically need to use `'ResponseVar'` when fitting a table or dataset array `tbl`.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

`'RobustOpts'` — Indicator of robust fitting type

`'off'` (default) | `'on'` | string | structure with string or function handle

Indicator of the robust fitting type to use, specified as the comma-separated pair consisting of `'RobustOpts'` and one of the following.

- `'off'` — No robust fitting. `fitlm` uses ordinary least squares.
- `'on'` — Robust fitting. When you use robust fitting, `'bisquare'` weight function is the default.
- String — Name of the robust fitting weight function from the following table. `fitlm` uses the corresponding default tuning constant in the table.
- Structure with the string `RobustWgtFun` containing the name of the robust fitting weight function from the following table and optional scalar `Tune` fields — `fitlm` uses the `RobustWgtFun` weight function and `Tune` tuning constant from the structure. You can choose the name of the robust fitting weight function from this table. If you do not supply a `Tune` field, the fitting function uses the corresponding default tuning constant.

Weight Function	Equation	Default Tuning Constant
`'andrews'`	`w = (abs(r)<pi) .* sin(r) ./ r`	1.339
`'bisquare'` (default)	`w = (abs(r)<1) .* (1 - r.^2).^2`	4.685
`'cauchy'`	`w = 1 ./ (1 + r.^2)`	2.385
`'fair'`	`w = 1 ./ (1 + abs(r))`	1.400
`'huber'`	`w = 1 ./ max(1, abs(r))`	1.345
`'logistic'`	`w = tanh(r) ./ r`	1.205
`'ols'`	Ordinary least squares (no weighting function)	None
`'talwar'`	`w = 1 * (abs(r)<1)`	2.795

Weight Function	Equation	Default Tuning Constant
'welsch'	w = exp(-(r.^2))	2.985

The value *r* in the weight functions is

r = resid/(tune*s*sqrt(1-h)),

where resid is the vector of residuals from the previous iteration, h is the vector of leverage values from a least-squares fit, and s is an estimate of the standard deviation of the error term given by

s = MAD/0.6745.

MAD is the median absolute deviation of the residuals from their median. The constant 0.6745 makes the estimate unbiased for the normal distribution. If there are *p* columns in X, the smallest *p* absolute deviations are excluded when computing the median.

Default tuning constants give coefficient estimates that are approximately 95% as statistically efficient as the ordinary least-squares estimates, provided the response has a normal distribution with no outliers. Decreasing the tuning constant increases the downweight assigned to large residuals; increasing the tuning constant decreases the downweight assigned to large residuals.

- Structure with the function handle RobustWgtFun and optional scalar Tune fields — You can specify a custom weight function. fitlm uses the RobustWgtFun weight function and Tune tuning constant from the structure. Specify RobustWgtFun as a function handle that accepts a vector of residuals, and returns a vector of weights the same size. The fitting function scales the residuals, dividing by the tuning constant (default 1) and by an estimate of the error standard deviation before it calls the weight function.

Example: 'RobustOpts','andrews'

'VarNames' — Names of variables in fit

{'x1','x2',...,'xn','y'} (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of 'VarNames' and a cell array of strings including the names for the columns of X first, and the name for the response variable y last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights

`ones(n,1)` (default) | *n*-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an *n*-by-1 vector of nonnegative scalar values, where *n* is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Linear model

`LinearModel` object

Linear model representing a least-squares fit of the response to the data, returned as a `LinearModel` object.

If the value of the `'RobustOpts'` name-value pair is not `[]` or `'ols'`, the model is not a least-squares fit, but uses the robust fitting function.

For properties and methods of the linear model object, `mdl`, see the `LinearModel` class page.

More About

Terms Matrix

A terms matrix is a *t*-by-(*p* + 1) matrix specifying terms in a model, where *t* is the number of terms, *p* is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

  ```
  load hospital
  ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
  hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
  ```

  Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

  ```
  T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
  ```

  ```
  T =

       0     0     0     0
       1     0     0     0
       0     0     1     0
       0     0     0     1
  ```

  Redefine the dataset array.

  ```
  ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
  hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
  ```

  Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

  ```
  T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
  ```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

  Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

  ```
  T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]

  T =

       0     0     0
       1     0     0
       0     1     0
       1     1     0
       0     2     0
  ```

  Fit a linear model.

  ```
  mdl = fitlm(X,MPG,T)

  mdl =

  Linear regression model:
      y ~ 1 + x1*x2 + x2^2

  Estimated Coefficients:
                      Estimate       SE            tStat      pValue
      (Intercept)         48.906        12.589     3.8847    0.00019665
      x1                 0.54418       0.57125    0.95261       0.34337
  ```

```
    x2              -0.012781     0.0060312    -2.1192      0.036857
    x1:x2          -0.00010892    0.00017925    -0.6076         0.545
    x2^2            9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)
```

```
1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *Y* is the response name.

- *terms* contains
  - Variable names
  - + means include the next variable
  - - means do not include the next variable
  - : defines an interaction, a product of terms
  - * defines an interaction **and all lower-order terms**
  - ^ raises the predictor to a power, exactly as in * repeated, so ^ includes lower order terms as well
  - ( ) groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include -1 in the formula.

For example,
'Y ~ A + B + C' means a three-variable linear model with intercept.
'Y ~ A + B + C - 1' is a three-variable linear model without intercept.
'Y ~ A + B + C + B^2' is a three-variable model with intercept and a B^2 term.
'Y ~ A + B^2 + C' is the same as the previous example because B^2 includes a B term.
'Y ~ A + B + C + A:B' includes an A*B term.
'Y ~ A*B + C' is the same as the previous example because A*B = A + B + A:B.
'Y ~ A*B*C - A:B:C' has all interactions among A, B, and C, except the three-way interaction.
'Y ~ A*(B + C + D)' has all linear terms, plus products of A with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
1	Constant (intercept) term
A^k, where k is a positive integer	A, A^2, ..., A^k

Wilkinson Notation	Factors in Standard Notation
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

- "Linear Regression" on page 9-11

See Also

`LinearModel` | `predict` | `stepwiselm`

fitlme

Fit linear mixed-effects model

Syntax

```
lme = fitlme(tbl,formula)
lme = fitlme(tbl,formula,Name,Value)
```

Description

`lme = fitlme(tbl,formula)` returns a linear mixed-effects model, specified by `formula`, fitted to the variables in the table or dataset array `tbl`.

`lme = fitlme(tbl,formula,Name,Value)` returns a linear mixed-effects model with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the covariance pattern of the random-effects terms, the method to use in estimating the parameters, or options for the optimization algorithm.

Examples

Fit Linear Mixed-Effects Model

Load the sample data.

```
load imports-85
```

Store the variables in a table.

```
tbl = table(X(:,12),X(:,14),X(:,24),'VariableNames',{'Horsepower','CityMPG','EngineType
```

Display the first five rows of the table.

```
tbl(1:5,:)
```

```
ans =

    Horsepower    CityMPG    EngineType
    __________    _______    __________
```

```
    111           21          13
    111           21          13
    154           19          37
    102           24          35
    115           18          35
```

Fit a linear mixed-effects model for miles per gallon in the city, with fixed effects for horsepower, and uncorrelated random effect for intercept and horsepower grouped by the engine type.

```
lme = fitlme(tbl,'CityMPG~Horsepower+(1|EngineType)+(Horsepower-1|EngineType)');
```

In this model, `CityMPG` is the response variable, horsepower is the predictor variable, and engine type is the grouping variable. The fixed-effects portion of the model corresponds to `1 + Horsepower`, because the intercept is included by default.

Since the random-effect terms for intercept and horsepower are uncorrelated, these terms are specified separately. Because the second random-effect term is only for horsepower, you must include a `–1` to eliminate the intercept from the second random-effect term.

Display the model.

```
lme
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             203
    Fixed effects coefficients           2
    Random effects coefficients         14
    Covariance parameters                3

Formula:
    CityMPG ~ 1 + Horsepower + (1 | EngineType) + (Horsepower | EngineType)

Model fit statistics:
    AIC       BIC     LogLikelihood    Deviance
    1099.5    1116    -544.73          1089.5

Fixed effects coefficients (95% CIs):
```

```
    Name                 Estimate    SE         tStat     DF     pValue         Lower
    '(Intercept)'          37.276     2.8556    13.054    201    1.3147e-28      31.645
    'Horsepower'         -0.12631    0.02284     -5.53    201    9.8848e-08    -0.17134

Random effects covariance parameters (95% CIs):
Group: EngineType (7 Levels)
    Name1                Name2                Type         Estimate    Lower     Upper
    '(Intercept)'        '(Intercept)'        'std'         5.7338      2.3773    13.829

Group: EngineType (7 Levels)
    Name1                Name2                Type         Estimate    Lower      Upper
    'Horsepower'         'Horsepower'         'std'        0.050357    0.02307    0.10992

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        3.226       2.9078    3.5789
```

Note that the random-effects covariance parameters for intercept and horsepower are separate in the display.

Now, fit a linear mixed-effects model for miles per gallon in the city, with the same fixed-effects term and potentially correlated random effect for intercept and horsepower grouped by the engine type.

```
lme2 = fitlme(tbl,'CityMPG~Horsepower+(Horsepower|EngineType)');
```

Because the random-effect term includes the intercept by default, you do not have to add `1`, the random effect term is equivalent to `(1 + Horsepower|EngineType)`.

Display the model.

```
lme2
```

```
lme2 =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             203
    Fixed effects coefficients           2
    Random effects coefficients         14
    Covariance parameters                4

Formula:
```

```
    CityMPG ~ 1 + Horsepower + (1 + Horsepower | EngineType)

Model fit statistics:
    AIC     BIC       LogLikelihood    Deviance
    1089    1108.9    -538.52          1077

Fixed effects coefficients (95% CIs):
    Name                Estimate    SE          tStat      DF     pValue         Lower
    '(Intercept)'         33.824      4.0181     8.4178    201    7.1678e-15     25.90
    'Horsepower'         -0.1087    0.032912    -3.3029    201     0.0011328    -0.173

Random effects covariance parameters (95% CIs):
Group: EngineType (7 Levels)
    Name1               Name2               Type          Estimate    Lower       Upp
    '(Intercept)'       '(Intercept)'       'std'           9.4952      4.7022
    'Horsepower'        '(Intercept)'       'corr'        -0.96843    -0.99568    -0.
    'Horsepower'        'Horsepower'        'std'         0.078874    0.039917     0.

Group: Error
    Name            Estimate    Lower     Upper
    'Res Std'       3.1845      2.8774    3.5243
```

Note that the random effects covariance parameters for intercept and horsepower are together in the display, and it includes the correlation (`'corr'`) between the intercept and horsepower.

Random Intercept Model

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables containing estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the Centers for Disease Control and Prevention, CDC).

To fit a linear-mixed effects model, your data must be in a properly formatted dataset array. To fit a linear mixed-effects model with the influenza rates as the responses, combine the nine columns corresponding to the regions into a tall array. The new dataset array, `flu2`, must have the new response variable `FluRate`, the nominal variable `Region` that shows which region each estimate is from, the nationwide estimate `WtdILI`, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
```

```
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Display the first six rows of `flu2`.

```
flu2(1:6,:)
```

```
ans =

    Date         WtdILI    Region       FluRate
    10/9/2005    1.182     NE            0.97
    10/9/2005    1.182     MidAtl       1.025
    10/9/2005    1.182     ENCentral    1.232
    10/9/2005    1.182     WNCentral    1.286
    10/9/2005    1.182     SAtl         1.082
    10/9/2005    1.182     ESCentral    1.457
```

Fit a linear mixed-effects model with a fixed-effects term for the nationwide estimate, `WtdILI`, and a random intercept that varies by `Date`. The model corresponds to

$$y_{im} = \beta_0 + \beta_1 WtdILI_{im} + b_{0m} + \varepsilon_{im}, \quad i = 1,2,\ldots,468, \quad m = 1,2,\ldots,52,$$

where y_{im} is the observation i for level m of grouping variable `Date`. b_{0m} is the random effect for level m of the grouping variable `Date` and ε_{im} is the observation error for observation i. The random effect has the prior distribution, $b \sim N(0,\sigma^2_b)$ and the error term has the distribution, $\varepsilon \sim N(0,\sigma^2)$.

```
lme = fitlme(flu2,'FluRate ~ 1 + WtdILI + (1|Date)')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             468
    Fixed effects coefficients           2
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    FluRate ~ 1 + WtdILI + (1 | Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
```

```
    286.24    302.83    -139.12          278.24

Fixed effects coefficients (95% CIs):
    Name                Estimate    SE          tStat     DF     pValue         Lower
    '(Intercept)'       0.16385     0.057525    2.8484    466     0.0045885     0.0508
    'WtdILI'             0.7236     0.032219    22.459    466    3.0502e-76      0.660

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1               Name2               Type         Estimate    Lower      Upper
    '(Intercept)'       '(Intercept)'       'std'        0.17146     0.13227    0.222

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.30201     0.28217    0.32324
```

Estimated covariance parameters are displayed in the section titled "Random effects covariance parameters". The estimated value of σ_b is 0.17146 and its 95% confidence interval is [0.13227, 0.22226]. Since this interval does not include 0, the random-effects term is significant. You can formally test the significance of any random-effects term using a likelihood ratio test via the `compare` method.

The estimated response at an observation is the sum of the fixed effects and the random-effect value at the grouping variable level corresponding to that observation. For example, the estimated flu rate for observation 28 is

$$\begin{aligned}\hat{y}_{28} &= \hat{\beta}_0 + \hat{\beta}_1 WtdILI_{28} + \hat{b}_{10/30/2005} \\ &= 0.1639 + 0.7236 * (1.343) + 0.3318 \\ &= 1.46749,\end{aligned}$$

where $\hat{b}$ is the estimated best linear unbiased predictor (BLUP) of the random effects for the intercept. You can compute this value as follows.

```
beta = fixedEffects(lme);
[~,~,STATS] = randomEffects(lme); % Compute the random-effects statistics (STATS)
STATS.Level = nominal(STATS.Level);
y_hat = beta(1) + beta(2)*flu2.WtdILI(28) + STATS.Estimate(STATS.Level=='10/30/2005')
```

```
y_hat =

    1.4674
```

You can display the fitted value using the `fitted` method.

```
F = fitted(lme);
F(28)

ans =

    1.4674
```

Randomized Block Design

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data shows the absolute deviations from the target quality characteristic measured from the products each of five operators manufacture during three shifts: morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the absolute deviations of the quality characteristics from the target value. This is simulated data.

Fit a linear mixed-effects model with a random intercept grouped by operator to assess if performance significantly differs according to the time of the shift. Use the restricted maximum likelihood method and `'effects'` contrasts.

`'effects'` contrasts mean that the coefficients sum to 0, and `fitlme` creates a matrix called a "fixed effects design matrix" to describe the effect of shift. This matrix has two columns, *Shift_Evening* and *Shift_Morning*, where

$$Shift\_Evening = \begin{cases} 0, & if\ Morning \\ 1, & if\ Evening \\ -1, & if\ Night \end{cases} \quad and \quad Shift\_Morning = \begin{cases} 1, & if\ Morning \\ 0, & if\ Evening \\ -1, & if\ Night \end{cases}.$$

The model corresponds to

$$\begin{aligned} &\text{Morning Shift: } QCDev_{im} = \beta_0 + \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \quad m = 1,2,\ldots,5, \\ &\text{Evening Shift: } QCDev_{im} = \beta_0 + \beta_1 Shift\_Evening_i + b_{0m} + \varepsilon_{im}, \\ &\text{Night Shift: } \quad QCDev_{im} = \beta_0 - \beta_1 Shift\_Evening_i - \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \end{aligned}$$

where $b \sim N(0,\sigma^2_b)$ and $\varepsilon \sim N(0,\sigma^2)$.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)',...
'FitMethod','REML','DummyVarCoding','effects')
```

```
lme =


Linear mixed-effects model fit by REML

Model information:
    Number of observations             15
    Fixed effects coefficients          3
    Random effects coefficients         5
    Covariance parameters               2

Formula:
    QCDev ~ 1 + Shift + (1 | Operator)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    58.913    61.337    -24.456          48.913

Fixed effects coefficients (95% CIs):
    Name                  Estimate    SE         tStat      DF    pValue       Lower
    '(Intercept)'           3.6525    0.94109     3.8812    12    0.0021832     1.602
    'Shift_Evening'        -0.53293   0.31206    -1.7078    12      0.11339    -1.212
    'Shift_Morning'        -0.91973   0.31206    -2.9473    12     0.012206    -1.599

Random effects covariance parameters (95% CIs):
Group: Operator (5 Levels)
    Name1               Name2               Type         Estimate    Lower      Upper
    '(Intercept)'       '(Intercept)'       'std'        2.0457      0.98207    4.261

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.85462     0.52357    1.395
```

Compute the best linear unbiased predictor (BLUP) estimates of random effects.

```
B = randomEffects(lme)
```

```
B =

    0.5775
```

```
    1.1757
   -2.1715
    2.3655
   -1.9472
```

The estimated absolute deviation from the target quality characteristics for the third operator working the evening shift is

$$\begin{aligned}\hat{y}_{Evening,Operator3} &= \hat{\beta}_0 + \hat{\beta}_1 Shift\_Evening + \hat{b}_{03} \\ &= 3.6525 - 0.53293 - 2.1715 \\ &= 0.94807.\end{aligned}$$

You can also display this value as follows.

```
F = fitted(lme);
F(shift.Shift=='Evening' & shift.Operator=='3')
```

```
ans =

    0.9481
```

Similarly, you can calculate the estimated absolute deviation from the target quality characteristics for the third operator working the morning shift as

$$\begin{aligned}\hat{y}_{Morning,Operator3} &= \hat{\beta}_0 + \hat{\beta}_2 Shift\_Morning + \hat{b}_{03} \\ &= 3.6525 - 0.91973 - 2.1715 \\ &= 0.56127.\end{aligned}$$

You can also display this value as follows.

```
F(shift.Shift=='Morning' & shift.Operator=='3')
```

```
ans =

    0.5613
```

The operator tends to make a smaller magnitude of error during the morning shift.

Split-Plot Experiment

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type) and the plots within blocks (tomato types within soil types) independently.

This model corresponds to

$$y_{imjk} = \beta_0 + \sum_{m=2}^{4} \beta_{1m} I[F]_{im} + \sum_{j=2}^{5} \beta_{2j} I[T]_{ij} + \sum_{j=2}^{5}\sum_{m=2}^{4} \beta_{3mj} I[F]_{im}\, I[T]_{ij} + b_{0k} S_k + b_{0jk} (S*T)_{jk} + \varepsilon_{imjk},$$

where $i = 1, 2, ..., 60$, index m corresponds to the fertilizer types, j corresponds to the tomato types, and $k = 1, 2, 3$ corresponds to the blocks (soil). S_k represents the kth soil type, and $(S*T)_{jk}$ represents the jth tomato type nested in the kth soil type. $I[F]_{im}$ is the dummy variable representing level m of the fertilizer. Similarly, $I[T]_{ij}$ is the dummy variable representing level j of the tomato type.

The random effects and observation error have these prior distributions: $b_{0k} \sim N(0,\sigma^2_S)$, $b_{0jk} \sim N(0,\sigma^2_{S*T})$, and $\varepsilon_{imjk} \sim N(0,\sigma^2)$.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)')
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             60
    Fixed effects coefficients         20
    Random effects coefficients        18
    Covariance parameters               3

Formula:
    Yield ~ 1 + Tomato*Fertilizer + (1 | Soil) + (1 | Soil:Tomato)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    522.57    570.74    -238.29          476.57

Fixed effects coefficients (95% CIs):
    Name                                 Estimate    SE         tStat       DF    pValu
    '(Intercept)'                             77     8.5836      8.9706     40    4.020
    'Tomato_Grape'                           -16     11.966     -1.3371     40       0
    'Tomato_Heirloom'                    -6.6667     11.966    -0.55714     40       0
    'Tomato_Plum'                         32.333     11.966      2.7022     40     0.0
    'Tomato_Vine'                            -13     11.966     -1.0864     40       0
    'Fertilizer_2'                        34.667      8.572      4.0442     40   0.000
    'Fertilizer_3'                        33.667      8.572      3.9275     40   0.000
    'Fertilizer_4'                        47.667      8.572      5.5607     40   1.956
    'Tomato_Grape:Fertilizer_2'          -2.6667     12.123    -0.21997     40       0
    'Tomato_Heirloom:Fertilizer_2'            -8     12.123    -0.65992     40       0
    'Tomato_Plum:Fertilizer_2'               -15     12.123     -1.2374     40       0
    'Tomato_Vine:Fertilizer_2'               -16     12.123     -1.3198     40       0
    'Tomato_Grape:Fertilizer_3'           16.667     12.123      1.3748     40       0
    'Tomato_Heirloom:Fertilizer_3'        3.3333     12.123     0.27497     40       0
    'Tomato_Plum:Fertilizer_3'            3.6667     12.123     0.30246     40       0
    'Tomato_Vine:Fertilizer_3'                 3     12.123     0.24747     40       0
    'Tomato_Grape:Fertilizer_4'           13.333     12.123      1.0999     40       0
    'Tomato_Heirloom:Fertilizer_4'           -19     12.123     -1.5673     40       0
    'Tomato_Plum:Fertilizer_4'           -2.6667     12.123    -0.21997     40       0
    'Tomato_Vine:Fertilizer_4'            8.6667     12.123     0.71492     40       0

Random effects covariance parameters (95% CIs):
Group: Soil (3 Levels)
```

```
    Name1                Name2                Type          Estimate    Lower      Upper
    '(Intercept)'        '(Intercept)'        'std'         2.5028      0.02771    226.0

Group: Soil:Tomato (15 Levels)
    Name1                Name2                Type          Estimate    Lower     Upper
    '(Intercept)'        '(Intercept)'        'std'         10.225      6.1497    17.001

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        10.499      8.5389    12.908
```

The *p*-values corresponding to the last 12 rows in the fixed-effects coefficients display (0.82701 to 0.47881) indicate that interaction coefficients between the tomato and fertilizer types are not significant. To test for the overall interaction between tomato and fertilizer, use the `anova` method after refitting the model using `'effects'` contrasts.

The confidence interval for the standard deviations of the random-effects terms ($\sigma^2 s$), where the intercept is grouped by soil, is very large. This term does not appear significant.

Refit the model after removing the interaction term `Tomato:Fertilizer` and the random-effects term `(1 | Soil)`.

```
lme = fitlme(ds,'Yield ~ Fertilizer + Tomato + (1|Soil:Tomato)')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             60
    Fixed effects coefficients          8
    Random effects coefficients        15
    Covariance parameters               2

Formula:
    Yield ~ 1 + Tomato + Fertilizer + (1 | Soil:Tomato)

Model fit statistics:
    AIC       BIC    LogLikelihood    Deviance
    511.06    532    -245.53          491.06

Fixed effects coefficients (95% CIs):
```

```
    Name                    Estimate    SE        tStat       DF    pValue        Lowe
    '(Intercept)'            77.733     7.3293      10.606    52    1.3108e-14     63.
    'Tomato_Grape'          -9.1667     9.6045    -0.95441    52       0.34429    -28.
    'Tomato_Heirloom'       -12.583     9.6045     -1.3102    52        0.1959    -31.
    'Tomato_Plum'            28.833     9.6045      3.0021    52     0.0041138     9.5
    'Tomato_Vine'           -14.083     9.6045     -1.4663    52       0.14858    -33.
    'Fertilizer_2'           26.333     4.5004      5.8514    52    3.3024e-07     17.
    'Fertilizer_3'               39     4.5004      8.6659    52    1.1459e-11     29.
    'Fertilizer_4'           47.733     4.5004      10.607    52     1.308e-14     38.

Random effects covariance parameters (95% CIs):
Group: Soil:Tomato (15 Levels)
    Name1               Name2               Type         Estimate    Lower     Upper
    '(Intercept)'       '(Intercept)'       'std'        10.02       6.0812    16.509

Group: Error
    Name            Estimate    Lower     Upper
    'Res Std'       12.325      10.024    15.153
```

You can compare the two models using the `compare` method with the simulated likelihood ratio test since both a fixed-effect and a random-effect term are tested.

Longitudinal Study with a Covariate

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs (A, B, C, D), and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

`fitlme` uses program A as a reference and creates the necessary dummy variables $I[.]$. Since the model already has an intercept, `fitlme` only creates dummy variables for programs B, C, and D. This is also known as the `'reference'` method of coding dummy variables. This model corresponds to

$$\begin{aligned} y_{im} &= \beta_0 + \beta_1 IW_i + \beta_2 Week_i + \beta_3 I[PB]_i + \beta_4 I[PC]_i + \beta_5 I[PD]_i \\ &\quad + \beta_6 \left(Week_i * I[PB]_i \right) + \beta_7 \left(Week_i * I[PC]_i \right) + \beta_8 \left(Week_i * I[PD]_i \right) \\ &\quad + b_{0m} + b_{1m} Week_{im} + \varepsilon_{im}, \end{aligned}$$

where $i = 1, 2, ..., 120$, and $m = 1, 2, ..., 20$. β_j are the fixed-effects coefficients, $j = 0, 1, ..., 8$, and b_{1m} and b_{1m} are random effects. IW stands for initial weight and I[.] is a dummy variable representing a type of program. For example, $I[PB]_i$ is the dummy variable representing program B. The random effects and observation error have these prior distributions: $b_{0m} \sim N(0,\sigma^2_0)$, $b_{1m} \sim N(0,\sigma^2_1)$, and $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           9
    Random effects coefficients         40
    Covariance parameters                4

Formula:
    y ~ 1 + InitialWeight + Program*Week + (1 + Week | Subject)

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -22.981    13.257    24.49            -48.981

Fixed effects coefficients (95% CIs):
    Name                  Estimate     SE           tStat       DF     pValue       l
    '(Intercept)'           0.66105      0.25892      2.5531     111     0.012034
    'InitialWeight'        0.0031879    0.0013814     2.3078     111     0.022863    (
    'Program_B'             0.36079      0.13139      2.746      111    0.0070394
    'Program_C'            -0.033263     0.13117     -0.25358    111      0.80029
    'Program_D'             0.11317      0.13132      0.86175    111      0.39068
```

```
    'Week'                    0.1732     0.067454      2.5677    111      0.011567
    'Program_B:Week'         0.038771    0.095394     0.40644    111       0.68521
    'Program_C:Week'         0.030543    0.095394     0.32018    111       0.74944
    'Program_D:Week'         0.033114    0.095394     0.34713    111       0.72915

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1               Name2               Type          Estimate    Lower      Upp
    '(Intercept)'       '(Intercept)'       'std'         0.18407     0.12281    0.27
    'Week'              '(Intercept)'       'corr'        0.66841     0.21076    0.88
    'Week'              'Week'              'std'         0.15033     0.11004    0.20

Group: Error
    Name            Estimate    Lower       Upper
    'Res Std'       0.10261     0.087882    0.11981
```

The *p*-values 0.022863 and 0.011567 indicate significant effects of subject initial weights and time in the amount of weight lost. The weight loss of subjects who are in program B is significantly different relative to the weight loss of subjects who are in program A. The lower and upper limits of the covariance parameters for the random effects do not include 0, thus they are significant. You can also test the significance of the random effects using the `compare` method.

Input Arguments

`tbl` — Input data

table | `dataset` array

Input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or `dataset` array. The predictor variables can be continuous or grouping variables (see “Grouping Variables” on page 2-52). You must specify the model for the variables using formula.

Data Types: `single` | `double` | `char` | `cell`

`formula` — Formula for model specification

string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`

Formula for model specification, specified as a string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`. The string is case sensitive. For a full description, see “Formula” on page 22-1731.

Example: `'y ~ treatment + (1|block)'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'CovariancePattern','Diagonal','Optimizer','fminunc','OptimizerOptions',opt` specifies a model, where the random-effects terms have a diagonal covariance matrix structure, and `fitlme` uses the `fminunc` optimization algorithm with the custom optimization parameters defined in variable `opt`.

`'CovariancePattern'` — Pattern of covariance matrix

`'FullCholesky'` (default) | string | square symmetric logical matrix | cell array of strings or logical matrices

Pattern of the covariance matrix of the random effects, specified as the comma-separated pair consisting of `'CovariancePattern'` and a string, a square symmetric logical matrix, or a cell array of strings or logical matrices.

If there are R random-effects terms, then the value of `'CovariancePattern'` must be a cell array of length R, where each element r of this cell array specifies the pattern of the covariance matrix of the random-effects vector associated with the rth random-effects term. The options for each element follow.

`'FullCholesky'`	Default. Full covariance matrix using the Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.
`'Full'`	Full covariance matrix, using the log-Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.
`'Diagonal'`	Diagonal covariance matrix. That is, off-diagonal elements of the covariance matrix are constrained to be 0.

$$\begin{pmatrix} \sigma_{b1}^2 & 0 & 0 \\ 0 & \sigma_{b2}^2 & 0 \\ 0 & 0 & \sigma_{b3}^2 \end{pmatrix}$$

`'Isotropic'`

Diagonal covariance matrix with equal variances. That is, off-diagonal elements of the covariance matrix are constrained to be 0, and the diagonal elements are constrained to be equal. For example, if there are three random-effects terms with an isotropic covariance structure, this covariance matrix looks like

$$\begin{pmatrix} \sigma_b^2 & 0 & 0 \\ 0 & \sigma_b^2 & 0 \\ 0 & 0 & \sigma_b^2 \end{pmatrix}$$

where σ^2_b is the common variance of the random-effects terms.

`'CompSymm'`	Compound symmetry structure. That is, common variance along diagonals and equal correlation between all random effects. For example, if there are three random-effects terms with a covariance matrix having a compound symmetry structure, this covariance matrix looks like $\begin{pmatrix} \sigma_{b1}^2 & \sigma_{b1,b2} & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1}^2 & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1,b2} & \sigma_{b1}^2 \end{pmatrix}$ where σ^2_{b1} is the common variance of the random-effects terms and $\sigma_{b1,b2}$ is the common covariance between any two random-effects term .
`PAT`	Square symmetric logical matrix. If `'CovariancePattern'` is defined by the matrix `PAT`, and if `PAT(a,b) = false`, then the `(a,b)` element of the corresponding covariance matrix is constrained to be 0.

Example: `'CovariancePattern','Diagonal'`

Example: `'CovariancePattern',{'Full','Diagonal'}`

`'FitMethod'` — Method for estimating parameters

`'ML'` (default) | `'REML'`

Method for estimating parameters of the linear mixed-effects model, specified as the comma-separated pair consisting of `'FitMethod'` and either of the following.

`'ML'`	Default. Maximum likelihood estimation
`'REML'`	Restricted maximum likelihood estimation

Example: `'FitMethod','REML'`

'Weights' — Observation weights

vector of scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and a vector of length n, where n is the number of observations.

Data Types: single | double

'Exclude' — Indices for rows to exclude

use all rows without NaNs (default) | vector of integer or logical values

Indices for rows to exclude from the linear mixed-effects model in the data, specified as the comma-separated pair consisting of 'Exclude' and a vector of integer or logical values.

For example, you can exclude the 13th and 67th rows from the fit as follows.

Example: 'Exclude',[13,67]

Data Types: single | double | logical

'DummyVarCoding' — Coding to use for dummy variables

'reference' (default) | 'effects' | 'full'

Coding to use for dummy variables created from the categorical variables, specified as the comma-separated pair consisting of 'DummyVarCoding' and one of the following.

'reference'	Default. Coefficient for first category set to 0.
'effects'	Coefficients sum to 0.
'full'	One dummy variable for each category.

Example: 'DummyVarCoding','effects'

'Optimizer' — Optimization algorithm

'quasinewton' (default) | 'fminunc'

Optimization algorithm, specified as the comma-separated pair consisting of 'Optimizer' and either of the following.

'quasinewton'	Default. Uses a trust region based quasi-Newton optimizer. Change

	the options of the algorithm using `statset('LinearMixedModel')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `statset('LinearMixedModel')`.
`'fminunc'`	You must have Optimization Toolbox to specify this option. Change the options of the algorithm using `optimoptions('fminunc')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.

Example: `'Optimizer','fminunc'`

`'OptimizerOptions'` — Options for optimization algorithm

structure returned by `statset` | object returned by `optimoptions`

Options for the optimization algorithm, specified as the comma-separated pair consisting of `'OptimizerOptions'` and a structure returned by `statset('LinearMixedModel')` or an object returned by `optimoptions('fminunc')`.

- If `'Optimizer'` is `'fminunc'`, then use `optimoptions('fminunc')` to change the options of the optimization algorithm. See `optimoptions` for the options `'fminunc'` uses. If `'Optimizer'` is `'fminunc'` and you do not supply `'OptimizerOptions'`, then the default for `LinearMixedModel` is the default options created by `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.
- If `'Optimizer'` is `'quasinewton'`, then use `statset('LinearMixedModel')` to change the optimization parameters. If you don't change the optimization parameters, then `LinearMixedModel` uses the default options created by `statset('LinearMixedModel')`:

The `'quasinewton'` optimizer uses the following fields in the structure created by `statset('LinearMixedModel')`.

`'TolFun'` — Relative tolerance on gradient of objective function

`1e-6` (default) | positive scalar value

Relative tolerance on the gradient of the objective function, specified as a positive scalar value.

`'TolX'` — Absolute tolerance on step size
`1e-12` (default) | positive scalar value

Absolute tolerance on the step size, specified as a positive scalar value.

`'MaxIter'` — Maximum number of iterations allowed
`10000` (default) | positive scalar value

Maximum number of iterations allowed, specified as a positive scalar value.

`'Display'` — Level of display
`'off'` (default) | `'iter'` | `'final'`

Level of display, specified as one of `'off'`, `'iter'`, or `'final'`.

`'StartMethod'` — Method to start iterative optimization
`'default'` (default) | `'random'`

Method to start iterative optimization, specified as the comma-separated pair consisting of `'StartMethod'` and either of the following.

`'default'`	Default. An internally defined default value.
`'random'`	A random initial value.

Example: `'StartMethod','random'`

`'Verbose'` — Indicator to display optimization process on screen
`false` (default) | `true`

Indicator to display the optimization process on screen, specified as the comma-separated pair consisting of `'Verbose'` and either `false` or `true`. Default is `false`.

The setting for `'Verbose'` overrides the field `'Display'` in `'OptimizerOptions'`.

Example: `'Verbose',true`

`'CheckHessian'` — Indicator to check positive definiteness of Hessian
`false` (default) | `true`

Indicator to check the positive definiteness of the Hessian of the objective function with respect to unconstrained parameters at convergence, specified as the comma-separated pair consisting of `'CheckHessian'` and either `false` or `true`. Default is `false`.

Specify `'CheckHessian'` as `true` to verify optimality of the solution or to determine if the model is overparameterized in the number of covariance parameters.

Example: `'CheckHessian',true`

Output Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Alternatives

If your model is not easily described using a formula, you can create matrices to define the fixed and random effects, and fit the model using `fitlmematrix(X,y,Z,G)`.

More About

Formula

In general, a formula for model specification is a string of the form `'y ~ terms'`. For the linear mixed-effects models, this formula is in the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` and `random` contain the fixed-effects and the random-effects terms.

Suppose a table `tbl` contains the following:

- A response variable, `y`
- Predictor variables, X_j, which can be continuous or grouping variables
- Grouping variables, g_1, g_2, ..., g_R,

where the grouping variables in X_j and g_r can be categorical, logical, character arrays, or cell arrays of strings.

Then, in a formula of the form, `'y ~ fixed + (random`$_1$`|g`$_1$`) + ... + (random`$_R$`|g`$_R$`)'`, the term `fixed` corresponds to a specification of the fixed-effects design matrix `X`, `random`$_1$ is a specification of the random-effects design matrix Z_1 corresponding to grouping variable g_1, and similarly `random`$_R$ is a specification of the random-effects design matrix Z_R corresponding to grouping variable g_R. You can express the `fixed` and `random` terms using Wilkinson notation.

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1.*X2 (elementwise multiplication of X1 and X2)`
`X1:X2`	`X1.*X2` only
`- X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`. Here are some examples for linear mixed-effects model specification.

Examples:

Formula	Description
`'y ~ X1 + X2'`	Fixed effects for the intercept, `X1` and `X2`. This is equivalent to `'y ~ 1 + X1 + X2'`.

Formula	Description
`'y ~ -1 + X1 + X2'`	No intercept and fixed effects for `X1` and `X2`. The implicit intercept term is suppressed by including `-1`.
`'y ~ 1 + (1 | g1)'`	Fixed effects for the intercept plus random effect for the intercept for each level of the grouping variable `g1`.
`'y ~ X1 + (1 | g1)'`	Random intercept model with a fixed slope.
`'y ~ X1 + (X1 | g1)'`	Random intercept and slope, with possible correlation between them. This is equivalent to `'y ~ 1 + X1 + (1 + X1| g1)'`.
`'y ~ X1 + (1 | g1) + (-1 + X1 | g1)'`	Independent random effects terms for intercept and slope.
`'y ~ 1 + (1 | g1) + (1 | g2) + (1 | g1:g2)'`	Random intercept model with independent main effects for `g1` and `g2`, plus an independent interaction effect.

Cholesky Parameterization

One of the assumptions of linear mixed-effects models is that the random effects have the following prior distribution.

$$b \sim N\left(0,\sigma^2 D(\theta)\right),$$

where D is a q-by-q symmetric and positive semidefinite matrix, parameterized by a variance component vector θ, q is the number of variables in the random-effects term, and σ^2 is the observation error variance. Since the covariance matrix of the random effects, D, is symmetric, it has $q(q+1)/2$ free parameters. Suppose L is the lower triangular Cholesky factor of $D(\theta)$ such that

$$D(\theta) = L(\theta)L(\theta)^T,$$

then the $q*(q+1)/2$-by-1 unconstrained parameter vector θ is formed from elements in the lower triangular part of L.

For example, if

$$L = \begin{bmatrix} L_{11} & 0 & 0 \\ L_{21} & L_{22} & 0 \\ L_{31} & L_{32} & L_{33} \end{bmatrix},$$

then

$$\theta = \begin{bmatrix} L_{11} \\ L_{21} \\ L_{31} \\ L_{22} \\ L_{32} \\ L_{33} \end{bmatrix}.$$

Log-Cholesky Parameterization

When the diagonal elements of L in Cholesky parameterization are constrained to be positive, then the solution for L is unique. Log-Cholesky parameterization is the same as Cholesky parameterization except that the logarithm of the diagonal elements of L are used to guarantee unique parameterization.

For example, for the 3-by-3 example in Cholesky parameterization, enforcing $L_{ii} \geq 0$,

$$\theta = \begin{bmatrix} \log(L_{11}) \\ L_{21} \\ L_{31} \\ \log(L_{22}) \\ L_{32} \\ \log(L_{33}) \end{bmatrix}.$$

References

[1] Pinherio, J. C., and D. M. Bates. “Unconstrained Parametrizations for Variance-Covariance Matrices”. *Statistics and Computing*, Vol. 6, 1996, pp. 289–296.

See Also

`LinearMixedModel` | `fitlmematrix`

fitlmematrix

Fit linear mixed-effects model

Syntax

```
lme = fitlmematrix(X,y,Z,[])
lme = fitlmematrix(X,y,Z,G)
lme = fitlmematrix(___,Name,Value)
```

Description

`lme = fitlmematrix(X,y,Z,[])` creates a linear mixed-effects model of the responses y using the fixed-effects design matrix `X` and random-effects design matrix or matrices in Z.

`[]` implies that there is one group. That is, the grouping variable G is `ones(n,1)`, where n is the number of observations. Using `fitlmematrix(X,Y,Z,[])` without a specified covariance pattern most likely results in a nonidentifiable model. This syntax is recommended only if you build the grouping information into the random effects design `Z` and specify a covariance pattern for the random effects using the `'CovariancePattern'` name-value pair argument.

`lme = fitlmematrix(X,y,Z,G)` creates a linear mixed-effects model of the responses y using the fixed-effects design matrix `X` and random-effects design matrix Z or matrices in `Z`, and the grouping variable or variables in `G`.

`lme = fitlmematrix(___,Name,Value)` also creates a linear mixed-effects model with additional options specified by one or more Name,Value pair arguments, using any of the previous input arguments.

For example, you can specify the names of the response, predictor, and grouping variables. You can also specify the covariance pattern, fitting method, or the optimization algorithm.

Examples

No Grouping Variable Specified

Load the sample data.

```
load carsmall
```

Fit a linear mixed-effects model, where miles per gallon (MPG) is the response, weight is the predictor variable, and the intercept varies by model year. First, define the design matrices. Then, fit the model using the specified design matrices.

```
y = MPG;
X = [ones(size(Weight)), Weight];
Z = ones(size(y));
lme = fitlmematrix(X,y,Z,Model_Year)
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             94
    Fixed effects coefficients          2
    Random effects coefficients         3
    Covariance parameters               2

Formula:
    y ~ x1 + x2 + (z11 | g1)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    486.09    496.26    -239.04          478.09

Fixed effects coefficients (95% CIs):
    Name        Estimate      SE           tStat      DF    pValue        Lower
    'x1'            43.575       2.3038     18.915    92    1.8371e-33           39
    'x2'        -0.0067097    0.0004242    -15.817    92    5.5373e-28    -0.0075522

Random effects covariance parameters (95% CIs):
Group: g1 (3 Levels)
    Name1        Name2        Type         Estimate    Lower     Upper
    'z11'        'z11'        'std'        3.301       1.4448    7.5421
```

```
Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        2.8997      2.5075    3.3532
```

Now, fit the same model by building the grouping into the Z matrix.

```
Z = double([Model_Year==70, Model_Year==76, Model_Year==82]);
lme = fitlmematrix(X,y,Z,[],'Covariancepattern','Isotropic')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             94
    Fixed effects coefficients          2
    Random effects coefficients         3
    Covariance parameters               2

Formula:
    y ~ x1 + x2 + (z11 + z12 + z13 | g1)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    486.09    496.26    -239.04          478.09

Fixed effects coefficients (95% CIs):
    Name        Estimate      SE           tStat      DF    pValue         Lower
    'x1'            43.575       2.3038     18.915    92    1.8371e-33           39
    'x2'        -0.0067097    0.0004242    -15.817    92    5.5373e-28    -0.0075522

Random effects covariance parameters (95% CIs):
Group: g1 (1 Levels)
    Name1        Name2        Type         Estimate    Lower     Upper
    'z11'        'z11'        'std'        3.301       1.4448    7.5421

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        2.8997      2.5075    3.3532
```

Longitudinal Study with a Covariate

Navigate to a folder containing sample data.

```
cd(matlabroot)
```

```
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned 4 exercise programs (A, B, C, D) and their weight loss is recorded over six 2-week time periods. This is simulated data.

Define `Subject` and `Program` as categorical variables. Create the design matrices for a linear mixed-effects model, with the initial weight, type of program, week, and the interaction between the week and type of program as the fixed effects. The intercept and coefficient of week vary by subject.

This model corresponds to

$$\begin{aligned} y_{im} &= \beta_0 + \beta_1 IW_i + \beta_2 Week_i + \beta_3 I[PB]_i + \beta_4 I[PC]_i + \beta_5 I[PD]_i \\ &\quad + \beta_6 \left(Week_i * I[PB]_i \right) + \beta_7 \left(Week_i * I[PC]_i \right) + \beta_8 \left(Week_i * I[PD]_i \right) \\ &\quad + b_{0m} + b_{1m} Week_{im} + \varepsilon_{im}, \end{aligned}$$

where $i = 1, 2, ..., 120$, and $m = 1, 2, ..., 20$. β_j are the fixed-effects coefficients, $j = 0, 1, ..., 8$, and b_{0m} and b_{1m} are random effects. IW stands for initial weight and I[.] is a dummy variable representing a type of program. For example, $I[PB]_i$ is the dummy variable representing program type B. The random effects and observation error have these prior distributions: $b_{0m} \sim N(0,\sigma^2_0)$, $b_{1m} \sim N(0,\sigma^2_1)$, and $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
Subject = nominal(Subject);
Program = nominal(Program);
D = dummyvar(Program); % Create dummy variables for Program
X = [ones(120,1), InitialWeight, D(:,2:4), Week,...
   D(:,2).*Week, D(:,3).*Week, D(:,4).*Week];
Z = [ones(120,1), Week];
G = Subject;
```

Since the model has an intercept, you only need the dummy variables for programs B, C, and D. This is also known as the `'reference'` method of coding dummy variables.

Fit the model using `fitlmematrix` with the defined design matrices and grouping variables.

```
lme = fitlmematrix(X,y,Z,G,'FixedEffectPredictors',...
{'Intercept','InitWeight','PrgB','PrgC','PrgD','Week','Week_PrgB','Week_PrgC','Week_Prg
```

```
'RandomEffectPredictors',{{'Intercept','Week'}},'RandomEffectGroups',{'Subject'})

lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           9
    Random effects coefficients         40
    Covariance parameters                4

Formula:
    Linear Mixed Formula with 10 predictors.

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -22.981    13.257    24.49            -48.981

Fixed effects coefficients (95% CIs):
    Name                Estimate     SE           tStat       DF     pValue       Lower
    'Intercept'           0.66105      0.25892      2.5531    111     0.012034       0.
    'InitWeight'        0.0031879    0.0013814      2.3078    111     0.022863    0.000
    'PrgB'                0.36079      0.13139       2.746    111    0.0070394       0.
    'PrgC'              -0.033263      0.13117    -0.25358    111      0.80029      -0.
    'PrgD'                0.11317      0.13132     0.86175    111      0.39068      -0.
    'Week'                 0.1732     0.067454      2.5677    111     0.011567       0.
    'Week_PrgB'          0.038771     0.095394     0.40644    111      0.68521      -0.
    'Week_PrgC'          0.030543     0.095394     0.32018    111      0.74944      -0.
    'Week_PrgD'          0.033114     0.095394     0.34713    111      0.72915      -0.

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1              Name2              Type          Estimate    Lower      Upper
    'Intercept'        'Intercept'        'std'         0.18407     0.12281    0.27587
    'Week'             'Intercept'        'corr'        0.66841     0.21076    0.88573
    'Week'             'Week'             'std'         0.15033     0.11004    0.20537

Group: Error
    Name            Estimate    Lower       Upper
    'Res Std'       0.10261     0.087882    0.11981
```

The p-values 0.0228 and 0.0115 indicate significant effects of the initial weights of the subjects and the time factor in the amount of weight lost. The weight loss of subjects who

are in program B is significantly different relative to the weight loss of subjects who are in program A. The lower and upper limits of the covariance parameters for the random effects do not include zero, thus they seem significant. You can also test the significance of the random-effects using the `compare` method.

Random Intercept Model

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables for estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the Centers for Disease Control and Prevention, CDC).

To fit a linear-mixed effects model, where the influenza rates are the responses, combine the nine columns corresponding to the regions into a tall array that has a single response variable, `FluRate`, and a nominal variable, `Region`, the nationwide estimate `WtdILI`, that shows which region each estimate is from, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Define the design matrices for a random-intercept linear mixed-effects model, where the intercept varies by `Date`. The corresponding model is

$$y_{im} = \beta_0 + \beta_1 WtdILI_{im} + b_{0m} + \varepsilon_{im}, \quad i = 1,2,\ldots,468, \quad m = 1,2,\ldots,52,$$

where y_{im} is the observation i for level m of grouping variable `Date`. b_{0m} is the random effect for level m of the grouping variable `Date` and ε_{im} is the observation error for observation i. The random effect has the prior distribution, $b_{0m} \sim N(0,\sigma^2_{FR})$ and the error term has the distribution, $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
y = flu2.FluRate;
X = [ones(468,1) flu2.WtdILI];
Z = [ones(468,1)];
G = flu2.Date;
```

Fit the linear mixed-effects model.

```
lme = fitlmematrix(X,y,Z,G,'FixedEffectPredictors',{'Intercept','NationalRate'},...
'RandomEffectPredictors',{{'Intercept'}},'RandomEffectGroups',{'Date'})

lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             468
    Fixed effects coefficients           2
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    y ~ Intercept + NationalRate + (Intercept | Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    286.24    302.83    -139.12          278.24

Fixed effects coefficients (95% CIs):
    Name                 Estimate    SE          tStat     DF     pValue        Lower
    'Intercept'          0.16385     0.057525    2.8484    466     0.0045885    0.0508
    'NationalRate'        0.7236     0.032219    22.459    466    3.0502e-76     0.660

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1              Name2              Type         Estimate    Lower      Upper
    'Intercept'        'Intercept'        'std'        0.17146     0.13227    0.22226

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.30201     0.28217    0.32324
```

The confidence limits of the standard deviation of the random-effects term $\sigma^2_{b_{0m}}$, do not include zero (0.13227, 0.22226), which indicates that the random-effects term is significant. You can also test the significance of the random-effects using `compare` method.

The estimated value of an observation is the sum of the fixed-effects values and value of the random effect at the grouping variable level corresponding to that observation. For example, the estimated flu rate for observation 28

$$\begin{aligned}\hat{y}_{28} &= \hat{\beta}_0 + \hat{\beta}_1 WtdILI_{28} + \hat{b}_{10/30/2005} \\ &= 0.1639 + 0.7236 * (1.343) + 0.3318 \\ &= 1.46749,\end{aligned}$$

where $\hat{b}$ is the best linear unbiased predictor (BLUP) of the random effects for the intercept. You can compute this value as follows.

```
beta = fixedEffects(lme);
[~,~,STATS] = randomEffects(lme); % compute the random effects statistics STATS
STATS.Level = nominal(STATS.Level);
y_hat = beta(1) + beta(2)*flu2.WtdILI(28) + STATS.Estimate(STATS.Level=='10/30/2005')
```

```
y_hat =

    1.4674
```

You can simply display the fitted value using the `fitted(lme)` method.

```
F = fitted(lme);
F(28)
```

```
ans =

    1.4674
```

Randomized Block Design

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data shows the deviations from the target quality characteristic measured from the products that five operators manufacture during three shifts: morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the deviations of the quality characteristics from the target value. This is simulated data.

Define the design matrices for a linear mixed-effects model with a random intercept grouped by operator, and shift as the fixed effects. Use the `'effects'` contrasts. `'effects'` contrasts mean that the coefficients sum to 0. You need to create two contrast coded variables in the fixed-effects design matrix, $X1$ and $X2$, where

$$Shift\_Evening = \begin{cases} 0, & if\ Morning \\ 1, & if\ Evening \\ -1, & if\ Night \end{cases} \quad and \quad Shift\_Morning = \begin{cases} 1, & if\ Morning \\ 0, & if\ Evening \\ -1, & if\ Night \end{cases}.$$

The model corresponds to

$$\begin{aligned} &\text{Morning Shift: } QCDev_{im} = \beta_0 + \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \quad m = 1,2,\ldots,5, \\ &\text{Evening Shift: } QCDev_{im} = \beta_0 + \beta_1 Shift\_Evening_i + b_{0m} + \varepsilon_{im}, \\ &\text{Night Shift: } \quad QCDev_{im} = \beta_0 - \beta_1 Shift\_Evening_i - \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \end{aligned}$$

where i represents the observations, and m represents the operators, i = 1, 2, ..., 15, and m = 1, 2, ..., 5. The random effects and the observation error have these distributions: $b_{0m} \sim N(0,\sigma^2_{b_{0m}})$ and $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
S = shift.Shift;
X1 = (S=='Morning') - (S=='Night');
X2 = (S=='Evening') - (S=='Night');
X = [ones(15,1), X1, X2];
y = shift.QCDev;
Z = ones(15,1);
G = shift.Operator;
```

Fit a linear mixed-effects model using the specified design matrices and restricted maximum likelihood method.

```
lme = fitlmematrix(X,y,Z,G,'FitMethod','REML','FixedEffectPredictors',....
{'Intercept','S_Morning','S_Evening'},'RandomEffectPredictors',{{'Intercept'}},...
'RandomEffectGroups',{'Operator'},'DummyVarCoding','effects')
```

```
lme =


Linear mixed-effects model fit by REML

Model information:
    Number of observations             15
    Fixed effects coefficients          3
```

```
    Random effects coefficients          5
    Covariance parameters                2

Formula:
    y ~ Intercept + S_Morning + S_Evening + (Intercept | Operator)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    58.913    61.337    -24.456          48.913

Fixed effects coefficients (95% CIs):
    Name              Estimate    SE         tStat      DF    pValue       Lower
    'Intercept'         3.6525    0.94109     3.8812    12    0.0021832     1.6021
    'S_Morning'        -0.91973   0.31206    -2.9473    12     0.012206    -1.5997
    'S_Evening'        -0.53293   0.31206    -1.7078    12      0.11339    -1.2129

Random effects covariance parameters (95% CIs):
Group: Operator (5 Levels)
    Name1             Name2             Type         Estimate    Lower      Upper
    'Intercept'       'Intercept'       'std'        2.0457      0.98207    4.2612

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.85462     0.52357    1.395
```

Compute the best linear unbiased predictor (BLUP) estimates of random effects.

```
B = randomEffects(lme)
```

```
B =

    0.5775
    1.1757
   -2.1715
    2.3655
   -1.9472
```

The estimated deviation from the target quality characteristics for the third operator working the evening shift is

$$\begin{aligned}\hat{y}_{Evening,Operator3} &= \hat{\beta}_0 + \hat{\beta}_1 Shift\_Evening + \hat{b}_{03} \\ &= 3.6525 - 0.53293 - 2.1715 \\ &= 0.94807.\end{aligned}$$

You can also display this value as follows.

```
F = fitted(lme);
F(shift.Shift=='Evening' & shift.Operator=='3')
```

```
ans =

    0.9481
```

Correlated and Uncorrelated Random-Effects Terms

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration and horsepower, and uncorrelated random effect for intercept and acceleration grouped by the model year. This model corresponds to

$$MPG_{im} = \beta_0 + \beta_1 Acc_i + \beta_2 HP + b_{0m} + b_{1m} Acc_{im} + \varepsilon_{im}, \quad m = 1,2,3,$$

with the random-effects terms having these distributions: $b_{0m} \sim N(0,\sigma^2_0)$, and $b_{1m} \sim N(0,\sigma^2_1)$. m represents the model year.

First, prepare the design matrices for fitting the linear mixed-effects model.

```
X = [ones(406,1) Acceleration Horsepower];
Z = {ones(406,1),Acceleration};
G = {Model_Year,Model_Year};
Model_Year = nominal(Model_Year);
```

Now, fit the model using `fitlmematrix` with the defined design matrices and grouping variables.

```
lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept'},{'Acceleration'}},'RandomEffectGroups',{'Model_Year','Model_Year'})
```

```
lme =


Linear mixed-effects model fit by ML
```

```
Model information:
    Number of observations             392
    Fixed effects coefficients           3
    Random effects coefficients         26
    Covariance parameters                3

Formula:
    y ~ Intercept + Acceleration + Horsepower + (Intercept | Model_Year) + (Acceleratio

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    2194.5    2218.3    -1091.3          2182.5

Fixed effects coefficients (95% CIs):
    Name                  Estimate    SE           tStat      DF     pValue        Lowe
    'Intercept'             49.839      2.0518      24.291    389    5.6168e-80      45
    'Acceleration'        -0.58565     0.10846     -5.3995    389    1.1652e-07     -0.
    'Horsepower'          -0.16534    0.0071227    -23.213    389    1.9755e-75    -0.1

Random effects covariance parameters (95% CIs):
Group: Model_Year (13 Levels)
    Name1              Name2              Type         Estimate      Lower    Upper
    'Intercept'        'Intercept'        'std'        8.0669e-07    NaN      NaN

Group: Model_Year (13 Levels)
    Name1                 Name2                 Type         Estimate    Lower      Upp
    'Acceleration'        'Acceleration'        'std'        0.18783     0.12523    0.2

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        3.7258      3.4698    4.0007
```

Note that the random effects covariance parameters for intercept and acceleration are separate in the display. The standard deviation of the random effect for the intercept does not seem significant.

Refit the model with potentially correlated random effects for intercept and acceleration. In this case, the random-effects terms has this prior distribution

$$b_m = \begin{pmatrix} b_{0m} \\ b_{1m} \end{pmatrix} \sim N\left(0, \begin{pmatrix} \sigma_0^2 & \sigma_{0,1} \\ \sigma_{0,1} & \sigma_1^2 \end{pmatrix}\right),$$

where m represents the model year.

First, prepare the random-effects design matrix and grouping variable.

```
Z = [ones(406,1) Acceleration];
G = Model_Year;

lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept','Acceleration'}},'RandomEffectGroups',{'Model_Year'})
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             392
    Fixed effects coefficients           3
    Random effects coefficients         26
    Covariance parameters                4

Formula:
    y ~ Intercept + Acceleration + Horsepower + (Intercept + Acceleration | Model_Year)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    2193.5    2221.3    -1089.7          2179.5

Fixed effects coefficients (95% CIs):
    Name                  Estimate    SE           tStat      DF     pValue        Lowe
    'Intercept'             50.133       2.2652     22.132    389    7.7727e-71      45
    'Acceleration'        -0.58327      0.13394    -4.3545    389    1.7075e-05    -0.8
    'Horsepower'          -0.16954    0.0072609     -23.35    389     5.188e-76    -0.1

Random effects covariance parameters (95% CIs):
Group: Model_Year (13 Levels)
    Name1                 Name2                Type          Estimate    Lower       U
    'Intercept'           'Intercept'          'std'           3.3475      1.2862
    'Acceleration'        'Intercept'          'corr'         -0.87971    -0.98501    -
    'Acceleration'        'Acceleration'       'std'           0.33789      0.1825

Group: Error
    Name            Estimate    Lower     Upper
    'Res Std'       3.6874      3.4298    3.9644
```

Note that the random effects covariance parameters for intercept and acceleration are together in the display, with an addition of the correlation between the intercept and acceleration. The confidence intervals for the standard deviations and the correlation between the random effects for intercept and acceleration do not include 0s, hence they seem significant. You can compare these two models using the `compare` method.

Specify the Covariance Pattern

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Define `Subject` and `Program` as categorical variables.

```
Subject = nominal(Subject);
Program = nominal(Program);
```

Create the design matrices for a linear mixed-effects model, with the initial weight, type of program, and week as the fixed effects.

```
D = dummyvar(Program);
X = [ones(120,1), InitialWeight, D(:,2:4), Week];
Z = [ones(120,1) Week];
G = Subject;
```

This model corresponds to

$$\begin{aligned} y_{im} &= \beta_0 + \beta_1 IW_i + \beta_2 Week_i + \beta_3 I[PB]_i + \beta_4 I[PC]_i + \beta_5 I[PD]_i \\ &\quad + b_{0m} + b_{1m} Week2_{im} + b_{2m} Week4_{im} + b_{3m} Week6_{im} + b_{4m} Week8_{im} \\ &\quad + b_{5m} Week10_{im} + b_{6m} Week12_{im} + \varepsilon_{im}, \end{aligned}$$

where i = 1, 2, ..., 120, and m = 1, 2, ..., 20.

β_j are the fixed-effects coefficients, j = 0, 1, ..., 8, and b_{1m} and b_{1m} are random effects. IW stands for initial weight and I[.] is a dummy variable representing a type of program. For

example, $I[PB]_i$ is the dummy variable representing program type B. The random effects and observation error have these prior distributions: b_{0m}~N(0,σ^2_0), b_{1m}~N(0,σ^2_1), and ε_{im} ~ N(0,σ^2).

Fit the model using `fitlmematrix` with the defined design matrices and grouping variables. Assume the repeated observations collected on a subject have common variance along diagonals.

```
lme = fitlmematrix(X,y,Z,G,'FixedEffectPredictors',...
{'Intercept','InitWeight','PrgB','PrgC','PrgD','Week'},...
'RandomEffectPredictors',{{'Intercept','Week'}},...
'RandomEffectGroups',{'Subject'},'CovariancePattern','Isotropic')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           6
    Random effects coefficients         40
    Covariance parameters                2

Formula:
    y ~ Intercept + InitWeight + PrgB + PrgC + PrgD + Week + (Intercept + Week | Subjec

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -24.783    -2.483    20.391           -40.783

Fixed effects coefficients (95% CIs):
    Name                Estimate     SE           tStat       DF     pValue        Lowe
    'Intercept'            0.4208      0.28169      1.4938    114       0.13799      -0.
    'InitWeight'        0.0045552    0.0015338      2.9699    114     0.0036324    0.00
    'PrgB'                0.36993      0.12119      3.0525    114     0.0028242       0.
    'PrgC'              -0.034009       0.1209    -0.28129    114       0.77899      -0.
    'PrgD'                  0.121      0.12111     0.99911    114       0.31986      -0.
    'Week'                0.19881     0.037134      5.3538    114    4.5191e-07       0.

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1              Name2              Type         Estimate    Lower      Upper
    'Intercept'        'Intercept'        'std'        0.16561     0.12896    0.21269
```

```
Group: Error
    Name             Estimate    Lower       Upper
    'Res Std'        0.10272     0.088014    0.11987
```

Input Arguments

X — Fixed-effects design matrix

n-by-*p* matrix

Fixed-effects design matrix, specified as an *n*-by-*p* matrix, where *n* is the number of observations, and *p* is the number of fixed-effects predictor variables. Each row of `X` corresponds to one observation, and each column of `X` corresponds to one variable.

Data Types: `single` | `double`

y — Response values

n-by-1 vector

Response values, specified as an *n*-by-1 vector, where *n* is the number of observations.

Data Types: `single` | `double`

Z — Random-effects design

n-by-*q* matrix | cell array of *R* *n*-by-*q*(*r*) matrices, *r* = 1, 2, ..., *R*

Random-effects design, specified as either of the following.

- If there is one random-effects term in the model, then `Z` must be an *n*-by-*q* matrix, where *n* is the number of observations and *q* is the number of variables in the random-effects term.
- If there are *R* random-effects terms, then `Z` must be a cell array of length *R*. Each cell of `Z` contains an *n*-by-*q*(*r*) design matrix `Z{r}`, *r* = 1, 2, ..., *R*, corresponding to each random-effects term. Here, *q*(*r*) is the number of random effects term in the *r*th random effects design matrix, `Z{r}`.

Data Types: `single` | `double` | `cell`

G — Grouping variable or variables

n-by-1 vector | cell array of *R* *n*-by-1 vectors

Grouping variable or variables, specified as either of the following.

- If there is one random-effects term, then `G` must be an n-by-1 vector corresponding to a single grouping variable with M levels or groups.

  `G` can be a categorical vector, numeric vector, character array, or cell array of strings.

- If there are multiple random-effects terms, then `G` must be a cell array of length R. Each cell of `G` contains a grouping variable `G{r}`, r = 1, 2, ..., R, with $M(r)$ levels.

  `G{r}` can be a categorical vector, numeric vector, character array, or cell array of strings.

Data Types: `single` | `double` | `char` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'CovariancePattern','Diagonal','DummyVarCoding','full','Optimizer','fminunc'` specifies a random-effects covariance pattern with zero off-diagonal elements, creates a dummy variable for each level of a categorical variable, and uses the `fminunc` optimization algorithm.

`'FixedEffectPredictors'` — Names of columns in fixed-effects design matrix

`{'x1','x2',...,'xP'}` (default) | cell array of length p

Names of columns in the fixed-effects design matrix `X`, specified as the comma-separated pair consisting of `'FixedEffectPredictors'` and a cell array of length p.

For example, if you have a constant term and two predictors, say `TimeSpent` and `Gender`, where `Female` is the reference level for `Gender`, as the fixed effects, then you can specify the names of your fixed effects in the following way. `Gender_Male` represents the dummy variable you must create for category `Male`. You can choose different names for these variables.

Example: `'FixedEffectPredictors',`
`{'Intercept','TimeSpent','Gender_Male'},`

Data Types: `cell`

`'RandomEffectPredictors'` — Names of columns in random-effects design matrix or cell array

cell array of length q | cell array of length R with elements of length $q(r)$, $r = 1, 2, ..., R$

Names of columns in the random-effects design matrix or cell array `Z`, specified as the comma-separated pair consisting of `'RandomEffectPredictors'` and either of the following:

- A cell array of length q when `Z` is an n-by-q design matrix. In this case, the default is `{'z1','z2',...,'zQ'}`.
- A cell array of length R, when `Z` is a cell array of length R with each element `Z{r}` of length $q(r)$, $r = 1, 2, ..., R$. In this case, the default is `{'z11','z12',...,'z1Q(1)'},...,{'zr1','zr2',...,'zrQ(r)'}`.

For example, suppose you have correlated random effects for intercept and a variable named `Acceleration`. Then, you can specify the random-effects predictor names as follows.

Example: `'RandomEffectPredictors',{'Intercept','Acceleration'}`

If you have two random effects terms, one for the intercept and the variable `Acceleration` grouped by variable `g1`, and the second for the intercept, grouped by the variable `g2`, then you specify the random-effects predictor names as follows.

Example: `'RandomEffectPredictors',{{'Intercept','Acceleration'},{'Intercept'}}`

Data Types: `cell`

`'ResponseVarName'` — Name of response variable

`'y'` (default) | string

Name of response variable, specified as the comma-separated pair consisting of `'ResponseVarName'` and a string.

For example, if your response variable name is `score`, then you can specify it as follows.

Example: `'ResponseVarName','score'`

Data Types: `char`

`'RandomEffectGroups'` — Names of random effects grouping variables

`'g'` or `{'g1','g2',...,'gR'}` (default) | string | cell array of strings

Names of random effects grouping variables, specified as the comma-separated pair `'RandomEffectGroups'` and either of the following:

- String — If there is only one random-effects term, that is, if G is a vector, then the value of `'RandomEffectGroups'` is a string containing the name for the grouping variable `G`. The default is `'g'`.
- Cell array of strings — If there are multiple random-effects terms, that is, if `G` is a cell array of length R, then the value of `'RandomEffectGroups'` is a cell array of length R, where each cell contains the name for the grouping variable `G{r}`. The default is `{'g1','g2',...,'gR'}`.

For example, if you have two random-effects terms, `z1` and `z2`, grouped by the grouping variables `sex` and `subject`, then you can specify the names of your grouping variables as follows.

Example: `'RandomEffectGroups',{'sex','subject'}`

Data Types: `char` | `cell`

`'CovariancePattern'` — Pattern of covariance matrix

`'FullCholesky'` (default) | string | square symmetric logical matrix | cell array of strings or logical matrices

Pattern of the covariance matrix of the random effects, specified as the comma-separated pair consisting of `'CovariancePattern'` and a string, a square symmetric logical matrix, or a cell array of strings or logical matrices.

If there are R random-effects terms, then the value of `'CovariancePattern'` must be a cell array of length R, where each element r of this cell array specifies the pattern of the covariance matrix of the random-effects vector associated with the rth random-effects term. The options for each element follow.

`'FullCholesky'`	Default. Full covariance matrix using the Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.
`'Full'`	Full covariance matrix, using the log-Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.

`'Diagonal'`

Diagonal covariance matrix. That is, off-diagonal elements of the covariance matrix are constrained to be 0.

$$\begin{pmatrix} \sigma_{b1}^2 & 0 & 0 \\ 0 & \sigma_{b2}^2 & 0 \\ 0 & 0 & \sigma_{b3}^2 \end{pmatrix}$$

`'Isotropic'`

Diagonal covariance matrix with equal variances. That is, off-diagonal elements of the covariance matrix are constrained to be 0, and the diagonal elements are constrained to be equal. For example, if there are three random-effects terms with an isotropic covariance structure, this covariance matrix looks like

$$\begin{pmatrix} \sigma_b^2 & 0 & 0 \\ 0 & \sigma_b^2 & 0 \\ 0 & 0 & \sigma_b^2 \end{pmatrix}$$

where σ^2_b is the common variance of the random-effects terms.

`'CompSymm'`	Compound symmetry structure. That is, common variance along diagonals and equal correlation between all random effects. For example, if there are three random-effects terms with a covariance matrix having a compound symmetry structure, this covariance matrix looks like $\begin{pmatrix} \sigma_{b1}^2 & \sigma_{b1,b2} & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1}^2 & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1,b2} & \sigma_{b1}^2 \end{pmatrix}$ where σ^2_{b1} is the common variance of the random-effects terms and $\sigma_{b1,b2}$ is the common covariance between any two random-effects term .
`PAT`	Square symmetric logical matrix. If `'CovariancePattern'` is defined by the matrix `PAT`, and if `PAT(a,b) = false`, then the `(a,b)` element of the corresponding covariance matrix is constrained to be 0.

Example: `'CovariancePattern','Diagonal'`

Example: `'CovariancePattern',{'Full','Diagonal'}`

`'FitMethod'` — Method for estimating parameters

`'ML'` (default) | `'REML'`

Method for estimating parameters of the linear mixed-effects model, specified as the comma-separated pair consisting of `'FitMethod'` and either of the following.

`'ML'`	Default. Maximum likelihood estimation
`'REML'`	Restricted maximum likelihood estimation

Example: `'FitMethod','REML'`

'Weights' — Observation weights

vector of scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and a vector of length n, where n is the number of observations.

Data Types: single | double

'Exclude' — Indices for rows to exclude

use all rows without NaNs (default) | vector of integer or logical values

Indices for rows to exclude from the linear mixed-effects model in the data, specified as the comma-separated pair consisting of 'Exclude' and a vector of integer or logical values.

For example, you can exclude the 13th and 67th rows from the fit as follows.

Example: 'Exclude',[13,67]

Data Types: single | double | logical

'DummyVarCoding' — Coding to use for dummy variables

'reference' (default) | 'effects' | 'full'

Coding to use for dummy variables created from the categorical variables, specified as the comma-separated pair consisting of 'DummyVarCoding' and one of the following.

'reference'	Default. Coefficient for first category set to 0.
'effects'	Coefficients sum to 0.
'full'	One dummy variable for each category.

Example: 'DummyVarCoding','effects'

'Optimizer' — Optimization algorithm

'quasinewton' (default) | 'fminunc'

Optimization algorithm, specified as the comma-separated pair consisting of 'Optimizer' and either of the following.

'quasinewton'	Default. Uses a trust region based quasi-Newton optimizer. Change

	the options of the algorithm using `statset('LinearMixedModel')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `statset('LinearMixedModel')`.
`'fminunc'`	You must have Optimization Toolbox to specify this option. Change the options of the algorithm using `optimoptions('fminunc')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.

Example: `'Optimizer','fminunc'`

`'OptimizerOptions'` — Options for optimization algorithm
structure returned by `statset` | object returned by `optimoptions`

Options for the optimization algorithm, specified as the comma-separated pair consisting of `'OptimizerOptions'` and a structure returned by `statset('LinearMixedModel')` or an object returned by `optimoptions('fminunc')`.

- If `'Optimizer'` is `'fminunc'`, then use `optimoptions('fminunc')` to change the options of the optimization algorithm. See `optimoptions` for the options `'fminunc'` uses. If `'Optimizer'` is `'fminunc'` and you do not supply `'OptimizerOptions'`, then the default for `LinearMixedModel` is the default options created by `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.
- If `'Optimizer'` is `'quasinewton'`, then use `statset('LinearMixedModel')` to change the optimization parameters. If you don't change the optimization parameters, then `LinearMixedModel` uses the default options created by `statset('LinearMixedModel')`:

The `'quasinewton'` optimizer uses the following fields in the structure created by `statset('LinearMixedModel')`.

`'TolFun'` — Relative tolerance on gradient of objective function
`1e-6` (default) | positive scalar value

Relative tolerance on the gradient of the objective function, specified as a positive scalar value.

`'TolX'` — Absolute tolerance on step size
`1e-12` (default) | positive scalar value

Absolute tolerance on the step size, specified as a positive scalar value.

`'MaxIter'` — Maximum number of iterations allowed
`10000` (default) | positive scalar value

Maximum number of iterations allowed, specified as a positive scalar value.

`'Display'` — Level of display
`'off'` (default) | `'iter'` | `'final'`

Level of display, specified as one of `'off'`, `'iter'`, or `'final'`.

`'StartMethod'` — Method to start iterative optimization
`'default'` (default) | `'random'`

Method to start iterative optimization, specified as the comma-separated pair consisting of `'StartMethod'` and either of the following.

`'default'`	Default. An internally defined default value.
`'random'`	A random initial value.

Example: `'StartMethod','random'`

`'Verbose'` — Indicator to display optimization process on screen
`false` (default) | `true`

Indicator to display the optimization process on screen, specified as the comma-separated pair consisting of `'Verbose'` and either `false` or `true`. Default is `false`.

The setting for `'Verbose'` overrides the field `'Display'` in `'OptimizerOptions'`.

Example: `'Verbose',true`

'CheckHessian' — Indicator to check positive definiteness of Hessian
false (default) | true

Indicator to check the positive definiteness of the Hessian of the objective function with respect to unconstrained parameters at convergence, specified as the comma-separated pair consisting of 'CheckHessian' and either false or true. Default is false.

Specify 'CheckHessian' as true to verify optimality of the solution or to determine if the model is overparameterized in the number of covariance parameters.

Example: 'CheckHessian',true

Output Arguments

lme — Linear mixed-effects model
LinearMixedModel object

Linear mixed-effects model, returned as a LinearMixedModel object.

For properties and methods of this object, see LinearMixedModel.

Alternative Functionality

You can also fit a linear mixed-effects model using fitlme(tbl,formula), where tbl is a table or dataset array containing the response y, the predictor variables X, and the grouping variables, and formula is of the form 'y ~ fixed + ($random_1|g_1$) + ... + ($random_R|g_R$)'.

More About

Cholesky Parameterization

One of the assumptions of linear mixed-effects models is that the random effects have the following prior distribution.

$$b \sim N\left(0,\sigma^2 D(\theta)\right),$$

where D is a q-by-q symmetric and positive semidefinite matrix, parameterized by a variance component vector θ, q is the number of variables in the random-effects term, and σ^2 is the observation error variance. Since the covariance matrix of the random effects, D, is symmetric, it has $q(q+1)/2$ free parameters. Suppose L is the lower triangular Cholesky factor of $D(\theta)$ such that

$$D(\theta) = L(\theta)L(\theta)^T,$$

then the $q*(q+1)/2$-by-1 unconstrained parameter vector θ is formed from elements in the lower triangular part of L.

For example, if

$$L = \begin{bmatrix} L_{11} & 0 & 0 \\ L_{21} & L_{22} & 0 \\ L_{31} & L_{32} & L_{33} \end{bmatrix},$$

then

$$\theta = \begin{bmatrix} L_{11} \\ L_{21} \\ L_{31} \\ L_{22} \\ L_{32} \\ L_{33} \end{bmatrix}.$$

Log-Cholesky Parameterization

When the diagonal elements of L in Cholesky parameterization are constrained to be positive, then the solution for L is unique. Log-Cholesky parameterization is the same as Cholesky parameterization except that the logarithm of the diagonal elements of L are used to guarantee unique parameterization.

For example, for the 3-by-3 example in Cholesky parameterization, enforcing $L_{ii} \geq 0$,

$$\theta = \begin{bmatrix} \log(L_{11}) \\ L_{21} \\ L_{31} \\ \log(L_{22}) \\ L_{32} \\ \log(L_{33}) \end{bmatrix}.$$

See Also

`compare` | `fitlme` | `LinearMixedModel`

fitrm

Fit repeated measures model

Syntax

```
rm = fitrm(t,modelspec)
rm = fitrm(t,modelspec,Name,Value)
```

Description

`rm = fitrm(t,modelspec)` returns a repeated measures model, specified by `modelspec`, fitted to the variables in the table or dataset array `t`.

`rm = fitrm(t,modelspec,Name,Value)` returns a repeated measures model, with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the hypothesis for the within-subject factors.

Examples

Fit a Repeated Measures Model

Load the sample data.

```
load fisheriris
```

The column vector `species` consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = table([1 2 3 4]','VariableNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas)

rm =

  RepeatedMeasuresModel with properties:

   Between Subjects:
         BetweenDesign: [150x5 table]
         ResponseNames: {'meas1'  'meas2'  'meas3'  'meas4'}
    BetweenFactorNames: {'species'}
          BetweenModel: '1 + species'

   Within Subjects:
         WithinDesign: [4x1 table]
    WithinFactorNames: {'Measurements'}
          WithinModel: 'separatemeans'

   Estimates:
    Coefficients: [3x4 table]
      Covariance: [4x4 table]
```

Display the coefficients.

```
rm.Coefficients

ans =

                          meas1       meas2      meas3      meas4
                        ________    ________    ______    ________

    (Intercept)           5.8433      3.0573     3.758     1.1993
    species_setosa       -0.83733     0.37067   -2.296    -0.95333
    species_versicolor   0.092667    -0.28733    0.502     0.12667
```

`fitrm` uses the `'effects'` contrasts which means that the coefficients sum to 0. The `rm.DesignMatrix` has one column of 1s for the intercept, and two other columns `species_setosa` and `species_versicolor`, which are as follows:

$$\text{species\_setosa} = \begin{cases} 1, & \textit{if setosa} \\ 0, & \textit{if versicolor} \\ -1, & \textit{if virginica} \end{cases} \quad \text{and} \quad \text{species\_versicolor} = \begin{cases} 0, & \textit{if setosa} \\ 1, & \textit{if versicolor} \\ -1, & \textit{if virginica} \end{cases}$$

Display the covariance matrix.

```
rm.Covariance

ans =

              meas1       meas2       meas3       meas4
            ________    ________    ________    ________

    meas1     0.26501    0.092721     0.16751    0.038401
    meas2    0.092721     0.11539    0.055244     0.03271
    meas3     0.16751    0.055244     0.18519    0.042665
    meas4    0.038401     0.03271    0.042665    0.041882
```

Specify the Within-Subject Hypothesis

Navigate to the folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load('longitudinalData')
```

The matrix `Y` contains response data for 16 individuals. The response is the blood level of a drug measured at five time points (time = 0, 2, 4, 6, and 8). Each row of `Y` corresponds to an individual, and each column corresponds to a time point. The first eight subjects are female, and the second eight subjects are male. This is simulated data.

Define a variable that stores gender information.

```
Gender = ['F' 'F' 'F' 'F' 'F' 'F' 'F' 'F' 'M' 'M' 'M' 'M' 'M' 'M' 'M' 'M']';
```

Store the data in a proper table array format to conduct repeated measures analysis.

```
t = table(Gender,Y(:,1),Y(:,2),Y(:,3),Y(:,4),Y(:,5),...
'VariableNames',{'Gender','t0','t2','t4','t6','t8'});
```

Define the within-subjects variable.

```
Time = [0 2 4 6 8]';
```

Fit a repeated measures model, where blood levels are the responses and gender is the predictor variable. Also define the hypothesis for within-subject factors.

```
rm = fitrm(t,'t0-t8 ~ Gender','WithinDesign',Time,'WithinModel','orthogonalcontrasts')
```

```
rm =

  RepeatedMeasuresModel with properties:

   Between Subjects:
         BetweenDesign: [16x6 table]
         ResponseNames: {'t0'  't2'  't4'  't6'  't8'}
    BetweenFactorNames: {'Gender'}
          BetweenModel: '1 + Gender'

   Within Subjects:
         WithinDesign: [5x1 table]
    WithinFactorNames: {'Time'}
          WithinModel: 'orthogonalcontrasts'

   Estimates:
    Coefficients: [2x5 table]
      Covariance: [5x5 table]
```

Fit a Model with Covariates

Load the sample data.

```
load repeatedmeas
```

The table `between` includes the eight repeated measurements `y1`–`y8` as responses and the between-subject factors `Group`, `Gender` , `IQ`, and `Age`. `IQ` and `Age` as continuous variables. The table `within` includes the within-subject factors `w1` and `w2`.

Fit a repeated measures model, where age, IQ, and group, gender are the predictor variables, and the model includes the interaction effect of group and gender. Also define the within-subject factors.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender+Age+IQ','WithinDesign',within)
```

```
rm =

  RepeatedMeasuresModel with properties:

   Between Subjects:
         BetweenDesign: [30x12 table]
         ResponseNames: {'y1'  'y2'  'y3'  'y4'  'y5'  'y6'  'y7'  'y8'}
    BetweenFactorNames: {'Age'  'IQ'  'Group'  'Gender'}
          BetweenModel: '1 + Age + IQ + Group*Gender'
```

```
   Within Subjects:
         WithinDesign: [8x2 table]
    WithinFactorNames: {'w1'  'w2'}
          WithinModel: 'separatemeans'

   Estimates:
    Coefficients: [8x8 table]
      Covariance: [8x8 table]
```

Display the coefficients.

```
rm.Coefficients
```

```
ans =
```

	y1	y2	y3	y4	y5
(Intercept)	141.38	195.25	9.8663	-49.154	157.77
Age	0.32042	-4.7672	-1.2748	0.6216	-1.0621
IQ	-1.2671	-1.1653	0.05862	0.4288	-1.4518
Group_A	-1.2195	-9.6186	22.532	15.303	12.602
Group_B	2.5186	1.417	-2.2501	0.50181	8.0907
Gender_Female	5.3957	-3.9719	8.5225	9.3403	6.0909
Group_A:Gender_Female	4.1046	10.064	-7.3053	-3.3085	4.6751
Group_B:Gender_Female	-0.48486	-2.9202	1.1222	0.69715	-0.065945

The display shows the coefficients for fitting the repeated measures as a function of the terms in the between-subjects model.

Input Arguments

`t` — Input data

table

Input data, which includes the values of the response variables and the between-subject factors to use as predictors in the repeated measures model, specified as a table.

Data Types: `table`

`modelspec` — Formula for model specification

string of the form `'y1-yk ~ terms'`

Formula for model specification, specified as a string of the form `'y1-yk ~ terms'`. The responses and terms are specified using Wilkinson notation. `fitrm` treats the variables used in model terms as categorical if they are categorical (nominal or ordinal), logical, char arrays, or a cell arrays of strings.

For example, if you have four repeated measures as responses and the factors `x1`, `x2`, and `x3` as the predictor variables, then you can define a repeated measures model as follows.

Example: `'y1-y4 ~ x1 + x2 * x3'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'WithinDesign','W','WithinModel','w1+w2'` specifies the matrix `w` as the design matrix for within-subject factors, and the model for within-subject factors `w1` and `w2` is `'w1+w2'`.

`'WithinDesign'` — Design for within-subject factors

numeric vector of length *r* (default) | *r*-by-*k* numeric matrix | *r*-by-*k* table

Design for within-subject factors, specified as the comma-separated pair consisting of `'WithinDesign'` and one of the following:

- Numeric vector of length *r*, where *r* is the number of repeated measures.

  In this case, `fitrm` treats the values in the vector as continuous, and these are typically time values.
- *r*-by-*k* numeric matrix of the values of the *k* within-subject factors, w_1, w_2, ..., w_k.

  In this case,`fitrm` treats all *k* variables as continuous.
- *r*-by-*k* table that contains the values of the *k* within-subject factors.

  In this case, `fitrm` treats all numeric variables as continuous, and all categorical variables as categorical.

For example, if the table `weeks` contains the values of the within-subject factors, then you can define the design table as follows.

Example: `'WithinDesign',weeks`

Data Types: `single` | `double` | `table`

`'WithinModel'` — Model specifying within-subject hypothesis test
`'separatemeans'` (default) | `'orthogonalcontrasts'` | string that defines a model

Model specifying the within-subject hypothesis test, specified as the comma-separated pair consisting of `'WithinModel'` and one of the following:

- `'separatemeans'` — Compute a separate mean for each group.
- `'orthogonalcontrasts'` — This is valid only when the within-subject model has a single numeric factor T. Responses are the average, the slope of centered T, and, in general, all orthogonal contrasts for a polynomial up to T^(p – 1), where p is the number if rows in the within-subject model.
- A string that defines a model specification in the within-subject factors. You can define the model based on the rules for the `terms` in modelspec.

For example, if there are three within-subject factors `w1`, `w2`, and `w3`, then you can specify a model for the within-subject factors as follows.

Example: `'WithinModel','w1+w2+w2*w3'`

Data Types: `single` | `double`

Output Arguments

`rm` — Repeated measures model
`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

More About

Model Specification Using Wilkinson Notation

Wilkinson notation describes the factors present in models. It does not describe the multipliers (coefficients) of those factors.

The following rules specify the responses in modelspec.

Wilkinson Notation	Meaning
`Y1,Y2,Y3`	Specific list of variables
`Y1-Y5`	All table variables from `Y1` through `Y5`

The following rules specify terms in modelspec.

Wilkinson notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1*X2`
`X1:X2`	`X1*X2` only
`-X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

See Also

`RepeatedMeasuresModel`

fitdist

Fit probability distribution object to data

Syntax

```
pd = fitdist(x,distname)
pd = fitdist(x,distname,Name,Value)

[pdca,gn,gl] = fitdist(x,distname,'By',groupvar)
[pdca,gn,gl] = fitdist(x,distname,'By',groupvar,Name,Value)
```

Description

`pd = fitdist(x,distname)` creates a probability distribution object by fitting the distribution specified by distname to the data in column vector x.

`pd = fitdist(x,distname,Name,Value)` creates the probability distribution object with additional options specified by one or more name-value pair arguments. For example, you can indicate censored data or specify control parameters for the iterative fitting algorithm.

`[pdca,gn,gl] = fitdist(x,distname,'By',groupvar)` creates probability distribution objects by fitting the distribution specified by distname to the data in x based on the grouping variable groupvar. It returns a cell array of fitted probability distribution objects, pdca, a cell array of group labels, gn, and a cell array of grouping variable levels, gl.

`[pdca,gn,gl] = fitdist(x,distname,'By',groupvar,Name,Value)` returns the above output arguments using additional options specified by one or more name-value pair arguments. For example, you can indicate censored data or specify control parameters for the iterative fitting algorithm.

Examples

Fit a Normal Distribution to Data

Load the sample data. Create a vector containing the patients' weight data.

```
load hospital
x = hospital.Weight;
```

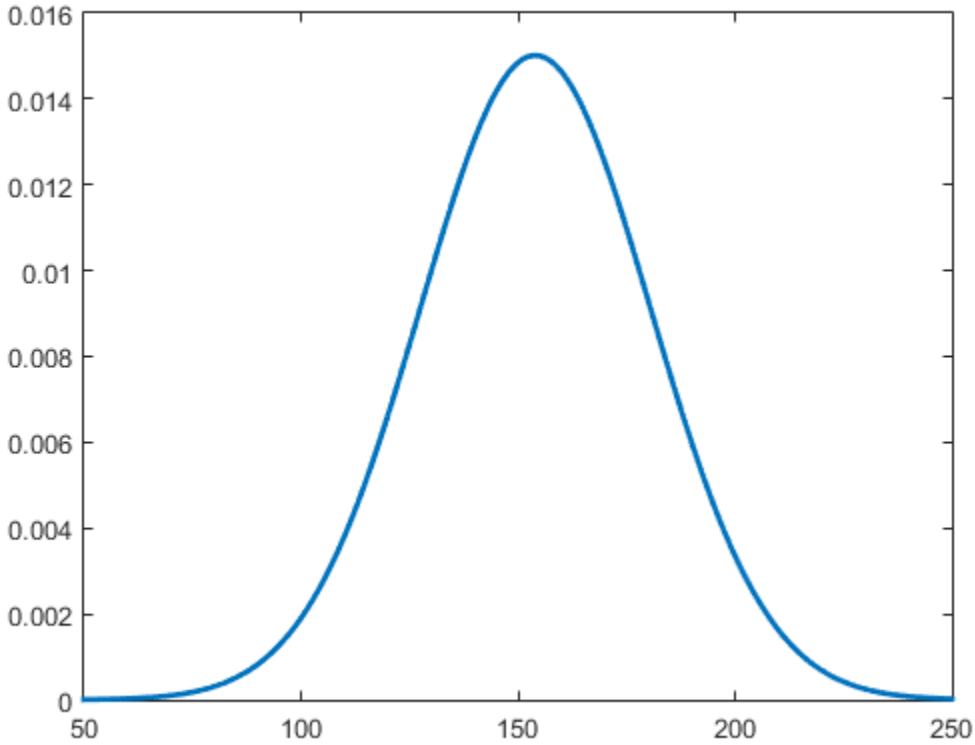
Create a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu =     154   [148.728, 159.272]
    sigma = 26.5714   [23.3299, 30.8674]
```

Plot the pdf of the distribution.

```
x_values = 50:1:250;
y = pdf(pd,x_values);
plot(x_values,y,'LineWidth',2)
```



Fit a Kernel Distribution to Data

Load the sample data. Create a vector containing the patients' weight data.

```
load hospital
x = hospital.Weight;
```

Create a kernel distribution object by fitting it to the data. Use the Epanechnikov kernel function.

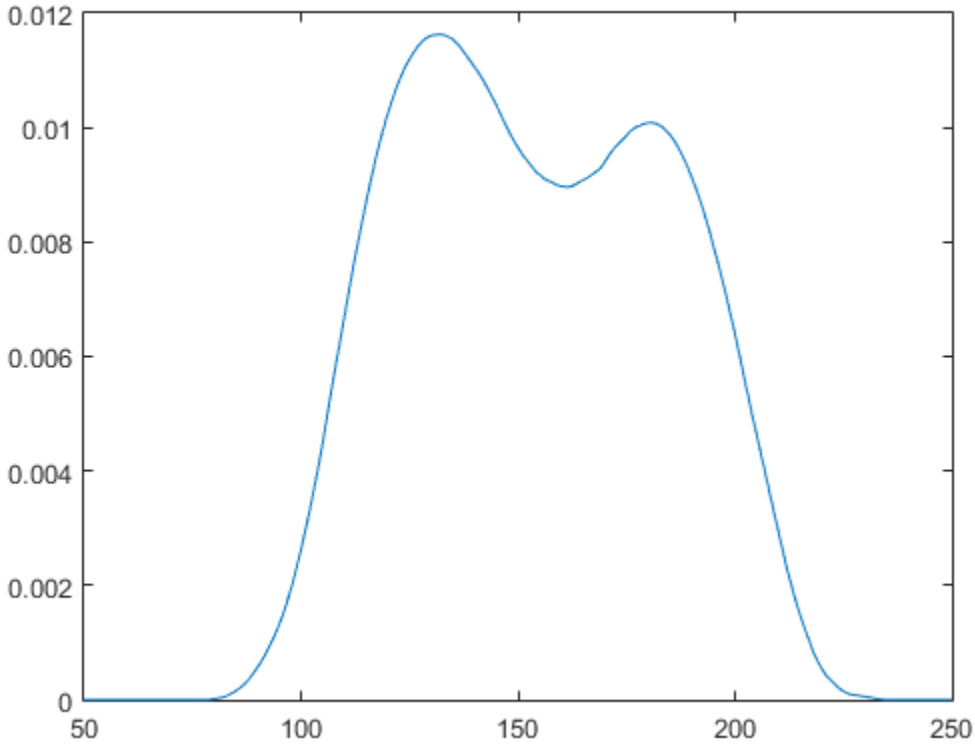
```
pd = fitdist(x,'Kernel','Kernel','epanechnikov')
```

```
pd =
```

```
  KernelDistribution

    Kernel = epanechnikov
    Bandwidth = 14.3792
    Support = unbounded
```

Plot the pdf of the distribution.

```
x_values = 50:1:250;
y = pdf(pd,x_values);
plot(x_values,y)
```



Fit Normal Distributions to Grouped Data

Load the sample data. Create a vector containing the patients' weight data.

```
load hospital
x = hospital.Weight;
```

Create normal distribution objects by fitting them to the data, grouped by patient gender.

```
gender = hospital.Sex;
[pdca,gn,gl] = fitdist(x,'Normal','By',gender)
```

```
pdca =
```

```
    [1x1 prob.NormalDistribution]    [1x1 prob.NormalDistribution]

gn =

    'Female'
    'Male'


gl =

    'Female'
    'Male'
```

The cell array `pdca` contains two probability distribution objects, one for each gender group. The cell array `gn` contains two strings of the group labels. The cell array `gl` contains two strings of the group levels.

View each distribution in the cell array `pdca` to compare the mean, `mu`, and the standard deviation, `sigma`, grouped by patient gender.

```
female = pdca{1}  % Distribution for females


female =

  NormalDistribution

  Normal distribution
       mu = 130.472   [128.183, 132.76]
    sigma = 8.30339   [6.96947, 10.2736]


male = pdca{2}  % Distribution for males


male =

  NormalDistribution

  Normal distribution
       mu = 180.532   [177.833, 183.231]
```

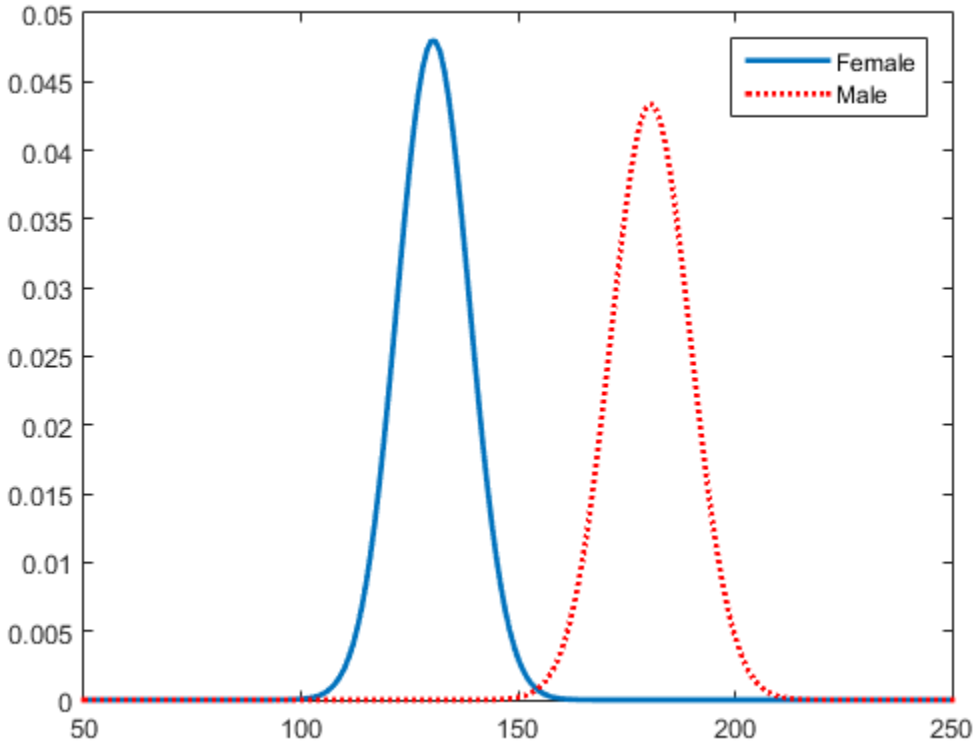
```
    sigma = 9.19322   [7.63933, 11.5466]
```

Compute the pdf of each distribution.

```
x_values = 50:1:250;
femalepdf = pdf(female,x_values);
malepdf = pdf(male,x_values);
```

Plot the pdfs for a visual comparison of weight distribution by gender.

```
figure
plot(x_values,femalepdf,'LineWidth',2)
hold on
plot(x_values,malepdf,'Color','r','LineStyle',':','LineWidth',2)
legend(gn,'Location','NorthEast')
hold off
```



Fit Kernel Distributions to Grouped Data

Load the sample data. Create a vector containing the patients' weight data.

```
load hospital
x = hospital.Weight;
```

Create kernel distribution objects by fitting them to the data, grouped by patient gender. Use a triangular kernel function.

```
gender = hospital.Sex;
[pdca,gn,gl] = fitdist(x,'Kernel','By',gender,'Kernel','triangle');
```

View each distribution in the cell array `pdca` to see the kernel distributions for each gender.

```
female = pdca{1}  % Distribution for females
```

```
female =

  KernelDistribution

    Kernel = triangle
    Bandwidth = 4.25894
    Support = unbounded
```

```
male = pdca{2}  % Distribution for males
```

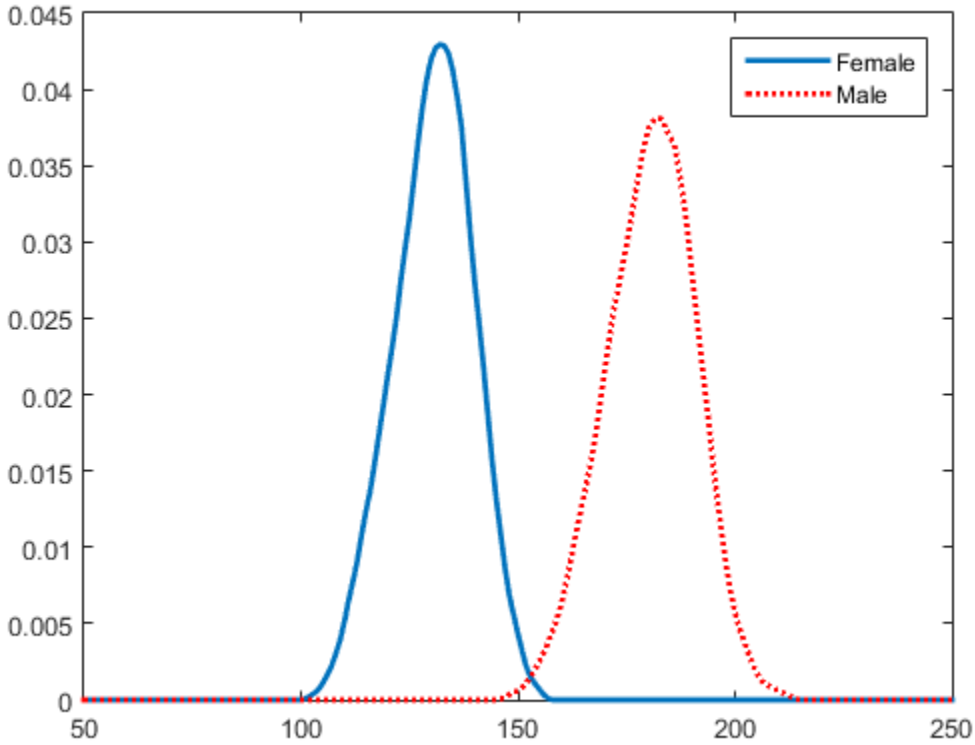
```
male =

  KernelDistribution

    Kernel = triangle
    Bandwidth = 5.08961
    Support = unbounded
```

Compute the pdf of each distribution.

```
x_values = 50:1:250;
femalepdf = pdf(female,x_values);
malepdf = pdf(male,x_values);
```

Plot the pdfs for a visual comparison of weight distribution by gender.

```
figure
plot(x_values,femalepdf,'LineWidth',2)
hold on
plot(x_values,malepdf,'Color','r','LineStyle',':','LineWidth',2)
legend(gn,'Location','NorthEast')
hold off
```



Input Arguments

x — Input data

column vector

Input data, specified as a column vector. `fitdist` ignores `NaN` values in x. Additionally, any `NaN` values in the censoring vector or frequency vector causes `fitdist` to ignore the corresponding values in x.

Data Types: `single` | `double`

`distname` — Distribution name

string

Distribution name, specified as one of the following strings. The distribution specified by `distname` determines the class type of the returned probability distribution object.

Distribution Name	Description	Distribution Class
`'Beta'`	Beta distribution	`prob.BetaDistribution`
`'Binomial'`	Binomial distribution	`prob.BinomialDistribution`
`'BirnbaumSaunders'`	Birnbaum-Saunders distribution	`prob.BirnbaumSaundersDistributio`
`'Burr'`	Burr distribution	`prob.BurrDistribution`
`'Exponential'`	Exponential distribution	`prob.ExponentialDistribution`
`'ExtremeValue'`	Extreme Value distribution	`prob.ExtremeValueDistribution`
`'Gamma'`	Gamma distribution	`prob.GammaDistribution`
`'GeneralizedExtremeVal`	Generalized Extreme Value distribution	`prob.GeneralizedExtremeValueDist`
`'GeneralizedPareto'`	Generalized Pareto distribution	`prob.GeneralizedParetoDistributi`
`'InverseGaussian'`	Inverse Gaussian distribution	`prob.InverseGaussianDistribution`
`'Kernel'`	Kernel distribution	`prob.KernelDistribution`
`'Logistic'`	Logistic distribution	`prob.LogisticDistribution`
`'Loglogistic'`	Loglogistic distribution	`prob.LoglogisticDistribution`
`'Lognormal'`	Lognormal distribution	`prob.LognormalDistribution`
`'Multinomial'`	Multinomial distribution	`prob.MultinomialDistribution`
`'Nakagami'`	Nakagami distribution	`prob.NakagamiDistribution`
`'NegativeBinomial'`	Negative Binomial distribution	`prob.NegativeBinomialDistributio`
`'Normal'`	Normal distribution	`prob.NormalDistribution`
`'Poisson'`	Poisson distribution	`prob.PoissonDistribution`
`'Rayleigh'`	Rayleigh distribution	`prob.RayleighDistribution`

Distribution Name	Description	Distribution Class
`'Rician'`	Rician distribution	`prob.RicianDistribution`
`'tLocationScale'`	*t* Location-Scale distribution	`prob.tLocationScaleDistribution`
`'Weibull'`	Weibull distribution	`prob.WeibullDistribution`

`groupvar` — Grouping variable

categorical array | logical or numeric vector | cell array of strings

Grouping variable, specified as a categorical array, logical or numeric vector, or cell array of strings. Each unique value in a grouping variable defines a group.

For example, if `Gender` is a cell array of strings with values `'Male'` and `'Female'`, you can use `Gender` as a grouping variable to fit a distribution to your data by gender.

More than one grouping variable can be used by specifying a cell array of grouping variable names. Observations are placed in the same group if they have common values of all specified grouping variables.

For example, if `Smoker` is a logical vector with values `0` for nonsmokers and `1` for smokers, then specifying the cell array `{Gender,Smoker}` divides observations into four groups: Male Smoker, Male Nonsmoker, Female Smoker, and Female Nonsmoker.

Example: `{Gender,Smoker}`

Data Types: `single` | `double` | `logical` | `cell` | `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `fitdist(x,'Kernel','Kernel','triangle')` fits a kernel distribution object to the data in `x` using a triangular kernel function.

`'Censoring'` — Logical flag for censored data

`0` (default) | vector of logical values

Logical flag for censored data, specified as the comma-separated pair consisting of `'Censoring'` and a vector of logical values that is the same size as input vector x. The

value is 1 when the corresponding element in x is a right-censored observation and 0 when the corresponding elements is an exact observation. The default is a vector of 0s, indicating that all observations are exact.

fitdist ignores any NaN values in this censoring vector. Additionally, any NaN values in x or the frequency vector causes fitdist to ignore the corresponding values in the censoring vector.

Data Types: logical

'Frequency' — Observation frequency

1 (default) | vector of nonnegative integer values

Observation frequency, specified as the comma-separated pair consisting of 'Frequency' and a vector of nonnegative integer values that is the same size as input vector x. Each element of the frequency vector specifies the frequencies for the corresponding elements in x. The default is a vector of 1s, indicating that each value in x only appears once.

fitdist ignores any NaN values in this frequency vector are ignored by the fitting calculations. Additionally, any NaN values in x or the censoring vector causes fitdist to ignore the corresponding values in the frequency vector.

Data Types: logical

'Options' — Control parameters

structure

Control parameters for the iterative fitting algorithm, specified as the comma-separated pair consisting of 'Options' and a structure you create using statset.

Data Types: struct

'NTrials' — Number of trials

positive integer value

Number of trials for the binomial distribution, specified as the comma-separated pair consisting of 'NTrials' and a positive integer value. You must specify distname as 'Binomial' to use this option.

Data Types: single | double

'Theta' — Threshold parameter

0 (default) | scalar value

Threshold parameter for the generalized Pareto distribution, specified as the comma-separated pair consisting of `'Theta'` and a scalar value. You must specify distname as `'GeneralizedPareto'` to use this option.

Data Types: `single` | `double`

`'Kernel'` — Kernel smoother type

`'normal'` (default) | `'box'` | `'triangle'` | `'epanechnikov'`

Kernel smoother type, specified as the comma-separated pair consisting of `'Kernel'` and one of the following:

- `'normal'`
- `'box'`
- `'triangle'`
- `'epanechnikov'`

You must specify distname as `'Kernel'` to use this option.

`'Support'` — Kernel density support

`'unbounded'` (default) | `'positive'` | two-element vector

Kernel density support, specified as the comma-separated pair consisting of `'Support'` and a string or two-element vector. The string must be one of the following.

`'unbounded'`	Density can extend over the whole real line.
`'positive'`	Density is restricted to positive values.

Alternatively, you can specify a two-element vector giving finite lower and upper limits for the support of the density.

You must specify distname as `'Kernel'` to use this option.

Data Types: `single` | `double`

`'Width'` — Bandwidth of kernel smoothing window

scalar value

Bandwidth of the kernel smoothing window, specified as the comma-separated pair consisting of `'Width'` and a scalar value. The default value used by `fitdist` is optimal for estimating normal densities, but you might want to choose a smaller value to reveal

features such as multiple modes. You must specify distname as `'Kernel'` to use this option.

Data Types: `single` | `double`

Output Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, returned as a probability distribution object. The distribution specified by `distname` determines the class type of the returned probability distribution object.

`pdca` — Probability distribution objects

cell array

Probability distribution objects of the type specified by distname, returned as a cell array.

`gn` — Group labels

cell array of strings

Group labels, returned as a cell array of strings.

`gl` — Grouping variable levels

cell array of strings

Grouping variable levels, returned as a cell array of strings containing one column for each grouping variable.

Alternative Functionality

App

The Distribution Fitting app opens a graphical user interface for you to import data from the workspace and interactively fit a probability distribution to that data. You can then save the distribution to the workspace as a probability distribution object. Open the Distribution Fitting app using `dfittool`, or click Distribution Fitting on the Apps tab.

More About

Algorithms

The `fitdist` function fits most distributions using maximum likelihood estimation. Two exceptions are the normal and lognormal distributions with uncensored data.

- For the uncensored normal distribution, the estimated value of the sigma parameter is the square root of the unbiased estimate of the variance.
- For the uncensored lognormal distribution, the estimated value of the sigma parameter is the square root of the unbiased estimate of the variance of the log of the data.

References

[1] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 1, Hoboken, NJ: Wiley-Interscience, 1993.

[2] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 2, Hoboken, NJ: Wiley-Interscience, 1994.

[3] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis*. New York: Oxford University Press, 1997.

See Also

`dfittool` | `makedist`

fitensemble

Fitted ensemble for classification or regression

Syntax

```
Ensemble = fitensemble(X,Y,Method,NLearn,Learners)
Ensemble = fitensemble(X,Y,Method,NLearn,Learners,Name,Value)
```

Description

`Ensemble = fitensemble(X,Y,Method,NLearn,Learners)` creates an ensemble model that predicts responses to data. The ensemble consists of models listed in Learners.

`Ensemble = fitensemble(X,Y,Method,NLearn,Learners,Name,Value)` creates an ensemble model with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`X`

Matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

For classification, `Y` is a categorical variable, character array, or cell array of strings. Each row of `Y` represents the classification of the corresponding row of `X`.

For regression, `Y` is a numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

`Method`

Case-insensitive string consisting of one of the following.

- For classification with two classes:
  - `'AdaBoostM1'`
  - `'LogitBoost'`
  - `'GentleBoost'`
  - `'RobustBoost'` (requires an Optimization Toolbox license)
  - `'LPBoost'` (requires an Optimization Toolbox license)
  - `'TotalBoost'` (requires an Optimization Toolbox license)
  - `'RUSBoost'`
  - `'Subspace'`
  - `'Bag'`
- For classification with three or more classes:
  - `'AdaBoostM2'`
  - `'LPBoost'` (requires an Optimization Toolbox license)
  - `'TotalBoost'` (requires an Optimization Toolbox license)
  - `'RUSBoost'`
  - `'Subspace'`
  - `'Bag'`
- For regression:
  - `'LSBoost'`
  - `'Bag'`

`'Bag'` applies to all methods. So when you use `'Bag'`, indicate whether you want a classifier or regressor with the `type` name-value pair set to `'classification'` or `'regression'`.

`NLearn`

Number of ensemble learning cycles, a positive integer (or the string `'AllPredictorCombinations'`, see the next paragraph). At every training cycle, `fitensemble` loops over all learner templates in `Learners` and trains one weak learner for every template. The total number of trained learners in Ensemble is `NLearn*numel(Learners)`.

If you set `Method` to `'Subspace'`, you can set `NLearn` to `'AllPredictorCombinations'`. With this setting, `fitensemble` constructs learners for all possible combinations of predictors taken `NPredToSample` at a time. This gives a total of `nchoosek(size(X,2),NPredToSample)` learners in the ensemble. You can use only one learner template for this setting.

`NLearn` for ensembles can vary from a few dozen to a few thousand. Usually, an ensemble with a good predictive power needs from a few hundred to a few thousand weak learners. You do not have to train an ensemble for that many cycles at once. You can start by growing a few dozen learners, inspect the ensemble performance and, if necessary, train more weak learners using the `resume` method of the ensemble.

`Learners`

One of the following:

- A string with the name of a weak learner:
  - `'Discriminant'` recommended for `'Subspace'`)
  - `'KNN'` (applies only to `'Subspace'`)
  - `'Tree'` (applies to all methods except `'Subspace'`)
- A single weak learner template you create with `templateTree`, `templateKNN`, or `templateDiscriminant`.
- A cell array of weak learner templates. Usually you should supply only one weak learner template.

Ensemble performance depends on the parameters of the weak learners, and you can get poor performance using weak learners with default parameters. Specify the parameters for the weak learners in the template. Specify parameters for the ensemble in the `fitensemble` name-value pairs.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

All Ensembles

`'CategoricalPredictors'`

List of categorical predictors. Pass `CategoricalPredictors` as one of:

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of `X` is a categorical variable.
- `'All'`, meaning all predictors are categorical.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in the `PredictorNames` property.
- A character matrix, where each row of the matrix is the name of a predictor variable. The names must match entries in the `PredictorNames` property. Pad the names with extra blanks so each row of the character matrix has the same length.

You can set `CategoricalPredictors` for these learners:

- `'Tree'`
- `'KNN'`, when all predictors are categorical

Default: `[ ]`

`'CrossVal'`

If `'On'`, grows a cross-validated learner with 10 folds. You can use `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` parameters to override this cross-validation setting. You can only use one of these four parameters (`'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`) at a time when creating a cross-validated learner.

Default: `'Off'`

`'CVPartition'`

Partition created with `cvpartition` to use in a cross-validated learner. You can only use one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'FResample'`

Fraction of the training set to be selected by resampling for every weak learner. A numeric scalar from `0` through `1`. This parameter has no effect unless you grow an

ensemble by bagging or set `'Resample'` to `'on'`. The default setting is the one used most often for an ensemble grown by resampling.

Default: `1`

`'Holdout'`

Holdout validation tests the specified fraction of the data, and uses the remaining data for training. Specify a numeric scalar from `0` to `1`. You can only use one of these four options at a time for creating a cross-validated learner: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'KFold'`

Number of folds to use in a cross-validated learner, a positive integer. You can only use one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Default: `10`

`'Leaveout'`

Use leave-one-out cross validation by setting to `'on'`. You can only use one of these four options at a time: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`'NPredToSample'`

Number of predictors in each random subspace learner, a positive integer from `1` to `size(X,2)`.

Default: `1`

`'NPrint'`

Printout frequency, a positive integer scalar. Set to `'Off'` for no printout. Use this parameter to track how many weak learners have been trained so far. This is useful when you train ensembles with many learners on large data sets. If you use one of the cross-validation options, this parameter defines the printout frequency per number of cross-validation folds.

Default: `'Off'`

'PredictorNames'

Cell array of names for the predictor variables, in the order in which they appear in X.

Default: {'x1','x2',...}

'Replace'

'On' or 'Off'. If 'On', sample with replacement. If 'Off', sample without replacement. This parameter has no effect unless you grow an ensemble by bagging or set Resample to 'On'. If you set Resample to 'On' and Replace to 'Off', fitensemble samples training observations assuming uniform weights, and boosts by reweighting observations.

Default: 'On'

'Resample'

'On' or 'Off'. If 'On', grow an ensemble by resampling, with the resampling fraction given by FResample, and sampling with or without replacement given by Replace.

- Boosting — When 'Off', the boosting algorithm reweights observations at every learning iteration. When 'On', the algorithm samples training observations using updated weights as the multinomial sampling probabilities.
- Bagging — You can use only the default value of this parameter ('On').

Default: 'Off' for boosting, 'On' for bagging

'ResponseName'

Name of the response variable Y, a string.

Default: 'Y'

'Type'

String, either 'Classification' or 'Regression'. Specify Type when the Method is 'Bag'.

'Weights'

Vector of observation weights. The length of Weights is the number of rows in X.

Default: `ones(size(X,1),1)`

Classification Ensembles

`'ClassNames'`

Array of class names. Specify a data type the same as exists in `Y`.

Use `ClassNames` to order the classes or to select a subset of classes for training.

Default: Class names that exist in `Y`

`'Cost'`

Square matrix `C`, where `C(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.

Alternatively, `cost` can be a structure `S` having two fields:

- `S.ClassNames` containing the group names as a categorical variable, character array, or cell array of strings
- `S.ClassificationCosts` containing the cost matrix `C`

If `Method` is `Bag`, `Type` is `Classification`, and `Cost` is highly skewed, then, for in-bag samples, the software oversamples unique observations from the class that has a large penalty. For smaller sample sizes, this might cause a very low relative frequency of out-of-bag observations from the class that has a large penalty. Therefore, the estimated out-of-bag error is highly variable, and might be difficult to interpret.

Default: `C(i,j) = 1` if `i ~= j`, and `C(i,j) = 0` if `i = j`

`'Prior'`

Prior probabilities for each class. Specify as one of:

- A string:
  - `'Empirical'` determines class probabilities from class frequencies in `Y`. If you pass observation weights, they are used to compute the class probabilities.
  - `'Uniform'` sets all class probabilities equal.

- A vector (one scalar value for each class). To specify the class order for the corresponding elements of `Prior`, additionally specify the ClassNames name-value pair argument.
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a categorical variable, character array, or cell array of strings
  - `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `Weights` and `Prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

If `Method` is `Bag`, `Type` is `Classification`, and `Prior` is highly skewed, then, for in-bag samples, the software oversamples unique observations from the class that has a large prior probability. For smaller sample sizes, this might cause a very low relative frequency of out-of-bag observations from the class that has a large prior probability. Therefore, the estimated out-of-bag error is highly variable, and might be difficult to interpret.

Default: `'Empirical'`

AdaBoostM1, AdaBoostM2, LogitBoost, GentleBoost, RUSBoost, and LSBoost

`'LearnRate'`

Learning rate for shrinkage, a numeric scalar from `0` to `1`. If you set the learning rate to less than `1`, the ensemble requires more learning iterations but often achieves a better accuracy. `0.1` is a popular choice for an ensemble grown with shrinkage.

Default: `1`

RUSBoost

`'RatioToSmallest'`

Either a numeric scalar or vector with `K` elements when there are `K` classes. Every element of this vector is the sampling proportion for this class with respect to the class

with fewest observations in Y. If you pass a scalar, the software uses this sampling proportion for all classes. For example, suppose you have class A with 100 observations and class B with 10 observations. If you pass [2 1] for 'RatioToSmallest', every learner in the ensemble is trained on 20 observations of class A and 10 observations of class B. If you pass 2 or [2 2], every learner is trained on 20 observations of class A and 20 observations of class B. If you specify class names by using the ClassNames name-value pair argument of the fitting function, then the software matches elements in the array of class names to elements in this vector.

Default: ones(K,1)

LPBoost and TotalBoost

'MarginPrecision'

Margin precision, a numeric scalar between 0 and 1. MarginPrecision affects the number of boosting iterations required for conversion. Use a small value to grow an ensemble with many learners, and use a large value to grow an ensemble with few learners.

Default: 0.01

RobustBoost

'RobustErrorGoal'

Target classification error for RobustBoost, a numeric scalar from 0 through 1. Usually there is an optimal range for this parameter for your training data. If you set the error goal too low or too high, RobustBoost can produce a model with poor classification accuracy.

Default: 0.1

'RobustMarginSigma'

Spread of the distribution of classification margins over the training set for RobustBoost, a numeric positive scalar. You should consult literature on RobustBoost before setting this parameter

Default: `0.1`

`'RobustMaxMargin'`

Maximal classification margin for `RobustBoost` in the training set, a nonnegative numeric scalar. `RobustBoost` minimizes the number of observations in the training set with classification margins below `RobustMaxMargin`.

Default: `0`

Output Arguments

`Ensemble`

Ensemble object for predicting characteristics. The class of Ensemble depends on settings. In the following table, cross-validation names are `CrossVal`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Settings	Class
`Resample` name-value pair is `'Off'`, and you don't set a cross-validation name-value pair argument.	`ClassificationEnsemble`
`Resample` name-value pair is `'Off'`, and you don't set a cross-validation name-value pair argument.	`RegressionEnsemble`
`Resample` name-value pair is `'On'`, `type` is `'classification'`, and you don't set a cross-validation name-value pair argument.	`ClassificationBaggedEnsemble`
`Resample` name-value pair is `'On'`, `type` is `'regression'`, and you don't set a cross-validation name-value pair argument.	`RegressionBaggedEnsemble`
Method is a classification method, and you set a cross-validation name-value pair argument.	`ClassificationPartitionedEnsemble`
Method is a regression method, and you set a cross-validation name-value pair argument.	`RegressionPartitionedEnsemble`

Examples

Estimate the Resubstitution Loss of a Boosting Ensemble

Estimate the resubstitution loss of a trained, boosting classification ensemble of decision trees.

Load the `ionosphere` data set.

```
load ionosphere;
```

Train a decision tree ensemble using AdaBoost, 100 learning cycles, and the entire data set.

```
ClassTreeEns = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
```

`ClassTreeEns` is a trained `ClassificationEnsemble` ensemble classifier.

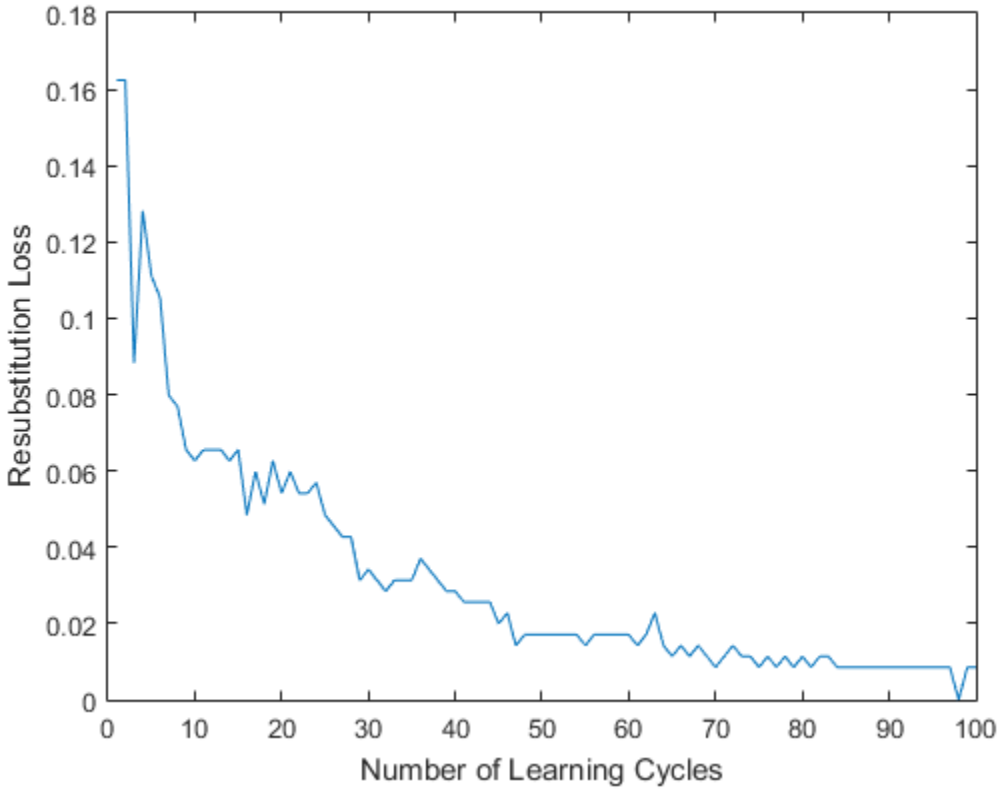
Determine the cumulative resubstitution losses (i.e., the cumulative misclassification error of the labels in the training data).

```
rsLoss = resubLoss(ClassTreeEns,'Mode','Cumulative');
```

`rsLoss` is a 100-by-1 vector, where element k contains the resubstition loss after the first k learning cycles.

Plot the cumulative resubstitution loss over the number of learning cycles.

```
plot(rsLoss);
xlabel('Number of Learning Cycles');
ylabel('Resubstitution Loss');
```



In general, as the number of decision trees in the trained classification ensemble increases, the resubstitution loss decreases.

A decrease in resubstitution loss might indicate that the software trained the ensemble sensibly. However, you cannot infer the predictive power of the ensemble by this decrease. To measure the predictive power of an ensemble, estimate the generalization error by:

1. Randomly partitioning the data into training and cross-validation sets. Do this by specifying `'holdout',holdoutProportion` when you train the ensemble using `fitensemble`.

2 Passing the trained ensemble to `kfoldLoss`, which estimates the generalization error.

Train a Regression Ensemble

Use a trained, boosted regression tree ensemble to predict the fuel economy of a car. Choose the number of cylinders, volume displaced by the cylinders, horsepower, and weight as predictors.

Load the `carsmall` data set. Set the predictors to `X`.

```
load carsmall
X = [Cylinders,Displacement,Horsepower,Weight];
xnames = {'Cylinders','Displacement','Horsepower','Weight'};
```

Specify a regression tree template that uses surrogate splits to impove predictive accuracy in the presence of `NaN` values.

```
RegTreeTemp = templateTree('Surrogate','On');
```

Train the regression tree ensemble using LSBoost and 100 learning cycles.

```
RegTreeEns = fitensemble(X,MPG,'LSBoost',100,RegTreeTemp,...
    'PredictorNames',xnames);
```

`RegTreeEns` is a trained `RegressionEnsemble` regression ensemble.

Use the trained regression ensemble to predict the fuel economy for a four-cylinder car with a 200-cubic inch displacement, 150 horsepower, and weighing 3000 lbs.

```
predMPG = predict(RegTreeEns,[4 200 150 3000])
```

```
predMPG =

   22.6290
```

The average fuel economy of a car with these specifications is 21.78 mpg.

Estimate the Generalization Error of a Boosting Ensemble

Estimate the generalization error of a trained, boosting classification ensemble of decision trees.

Load the `ionosphere` data set.

```
load ionosphere;
```

Train a decision tree ensemble using AdaBoostM1, 100 learning cycles, and half of the data chosen randomly. The software validates the algorithm using the remaining half.

```
rng(2); % For reproducibility
ClassTreeEns = fitensemble(X,Y,'AdaBoostM1',100,'Tree',...
    'Holdout',0.5);
```

`ClassTreeEns` is a trained `ClassificationEnsemble` ensemble classifier.

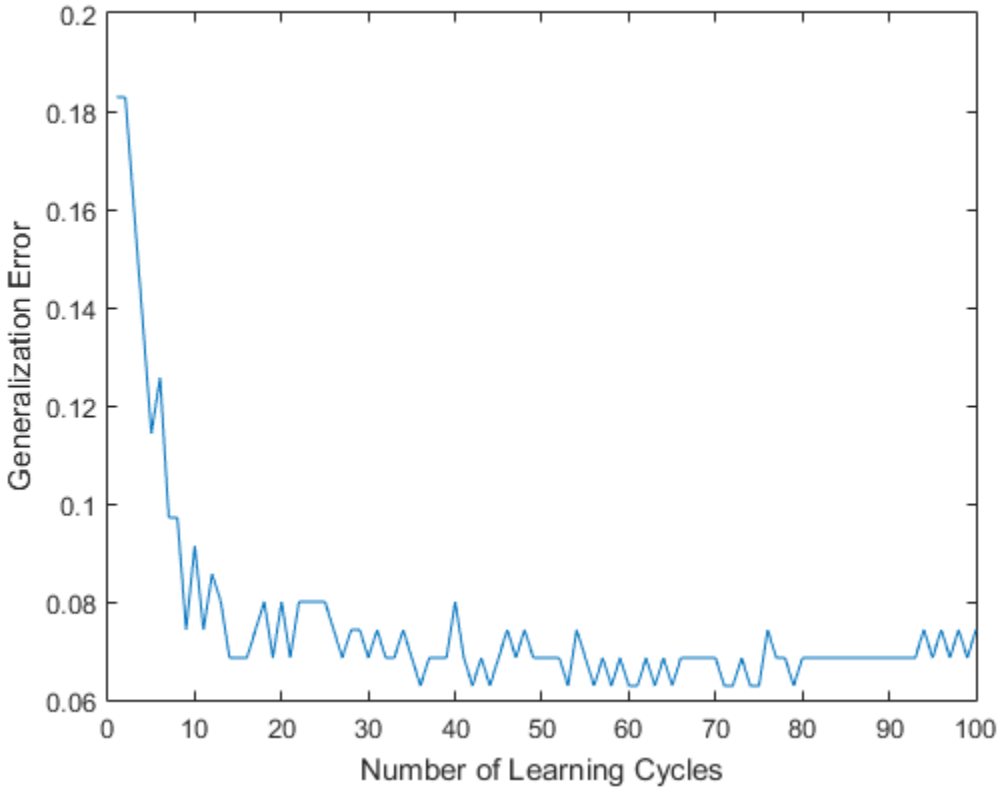
Determine the cumulative generalization error, i.e., the cumulative misclassification error of the labels in the validation data).

```
genError = kfoldLoss(ClassTreeEns,'Mode','Cumulative');
```

`genError` is a 100-by-1 vector, where element k contains the generalization error after the first k learning cycles.

Plot the generalization error over the number of learning cycles.

```
plot(genError);
xlabel('Number of Learning Cycles');
ylabel('Generalization Error');
```



The cumulative generalization error decreases to approximately 7% when 25 weak learners compose the ensemble classifier.

Find the Optimal Number of Splits and Trees for an Ensemble

You can control the depth of the trees in an ensemble of decision trees. You can also control the tree depth in an ECOC model containing decision tree binary learners using the `MaxNumSplits`, `MinLeafSize`, or `MinParentSize` name-value pair parameters.

- When bagging decision trees, `fitensemble` grows deep decision trees by default. You can grow shallower trees to reduce model complexity or computation time.
- When boosting decision trees, fitensemble grows stumps (a tree with one split) by default. You can grow deeper trees for better accuracy.

Load the `carsmall` data set. Specify the variables `Acceleration`, `Displacement`, `Horsepower`, and `Weight` as predictors, and `MPG` as the response.

```
load carsmall
X = [Acceleration Displacement Horsepower Weight];
Y = MPG;
```

The default values of the tree depth controllers for boosting regression trees are:

- `1` for `MaxNumSplits`. This option grows stumps.
- `5` for `MinLeafSize`
- `10` for `MinParentSize`

To search for the optimal number of splits:

1. Train a set of ensembles. Exponentially increase the maximum number of splits for subsequent ensembles from stump to at most n - 1 splits. Also, decrease the learning rate for each ensemble from 1 to 0.1.
2. Cross validate the ensembles.
3. Estimate the cross-validated mean-squared error (MSE) for each ensemble.
4. Compare the cross-validated MSEs. The ensemble with the lowest one performs the best, and indicates the optimal maximum number of splits, number of trees, and learning rate for the data set.

Grow and cross validate a deep classification tree and a stump. Specify to use surrogate splits because the data contain missing values. These serve as benchmarks.

```
MdlDeep = fitrtree(X,Y,'CrossVal','on','MergeLeaves','off',...
    'MinParentSize',1,'Surrogate','on');
MdlStump = fitrtree(X,Y,'MaxNumSplits',1,'CrossVal','on','Surrogate','on');
```

Train the boosting ensembles using 200 regression trees. Cross validate the ensemble using 10-fold cross validation. Vary the maximum number of splits using the values in the sequence $\{2^0, 2^1, ..., 2^m\}$, where m is such that 2^m is no greater than n - 1. For each variant, adjust the learning rate to each value in the set {0.1, 0.25, 0.5, 1};

```
n = size(X,1);
m = floor(log2(n - 1));
lr = [0.1 0.25 0.5 1];
maxNumSplits = 2.^(0:m);
```

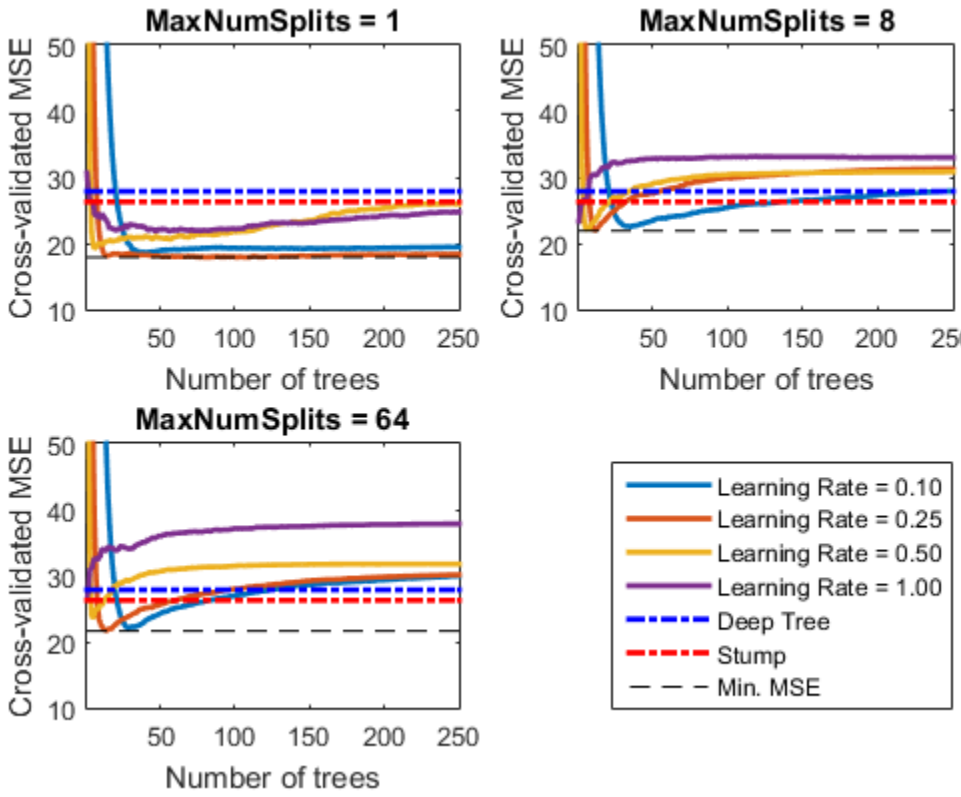
```
numTrees = 250;
Mdl = cell(numel(maxNumSplits),numel(lr));
rng(1); % For reproducibility
for k = 1:numel(lr);
    for j = 1:numel(maxNumSplits);
        t = templateTree('MaxNumSplits',maxNumSplits(j),'Surrogate','on');
        Mdl{j,k} = fitensemble(X,Y,'LSBoost',numTrees,t,...
            'Type','regression','CrossVal','on','LearnRate',lr(k));
    end;
end;
```

Compute the cross-validated MSE for each ensemble.

```
kflAll = @(x)kfoldLoss(x,'Mode','cumulative');
errorCell = cellfun(kflAll,Mdl,'Uniform',false);
error = reshape(cell2mat(errorCell),[numTrees numel(maxNumSplits) numel(lr)]);
errorDeep = kfoldLoss(MdlDeep);
errorStump = kfoldLoss(MdlStump);
```

Plot how the cross-validated classification error behaves as the number of trees in the ensemble increases for a few of the ensembles, the deep tree, and the stump. Plot the curves with respect to learning rate in the same plot, and plot separate plots for varying tree complexities. Choose a subset of tree complexity levels.

```
mnsPlot = [1 round(numel(maxNumSplits)/2) numel(maxNumSplits)];
figure;
for k = 1:3;
    subplot(2,2,k);
    plot(squeeze(error(:,mnsPlot(k),:)),'LineWidth',2);
    axis tight;
    hold on;
    h = gca;
    plot(h.XLim,[errorDeep errorDeep],'-.b','LineWidth',2);
    plot(h.XLim,[errorStump errorStump],'-.r','LineWidth',2);
    plot(h.XLim,min(min(error(:,mnsPlot(k),:))).*[1 1],'--k');
    h.YLim = [10 50];
    xlabel 'Number of trees';
    ylabel 'Cross-validated MSE';
    title(sprintf('MaxNumSplits = %0.3g', maxNumSplits(mnsPlot(k))));
    hold off;
end;
hL = legend([cellstr(num2str(lr','Learning Rate = %0.2f'));...
        'Deep Tree';'Stump';'Min. MSE']);
hL.Position(1) = 0.6;
```



Each curve contains a minimum cross-validated MSE occuring at the optimal number of trees in the ensemble.

Identify the maximum number of splits, number of trees, and learning rate that yields the lowest MSE overall.

```
[minErr minErrIdxLin] = min(error(:));
[idxNumTrees idxMNS idxLR] = ind2sub(size(error),minErrIdxLin);

fprintf('\nMin. MSE = %0.5f',minErr)
fprintf('\nOptimal Parameter Values:\nNum. Trees = %d',idxNumTrees);
fprintf('\nMaxNumSplits = %d\nLearning Rate = %0.2f\n',...
    maxNumSplits(idxMNS),lr(idxLR))
```

```
Min. MSE = 17.87423
Optimal Parameter Values:
Num. Trees = 79
MaxNumSplits = 1
Learning Rate = 0.25
```

More About

Tips

Avoid large estimated out-of-bag error variances by setting a more balanced misclassification cost matrix or a less skewed prior probability vector. This is particularly important if you train using a small sample size.

Algorithms

- For details of boosting and bagging algorithms, see “Ensemble Algorithms” on page 16-155.
- `fitensemble` generates in-bag samples by oversampling classes with large misclassification costs and undersampling classes with small misclassification costs. Consequently, out-of-bag samples have fewer observations from classes with large misclassification costs and more observations from classes with small misclassification costs. If you train a classification ensemble using a small data set and a highly skewed cost matrix, then the number of out-of-bag observations per class might be very low. Therefore, the estimated out-of-bag error might have a large variance and might be difficult to interpret. The same phenomenon can occur for classes with large prior probabilities.
- For ensembles of decision trees, and for dual-core systems and above, `fitensemble` parallelizes training using Intel Threading Building Blocks (TBB). For details on Intel TBB, see https://software.intel.com/en-us/intel-tbb.

- “Supervised Learning Workflow and Algorithms” on page 16-2
- “Ensemble Methods” on page 16-68

See Also

`RegressionEnsemble` | `RegressionBaggedEnsemble` | `ClassificationPartitionedEnsemble` | `RegressionPartitionedEnsemble`

```
| ClassificationEnsemble | ClassificationBaggedEnsemble |
templateDiscriminant | templateKNN | templateTree
```

fitnlm

Fit nonlinear regression model

Syntax

```
mdl = fitnlm(tbl,modelfun,beta0)
mdl = fitnlm(X,y,modelfun,beta0)
mdl = fitnlm(___,modelfun,beta0,Name,Value)
```

Description

`mdl = fitnlm(tbl,modelfun,beta0)` fits the model specified by `modelfun` to variables in the table or dataset array `tbl`, and returns the nonlinear model `mdl`.

`fitnlm` estimates model coefficients using an iterative procedure starting from the initial values in `beta0`.

`mdl = fitnlm(X,y,modelfun,beta0)` fits a nonlinear regression model using the column vector `y` as a response variable and the columns of the matrix `X` as predictor variables.

`mdl = fitnlm(___,modelfun,beta0,Name,Value)` fits a nonlinear regression model with additional options specified by one or more Name,Value pair arguments.

Examples

Nonlinear Model from a Table

Create a nonlinear model for auto mileage based on the `carbig` data.

Load the data and create a nonlinear model.

```
load carbig
tbl = table(Horsepower,Weight,MPG);
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
mdl = fitnlm(tbl,modelfun,beta0)
```

```
mdl =


Nonlinear regression model:
    MPG ~ b1 + b2*Horsepower^b3 + b4*Weight^b5

Estimated Coefficients:
          Estimate      SE        tStat       pValue
          ________    _______    ________    ________

    b1      -49.383     119.97    -0.41164     0.68083
    b2       376.43     567.05     0.66384     0.50719
    b3    -0.78193    0.47168     -1.6578    0.098177
    b4       422.37     776.02     0.54428     0.58656
    b5    -0.24127    0.48325    -0.49926     0.61788


Number of observations: 392, Error degrees of freedom: 387
Root Mean Squared Error: 3.96
R-Squared: 0.745,  Adjusted R-Squared 0.743
F-statistic vs. constant model: 283, p-value = 1.79e-113
```

Nonlinear Model from Matrix Data

Create a nonlinear model for auto mileage based on the `carbig` data.

Load the data and create a nonlinear model.

```
load carbig
X = [Horsepower,Weight];
y = MPG;
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
mdl = fitnlm(X,y,modelfun,beta0)

mdl =


Nonlinear regression model:
    y ~ b1 + b2*x1^b3 + b4*x2^b5

Estimated Coefficients:
          Estimate    SE         tStat       pValue
    b1      -49.383     119.97    -0.41164     0.68083
```

```
    b2      376.43      567.05      0.66384      0.50719
    b3    -0.78193     0.47168      -1.6578     0.098177
    b4      422.37      776.02      0.54428      0.58656
    b5    -0.24127     0.48325     -0.49926      0.61788


Number of observations: 392, Error degrees of freedom: 387
Root Mean Squared Error: 3.96
R-Squared: 0.745,  Adjusted R-Squared 0.743
F-statistic vs. constant model: 283, p-value = 1.79e-113
```

Adjust Fitting Options in the Nonlinear Model

Create a nonlinear model for auto mileage based on the `carbig` data. Strive for more accuracy by lowering the `TolFun` option, and observe the iterations by setting the `Display` option.

Load the data and create a nonlinear model.

```
load carbig
X = [Horsepower,Weight];
y = MPG;
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
```

Create options to lower `TolFun` and to report iterative display, and create a model using the options.

```
opts = statset('Display','iter','TolFun',1e-10);
mdl = fitnlm(X,y,modelfun,beta0,'Options',opts);
```

```
                                 Norm of         Norm of
   Iteration            SSE      Gradient           Step
  ----------------------------------------------------------
           0     1.82248e+06
           1          678600          788810        1691.07
           2          616716     6.12739e+06        45.4738

%%%     Many iterations deleted   %%%

         122         6068.48         1.56393       0.629325
         123         6068.48         1.13809       0.432543
         124         6068.48        0.295962       0.297511
Iterations terminated: relative change in SSE less than OPTIONS.TolFun
```

Specify Nonlinear Regression Using Model String Syntax

Specify a nonlinear regression model for estimation using a function handle or model string syntax.

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Use a function handle to specify the Hougen-Watson model for the rate data.

```
mdl = fitnlm(X,y,@hougen,beta0)
```

```
mdl =


Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1      1.2526     0.86701    1.4447    0.18654
    b2    0.062776    0.043561    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075157    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.193
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 3.91e+03, p-value = 2.54e-13
```

Alternatively, you can use a string expression to specify the Hougen-Watson model for the rate data.

```
myfun = 'y~(b1*x2-x3/b5)/(1+b2*x1+b3*x2+b4*x3)';
mdl2 = fitnlm(X,y,myfun,beta0)
```

```
mdl2 =


Nonlinear regression model:
    y ~ (b1*x2 - x3/b5)/(1 + b2*x1 + b3*x2 + b4*x3)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
```

```
    b1      1.2526     0.86701    1.4447    0.18654
    b2    0.062776    0.043561    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075157    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.193
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 3.91e+03, p-value = 2.54e-13
```

Estimate Nonlinear Regression Using Robust Fitting Options

Generate sample data from the nonlinear regression model

$$y = b_1 + b_2 \exp\{-b_3 x\} + \varepsilon,$$

where b_1, b_2, and b_3 are coefficients, and the error term is normally distributed with mean 0 and standard deviation 0.5.

```
modelfun = @(b,x)(b(1)+b(2)*exp(-b(3)*x));

rng('default') % for reproducibility
b = [1;3;2];
x = exprnd(2,100,1);
y = modelfun(b,x) + normrnd(0,0.5,100,1);
```

Set robust fitting options.

```
opts = statset('nlinfit');
opts.RobustWgtFun = 'bisquare';
```

Fit the nonlinear model using the robust fitting options. Here, use a string expression to specify the model.

```
b0 = [2;2;2];
modelstr = 'y ~ b1 + b2*exp(-b3*x)';

mdl = fitnlm(x,y,modelstr,b0,'Options',opts)

mdl =
```

```
Nonlinear regression model (robust fit):
    y ~ b1 + b2*exp( - b3*x)

Estimated Coefficients:
          Estimate    SE         tStat     pValue
    b1    1.0218      0.07202    14.188    2.1344e-25
    b2    3.6619      0.25429    14.401     7.974e-26
    b3    2.9732      0.38496    7.7232    1.0346e-11


Number of observations: 100, Error degrees of freedom: 97
Root Mean Squared Error: 0.501
R-Squared: 0.807,  Adjusted R-Squared 0.803
F-statistic vs. constant model: 203, p-value = 2.34e-35
```

Fit Nonlinear Regression Model Using Weights Function Handle

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Specify a function handle for observation weights. The function accepts the model fitted values as input, and returns a vector of weights.

```
 a = 1; b = 1;
 weights = @(yhat) 1./((a + b*abs(yhat)).^2);
```

Fit the Hougen-Watson model to the rate data using the specified observation weights function.

```
mdl = fitnlm(X,y,@hougen,beta0,'Weights',weights)

mdl =


Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1     0.83085     0.58224     1.427    0.19142
    b2     0.04095    0.029663    1.3805    0.20477
```

```
    b3    0.025063    0.019673     1.274    0.23842
    b4    0.080053    0.057812    1.3847    0.20353
    b5      1.8261       1.281    1.4256    0.19183


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 0.037
R-Squared: 0.998,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 1.14e+03, p-value = 3.49e-11
```

Nonlinear Regression Model Using Nonconstant Error Model

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Fit the Hougen-Watson model to the rate data using the combined error variance model.

```
mdl = fitnlm(X,y,@hougen,beta0,'ErrorModel','combined')
```

```
mdl =


Nonlinear regression model:
    y ~ hougen(b,X)

Estimated Coefficients:
          Estimate    SE          tStat     pValue
    b1      1.2526     0.86702    1.4447    0.18654
    b2    0.062776    0.043561    1.4411    0.18753
    b3    0.040048    0.030885    1.2967    0.23089
    b4     0.11242    0.075158    1.4957    0.17309
    b5      1.1914     0.83671    1.4239     0.1923


Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 1.27
R-Squared: 0.999,  Adjusted R-Squared 0.998
F-statistic vs. zero model: 3.91e+03, p-value = 2.54e-13
```

- “Examine Quality and Adjust the Fitted Nonlinear Model” on page 11-7
- “Predict or Simulate Responses Using a Nonlinear Model” on page 11-10

- "Nonlinear Regression Workflow" on page 11-14

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. If you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables and response variable must be numeric.

You specify the response and predictor names in your model string. If you do not provide a model string, you can set a different column as the response variable by using the ResponseVar name-value pair argument. You can select a subset of the columns as predictors by using the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelfun` — Functional form of the model

function handle | string of the form `'y ~ f(b1,b2,...,bj,x1,x2,...,xk)'`

Functional form of the model, specified as either of the following.

- Function handle `@modelfun` or `@(b,x)modelfun`, where

- `b` is a coefficient vector with the same number of elements as `beta0`.
- `x` is a matrix with the same number of columns as `X` or the number of predictor variable columns of `tbl`.

`modelfun(b,x)` returns a column vector that contains the same number of rows as `x`. Each row of the vector is the result of evaluating `modelfun` on the corresponding row of `x`. In other words, `modelfun` is a vectorized function, one that operates on all data rows and returns all evaluations in one function call. `modelfun` should return real numbers to obtain meaningful coefficients.

- String of the form `'y ~ f(b1,b2,...,bj,x1,x2,...,xk)'`, where `f` represents a scalar function of the scalar coefficient variables `b1`,...,`bj` and the scalar data variables `x1`,...,`xk`.

`beta0` — Coefficients

numeric vector

Coefficients for the nonlinear model, specified as a numeric vector. `NonLinearModel` starts its search for optimal coefficients from `beta0`.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'ErrorModel','combined','Exclude',2,'Options',opt` specifies the error model as the combined model, excludes the second observation from the fit, and uses the options defined in the structure `opt` to control the iterative fitting procedure.

`'CoefficientNames'` — Names of the model coefficients

`{'b1','b2',...,'bk'}` (default) | cell array of strings

Names of the model coefficients, specified as a cell array of strings.

Data Types: `char`

`'ErrorModel'` — Form of the error variance model

`'constant'` (default) | `'proportional'` | `'combined'`

Form of the error variance model, specified as one of the following. Each model defines the error using a standard mean-zero and unit-variance variable e in combination with independent components: the function value f, and one or two parameters a and b

`'constant'` (default)	$y = f + ae$
`'proportional'`	$y = f + bfe$
`'combined'`	$y = f + \left(a + b\left\|f\right\|\right)e$

The only allowed error model when using Weights is `'constant'`.

Note: `options.RobustWgtFun` must have value `[]` when using an error model other than `'constant'`.

Example: `'ErrorModel','proportional'`

`'ErrorParameters'` — Initial estimates of the error model parameters

numeric array

Initial estimates of the error model parameters for the chosen ErrorModel, specified as a numeric array.

Error Model	Parameters	Default Values
`'constant'`	a	`1`
`'proportional'`	b	`1`
`'combined'`	a, b	`[1,1]`

You can only use the `'constant'` error model when using Weights.

Note: `options.RobustWgtFun` must have value `[]` when using an error model other than `'constant'`.

For example, if `'ErrorModel'` has the value `'combined'`, you can specify the starting value 1 for a and the starting value 2 for b as follows.

Example: `'ErrorParameters',[1,2]`

Data Types: `single` | `double`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Options'` — Options for controlling the iterative fitting procedure

[ ] (default) | structure

Options for controlling the iterative fitting procedure, specified as a structure created by `statset`. The relevant fields are the nonempty fields in the structure returned by the call `statset('fitnlm')`.

Option	Meaning	Default
`DerivStep`	Relative difference used in finite difference derivative calculations. A positive scalar, or a vector of positive scalars the same size as the vector of parameters estimated by the Statistics and Machine Learning Toolbox function using the options structure.	`eps^(1/3)`
`Display`	Amount of information displayed by the fitting algorithm. • `'off'` — Displays no information. • `'final'` — Displays the final output. • `'iter'` — Displays iterative output to the Command Window.	`'off'`
`FunValCheck`	String indicating to check for invalid values, such as `NaN` or `Inf`, from the model function.	`'on'`

Option	Meaning	Default
`MaxIter`	Maximum number of iterations allowed. Positive integer.	`200`
`RobustWgtFun`	Weight function for robust fitting. Can also be a function handle that accepts a normalized residual as input and returns the robust weights as output. If you use a function handle, give a `Tune` constant. See “Robust Options” on page 22-1820	`[]`
`Tune`	Tuning constant used in robust fitting to normalize the residuals before applying the weight function. A positive scalar. Required if the weight function is specified as a function handle.	See “Robust Options” on page 22-1820 for the default, which depends on `RobustWgtFun`.
`TolFun`	Termination tolerance for the objective function value. Positive scalar.	`1e-8`
`TolX`	Termination tolerance for the parameters. Positive scalar.	`1e-8`

Data Types: `struct`

`'PredictorVars'` — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

`'ResponseVar'` — Response variable

last column of `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset array `tbl`, or a logical or numeric index vector indicating which column is the response variable.

If you supply a model string, it specifies the response variable. Otherwise, when fitting a table or dataset array, `'ResponseVar'` indicates which variable `fitnlm` should use as the response.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

`'VarNames'` — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights

`ones(n,1)` (default) | vector of nonnegative scalar values | function handle

Observation weights, specified as a vector of nonnegative scalar values or function handle.

- If you specify a vector, then it must have n elements, where n is the number of rows in `tbl` or `y`.
- If you specify a function handle, then the function must accept a vector of predicted response values as input, and return a vector of real positive weights as output.

Given weights, `W`, `NonLinearModel` estimates the error variance at observation `i` by `MSE*(1/W(i))`, where MSE is the mean squared error.

Data Types: `single` | `double` | `function_handle`

Output Arguments

`mdl` — Nonlinear model

`NonLinearModel` object

Nonlinear model representing a least-squares fit of the response to the data, returned as a `NonLinearModel` object.

If the `Options` structure contains a nonempty `RobustWgtFun` field, the model is not a least-squares fit, but uses the `RobustWgtFun` robust fitting function.

For properties and methods of the nonlinear model object, `mdl`, see the `NonLinearModel` class page.

More About

Robust Options

Weight Function	Equation	Default Tuning Constant
`'andrews'`	`w = (abs(r)<pi) .* sin(r) ./ r`	1.339
`'bisquare'` (default)	`w = (abs(r)<1) .* (1 - r.^2).^2`	4.685
`'cauchy'`	`w = 1 ./ (1 + r.^2)`	2.385

Weight Function	Equation	Default Tuning Constant
`'fair'`	`w = 1 ./ (1 + abs(r))`	1.400
`'huber'`	`w = 1 ./ max(1, abs(r))`	1.345
`'logistic'`	`w = tanh(r) ./ r`	1.205
`'talwar'`	`w = 1 * (abs(r)<1)`	2.795
`'welsch'`	`w = exp(-(r.^2))`	2.985
`[]`	No robust fitting	—

Algorithms

`fitnlm` uses the same fitting algorithm as `nlinfit`.

- "Nonlinear Regression" on page 11-2

References

[1] Seber, G. A. F., and C. J. Wild. *Nonlinear Regression*. Hoboken, NJ: Wiley-Interscience, 2003.

[2] DuMouchel, W. H., and F. L. O'Brien. "Integrating a Robust Option into a Multiple Regression Computing Environment." *Computer Science and Statistics: Proceedings of the 21st Symposium on the Interface*. Alexandria, VA: American Statistical Association, 1989.

[3] Holland, P. W., and R. E. Welsch. "Robust Regression Using Iteratively Reweighted Least-Squares." *Communications in Statistics: Theory and Methods*, *A6*, 1977, pp. 813–827.

See Also

`nlinfit` | `NonLinearModel`

LinearMixedModel.fitmatrix

Class: LinearMixedModel

Fit linear mixed-effects model using design matrices

Compatibility

`LinearMixedModel.fitmatrix` will be removed in a future release. Use `fitlmematrix` instead.

Syntax

```
lme = LinearMixedModel.fitmatrix(X,y,Z,[])
lme = LinearMixedModel.fitmatrix(X,y,Z,G)
lme = LinearMixedModel.fitmatrix(___,Name,Value)
```

Description

`lme = LinearMixedModel.fitmatrix(X,y,Z,[])` creates a linear mixed-effects model of the responses y using the fixed-effects design matrix `X` and random-effects design matrix or matrices in Z.

`[]` implies that there is one group. That is, the grouping variable G is `ones(n,1)`, where n is the number of observations. Using `LinearMixedModel.fitmatrix(X,Y,Z,[])` without a specified covariance pattern most likely will result in a non-identifiable model. This syntax is recommended only if you build the grouping information into the random effects design `Z` and specify a covariance pattern for the random effects using `'CovariancePattern'` name-value pair argument.

`lme = LinearMixedModel.fitmatrix(X,y,Z,G)` creates a linear mixed-effects model of the responses y using the fixed-effects design matrix `X` and random-effects design matrix Z or matrices in `Z`, and the grouping variable or variables in `G`.

`lme = LinearMixedModel.fitmatrix(___,Name,Value)` also creates a linear mixed-effects model with additional options specified by one or more Name,Value pair arguments, using any of the previous input arguments.

For example, you can specify the names of the response, predictor, and grouping variables. You can also specify the covariance pattern, fitting method, or the optimization algorithm.

Tips

- If your model is not easily described using a formula, you can create matrices to define the fixed and random effects, and fit the model using `fitlmematrix`.

Input Arguments

X — Fixed-effects design matrix

n-by-*p* matrix

Fixed-effects design matrix, specified as an *n*-by-*p* matrix, where *n* is the number of observations, and *p* is the number of fixed-effects predictor variables. Each row of `X` corresponds to one observation, and each column of `X` corresponds to one variable.

Data Types: `single | double`

y — Response values

n-by-1 vector

Response values, specified as an *n*-by-1 vector, where *n* is the number of observations.

Data Types: `single | double`

Z — Random-effects design

n-by-*q* matrix | cell array of *R* *n*-by-*q*(*r*) matrices, *r* = 1, 2, ..., *R*

Random-effects design, specified as either of the following.

- If there is one random-effects term in the model, then `Z` must be an *n*-by-*q* matrix, where *n* is the number of observations and *q* is the number of variables in the random-effects term.
- If there are *R* random-effects terms, then `Z` must be a cell array of length *R*. Each cell of `Z` contains an *n*-by-*q*(*r*) design matrix `Z{r}`, *r* = 1, 2, ..., *R*, corresponding to each random-effects term. Here, *q*(*r*) is the number of random effects term in the *r*th random effects design matrix, `Z{r}`.

Data Types: `single` | `double` | `cell`

`G` — Grouping variable or variables

n-by-1 vector | cell array of *R* *n*-by-1 vectors

Grouping variable or variables, specified as either of the following.

- If there is one random-effects term, then `G` must be an *n*-by-1 vector corresponding to a single grouping variable with *M* levels or groups.

  `G` can be a categorical vector, numeric vector, character array, or cell array of strings.
- If there are multiple random-effects terms, then `G` must be a cell array of length *R*. Each cell of `G` contains a grouping variable `G{r}`, *r* = 1, 2, ..., *R*, with *M*(*r*) levels.

  `G{r}` can be a categorical vector, numeric vector, character array, or cell array of strings.

Data Types: `single` | `double` | `char` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'FixedEffectPredictors'` — Names of columns in fixed-effects design matrix

`{'x1','x2',...,'xP'}` (default) | cell array of length *p*

Names of columns in the fixed-effects design matrix `X`, specified as the comma-separated pair consisting of `'FixedEffectPredictors'` and a cell array of length *p*.

For example, if you have a constant term and two predictors, say `TimeSpent` and `Gender`, where `Female` is the reference level for `Gender`, as the fixed effects, then you can specify the names of your fixed effects in the following way. `Gender_Male` represents the dummy variable you must create for category `Male`. You can choose different names for these variables.

Example: `'FixedEffectPredictors',`
`{'Intercept','TimeSpent','Gender_Male'},`

Data Types: `cell`

'RandomEffectPredictors' — Names of columns in random-effects design matrix or cell array

cell array of length q | cell array of length R with elements of length $q(r)$, $r = 1, 2, ..., R$

Names of columns in the random-effects design matrix or cell array `Z`, specified as the comma-separated pair consisting of `'RandomEffectPredictors'` and either of the following:

- A cell array of length q when `Z` is an n-by-q design matrix. In this case, the default is `{'z1','z2',...,'zQ'}`.
- A cell array of length R, when `Z` is a cell array of length R with each element `Z{r}` of length $q(r)$, $r = 1, 2, ..., R$. In this case, the default is `{'z11','z12',...,'z1Q(1)'},...,{'zr1','zr2',...,'zrQ(r)'}`.

For example, suppose you have correlated random effects for intercept and a variable named `Acceleration`. Then, you can specify the random-effects predictor names as follows.

Example: `'RandomEffectPredictors',{'Intercept','Acceleration'}`

If you have two random effects terms, one for the intercept and the variable `Acceleration` grouped by variable `g1`, and the second for the intercept, grouped by the variable `g2`, then you specify the random-effects predictor names as follows.

Example: `'RandomEffectPredictors',{{'Intercept','Acceleration'}, {'Intercept'}}`

Data Types: `cell`

'ResponseVarName' — Name of response variable

`'y'` (default) | string

Name of response variable, specified as the comma-separated pair consisting of `'ResponseVarName'` and a string.

For example, if your response variable name is `score`, then you can specify it as follows.

Example: `'ResponseVarName','score'`

Data Types: `char`

'RandomEffectGroups' — Names of random effects grouping variables

`'g'` or `{'g1','g2',...,'gR'}` (default) | string | cell array of strings

Names of random effects grouping variables, specified as the comma-separated pair `'RandomEffectGroups'` and either of the following:

- String — If there is only one random-effects term, that is, if G is a vector, then the value of `'RandomEffectGroups'` is a string containing the name for the grouping variable `G`. The default is `'g'`.
- Cell array of strings — If there are multiple random-effects terms, that is, if `G` is a cell array of length R, then the value of `'RandomEffectGroups'` is a cell array of length R, where each cell contains the name for the grouping variable `G{r}`. The default is `{'g1','g2',...,'gR'}`.

For example, if you have two random-effects terms, `z1` and `z2`, grouped by the grouping variables `sex` and `subject`, then you can specify the names of your grouping variables as follows.

Example: `'RandomEffectGroups',{'sex','subject'}`

Data Types: `char` | `cell`

`'CovariancePattern'` — Pattern of covariance matrix

`'FullCholesky'` (default) | string | square symmetric logical matrix | cell array of strings or logical matrices

Pattern of the covariance matrix of the random effects, specified as the comma-separated pair consisting of `'CovariancePattern'` and a string, a square symmetric logical matrix, or a cell array of strings or logical matrices.

If there are R random-effects terms, then the value of `'CovariancePattern'` must be a cell array of length R, where each element r of this cell array specifies the pattern of the covariance matrix of the random-effects vector associated with the rth random-effects term. The options for each element follow.

`'FullCholesky'`	Default. Full covariance matrix using the Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.
`'Full'`	Full covariance matrix, using the log-Cholesky parameterization. `fitlme` estimates all elements of the covariance matrix.

`'Diagonal'`	Diagonal covariance matrix. That is, off-diagonal elements of the covariance matrix are constrained to be 0. $\begin{pmatrix} \sigma_{b1}^2 & 0 & 0 \\ 0 & \sigma_{b2}^2 & 0 \\ 0 & 0 & \sigma_{b3}^2 \end{pmatrix}$
`'Isotropic'`	Diagonal covariance matrix with equal variances. That is, off-diagonal elements of the covariance matrix are constrained to be 0, and the diagonal elements are constrained to be equal. For example, if there are three random-effects terms with an isotropic covariance structure, this covariance matrix looks like $\begin{pmatrix} \sigma_b^2 & 0 & 0 \\ 0 & \sigma_b^2 & 0 \\ 0 & 0 & \sigma_b^2 \end{pmatrix}$ where σ^2_b is the common variance of the random-effects terms.

`'CompSymm'`	Compound symmetry structure. That is, common variance along diagonals and equal correlation between all random effects. For example, if there are three random-effects terms with a covariance matrix having a compound symmetry structure, this covariance matrix looks like $$\begin{pmatrix} \sigma_{b1}^2 & \sigma_{b1,b2} & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1}^2 & \sigma_{b1,b2} \\ \sigma_{b1,b2} & \sigma_{b1,b2} & \sigma_{b1}^2 \end{pmatrix}$$ where σ^2_{b1} is the common variance of the random-effects terms and $\sigma_{b1,b2}$ is the common covariance between any two random-effects term .
`PAT`	Square symmetric logical matrix. If `'CovariancePattern'` is defined by the matrix `PAT`, and if `PAT(a,b) = false`, then the `(a,b)` element of the corresponding covariance matrix is constrained to be 0.

Example: `'CovariancePattern','Diagonal'`

Example: `'CovariancePattern',{'Full','Diagonal'}`

`'FitMethod'` — Method for estimating parameters

`'ML'` (default) | `'REML'`

Method for estimating parameters of the linear mixed-effects model, specified as the comma-separated pair consisting of `'FitMethod'` and either of the following.

`'ML'`	Default. Maximum likelihood estimation
`'REML'`	Restricted maximum likelihood estimation

Example: `'FitMethod','REML'`

'Weights' — Observation weights

vector of scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and a vector of length n, where n is the number of observations.

Data Types: single | double

'Exclude' — Indices for rows to exclude

use all rows without NaNs (default) | vector of integer or logical values

Indices for rows to exclude from the linear mixed-effects model in the data, specified as the comma-separated pair consisting of 'Exclude' and a vector of integer or logical values.

For example, you can exclude the 13th and 67th rows from the fit as follows.

Example: 'Exclude',[13,67]

Data Types: single | double | logical

'DummyVarCoding' — Coding to use for dummy variables

'reference' (default) | 'effects' | 'full'

Coding to use for dummy variables created from the categorical variables, specified as the comma-separated pair consisting of 'DummyVarCoding' and one of the following.

'reference'	Default. Coefficient for first category set to 0.
'effects'	Coefficients sum to 0.
'full'	One dummy variable for each category.

Example: 'DummyVarCoding','effects'

'Optimizer' — Optimization algorithm

'quasinewton' (default) | 'fminunc'

Optimization algorithm, specified as the comma-separated pair consisting of 'Optimizer' and either of the following.

'quasinewton'	Default. Uses a trust region based quasi-Newton optimizer. Change

	the options of the algorithm using `statset('LinearMixedModel')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `statset('LinearMixedModel')`.
`'fminunc'`	You must have Optimization Toolbox to specify this option. Change the options of the algorithm using `optimoptions('fminunc')`. If you don't specify the options, then `LinearMixedModel` uses the default options of `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.

Example: `'Optimizer','fminunc'`

`'OptimizerOptions'` — Options for optimization algorithm
structure returned by `statset` | object returned by `optimoptions`

Options for the optimization algorithm, specified as the comma-separated pair consisting of `'OptimizerOptions'` and a structure returned by `statset('LinearMixedModel')` or an object returned by `optimoptions('fminunc')`.

- If `'Optimizer'` is `'fminunc'`, then use `optimoptions('fminunc')` to change the options of the optimization algorithm. See `optimoptions` for the options `'fminunc'` uses. If `'Optimizer'` is `'fminunc'` and you do not supply `'OptimizerOptions'`, then the default for `LinearMixedModel` is the default options created by `optimoptions('fminunc')` with `'Algorithm'` set to `'quasi-newton'`.
- If `'Optimizer'` is `'quasinewton'`, then use `statset('LinearMixedModel')` to change the optimization parameters. If you don't change the optimization parameters, then `LinearMixedModel` uses the default options created by `statset('LinearMixedModel')`:

The `'quasinewton'` optimizer uses the following fields in the structure created by `statset('LinearMixedModel')`.

`'TolFun'` — Relative tolerance on gradient of objective function
`1e-6` (default) | positive scalar value

Relative tolerance on the gradient of the objective function, specified as a positive scalar value.

`'TolX'` — Absolute tolerance on step size
`1e-12` (default) | positive scalar value

Absolute tolerance on the step size, specified as a positive scalar value.

`'MaxIter'` — Maximum number of iterations allowed
`10000` (default) | positive scalar value

Maximum number of iterations allowed, specified as a positive scalar value.

`'Display'` — Level of display
`'off'` (default) | `'iter'` | `'final'`

Level of display, specified as one of `'off'`, `'iter'`, or `'final'`.

`'StartMethod'` — Method to start iterative optimization
`'default'` (default) | `'random'`

Method to start iterative optimization, specified as the comma-separated pair consisting of `'StartMethod'` and either of the following.

`'default'`	Default. An internally defined default value.
`'random'`	A random initial value.

Example: `'StartMethod','random'`

`'Verbose'` — Indicator to display optimization process on screen
`false` (default) | `true`

Indicator to display the optimization process on screen, specified as the comma-separated pair consisting of `'Verbose'` and either `false` or `true`. Default is `false`.

The setting for `'Verbose'` overrides the field `'Display'` in `'OptimizerOptions'`.

Example: `'Verbose',true`

`'CheckHessian'` — Indicator to check positive definiteness of Hessian
`false` (default) | `true`

Indicator to check the positive definiteness of the Hessian of the objective function with respect to unconstrained parameters at convergence, specified as the comma-separated pair consisting of `'CheckHessian'` and either `false` or `true`. Default is `false`.

Specify `'CheckHessian'` as `true` to verify optimality of the solution or to determine if the model is overparameterized in the number of covariance parameters.

Example: `'CheckHessian',true`

Output Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Examples

No Grouping Variable Specified

Load the sample data.

```
load carsmall
```

Fit a linear mixed-effects model, where MPG is the response, weight is the predictor variable, and the intercept varies by model year. First, define the design matrices. Then, fit the model using the specified design matrices.

```
y = MPG;
X = [ones(size(Weight)), Weight];
Z = ones(size(y));
lme = LinearMixedModel.fitmatrix(X,y,Z,Model_Year)
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             94
```

```
    Fixed effects coefficients           2
    Random effects coefficients          3
    Covariance parameters                2

Formula:
    y ~ x1 + x2 + (z11 | g1)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    486.09    496.26    -239.04          478.09

Fixed effects coefficients (95% CIs):
    Name        Estimate      SE           tStat      DF    pValue         Lower
    'x1'            43.575       2.3038     18.915    92    1.8371e-33           39
    'x2'        -0.0067097    0.0004242    -15.817    92    5.5373e-28    -0.0075522

Random effects covariance parameters (95% CIs):
Group: g1 (3 Levels)
    Name1        Name2        Type         Estimate    Lower     Upper
    'z11'        'z11'        'std'        3.301       1.4448    7.5421

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        2.8997      2.5075    3.3532
```

Now fit the same model by building the grouping into the Z matrix.

```
Z = double([Model_Year==70, Model_Year==76, Model_Year==82]);
lme = LinearMixedModel.fitmatrix(X,y,Z,[],...
'Covariancepattern','Isotropic')

lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             94
    Fixed effects coefficients          2
    Random effects coefficients         3
    Covariance parameters               2

Formula:
    y ~ x1 + x2 + (z11 + z12 + z13 | g1)
```

```
Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    486.09    496.26    -239.04          478.09

Fixed effects coefficients (95% CIs):
    Name        Estimate      SE           tStat      DF    pValue         Lower
    'x1'            43.575       2.3038     18.915    92    1.8371e-33            39
    'x2'        -0.0067097    0.0004242    -15.817    92    5.5373e-28    -0.0075522

Random effects covariance parameters (95% CIs):
Group: g1 (1 Levels)
    Name1        Name2        Type         Estimate    Lower     Upper
    'z11'        'z11'        'std'        3.301       1.4448    7.5421

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        2.8997      2.5075    3.3532
```

Longitudinal Study with Covariate

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned 4 exercise programs (A, B, C, D) and their weight loss is recorded over six two-week time periods. This is simulated data.

Define `Subject` and `Program` as categorical variables. Create the design matrices for a linear mixed-effects model, with the initial weight, type of program, week, and the interaction between the week and type of program as the fixed effects. The intercept and coefficient of week vary by subject.

This model corresponds to

$$\begin{aligned} y_{im} &= \beta_0 + \beta_1 IW_i + \beta_2 Week_i + \beta_3 I[PB]_i + \beta_4 I[PC]_i + \beta_5 I[PD]_i \\ &\quad + \beta_6 \left(Week_i * I[PB]_i \right) + \beta_7 \left(Week_i * I[PC]_i \right) + \beta_8 \left(Week_i * I[PD]_i \right) \\ &\quad + b_{0m} + b_{1m} Week_{im} + \varepsilon_{im}, \end{aligned}$$

where $i = 1, 2, ..., 120$, and $m = 1, 2, ..., 20$. β_j are the fixed-effects coefficients, $j = 0, 1, ...,8$, and b_{0m} and b_{1m} are random effects. *IW* stands for initial weight and I[.] is a dummy variable representing a type of program. For example, $I[PB]_i$ is the dummy variable representing program type B. The random effects and observation error have the following prior distributions: $b_{0m} \sim N(0,\sigma^2_0)$, $b_{1m} \sim N(0,\sigma^2_1)$, and $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
Subject = nominal(Subject);
Program = nominal(Program);
D = dummyvar(Program); % Create dummy variables for Program
X = [ones(120,1), InitialWeight, D(:,2:4), Week,...
   D(:,2).*Week, D(:,3).*Week, D(:,4).*Week];
Z = [ones(120,1), Week];
G = Subject;
```

Since the model has an intercept, you only need the dummy variables for programs B, C, and D. This is also known as the `'reference'` method of coding dummy variables.

Fit the model using `LinearMixedModel.fitmatrix` with the defined design matrices and grouping variables.

```
lme = LinearMixedModel.fitmatrix(X,y,Z,G,'FixedEffectPredictors',...
{'Intercept','InitWeight','PrgB','PrgC','PrgD','Week','Week_PrgB','Week_PrgC','Week_Prg
'RandomEffectPredictors',{{'Intercept','Week'}},'RandomEffectGroups',{'Subject'})
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           9
    Random effects coefficients         40
    Covariance parameters                4

Formula:
    Linear Mixed Formula with 10 predictors.

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -22.981    13.257    24.49            -48.981

Fixed effects coefficients (95% CIs):
    Name                Estimate     SE           tStat       DF     pValue       Lower
```

```
    'Intercept'          0.66105      0.25892      2.5531    111      0.012034       0
    'InitWeight'       0.0031879    0.0013814      2.3078    111      0.022863    0.000
    'PrgB'               0.36079      0.13139       2.746    111     0.0070394       0
    'PrgC'              -0.033263      0.13117    -0.25358    111       0.80029      -0
    'PrgD'               0.11317      0.13132     0.86175    111       0.39068      -0
    'Week'                0.1732     0.067454      2.5677    111      0.011567       0.0
    'Week_PrgB'          0.038771     0.095394     0.40644    111       0.68521      -0
    'Week_PrgC'          0.030543     0.095394     0.32018    111       0.74944      -0
    'Week_PrgD'          0.033114     0.095394     0.34713    111       0.72915      -0

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1              Name2              Type          Estimate    Lower      Upper
    'Intercept'        'Intercept'        'std'         0.18407     0.12281    0.27587
    'Week'             'Intercept'        'corr'        0.66841     0.21076    0.88573
    'Week'             'Week'             'std'         0.15033     0.11004    0.20537

Group: Error
    Name             Estimate    Lower       Upper
    'Res Std'        0.10261     0.087882    0.11981
```

The *p*-values 0.0228 and 0.0115 indicate significant effects of the initial weights of the subjects and the time factor in the amount of weight lost. The weight loss of subjects that are in program B is significantly different relative to the weight loss of subjects that are in program A. The lower and upper limits of the covariance parameters for the random effects do not include zero, thus they seem significant. You can also test the significance of the random-effects using the `compare` method.

Random-Intercept Model

Load the sample data.

```
load flu
```

`flu` dataset array has a `Date` variable, and 10 variables for estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the CDC).

To fit a linear-mixed effects model, where the influenza rates are the responses, combine the nine columns corresponding to the regions into a tall array that has a single response variable, `FluRate`, and a nominal variable, `Region`, the nationwide estimate `WtdILI`, that shows which region each estimate is from, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
```

```
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Define the design matrices for a random-intercept linear mixed-effects model, where the intercept varies by `Date`. The corresponding model is

$$y_{im} = \beta_0 + \beta_1 WtdILI_{im} + b_{0m} + \varepsilon_{im}, \quad i = 1,2,\ldots,468, \quad m = 1,2,\ldots,52,$$

where y_{im} is the observation i for level m of grouping variable `Date`. b_{0m} is the random effect for level m of the grouping variable `Date` and ε_{im} is the observation error for observation i. The random effect has the prior distribution, $b_{0m} \sim N(0,\sigma^2_{FR})$ and the error term has the distribution, $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
y = flu2.FluRate;
X = [ones(468,1) flu2.WtdILI];
Z = [ones(468,1)];
G = flu2.Date;
```

Fit the linear mixed-effects model.

```
lme = LinearMixedModel.fitmatrix(X,y,Z,G,'FixedEffectPredictors',{'Intercept','National
'RandomEffectPredictors',{{'Intercept'}},'RandomEffectGroups',{'Date'})
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             468
    Fixed effects coefficients           2
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    y ~ Intercept + NationalRate + (Intercept | Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    286.24    302.83    -139.12          278.24

Fixed effects coefficients (95% CIs):
    Name                  Estimate    SE          tStat     DF     pValue        Lower
```

```
    'Intercept'           0.16385     0.057525    2.8484    466     0.0045885    0.0508
    'NationalRate'         0.7236     0.032219    22.459    466    3.0502e-76     0.660

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1              Name2              Type         Estimate    Lower      Upper
    'Intercept'        'Intercept'        'std'        0.17146     0.13227    0.22226

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.30201     0.28217    0.32324
```

The confidence limits of the standard deviation of the random-effects term $\sigma^2_{b_{0m}}$, do not include zero (0.13227, 0.22226), which indicates that the random-effects term is significant. You can also test the significance of the random-effects using `compare` method.

The estimated value of an observation is the sum of the fixed-effects values and value of the random effect at the grouping variable level corresponding to that observation. For example, the estimated flu rate for observation 28

$$\begin{aligned}\hat{y}_{28} &= \hat{\beta}_0 + \hat{\beta}_1 WtdILI_{28} + \hat{b}_{10/30/2005} \\ &= 0.1639 + 0.7236 * (1.343) + 0.3318 \\ &= 1.46749,\end{aligned}$$

where $\hat{b}$ is the BLUP of the random effects for the intercept. You can compute this value in the following way.

```
beta = fixedEffects(lme);
[~,~,STATS] = randomEffects(lme); % compute the random effects statistics STATS
STATS.Level = nominal(STATS.Level);
y_hat = beta(1) + beta(2)*flu2.WtdILI(28) + STATS.Estimate(STATS.Level=='10/30/2005')

y_hat =

    1.4674
```

You can simply display the fitted value using the `fitted(lme)` method.

```
F = fitted(lme);
F(28)
```

```
ans =

    1.4674
```

Randomized-Block Design

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data set shows the deviations from the target quality characteristic measured from the products each of five operators manufacture over three different shifts, morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the deviations of the quality characteristics from the target value. This is simulated data.

Define the design matrices for a linear mixed-effects model with a random intercept grouped by operator, and shift as the fixed effects. Use the `'effects'` contrasts. `'effects'` contrasts mean that the coefficients sum to zero. You need to create two contrast coded variables in the fixed-effects design matrix, $X1$ and $X2$, where

$$Shift\_Evening = \begin{cases} 0, & if\ Morning \\ 1, & if\ Evening \\ -1, & if\ Night \end{cases} \quad and \quad Shift\_Morning = \begin{cases} 1, & if\ Morning \\ 0, & if\ Evening \\ -1, & if\ Night \end{cases}.$$

The model corresponds to

$$\begin{aligned} &\text{Morning Shift: } QCDev_{im} = \beta_0 + \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \quad m = 1,2,\ldots,5, \\ &\text{Evening Shift: } QCDev_{im} = \beta_0 + \beta_1 Shift\_Evening_i + b_{0m} + \varepsilon_{im}, \\ &\text{Night Shift: } \quad QCDev_{im} = \beta_0 - \beta_1 Shift\_Evening_i - \beta_2 Shift\_Morning_i + b_{0m} + \varepsilon_{im}, \end{aligned}$$

where i represents the observations, and m represents the operators, i = 1, 2, ..., 15, and m = 1, 2, ..., 5. The random effects and the observation error have the following distributions: $b_{0m} \sim N(0,\sigma^2_{b_{0m}})$ and $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
S = shift.Shift;
X1 = (S=='Morning') - (S=='Night');
X2 = (S=='Evening') - (S=='Night');
X = [ones(15,1), X1, X2];
y = shift.QCDev;
Z = ones(15,1);
G = shift.Operator;
```

Fit a linear mixed-effects model using the specified design matrices and restricted maximum likelihood method.

```
lme = LinearMixedModel.fitmatrix(X,y,Z,G,'FitMethod','REML','FixedEffectPredictors',...
{'Intercept','S_Morning','S_Evening'},'RandomEffectPredictors',{{'Intercept'}},...
'RandomEffectGroups',{'Operator'},'DummyVarCoding','effects')
```

```
lme =


Linear mixed-effects model fit by REML

Model information:
    Number of observations             15
    Fixed effects coefficients          3
    Random effects coefficients         5
    Covariance parameters               2

Formula:
    y ~ Intercept + S_Morning + S_Evening + (Intercept | Operator)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    58.913    61.337    -24.456          48.913

Fixed effects coefficients (95% CIs):
    Name               Estimate    SE         tStat      DF    pValue       Lower
    'Intercept'          3.6525    0.94109     3.8812    12    0.0021832     1.6021
    'S_Morning'        -0.91973    0.31206    -2.9473    12     0.012206    -1.5997
    'S_Evening'        -0.53293    0.31206    -1.7078    12      0.11339    -1.2129

Random effects covariance parameters (95% CIs):
Group: Operator (5 Levels)
    Name1              Name2              Type         Estimate    Lower      Upper
    'Intercept'        'Intercept'        'std'        2.0457      0.98207    4.2612

Group: Error
```

```
    Name             Estimate    Lower      Upper
    'Res Std'        0.85462     0.52357    1.395
```

Compute the best linear unbiased predictor (BLUP) estimates of random effects.

```
B = randomEffects(lme)
```

```
B =

    0.5775
    1.1757
   -2.1715
    2.3655
   -1.9472
```

The estimated deviation from the target quality characteristics for the third operator working in the evening shift is

$$\begin{aligned}\hat{y}_{Evening,Operator3} &= \hat{\beta}_0 + \hat{\beta}_1 Shift\_Evening + \hat{b}_{03} \\ &= 3.6525 - 0.53293 - 2.1715 \\ &= 0.94807.\end{aligned}$$

You can also display this value in the following way.

```
F = fitted(lme);
F(shift.Shift=='Evening' & shift.Operator=='3')
```

```
ans =

    0.9481
```

Correlated and Uncorrelated Random-Effects Terms

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower and the cylinders, and uncorrelated random-effect for intercept and acceleration grouped by the model year. This model corresponds to

$$MPG_{im} = \beta_0 + \beta_1 Acc_i + \beta_2 HP + b_{0m} + b_{1m} Acc_{im} + \varepsilon_{im}, \quad m = 1,2,3,$$

with the random-effects terms having the following prior distributions: $b_{0m} \sim N(0,\sigma^2_0)$, and $b_{1m} \sim N(0,\sigma^2_1)$. m represents the model year.

First, prepare the design matrices for fitting the linear mixed-effects model.

```
X = [ones(406,1) Acceleration Horsepower];
Z = {ones(406,1),Acceleration};
G = {Model_Year,Model_Year};
Model_Year = nominal(Model_Year);
```

Now, fit the model using `LinearMixedModel.fitmatrix` with the defined design matrices and grouping variables.

```
lme = LinearMixedModel.fitmatrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept'},{'Acceleration'}},'RandomEffectGroups',{'Model_Year','Model_Year'})
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             392
    Fixed effects coefficients           3
    Random effects coefficients         26
    Covariance parameters                3

Formula:
    y ~ Intercept + Acceleration + Horsepower + (Intercept | Model_Year) + (Acceleratio

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    2194.5    2218.3    -1091.3          2182.5

Fixed effects coefficients (95% CIs):
    Name                  Estimate    SE           tStat      DF     pValue        Lowe
    'Intercept'             49.839      2.0518      24.291    389    5.6168e-80      45
    'Acceleration'        -0.58565     0.10846    -5.3995    389    1.1652e-07     -0.
    'Horsepower'          -0.16534    0.0071227    -23.213    389    1.9755e-75    -0.1

Random effects covariance parameters (95% CIs):
Group: Model_Year (13 Levels)
    Name1              Name2              Type         Estimate      Lower    Upper
```

```
    'Intercept'        'Intercept'        'std'        8.0669e-07    NaN      NaN

Group: Model_Year (13 Levels)
    Name1                Name2                Type         Estimate    Lower      Upp
    'Acceleration'       'Acceleration'       'std'        0.18783     0.12523    0.2

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        3.7258      3.4698    4.0007
```

The standard deviation of the random effect for the intercept does not seem significant.

Refit the model with potentially correlated random effects for intercept and acceleration. In this case the random-effects terms have the following prior distribution

$$b_m = \begin{pmatrix} b_{0m} \\ b_{1m} \end{pmatrix} \sim N\left(0, \begin{pmatrix} \sigma_0^2 & \sigma_{0,1} \\ \sigma_{0,1} & \sigma_1^2 \end{pmatrix}\right),$$

where m represents the model year.

First prepare the random-effects design matrix and grouping variable.

```
Z = [ones(406,1) Acceleration];
G = Model_Year;

lme = LinearMixedModel.fitmatrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept','Acceleration'}},'RandomEffectGroups',{'Model_Year'})

lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             392
    Fixed effects coefficients           3
    Random effects coefficients         26
    Covariance parameters                4

Formula:
    y ~ Intercept + Acceleration + Horsepower + (Intercept + Acceleration | Model_Year)
```

```
Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    2193.5    2221.3    -1089.7          2179.5

Fixed effects coefficients (95% CIs):
    Name                 Estimate    SE           tStat      DF     pValue         Lowe
    'Intercept'            50.133       2.2652     22.132    389    7.7727e-71       45
    'Acceleration'        -0.58327      0.13394    -4.3545    389    1.7075e-05    -0.8
    'Horsepower'          -0.16954    0.0072609     -23.35    389     5.188e-76    -0.1

Random effects covariance parameters (95% CIs):
Group: Model_Year (13 Levels)
    Name1                Name2                Type          Estimate    Lower       U
    'Intercept'          'Intercept'          'std'           3.3475      1.2862
    'Acceleration'       'Intercept'          'corr'         -0.87971    -0.98501    -
    'Acceleration'       'Acceleration'       'std'           0.33789      0.1825

Group: Error
    Name            Estimate    Lower     Upper
    'Res Std'       3.6874      3.4298    3.9644
```

The confidence intervals for the standard deviations and the correlation between the random effects for intercept and acceleration do not include zeros, hence they seem significant. You can compare these two models using the `compare` method.

Specify the Covariance Pattern

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned 4 exercise programs, and their weight loss is recorded over six two-week time periods. This is simulated data.

Define `Subject` and `Program` as categorical variables.

```
Subject = nominal(Subject);
Program = nominal(Program);
```

Create the design matrices for a linear mixed-effects model, with the initial weight, type of program, and week are the fixed effects.

```
D = dummyvar(Program);
X = [ones(120,1), InitialWeight, D(:,2:4), Week];
Z = [ones(120,1) Week];
G = Subject;
```

This model corresponds to

$$\begin{aligned} y_{im} &= \beta_0 + \beta_1 IW_i + \beta_2 Week_i + \beta_3 I[PB]_i + \beta_4 I[PC]_i + \beta_5 I[PD]_i \\ &\quad + b_{0m} + b_{1m} Week2_{im} + b_{2m} Week4_{im} + b_{3m} Week6_{im} + b_{4m} Week8_{im} \\ &\quad + b_{5m} Week10_{im} + b_{6m} Week12_{im} + \varepsilon_{im}, \end{aligned}$$

where i = 1, 2, ..., 120, and m = 1, 2, ..., 20.

β_j are the fixed-effects coefficients, j = 0, 1, ...,8, and b_{1m} and b_{1m} are random effects. IW stands for initial weight and I[.] is a dummy variable representing a type of program. For example, $I[PB]_i$ is the dummy variable representing program type B. The random effects and observation error have the following prior distributions: $b_{0m} \sim N(0,\sigma^2_0)$, $b_{1m} \sim N(0,\sigma^2_1)$, and $\varepsilon_{im} \sim N(0,\sigma^2)$.

Fit the model using `LinearMixedModel.fitmatrix` with the defined design matrices and grouping variables. Assume the repeated observations collected on a subject have common variance along diagonals.

```
lme = LinearMixedModel.fitmatrix(X,y,Z,G,'FixedEffectPredictors',...
{'Intercept','InitWeight','PrgB','PrgC','PrgD','Week'},...
'RandomEffectPredictors',{{'Intercept','Week'}},...
'RandomEffectGroups',{'Subject'},'CovariancePattern','Isotropic')
```

```
lme =


Linear mixed-effects model fit by ML

Model information:
    Number of observations             120
    Fixed effects coefficients           6
    Random effects coefficients         40
    Covariance parameters                2
```

```
Formula:
    y ~ Intercept + InitWeight + PrgB + PrgC + PrgD + Week + (Intercept + Week | Subjec

Model fit statistics:
    AIC        BIC       LogLikelihood    Deviance
    -24.783    -2.483    20.391           -40.783

Fixed effects coefficients (95% CIs):
    Name                Estimate     SE           tStat       DF     pValue        Lowe
    'Intercept'            0.4208      0.28169      1.4938    114       0.13799     -0.
    'InitWeight'        0.0045552    0.0015338      2.9699    114     0.0036324    0.00
    'PrgB'                 0.36993      0.12119      3.0525    114     0.0028242       0
    'PrgC'              -0.034009       0.1209    -0.28129    114       0.77899     -0.
    'PrgD'                  0.121      0.12111     0.99911    114       0.31986     -0.
    'Week'                0.19881     0.037134      5.3538    114    4.5191e-07       0.

Random effects covariance parameters (95% CIs):
Group: Subject (20 Levels)
    Name1              Name2              Type         Estimate    Lower      Upper
    'Intercept'        'Intercept'        'std'        0.16561     0.12896    0.21269

Group: Error
    Name             Estimate    Lower       Upper
    'Res Std'        0.10272     0.088014    0.11987
```

Definitions

Cholesky Parameterization

One of the assumptions of linear mixed-effects models is that the random effects have the following prior distribution.

$$b \sim N\left(0,\sigma^2 D(\theta)\right),$$

where D is a q-by-q symmetric and positive semidefinite matrix, parameterized by a variance component vector θ, q is the number of variables in the random-effects term, and σ^2 is the observation error variance. Since the covariance matrix of the random effects, D, is symmetric, it has $q(q+1)/2$ free parameters. Suppose L is the lower triangular Cholesky factor of $D(\theta)$ such that

$$D(\theta) = L(\theta)L(\theta)^T,$$

then the q*(q+1)/2-by-1 unconstrained parameter vector θ is formed from elements in the lower triangular part of L.

For example, if

$$L = \begin{bmatrix} L_{11} & 0 & 0 \\ L_{21} & L_{22} & 0 \\ L_{31} & L_{32} & L_{33} \end{bmatrix},$$

then

$$\theta = \begin{bmatrix} L_{11} \\ L_{21} \\ L_{31} \\ L_{22} \\ L_{32} \\ L_{33} \end{bmatrix}.$$

Log-Cholesky Parameterization

When the diagonal elements of L in Cholesky parameterization are constrained to be positive, then the solution for L is unique. Log-Cholesky parameterization is the same as Cholesky parameterization except that the logarithm of the diagonal elements of L are used to guarantee unique parameterization.

For example, for the 3-by-3 example in Cholesky parameterization, enforcing $L_{ii} \geq 0$,

$$\theta = \begin{bmatrix} \log(L_{11}) \\ L_{21} \\ L_{31} \\ \log(L_{22}) \\ L_{32} \\ \log(L_{33}) \end{bmatrix}.$$

Alternatives

You can also fit a linear mixed-effects model using `fitlme(tbl,formula)`, where `tbl` is a table or dataset array containing the response `y`, the predictor variables `X`, and the grouping variables, and `formula` is of the form `'y ~ fixed + (random`$_1$`|g`$_1$`) + ... + (random`$_R$`|g`$_R$`)'`.

If your model is not easily described using a formula, you can create matrices to define the fixed and random effects, and fit the model using `fitlmematrix(X,y,Z,G)`.

See Also

`fitlme` | `LinearMixedModel`

fitNaiveBayes

Train naive Bayes classifier

Compatibility

`fitNaiveBayes` will be removed in a future release. Use `fitcnb` instead.

Syntax

```
NBModel = fitNaiveBayes(X,Y)
NBModel = fitNaiveBayes(X,Y,Name,Value)
```

Description

`NBModel = fitNaiveBayes(X,Y)` returns a naive Bayes classifier NBModel, trained by predictors X and class labels Y for *K*-level classification.

Predict labels for new data by passing the data and `NBModel` to `predict`.

`NBModel = fitNaiveBayes(X,Y,Name,Value)` returns a naive Bayes classifier with additional options specified by one or more Name,Value pair arguments.

For example, you can specify a distribution to model the data, prior probabilities for the classes, or the kernel smoothing window bandwidth.

Examples

Train a Naive Bayes Classifier

Load Fisher's iris data set.

```
load fisheriris
X = meas(:,3:4);
Y = species;
tabulate(Y)
```

```
      Value    Count   Percent
     setosa       50     33.33%
 versicolor       50     33.33%
  virginica       50     33.33%
```

The software can classify data with more than two classes using naive Bayes methods.

Train a naive Bayes classifier.

```
NBModel = fitNaiveBayes(X,Y)
```

```
NBModel =

Naive Bayes classifier with 3 classes for 2 dimensions.
Feature Distribution(s):normal
Classes:setosa, versicolor, virginica
```

`NBModel` is a trained `NaiveBayes` classifier.

By default, the software models the predictor distribution within each class using a Gaussian distribution having some mean and standard deviation. Use dot notation to display the parameters of a particular Gaussian fit, e.g., display the fit for the first feature within `setosa`.

```
setosaIndex = strcmp(NBModel.ClassLevels,'setosa');
estimates = NBModel.Params{setosaIndex,1}
```

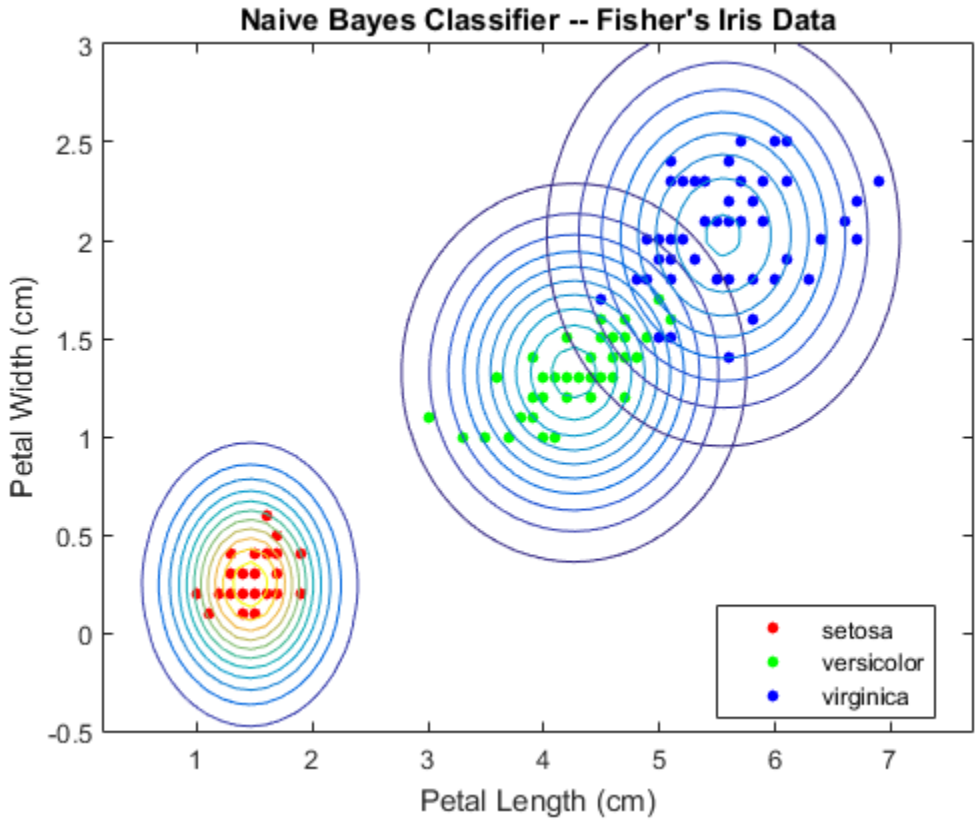
```
estimates =

    1.4620
    0.1737
```

The mean is `1.4620` and the standard deviation is `0.1737`.

Plot the Gaussian contours.

```
figure
gscatter(X(:,1),X(:,2),Y);
h = gca;
xylim = [h.XLim h.YLim];
```

```
hold on
Params = cell2mat(NBModel.Params);
Mu = Params(2*(1:3)-1,1:2); % Extracts the means
Sigma = zeros(2,2,3);
for j = 1:3
    Sigma(:,:,j) = diag(Params(2*j,:)); % Extracts the standard deviations
    ezcontour(@(x1,x2)mvnpdf([x1,x2],Mu(j,:),Sigma(:,:,j)),...
        xylim+0.5*[-1,1,-1,1]) ...
        % Draws contours for the multivariate normal distributions
end
title('Naive Bayes Classifier -- Fisher''s Iris Data')
xlabel('Petal Length (cm)')
ylabel('Petal Width (cm)')
hold off
```



You can change the default distribution using the name-value pair argument `'Distribution'`. For example, If some predictors are count based, then you can specify that they are multinomial random variables using `'Distribution','mn'` .

Specify Predictor Distributions for Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

Train a naive Bayes classifier using every predictor.

```
NBModel1 = fitNaiveBayes(X,Y);
NBModel1.ClassLevels % Display the class order
NBModel1.Params
NBModel1.Params{1,2}
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

    [2x1 double]    [2x1 double]    [2x1 double]    [2x1 double]
    [2x1 double]    [2x1 double]    [2x1 double]    [2x1 double]
    [2x1 double]    [2x1 double]    [2x1 double]    [2x1 double]


ans =

    3.4280
    0.3791
```

By default, the software models the predictor distribution within each class as a Gaussian with some mean and standard deviation. There are four predictors and three class levels. Each cell in `NBModel1.Params` corresponds to a numeric vector containing the mean and standard deviation of each distribution, e.g., the mean and standard deviation for setosa iris sepal widths are `3.4280` and `0.3791`, respectively.

Estimate the confusion matrix for `NBModel1`.

```
predictLabels1 = predict(NBModel1,X);
[ConfusionMat1,labels] = confusionmat(Y,predictLabels1)
```

```
ConfusionMat1 =

    50     0     0
     0    47     3
     0     3    47


labels =

    'setosa'
    'versicolor'
    'virginica'
```

Element (*j*, *k*) of `ConfusionMat1` represents the number of observations that the software classifies as *k*, but the data show as being in class *j*.

Retrain the classifier using the Gaussian distribution for predictors 1 and 2 (the sepal lengths and widths), and the default normal kernel density for predictors 3 and 4 (the petal lengths and widths).

```
NBModel2 = fitNaiveBayes(X,Y,...
    'Distribution',{'normal','kernel','normal','kernel'});
NBModel2.Params{1,2}
```

```
ans =

  KernelDistribution

    Kernel = normal
    Bandwidth = 0.179536
    Support = unbounded
```

The software does not train parameters to the kernel density. Rather, the software chooses an optimal width. However, you can specify a width using the `'KSWidth'` name-value pair argument.

Estimate the confusion matrix for `NBModel2`.

```
predictLabels2 = predict(NBModel2,X);
ConfusionMat2 = confusionmat(Y,predictLabels2)
```

```
ConfusionMat2 =

    50     0     0
     0    47     3
     0     3    47
```

Based on the confusion matrices, the two classifiers perform similarly in the training sample.

Train Naive Bayes Classifiers Using Multinomial Predictors

Some spam filters classify an incoming email as spam based on how many times a word or puncutation (called tokens) occurs in an email. The predictors are the frequencies of particular words or punctuations in an email. Therefore, the predictors compose multinomial random variables.

This example illustrates classification using naive Bayes and mutlinomial predictors.

Suppose you observed 1000 emails and classified them as spam or not spam. Do this by randomly assigning -1 or 1 to `y` for each email.

```
n = 1000;                          % Sample size
rng(1);                            % For reproducibility
y = randsample([-1 1],n,true);  % Random labels
```

To build the predictor data, suppose that there are five tokens in the vocabulary, and 20 observed tokens per email. Generate predictor data from the five tokens by drawing multinomial deviates. The relative frequencies for tokens corresponding to spam emails should differ from emails that are not spam.

```
tokenProbs = [0.2 0.3 0.1 0.15 0.25;...
    0.4 0.1 0.3 0.05 0.15];             % Token relative frequencies
tokensPerEmail = 20;
X = zeros(n,5);
X(y == 1,:) = mnrnd(tokensPerEmail,tokenProbs(1,:),sum(y == 1));
X(y == -1,:) = mnrnd(tokensPerEmail,tokenProbs(2,:),sum(y == -1));
```

Train a naive Bayes classifier. Specify that the predictors are multinomial.

```
NBModel = fitNaiveBayes(X,y,'Distribution','mn');
```

`NBModel` is a trained `NaiveBayes` classifier.

Assess the in-sample performance of `NBModel` by estimating the misclassification rate.

```
predSpam = predict(NBModel,X);
misclass = sum(y'~=predSpam)/n
```

```
misclass =

    0.0200
```

The in-sample misclassification rate is 2%.

Randomly generate deviates that represent a new batch of emails.

```
nOut = 500;
yOut = randsample([-1 1],nOut,true);
XOut = zeros(nOut,5);
XOut(yOut == 1,:) = mnrnd(tokensPerEmail,tokenProbs(1,:),...
    sum(yOut == 1));
XOut(yOut == -1,:) = mnrnd(tokensPerEmail,tokenProbs(2,:),...
    sum(yOut == -1));
```

Classify the new emails using the trained naive Bayes classifier `NBModel`, and determine whether the algorithm generalizes.

```
predSpamOut = predict(NBModel,XOut);
genRate = sum(yOut'~=predSpamOut)/nOut
```

```
genRate =

    0.0260
```

The out-of-sample misclassification rate is 2.6% indicating that the classifier generalizes fairly well.

Input Arguments

X — Predictor data

matrix of numeric values

Predictor data to which the naive Bayes classifier is trained, specified as a matrix of numeric values.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature).

The length of `Y` and the number of rows of `X` must be equivalent.

Data Types: `double`

Y — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels to which the naive Bayes classifier is trained, specified as a categorical or character array, logical or numeric vector, or cell array of strings. Each element of `Y` defines the class membership of the corresponding row of `X`. `Y` supports K class levels.

If `Y` is a character array, then each row must correspond to one class label.

The length of `Y` and the number of rows of `X` must be equivalent.

Data Types: `cell` | `char` | `double` | `logical`

Note: The software treats `NaN`, empty string (`''`), and `<undefined>` elements as missing values.

- If `Y` contains missing values, then the software removes them and the corresponding rows of `X`.
- If `X` contains any rows composed entirely of missing values, then the software removes those rows and the corresponding elements of `Y`.

- If `X` contains missing values and you set `'Distribution','mn'`, then the software removes those rows of `X` and the corresponding elements of `Y`.

- If a predictor is not represented in a class, that is, if all of its values are `NaN` within a class, then the software returns an error.

Removing rows of `X` and corresponding elements of `Y` decreases the effective training or cross-validation sample size.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Distribution','mn','Prior','uniform','KSWidth',0.5` specifies the following: the data distribution is multinomial, the prior probabilities for all classes are equal, and the kernel smoothing window bandwidth for all classes is `0.5` units.

`'Distribution'` — Data distributions

`'normal'` (default) | `'kernel'` | `'mn'` | `'mvmn'` | cell array of strings

Data distributions `fitNaiveBayes` uses to model the data, specified as the comma-separated pair consisting of `'Distribution'` and a string or cell array of strings.

This table summarizes the available distributions.

Value	Description
`'kernel'`	Kernel smoothing density estimate.
`'mn'`	Multinomial distribution. If you specify `mn`, then all features are components of a multinomial distribution. Therefore, you cannot include `'mn'` as an element of a cell array of strings. For details, see “Algorithms” on page 22-1862.
`'mvmn'`	Multivariate multinomial distribution. For details, see “Algorithms” on page 22-1862.
`'normal'`	Normal (Gaussian) distribution.

If you specify a string, then the software models all the features using that distribution. If you specify a 1-by-*D* cell array of strings, then the software models feature *j* using the distribution in element *j* of the cell array.

Example: `'Distribution',{'kernel','normal'}`

Data Types: `cell` | `char`

`'KSSupport'` — Kernel smoothing density support

`'unbounded'` (default) | `'positive'` | cell array | numeric row vector

Kernel smoothing density support, specified as the comma-separated pair consisting of `'KSSupport'` and a numeric row vector, a string, or a cell array. The software applies the kernel smoothing density to this region.

If you do not specify `'Distribution','kernel'`, then the software ignores the values of `'KSSupport'`, `'KSType'`, and `'KSWidth'`.

This table summarizes the available options for setting the kernel smoothing density region.

Value	Description
1-by-2 numeric row vector	For example, `[L,U]`, where `L` and `U` are the finite lower and upper bounds, respectively, for the density support.
`'positive'`	The density support is all positive real values.
`'unbounded'`	The density support is all real values.

If you specify a 1-by-*D* cell array, with each cell containing any value in the table, then the software trains the classifier using the kernel support in cell *j* for feature *j* in X.

Example: `'KSSupport',{[-10,20],'unbounded'}`

Data Types: `cell` | `char` | `double`

`'KSType'` — Kernel smoother type

`'normal'` (default) | `'box'` | `'epanechnikov'` | `'triangle'` | cell array of strings

Kernel smoother type, specified as the comma-separated pair consisting of `'KSType'` and a string or cell array of strings.

If you do not specify `'Distribution','kernel'`, then the software ignores the values of `'KSSupport'`, `'KSType'`, and `'KSWidth'`.

This table summarizes the available options for setting the kernel smoothing density region. Let $I\{u\}$ denote the indictor function.

Value	Kernel	Formula
`'box'`	Box (uniform)	$f(x) = 0.5I\{\|x\| \le 1\}$
`'epanechni`	Epanechnikov	$f(x) = 0.75\left(1 - x^2\right)I\{\|x\| \le 1\}$
`'normal'`	Gaussian	$f(x) = \frac{1}{\sqrt{2\pi}}\exp\left(-0.5x^2\right)$
`'triangle'`	Triangular	$f(x) = \left(1 - \|x\|\right)I\{\|x\| \le 1\}$

If you specify a 1-by-D cell array, with each cell containing any value in the table, then the software trains the classifier using the kernel smoother type in cell j for feature j in X.

Example: `'KSType',{'epanechnikov','normal'}`

Data Types: `cell` | `char`

`'KSWidth'` — Kernel smoothing window bandwidth

matrix of numeric values (default) | numeric column vector | numeric row vector | scalar | structure array

Kernel smoothing window bandwidth, specified as the comma-separated pair consisting of `'KSWidth'` and a matrix of numeric values, numeric row vector, numeric column vector, scalar, or structure array.

If you do not specify `'Distribution','kernel'`, then the software ignores the values of `'KSSupport'`, `'KSType'`, and `'KSWidth'`.

Suppose there are K class levels and D predictors. This table summarizes the available options for setting the kernel smoothing window bandwidth.

Value	Description
K-by-D matrix of numeric values	Element (k,d) specifies the bandwidth for predictor d in class k.

Value	Description
K-by-1 numeric column vector	Element *k* specifies the bandwidth for all predictors in class *k*.
1-by-*D* numeric row vector	Element *d* specifies the bandwidth in all class levels for predictor *d*.
scalar	Specifies the bandwidth for all features in all classes.
structure array	A structure array `S` containing class levels and their bandwidths. `S` must have two fields: • `S.width`: A numeric row vector of bandwidths, or a matrix of numeric values with *D* columns. • `S.group`: A vector of the same type as `Y`, containing unique class levels indicating the class for the corresponding element of `S.width`.

By default, the software selects a default bandwidth automatically for each combination of feature and class by using a value that is optimal for a Gaussian distribution.

Example: `'KSWidth',struct('width',[0.5,0.25],'group',{{'b';'g'}})`

Data Types: `double` | `struct`

`'Prior'` — Class prior probabilities

`'empirical'` (default) | `'uniform'` | numeric vector | structure array

Class prior probabilities, specified as the comma-separated pair consisting of `'Prior'` and a numeric vector, structure array, or string.

This table summarizes the available options for setting prior probabilities.

Value	Description
`'empirical'`	The software uses the class relative frequencies distribution for the prior probabilities.
numeric vector	A numeric vector of length *K* specifying the prior probabilities for each class. The order of the elements of `Prior` should correspond to the order of the class levels. For details on the order of the classes, see “Algorithms” on page 22-1862. The software normalizes prior probabilities to sum to `1`.

Value	Description
structure array	A structure array `S` containing class levels and their prior probabilities. `S` must have two fields: • `S.prob`: A numeric vector of prior probabilities. The software normalizes prior probabilities to sum to `1`. • `S.group`: A vector of the same type as Y containing unique class levels indicating the class for the corresponding element of `S.prob`. `S.class` must contain all the *K* levels in `Y`. It can also contain classes that do not appear in `Y`. This can be useful if X is a subset of a larger training set. The software ignores any classes that appear in `S.group` but not in `Y`.
`'uniform'`	The prior probabilities are equal for all classes.

Example: `'Prior',struct('prob',[1,2],'group',{{'b';'g'}})`

Data Types: `char` | `double` | `struct`

Output Arguments

`NBModel` — Trained naive Bayes classifier

`NaiveBayes` classifier

Trained naive Bayes classifier, returned as a `NaiveBayes` classifier.

More About

Bag-of-Tokens Model

In the bag-of-tokens model, the value of predictor *j* is the nonnegative number of occurrences of token *j* in this observation. The number of categories (bins) in this multinomial model is the number of distinct tokens, that is, the number of predictors.

Tips

- For classifying count-based data, such as the bag-of-tokens model, use the multinomial distribution (e.g., set `'Distribution','mn'`).

- This list defines the order of the classes. It is useful when you specify prior probabilities by setting `'Prior',prior`, where `prior` is a numeric vector.
  - If `Y` is a categorical array, then the order of the class levels matches the output of `categories(Y)`.
  - If `Y` is a numeric or logical vector, then the order of the class levels matches the output of `sort(unique(Y))`.
  - For cell arrays of string and character arrays, the order of the class labels is the order which each label appears in `Y`.

Algorithms

- If you specify `'Distribution','mn'`, then the software considers each observation as multiple trials of a multinomial distribution, and considers each occurrence of a token as one trial (see "Bag-of-Tokens Model" on page 22-1861).
- If you specify `'Distribution','mvmn'`, then the software assumes each individual predicator follows a multinomial model within a class. The parameters for a predictor include the probabilities of all possible values that the corresponding feature can take.

- "Naive Bayes Classification" on page 15-31
- "Grouping Variables" on page 2-52

See Also

`NaiveBayes` | `posterior` | `predict`

fitPosterior

Class: ClassificationSVM

Fit posterior probabilities

Syntax

```
ScoreSVMModel = fitPosterior(SVMModel)
[ScoreSVMModel,ScoreTransform] = fitPosterior(SVMModel)
[ScoreSVMModel,ScoreTransform] = fitPosterior(SVMModel,Name,Value)
```

Description

`ScoreSVMModel = fitPosterior(SVMModel)` returns a trained support vector machine (SVM) classifier `ScoreSVMModel` containing the optimal score-to-posterior-probability transformation function for two-class learning.

The software fits the appropriate score-to-posterior-probability transformation function using the SVM classifier `SVMModel`, and by conducting 10-fold cross validation using the stored predictor data (`SVMModel.X`) and the class labels (`SVMModel.Y`) as outlined in [1]. The transformation function computes the posterior probability that an observation is classified into the positive class (`SVMModel.Classnames(2)`).

- If the classes are inseparable, then the transformation function is the sigmoid function.
- If the classes are perfectly separable, then the transformation function is the step function.
- In two-class learning, if one of the two classes has a relative frequency of 0, then the transformation function is the constant function. `fitPosterior` is not appropriate for one-class learning.
- The software stores the optimal score transformation function in `ScoreSVMModel.ScoreTransform`.

`[ScoreSVMModel,ScoreTransform] = fitPosterior(SVMModel)` additionally returns the optimal score-to-posterior-probability transformation function parameters (`ScoreTransform`).

`[ScoreSVMModel,ScoreTransform] = fitPosterior(SVMModel,Name,Value)` returns the optimal score-to-posterior-probability transformation function and its parameters with additional options specified by one or more Name,Value pair arguments.

Tips

Here is one way to predict positive class posterior probabilities.

1. Train an SVM classifier by passing the data to `fitcsvm`. The result is a trained SVM classifier, such as, `SVMModel`, that stores the data. The software sets the score transformation function property (`SVMModel.ScoreTransformation`) to `none`.
2. Pass the trained SVM classifier `SVMModel` to `fitSVMPosterior` or `fitPosterior`. The result, for example, `ScoreSVMModel`, is the same, trained SVM classifier as `SVMModel`, except the software sets `ScoreSVMModel.ScoreTransformation` to the optimal score transformation function.

   If you skip step 2, then `predict` returns the positive class score rather than the positive class posterior probability.
3. Pass the trained SVM classifier containing the optimal score transformation function (`ScoreSVMModel`) and predictor data matrix to `predict`. The second column of the second output argument stores the positive class posterior probabilities corresponding to each row of the predictor data matrix.

Input Arguments

`SVMModel` — Trained SVM classifier

`ClassificationSVM` classifier

Trained SVM classifier, specified as a `ClassificationSVM`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CVPartition'` — Cross-validation partition

`[]` (default) | `cvpartition` partition

Cross-validation partition used to compute the transformation function, specified as the comma-separated pair consisting of `'CVPartition'` and a `cvpartition` partition as created by `cvpartition`. You can use only one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`crossval` splits the data into subsets using `cvpartition`.

`'Holdout'` — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data for holdout validation used to compute the transformation function, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). Holdout validation tests the specified fraction of the data, and uses the remaining data for training.

You can use only one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'Holdout',0.1`

Data Types: `double` | `single`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use when computing the transformation function, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

You can use only one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag indicating whether to use leave-one-out cross validation to compute the transformation function, specified as the comma-separated

pair consisting of 'Leaveout' and 'on' or 'off'. Use leave-one-out cross validation by using 'on'.

You can use only one of these four options at a time for creating a cross-validated model: 'KFold', 'Holdout', 'Leaveout', or 'CVPartition'.

Example: 'Leaveout','on'

Output Arguments

ScoreSVMModel — Trained SVM classifier

ClassificationSVM classifier

Trained SVM classifier containing the estimated score-to-posterior-probability transformation function, returned as a ClassificationSVM classifier.

To estimate posterior probabilities for the training set observations, pass ScoreSVMModel to resubPredict.

To estimate posterior probabilities for new observations, then pass them and ScoreSVMModel to predict. If you set 'Standardize',true in fitcsvm to train SVMModel, then predict standardizes the columns of X using the corresponding means in SVMModel.Mu and standard deviations in SVMModel.Sigma.

ScoreTransform — Optimal score transformation function parameters

structure array

Optimal score-to-posterior-probability transformation function parameters, returned as a structure array.

- If field Type is sigmoid, then ScoreTransform has the following other fields:
  - Slope: The value of A in the sigmoid function
  - Intercept: The value of B in the sigmoid function
- If field Type is step, then ScoreTransform has the following other fields:
  - PositiveClassProbability: The value of π in the step function. It represents the probability that an observation is in the positive class. Also, the posterior probability that an observation is in the positive class given that its score is in the interval (LowerBound,UpperBound).

- `LowerBound`: The value $\max_{y_n=-1} s_n$ in the step function. It represents the lower bound of the score interval that assigns observations with scores in the interval the posterior probability of being in the positive class `PositiveClassProbability`. Any observation with a score less than `LowerBound` has the posterior probability of being the positive class `0`.
- `UpperBound`: The value $\min_{y_n=+1} s_n$ in the step function. It represents the upper bound of the score interval that assigns observations with scores in the interval the posterior probability of being in the positive class `PositiveClassProbability`. Any observation with a score greater than `UpperBound` has the posterior probability of being the positive class `1`.

- If field `Type` is `constant`, then `ScoreTransform.PredictedClass` contains the name of the class prediction.

  This result is the same as `SVMModel.ClassNames`. The posterior probability of an observation being in `ScoreTransform.PredictedClass` is always `1`.

Definitions

Sigmoid Function

The sigmoid function that maps score s_j corresponding to observation j to the positive class posterior probability is

$$P(s_j) = \frac{1}{1+\exp(As_j + B)}.$$

If the output argument `ScoreTransform.Type` is `sigmoid`, then parameters A and B correspond to the fields `Scale` and `Intercept` of `ScoreTransform`, respectively.

Step Function

The step function that maps score s_j corresponding to observation j to the positive class posterior probability is

$$P\left(s_j\right)=\begin{cases}0; & s<\max\limits_{y_k=-1}s_k\\ \pi; & \max\limits_{y_k=-1}s_k\le s_j\le\min\limits_{y_k=+1}s_k\\ 1; & s_j>\min\limits_{y_k=+1}s_k\end{cases},$$

where:

- s_j the score of observation j.
- +1 and –1 denote the positive and negative classes, respectively.
- π is the prior probability that an observation is in the positive class.

If the output argument `ScoreTransform.Type` is `step`, then the quantities $\max\limits_{y_k=-1}s_k$ and $\min\limits_{y_k=+1}s_k$ correspond to the fields `LowerBound` and `UpperBound` of `ScoreTransform`, respectively.

Constant Function

The constant function maps all scores in a sample to posterior probabilities 1 or 0.

If all observations have posterior probability 1, then they are expected to come from the positive class.

If all observations have posterior probability 0, then they are not expected to come from the positive class.

Examples

Estimate In-Sample Posterior Probabilities of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to specify the class order and standardize the data.

```
SVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier. The positive class is `'g'`.

Fit the optimal score-to-posterior-probability transformation function.

```
rng(1); % For reproducibility
ScoreSVMModel = fitPosterior(SVMModel)
```

```
ScoreSVMModel =

  ClassificationSVM
      PredictorNames: {1x34 cell}
        ResponseName: 'Y'
          ClassNames: {'b'  'g'}
      ScoreTransform: '@(S)sigmoid(S,-9.481802e-01,-1.218745e-01)'
     NumObservations: 351
               Alpha: [90x1 double]
                Bias: -0.1343
    KernelParameters: [1x1 struct]
                  Mu: [1x34 double]
               Sigma: [1x34 double]
      BoxConstraints: [351x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [351x1 logical]
              Solver: 'SMO'
```

Since the classes are inseparable, the score transformation function (`ScoreSVMModel.ScoreTransform`) is the sigmoid function.

Estimate scores and positive class posterior probabilities for the training data. Display the results for the first 10 observations.

```
[label,scores] = resubPredict(SVMModel);
[~,postProbs] = resubPredict(ScoreSVMModel);
table(Y(1:10),label(1:10),scores(1:10,2),postProbs(1:10,2),'VariableNames',...
    {'TrueLabel','PredictedLabel','Score','PosteriorProbability'})
```

```
ans =

    TrueLabel    PredictedLabel     Score     PosteriorProbability
    _________    ______________    _______    ____________________

    'g'          'g'                1.4861      0.82215
    'b'          'b'               -1.0004      0.30436
    'g'          'g'                1.8685      0.86916
    'b'          'b'               -2.6458     0.084183
    'g'          'g'                1.2805      0.79184
    'b'          'b'               -1.4617      0.22028
    'g'          'g'                2.1672      0.89814
    'b'          'b'               -5.7085    0.0050122
    'g'          'g'                2.4797      0.92223
    'b'          'b'               -2.7811     0.074805
```

Plot Posterior Probability Contours for Multiple Classes Using SVM

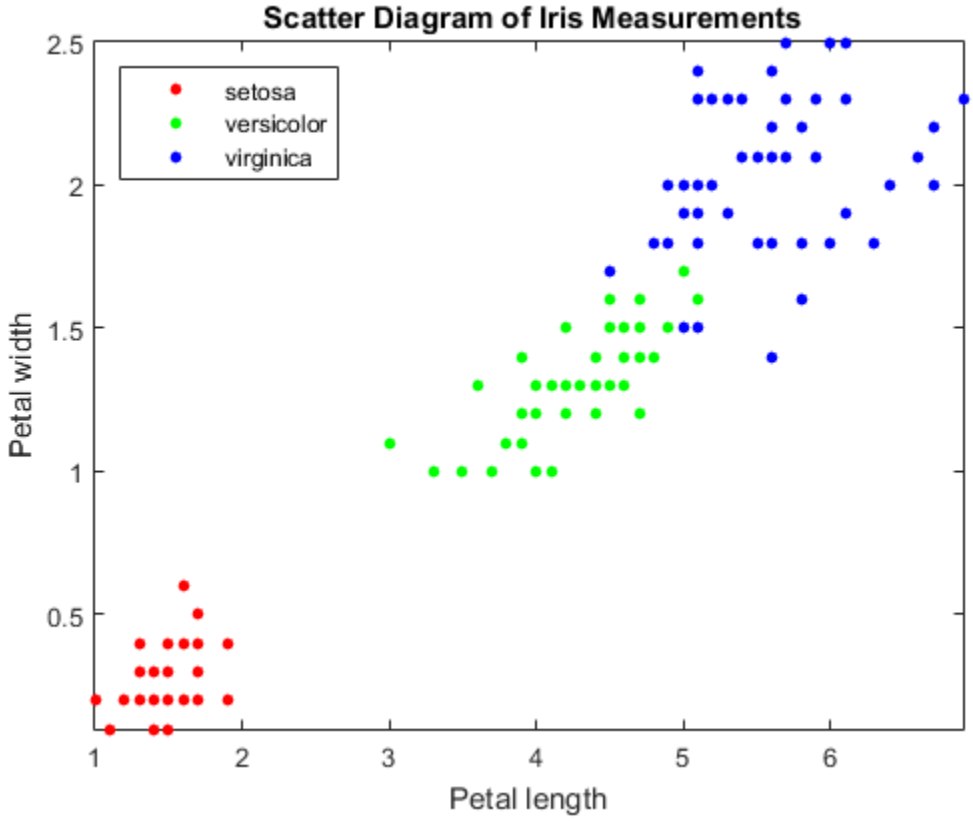
This example steps through the process of one-versus-all (OVA) classification to train a multiclass SVM classifier, and then plots probability contours for each class. To implement OVA directly, see fitcecoc.

Load Fisher's iris data set. Use the petal lengths and widths.

```
load fisheriris
X = meas(:,3:4);
Y = species;
```

Examine a scatter plot of the data.

```
figure
gscatter(X(:,1),X(:,2),Y);
title('{\bf Scatter Diagram of Iris Measurements}');
xlabel('Petal length');
ylabel('Petal width');
legend('Location','Northwest');
axis tight
```



Train three binary SVM classifiers that separate each type of iris from the others. Assume that a radial basis function is an appropriate kernel for each, and allow the algorithm to choose a kernel scale. It is good practice to define the class order and standardize the predictors.

```
classNames = {'setosa'; 'virginica'; 'versicolor'};
numClasses = size(classNames,1);
inds = cell(3,1); % Preallocation
SVMModel = cell(3,1);

rng(1); % For reproducibility
for j = 1:numClasses
    inds{j} = strcmp(Y,classNames{j});  % OVA classification
    SVMModel{j} = fitcsvm(X,inds{j},'ClassNames',[false true],...
```

```
        'Standardize',true,'KernelFunction','rbf','KernelScale','auto');
end
```

`fitcsvm` uses a heuristic procedure that involves subsampling to compute the value of the kernel scale.

Fit the optimal score-to-posterior-probability transformation function for each classifier.

```
for j = 1:numClasses
    SVMModel{j} = fitPosterior(SVMModel{j});
end
```

```
Warning: Classes are perfectly separated. The optimal score-to-posterior
transformation is a step function.
```

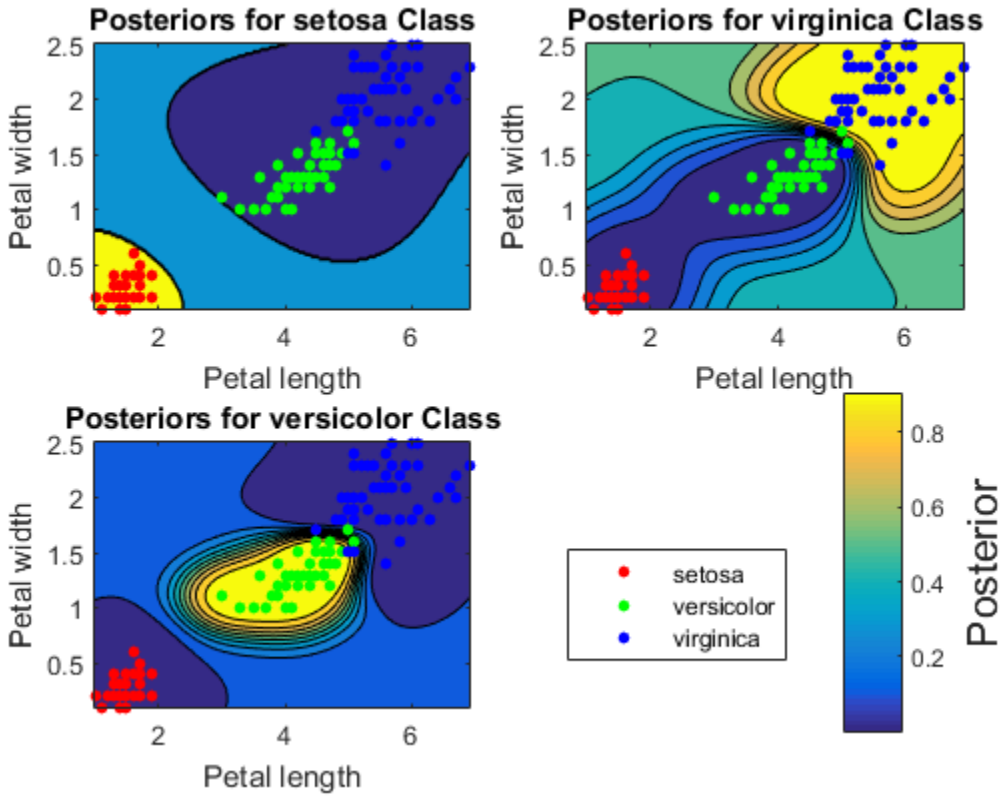
Define a grid to plot the posterior probability contours. Estimate the posterior probabilities over the grid for each classifier.

```
d = 0.02;
[x1Grid,x2Grid] = meshgrid(min(X(:,1)):d:max(X(:,1)),...
    min(X(:,2)):d:max(X(:,2)));
xGrid = [x1Grid(:),x2Grid(:)];

posterior = cell(3,1);
for j = 1:numClasses
    [~,posterior{j}] = predict(SVMModel{j},xGrid);
end
```

For each SVM classifier, plot the posterior probability contour under the scatter plot of the data.

```
figure
h = zeros(numClasses + 1,1); % Preallocation for graphics handles
for j = 1:numClasses
subplot(2,2,j)
contourf(x1Grid,x2Grid,reshape(posterior{j}(:,2),size(x1Grid,1),size(x1Grid,2)));
hold on
h(1:numClasses) = gscatter(X(:,1),X(:,2),Y);
title(sprintf('Posteriors for %s Class',classNames{j}));
xlabel('Petal length');
ylabel('Petal width');
legend off
axis tight
hold off
end
h(numClasses + 1) = colorbar('Location','EastOutside',...
```

```
    'Position',[[0.8,0.1,0.05,0.4]]);
set(get(h(numClasses + 1),'YLabel'),'String','Posterior','FontSize',16);
legend(h(1:numClasses),'Location',[0.6,0.2,0.1,0.1]);
```



Fit Optimal Posterior Probability Function Using Holdout Cross Validation

Platt (2000) outlines a bias-reducing method of estimating the score-to-posterior-probability transformation function. This method estimates the transformation function after the SVM classifer is trained, and uses cross validation to reduce bias. By default, `fitPosterior` and `fitSVMPosterior` use 10-fold cross validation when they estimate the transformation function. To reduce run time for larger data sets, you can specify to use holdout cross validation instead.

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to specify the class order and standardize the data.

```
SVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier. The positive class is `'g'`.

Fit the optimal score-to-posterior-probability transformation function. For comparison, use 10-fold cross validation (default) and specify a 10% holdout test sample.

```
rng(1); % For reproducibility

tic;    % Start the stopwatch
SVMModel_10FCV = fitPosterior(SVMModel);
toc     % Stop the stopwatch and display the run time

tic;
SVMModel_HO = fitPosterior(SVMModel,'Holdout',0.10);
toc
```

```
Elapsed time is 0.878663 seconds.
Elapsed time is 0.166979 seconds.
```

Though both runtimes are short because the data set is relatively small, `SVMModel_HO` fitted the score tansformation function much faster than `SVMModel_10FCV`.

Algorithms

If you reestimate the score-to-posterior-probability transformation function, that is, if you pass an SVM classifier to `fitPosterior` or `fitSVMPosterior` and its `ScoreTransform` property is not `none`, then the software:

- Displays a warning
- Resets the original transformation function to `'none'` before estimating the new one

Alternatives

You can also fit the posterior probability function using `fitSVMPosterior`. This function is similar to `fitPosterior`, except it is more broad since it accepts a wider range of SVM classifer types.

References

[1] Platt, J. “Probabilistic outputs for support vector machines and comparisons to regularized likelihood methods”. In: *Advances in Large Margin Classifiers*. Cambridge, MA: The MIT Press, 2000, pp. 61–74.

See Also

`ClassificationSVM` | `fitcsvm` | `fitSVMPosterior` | `predict`

fitPosterior

Class: CompactClassificationSVM

Fit posterior probabilities

Syntax

```
ScoreSVMModel = fitPosterior(SVMModel,X,Y)
[ScoreSVMModel,ScoreTransform] = fitPosterior(SVMModel,X,Y)
```

Description

`ScoreSVMModel = fitPosterior(SVMModel,X,Y)` returns a trained support vector machine (SVM) classifier `ScoreSVMModel` containing the optimal score-to-posterior-probability transformation function for two-class learning.

The software fits the appropriate score-to-posterior-probability transformation function using the SVM classifier `SVMModel`, and by conducting 10-fold cross validation using the stored predictor data (`SVMModel.X`) and the class labels (`SVMModel.Y`) as outlined in [1]. The transformation function computes the posterior probability that an observation is classified into the positive class (`SVMModel.Classnames(2)`).

- If the classes are inseparable, then the transformation function is the sigmoid function.
- If the classes are perfectly separable, the transformation function is the step function.
- In two-class learning, if one of the two classes has a relative frequency of 0, then the transformation function is the constant function. `fitPosterior` is not appropriate for one-class learning.
- The software stores the optimal score-to-posterior-probability transformation function in `ScoreSVMModel.ScoreTransform`.

`[ScoreSVMModel,ScoreTransform] = fitPosterior(SVMModel,X,Y)` additionally returns the optimal score-to-posterior-probability transformation function parameters (`ScoreTransform`)

Tips

Here is one way to predict positive class posterior probabilities.

1. Train an SVM classifier by passing the data to `fitcsvm`. The result is a trained SVM classifier, such as, `SVMModel`, that stores the data. The software sets the score transformation function property (`SVMModel.ScoreTransformation`) to `none`.
2. Pass the trained SVM classifier `SVMModel` to `fitSVMPosterior` or `fitPosterior`. The result, for example, `ScoreSVMModel`, is the same, trained SVM classifier as `SVMModel`, except the software sets `ScoreSVMModel.ScoreTransformation` to the optimal score transformation function.

   If you skip step 2, then `predict` returns the positive class score rather than the positive class posterior probability.
3. Pass the trained SVM classifier containing the optimal score transformation function (`ScoreSVMModel`) and predictor data matrix to `predict`. The second column of the second output argument stores the positive class posterior probabilities corresponding to each row of the predictor data matrix.

Input Arguments

`SVMModel` — Trained, compact SVM classifier

`CompactClassificationSVM` classifier

Trained, compact SVM classifier, specified as a `CompactClassificationSVM`.

`X` — Predictor data

matrix

Predictor data used to estimate the score-to-posterior-probability transformation function, specified as a matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature).

The length of `Y` and the number of rows of `X` must be equal.

If you set `'Standardize',true` in `fitcsvm` to train `SVMModel`, then the software standardizes the columns of `X` using the corresponding means in `SVMModel.Mu` and

standard deviations in `SVMModel.Sigma`. If the software fits the transformation-function parameter estimates using standardized data, then the estimates might differ from estimation without standardized data.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels used to estimate the score-to-posterior-probability transformation function, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `Y` is a character array, then each element must correspond to one class label.

The length of `Y` and the number of rows of `X` must be equal.

Output Arguments

`ScoreSVMModel` — Trained, compact SVM classifier

`CompactClassificationSVM` classifier

Trained, compact SVM classifier containing the estimated score-to-posterior-probability transformation function, returned as a `CompactClassificationSVM` classifier.

To estimate posterior probabilities, pass `ScoreSVMModel` and predictor data to `predict`. If you set `'Standardize',true` in `fitcsvm` to train `SVMModel`, then `predict` standardizes the columns of `X` using the corresponding means in `SVMModel.Mu` and standard deviations in `SVMModel.Sigma`.

`ScoreTransform` — Optimal score transformation function parameters

structure array

Optimal score-to-posterior-probability transformation function parameters, returned as a structure array.

- If field `Type` is `sigmoid`, then `ScoreTransform` has the following other fields:
  - `Slope`: The value of A in the sigmoid function
  - `Intercept`: The value of `B` in the sigmoid function

- If field `Type` is `step`, then `ScoreTransform` has the following other fields:
  - `PositiveClassProbability`: The value of π in the step function. It represents the probability that an observation is in the positive class. Also, the posterior probability that an observation is in the positive class given that its score is in the interval (`LowerBound`,`UpperBound`).
  - `LowerBound`: The value $\max_{y_n=-1} s_n$ in the step function. It represents the lower bound of the score interval that assigns observations with scores in the interval the posterior probability of being in the positive class `PositiveClassProbability`. Any observation with a score less than `LowerBound` has the posterior probability of being the positive class `0`.
  - `UpperBound`: The value $\min_{y_n=+1} s_n$ in the step function. It represents the upper bound of the score interval that assigns observations with scores in the interval the posterior probability of being in the positive class `PositiveClassProbability`. Any observation with a score greater than `UpperBound` has the posterior probability of being the positive class `1`.
- If field `Type` is `constant`, then `ScoreTransform.PredictedClass` contains the name of the class prediction.

  This result is the same as `SVMModel.ClassNames`. The posterior probability of an observation being in `ScoreTransform.PredictedClass` is always `1`.

Definitions

Sigmoid Function

The sigmoid function that maps score s_j corresponding to observation j to the positive class posterior probability is

$$P(s_j) = \frac{1}{1+\exp(As_j + B)}.$$

If the output argument `ScoreTransform.Type` is `sigmoid`, then parameters A and B correspond to the fields `Scale` and `Intercept` of `ScoreTransform`, respectively.

Step Function

The step function that maps score s_j corresponding to observation j to the positive class posterior probability is

$$P\left(s_j\right)=\begin{cases}0; & s<\max\limits_{y_k=-1}s_k\\ \pi; & \max\limits_{y_k=-1}s_k\le s_j\le\min\limits_{y_k=+1}s_k\\ 1; & s_j>\min\limits_{y_k=+1}s_k\end{cases},$$

where:

- s_j the score of observation j.
- +1 and –1 denote the positive and negative classes, respectively.
- π is the prior probability that an observation is in the positive class.

If the output argument `ScoreTransform.Type` is `step`, then the quantities $\max\limits_{y_k=-1}s_k$ and $\min\limits_{y_k=+1}s_k$ correspond to the fields `LowerBound` and `UpperBound` of `ScoreTransform`, respectively.

Constant Function

The constant function maps all scores in a sample to posterior probabilities 1 or 0.

If all observations have posterior probability 1, then they are expected to come from the positive class.

If all observations have posterior probability 0, then they are not expected to come from the positive class.

Examples

Estimate Posterior Probabilities for New Data When Classes Are Inseparable

Load the `ionosphere` data set. Reserve 20 random observations of the data, and consider this set new data.

```
load ionosphere
n = size(X,1);
rng(1);  % For reproducibility

indx = ~ismember([1:n],randsample(n,20)); % Indices for the training data
```

The classes of this data set are inseparable.

Train an SVM classifier using the training data. It is good practice to specify the class order and standardize the data.

```
SVMModel = fitcsvm(X(indx,:),Y(indx),'ClassNames',{'b','g'},...
    'Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier.

Use the new data set to estimate the optimal score-to-posterior-probability transformation function for mapping scores to the posterior probability of an observation being classified as `g`. For efficiency, make a compact version of the SVM classifier `SVMModel`, and pass it and the new data to `fitPosterior`.

```
CompactSVMModel = compact(SVMModel);
[ScoreCSVMModel,ScoreParameters] = fitPosterior(CompactSVMModel,...
    X(~indx,:),Y(~indx));

ScoreTransform = ScoreCSVMModel.ScoreTransform
ScoreParameters


ScoreTransform =

@(S)sigmoid(S,-1.098922e+00,4.519963e-01)


ScoreParameters =

         Type: 'sigmoid'
        Slope: -1.0989
    Intercept: 0.4520
```

`ScoreTransform` is the optimal score transform function. `ScoreParameters` is a structure array having three fields: the score transformation function name (`Type`), the sigmoid slope (`Slope`) and sigmoid intercept (`Intercept`) estimates.

Alternatively, you can pass `SVMModel` and the new data to `fitSVMPosterior`, but this does not have the benefit of efficiency.

Estimate the posterior probabilities that the observations in the new data are in class `g`.

```
[labels,postProbs] = predict(ScoreCSVMModel,X(~indx,:));
table(Y(~indx),labels,postProbs(:,2),...
    'VariableNames',{'TrueLabel','PredictedLabel','PosteriorProbability'})
```

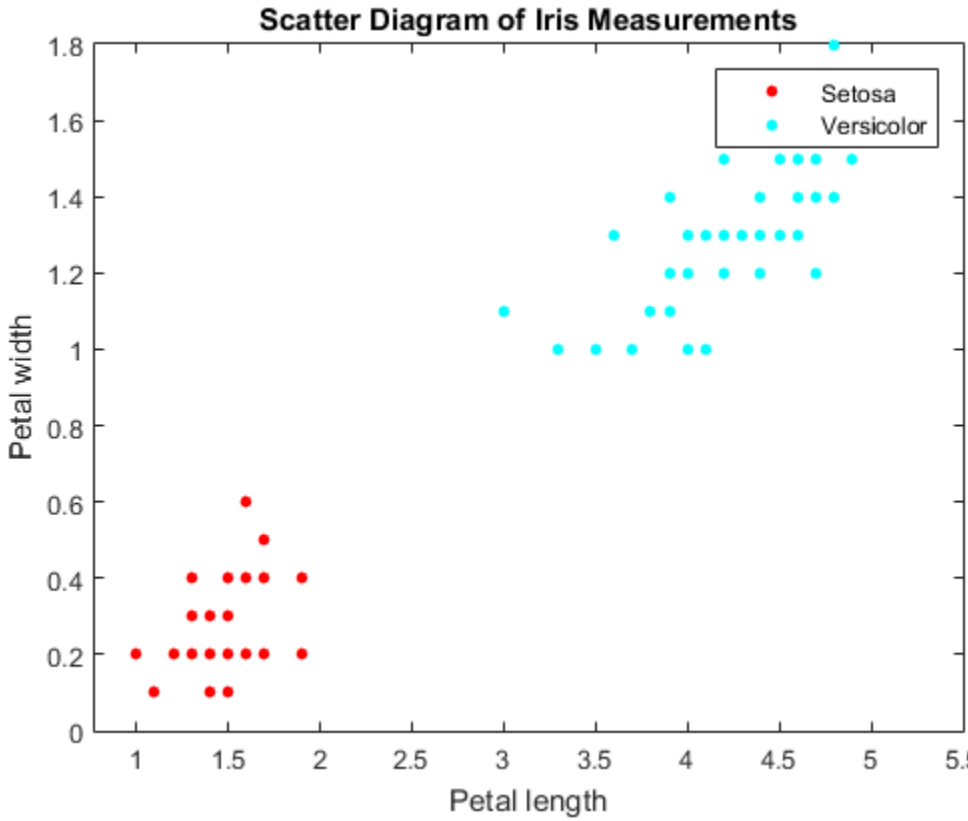
```
ans =

    TrueLabel    PredictedLabel    PosteriorProbability
    _________    ______________    ____________________

    'g'          'g'                  0.78437
    'b'          'b'                 0.024588
    'g'          'g'                  0.82399
    'b'          'b'                0.0061637
    'b'          'b'               3.6118e-06
    'b'          'b'                  0.15688
    'b'          'g'                   0.9622
    'b'          'b'               6.1348e-09
    'b'          'b'                0.0019646
    'g'          'g'                   0.7251
    'g'          'g'                  0.70263
    'b'          'b'                 0.075298
    'g'          'g'                  0.90691
    'g'          'g'                  0.82849
    'b'          'b'                 0.051193
    'g'          'g'                  0.95331
    'b'          'b'                0.0031877
    'b'          'b'                  0.16015
    'g'          'g'                  0.92008
    'g'          'g'                  0.91349
```

Estimate Posterior Probabilities for New Data When Classes Are Separable

Load Fisher's iris data set. Use the petal lengths and widths, and remove the virginica species from the data. Reserve 10 random observations of the data, and consider this set new data.

```
load fisheriris
```

```
classKeep = ~strcmp(species,'virginica');
X = meas(classKeep,3:4);
Y = species(classKeep);

rng(1);  % For reproducibility
indx1 = 1:numel(species);
indx2 = indx1(classKeep);
indx = ~ismember(indx2,randsample(indx2,10)); % Indices for the training data

gscatter(X(indx,1),X(indx,2),Y(indx));
title('Scatter Diagram of Iris Measurements')
xlabel('Petal length')
ylabel('Petal width')
legend('Setosa','Versicolor')
```



The classes are perfectly separable. Therefore, the score-to-posterior-probability transformation function is a step function.

Train an SVM classifier. It is good practice to specify the class order and standardize the data.

```
SVMModel = fitcsvm(X(indx,:),Y(indx),...
    'ClassNames',{'setosa','versicolor'},'Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier.

Use the new data set to estimate the optimal score-to-posterior-probability transformation function for mapping scores to the posterior probability of an observation being classified as `versicolor`. For efficiency, make a compact version of the SVM classifier `SVMModel`, and pass it and the new data to `fitPosterior`.

```
CompactSVMModel = compact(SVMModel);
[ScoreCSVMModel,ScoreParameters] = fitPosterior(CompactSVMModel,...
    X(~indx,:),Y(~indx));

ScoreTransform = ScoreCSVMModel.ScoreTransform
```

```
Warning: Classes are perfectly separated. The optimal score-to-posterior
transformation is a step function.

ScoreTransform =

@(S)step(S,-1.338450e+00,2.012495e+00,5.333333e-01)
```

`fitPosterior` displays a warning whenever the classes are separable, and stores the step function in `ScoreSVMModel.ScoreTransform`.

Display the score function type and its estimated values.

```
ScoreParameters
```

```
ScoreParameters =

                      Type: 'step'
                LowerBound: -1.3385
                UpperBound: 2.0125
```

```
    PositiveClassProbability: 0.5333
```

`ScoreParameters` is a structure array having four fields:

- The score transformation function type (`Type`)
- The score corresponding to negative class boundary (`LowerBound`)
- The score corresponding to positive class boundary (`UpperBound`)
- The positive class probability (`PositiveClassProbability`)

Alternatively, you can pass `SVMModel` and the new data to `fitSVMPosterior`, but this does not have the benefit of efficiency.

Estimate the posterior probabilities that the observations in the new data are versicolor irises.

```
[labels,postProbs] = predict(ScoreCSVMModel,X(~indx,:));
table(Y(~indx),labels,postProbs(:,2),...
    'VariableNames',{'TrueLabel','PredictedLabel','PosteriorProbability'})
```

```
ans =

     TrueLabel      PredictedLabel    PosteriorProbability
    ____________    ______________    ____________________

    'setosa'        'setosa'          0
    'setosa'        'setosa'          0
    'setosa'        'setosa'          0
    'setosa'        'setosa'          0
    'setosa'        'setosa'          0
    'setosa'        'setosa'          0
    'setosa'        'setosa'          0
    'setosa'        'setosa'          0
    'versicolor'    'versicolor'      1
    'versicolor'    'versicolor'      1
```

Since the classes are separable, the step function transforms the positive-class score to:

- `0`, if the score is less than `ScoreParameters.LowerBound`
- `1`, if the score is greater than `ScoreParameters.UpperBound`

- `ScoreParameters.PositiveClassProbability`, if the score is in the interval [`ScoreParameters.LowerBound` , `ScoreParameters.LowerBound`]

Algorithms

If you reestimate the score-to-posterior-probability transformation function, that is, if you pass an SVM classifier to `fitPosterior` or `fitSVMPosterior` and its `ScoreTransform` property is not `none`, then the software:

- Displays a warning
- Resets the original transformation function to `'none'` before estimating the new one

Alternatives

You can also estimate the optimal score-to-posterior-probability function using `fitSVMPosterior`. This function is similar to `fitPosterior`, except it is more broad since it accepts a wider range of SVM classifer types.

References

[1] Platt, J. “Probabilistic outputs for support vector machines and comparisons to regularized likelihood methods”. In: *Advances in Large Margin Classifiers*. Cambridge, MA: The MIT Press, 2000, pp. 61–74.

See Also

`CompactClassificationSVM` | `fitcsvm` | `fitSVMPosterior` | `predict`

fitrtree

Binary decision tree for regression

Syntax

```
tree = fitrtree(x,y)
tree = fitrtree(x,y,Name,Value)
```

Description

`tree = fitrtree(x,y)` returns a regression tree based on the input variables (also known as predictors, features, or attributes) x and output (response) y. The returned tree is a binary tree where each branching node is split based on the values of a column of x.

`tree = fitrtree(x,y,Name,Value)` fits a tree with additional options specified by one or more name-value pair arguments. For example, you can grow a cross-validated tree, hold out a fraction of data for validation, or specify observation weights.

Examples

Construct a Regression Tree

Load the sample data.

```
load carsmall;
```

Construct a regression tree using the sample data.

```
tree = fitrtree([Weight, Cylinders],MPG,...
                'categoricalpredictors',2,'MinParentSize',20,...
                'PredictorNames',{'W','C'})
```

```
tree =
```

```
  RegressionTree
           PredictorNames: {'W'   'C'}
             ResponseName: 'Y'
        ResponseTransform: 'none'
      CategoricalPredictors: 2
            NumObservations: 94
```

Predict the mileage of 4,000-pound cars with 4, 6, and 8 cylinders.

```
mileage4K = predict(tree,[4000 4; 4000 6; 4000 8])
```

```
mileage4K =

   19.2778
   19.2778
   14.3889
```

Control Regression Tree Depth

You can control the depth of trees using the `MaxNumSplits`, `MinLeafSize`, or `MinParentSize` name-value pair parameters. `fitrtree` grows deep decision trees by default. You can grow shallower trees to reduce model complexity or computation time.

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
X = [Displacement Horsepower Weight];
```

The default values of the tree-depth controllers for growing regression trees are:

- `n - 1` for `MaxNumSplits`. `n` is the training sample size.
- `1` for `MinLeafSize`.
- `10` for `MinParentSize`.

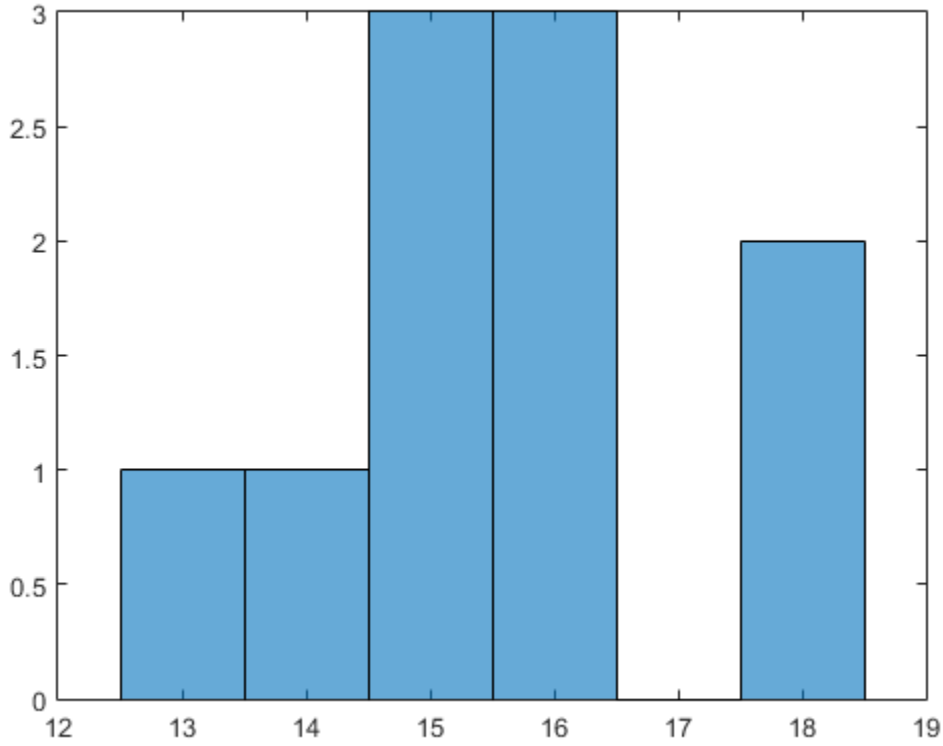
These default values tend to grow deep trees for large training sample sizes.

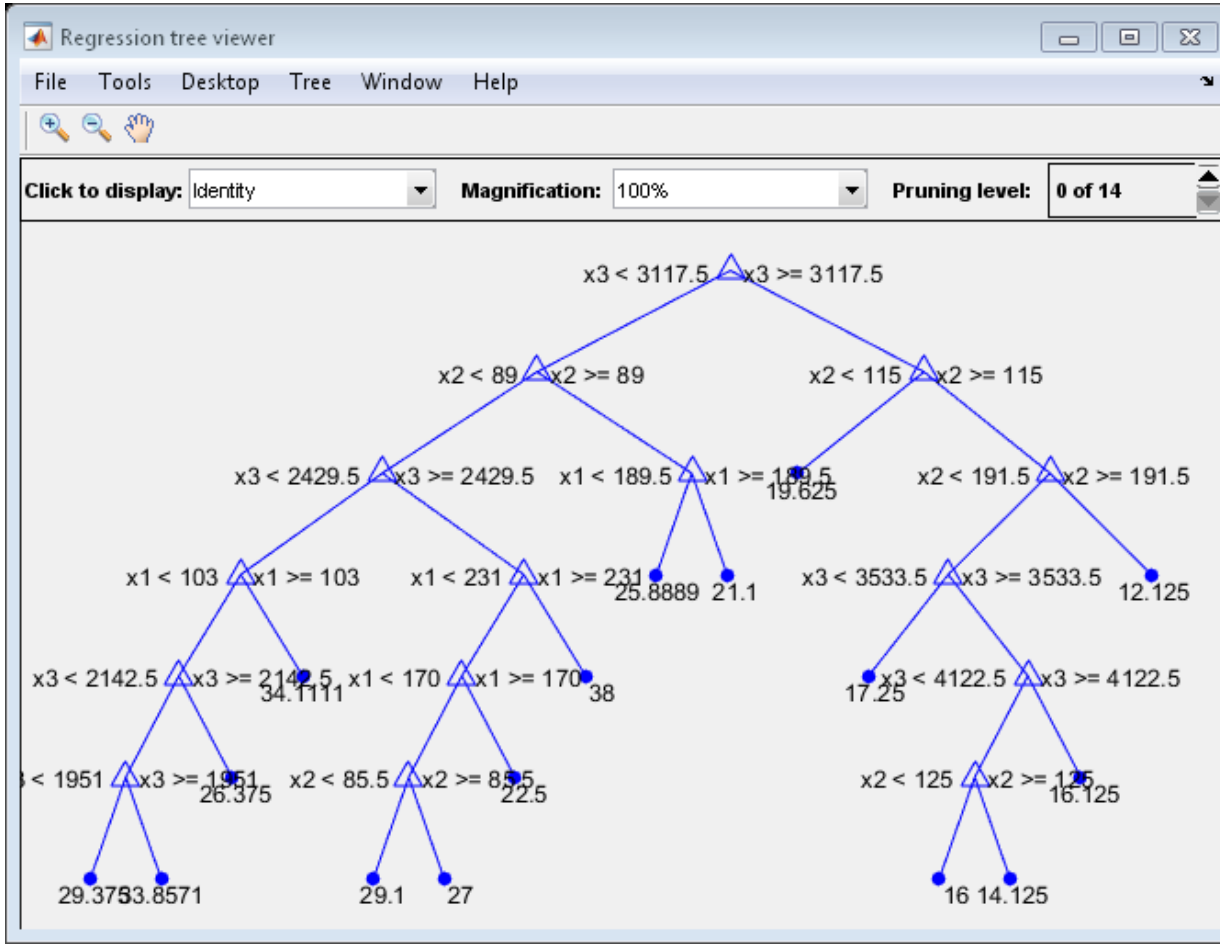
Train a regression tree using the default values for tree-depth control. Cross validate the model using 10-fold cross validation.

```
rng(1); % For reproducibility
MdlDefault = fitrtree(X,MPG,'CrossVal','on');
```

Draw a histogram of the number of imposed on the trees. The number of imposed splits is one less than the number of leaves. Also, view one of the trees.

```
numBranches = @(x)sum(x.IsBranch);
mdlDefaultNumSplits = cellfun(numBranches, MdlDefault.Trained);

figure;
histogram(mdlDefaultNumSplits)

view(MdlDefault.Trained{1},'Mode','graph')
```

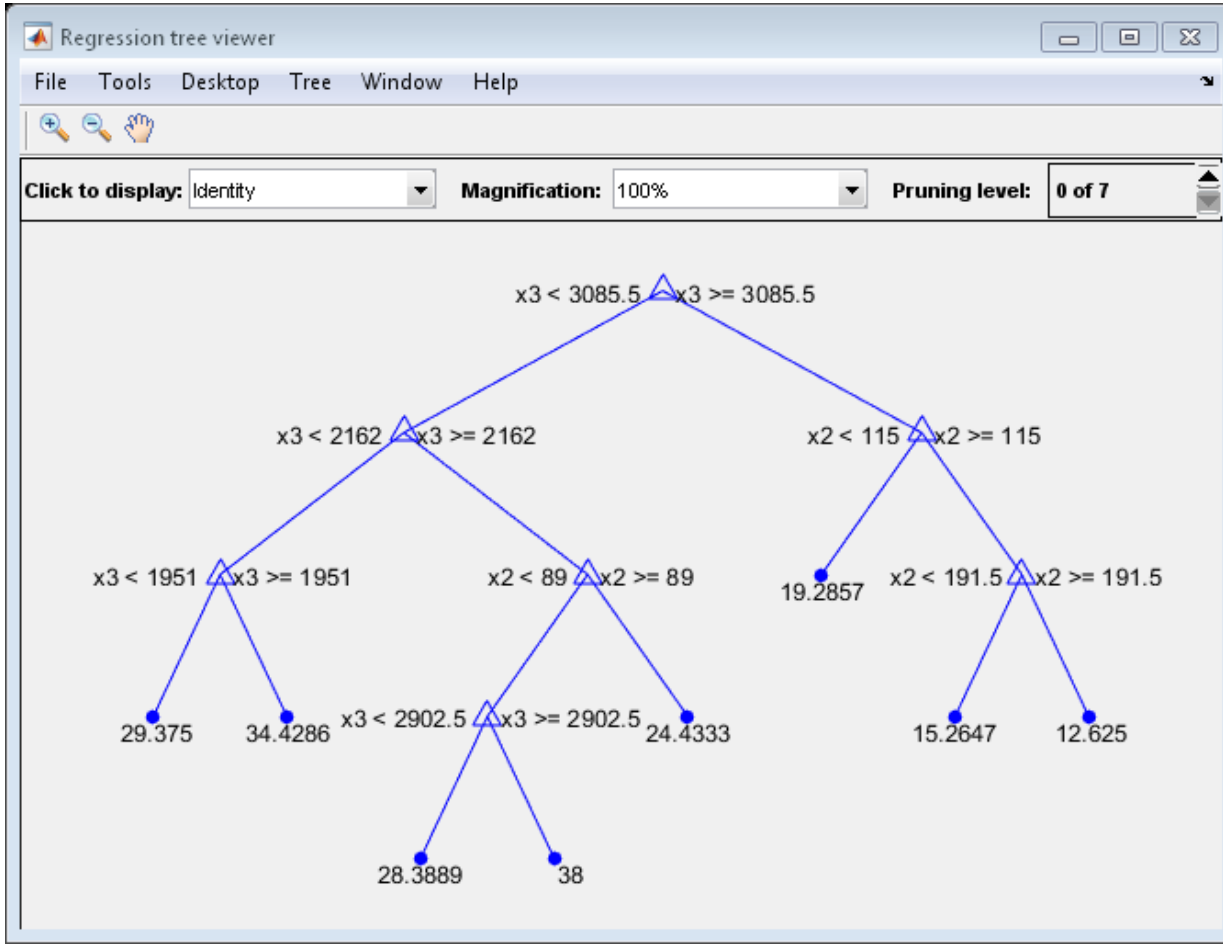




The average number of splits is between 14 and 15.

Suppose that you want a regression tree that is not as complex (deep) as the ones trained using the default number of splits. Train another regression tree, but set the maximum number of splits at 7, which is about half the mean number of splits from the default regression tree. Cross validate the model using 10-fold cross validation.

```
Mdl7 = fitrtree(X,MPG,'MaxNumSplits',7,'CrossVal','on');
view(Mdl7.Trained{1},'Mode','graph')
```



Compare the cross validation MSEs of the models.

```
mseDefault = kfoldLoss(MdlDefault)
mse7 = kfoldLoss(Mdl7)
```

```
mseDefault =

   27.7277
```

```
mse7 =

   28.3833
```

`Mdl7` is much less complex and performs only slightly worse than `MdlDefault`.

Input Arguments

x — Predictor values

matrix of scalar values

Predictor values, specified as a matrix of scalar values. Each column of x represents one variable, and each row represents one observation.

`fitrtree` considers `NaN` values in x as missing values. `fitrtree` does not use observations with all missing values for x in the fit. `fitrtree` uses observations with some missing values for x to find splits on variables for which these observations have valid values.

Data Types: `single | double`

y — Response values

vector of scalar values

Response values, specified as a vector of scalar values with the same number of rows as x. Each entry in y is the response to the data in the corresponding row of x.

`fitrtree` considers `NaN` values in y to be missing values. `fitrtree` does not use observations with missing values for y in the fit.

Data Types: `single | double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'CrossVal','on','MinParentSize',30` specifies a cross-validated regression tree with a minimum of 30 observations per branch node.

'CategoricalPredictors' — Categorical predictors list

numeric or logical vector | cell array of strings | character matrix | 'all'

Categorical predictors list, specified as the comma-separated pair consisting of 'CategoricalPredictors' and one of the following:

- A numeric vector with indices from 1 through p, where p is the number of columns of x.
- A logical vector of length p, where a true entry means that the corresponding column of x is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in the PredictorNames property.
- A character matrix, where each row of the matrix is a name of a predictor variable. Pad the names with extra blanks so each row of the character matrix has the same length.
- 'all', meaning all predictors are categorical.

Data Types: single | double | logical | char | cell

'CrossVal' — Cross-validation flag

'off' (default) | 'on'

Cross-validation flag, specified as the comma-separated pair consisting of 'CrossVal' and either 'on' or 'off'.

If 'on', fitrtree grows a cross-validated decision tree with 10 folds. You can override this cross-validation setting using one of the 'KFold', 'Holdout', 'Leaveout', or 'CVPartition' name-value pair arguments. You can only use one of these arguments at a time when creating a cross-validated tree.

Alternatively, cross validate tree later using the crossval method.

Example: 'CrossVal','on'

'CVPartition' — Partition for cross-validated tree

cvpartition object

Partition for cross-validated tree, specified as the comma-separated pair consisting of 'CVPartition' and an object created using cvpartition.

If you use 'CVPartition', you cannot use any of the 'KFold', 'Holdout', or 'Leaveout' name-value pair arguments.

'Holdout' — Fraction of data for holdout validation

0 (default) | scalar value in the range [0,1]

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of 'Holdout' and a scalar value in the range [0,1]. Holdout validation tests the specified fraction of the data, and uses the rest of the data for training.

If you use 'Holdout', you cannot use any of the 'CVPartition', 'KFold', or 'Leaveout' name-value pair arguments.

Example: 'Holdout',0.1

Data Types: single | double

'KFold' — Number of folds

10 (default) | positive integer value

Number of folds to use in a cross-validated tree, specified as the comma-separated pair consisting of 'KFold' and a positive integer value.

If you use 'KFold', you cannot use any of the 'CVPartition', 'Holdout', or 'Leaveout' name-value pair arguments.

Example: 'KFold',8

Data Types: single | double

'Leaveout' — Leave-one-out cross-validation flag

'off' (default) | 'on'

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of 'Leaveout' and either 'on' or 'off'. Specify 'on' to use leave-one-out cross validation.

If you use 'Leaveout', you cannot use any of the 'CVPartition', 'Holdout', or 'KFold' name-value pair arguments.

Example: 'Leaveout','on'

'MaxNumSplits' — Maximal number of decision splits

size(X,1) - 1 (default) | positive integer

Maximal number of decision splits (or branch nodes), specified as the comma-separated pair consisting of 'MaxNumSplits' and a positive integer. fitrtree splits

`MaxNumSplits` or fewer branch nodes. For more details on splitting behavior, see Algorithms.

Example: `'MaxNumSplits',5`

Data Types: `single` | `double`

`'MergeLeaves'` — Leaf merge flag

`'on'` (default) | `'off'`

Leaf merge flag, specified as the comma-separated pair consisting of `'MergeLeaves'` and either `'on'` or `'off'`.

If `MergeLeaves` is `'on'`, then `fitrtree` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. Otherwise, `fitrtree` does not merge leaves.

Example: `'MergeLeaves','off'`

`'MinLeafSize'` — Minimum number of leaf node observations

`1` (default) | positive integer value

Minimum number of leaf node observations, specified as the comma-separated pair consisting of `'MinLeafSize'` and a positive integer value. Each leaf has at least `MinLeafSize` observations per tree leaf. If you supply both `MinParentSize` and `MinLeafSize`, `fitrtree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinLeafSize',3`

Data Types: `single` | `double`

`'MinParentSize'` — Minimum number of branch node observations

`10` (default) | positive integer value

Minimum number of branch node observations, specified as the comma-separated pair consisting of `'MinParentSize'` and a positive integer value. Each branch node in the tree has at least `MinParentSize` observations. If you supply both `MinParentSize` and `MinLeafSize`, `fitrtree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinParentSize',8`

Data Types: `single` | `double`

'NumVariablesToSample' — Number of predictors to select at random for each split
'all' (default) | positive integer value

Number of predictors to select at random for each split, specified as the comma-separated pair consisting of 'NumVariablesToSample' and a positive integer value. You can also specify 'all' to use all available predictors.

Example: 'NumVariablesToSample',3

Data Types: single | double

'PredictorNames' — Predictor variable names
{'x1','x2',...} (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of 'PredictorNames' and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

Data Types: cell

'Prune' — Flag to estimate the optimal sequence of pruned subtrees
'on' (default) | 'off'

Flag to estimate the optimal sequence of pruned subtrees, specified as the comma-separated pair consisting of 'Prune' and either 'on' or 'off'.

If Prune is 'on', then fitrtree grows the regression tree and estimates the optimal sequence of pruned subtrees, but does not prune the regression tree. Otherwise, fitrtree grows the regression tree without estimating the optimal sequence of pruned subtrees.

To prune a trained RegressionTree model, pass it to prune.

Example: 'Prune','off'

'PruneCriterion' — Pruning criterion
'mse'

Pruning criterion, specified as the comma-separated pair consisting of 'PruneCriterion' and 'mse'.

Example: 'PruneCriterion','mse'

'QuadraticErrorTolerance' — Quadratic error tolerance
1e-6 (default) | positive scalar value

Quadratic error tolerance per node, specified as the comma-separated pair consisting of `'QuadraticErrorTolerance'` and a positive scalar value. Splitting nodes stops when the quadratic error per node drops below `QuadraticErrorTolerance*QED`, where `QED` is the quadratic error for all data computed before the decision tree is grown.

Example: `'QuadraticErrorTolerance',1e-4`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable in y.

Example: `'ResponseName','Response'`

Data Types: `char`

`'ResponseTransform'` — Response transform function

`'none'` (default) | function handle

Response transform function for transforming the raw response values, specified as the comma-separated pair consisting of `'ResponseTransform'` and either a function handle or `'none'`. The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function using dot notation:

```
tree.ResponseTransform = @function
```

Data Types: `function_handle`

`'SplitCriterion'` — Split criterion

`'MSE'`

Split criterion, specified as the comma-separated pair consisting of `'SplitCriterion'` and `'MSE'`, meaning mean squared error.

Example: `'SplitCriterion','MSE'`

`'Surrogate'` — Surrogate decision splits flag

`'off'` | `'on'` | `'all'` | positive integer value

Surrogate decision splits flag, specified as the comma-separated pair consisting of `'Surrogate'` and one of `'on'`, `'off'`, `'all'`, or a positive integer value.

- When `'on'`, `fitrtree` finds at most 10 surrogate splits at each branch node.
- When set to a positive integer value, `fitrtree` finds at most the specified number of surrogate splits at each branch node.
- When set to `'all'`, `fitrtree` finds all surrogate splits at each branch node. The `'all'` setting can use considerable time and memory.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also lets you compute measures of predictive association between predictors.

Example: `'Surrogate','on'`

Data Types: `single` | `double`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of scalar values. The length of `Weights` is the number of rows in x.

Data Types: `single` | `double`

Output Arguments

`tree` — Regression tree

regression tree object

Regression tree, returned as a regression tree object. Note that using the `'Crossval'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a tree of class `RegressionPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, `tree` is of class `RegressionTree`, and you can use the `predict` method to make predictions.

More About

Tips

By default, Prune is `'on'`. However, this specification does not prune the regression tree. To prune a trained regression tree, pass the regression tree to `prune`.

Algorithms

- If MergeLeaves is `'on'` and PruneCriterion is `'error'` (which are the default values for these name-value pair arguments), then the software applies pruning only to the leaves and by using classification error. This specification amounts to merging leaves that share the most popular class per leaf.
- To accommodate `MaxNumSplits`, `fitrtree` splits all nodes in the current *layer*, and then counts the number of branch nodes. A layer is the set of nodes that are equidistant from the root node. If the number of branch nodes exceeds `MaxNumSplits`, `fitrtree` follows this procedure:

  1. Determine how many branch nodes in the current layer must be unsplit so that there are at most `MaxNumSplits` branch nodes.
  2. Sort the branch nodes by their impurity gains.
  3. Unsplit the number of least successful branches.
  4. Return the decision tree grown so far.

  This procedure produces maximally balanced trees.
- The software splits branch nodes layer by layer until at least one of these events occurs:

  - There are MaxNumSplits branch nodes.
  - A proposed split causes the number of observations in at least one branch node to be fewer than MinParentSize.
  - A proposed split causes the number of observations in at least one leaf node to be fewer than MinLeafSize.
  - The algorithm cannot find a good split within a layer (i.e., the pruning criterion (see PruneCriterion), does not improve for all proposed splits in a layer). A special case is when all nodes are pure (i.e., all observations in the node have the same class).

  `MaxNumSplits` and `MinLeafSize` do not affect splitting at their default values. Therefore, if you set `'MaxNumSplits'`, splitting might stop due to the value of `MinParentSize`, before `MaxNumSplits` splits occur.
- For dual-core systems and above, `fitrtree` parallelizes training decision trees using Intel Threading Building Blocks (TBB). For details on Intel TBB, see https://software.intel.com/en-us/intel-tbb.

- "Splitting Categorical Predictors" on page 16-65

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`predict` | `prune` | `RegressionPartitionedModel` | `RegressionTree`

fitSVMPosterior

Fit posterior probabilities

Syntax

```
ScoreSVMModel = fitSVMPosterior(SVMModel)
ScoreSVMModel = fitSVMPosterior(SVMModel,Name,Value)
ScoreSVMModel = fitSVMPosterior(SVMModel,X,Y)
[ScoreSVMModel,ScoreTransform] = fitSVMPosterior(___)
```

Description

`ScoreSVMModel = fitSVMPosterior(SVMModel)` returns `ScoreSVMModel`, which is a trained, support vector machine (SVM) classifier containing the optimal score-to-posterior-probability transformation function for two-class learning.

The software fits the appropriate score-to-posterior-probability transformation function using the SVM classifier`SVMModel`, and by cross validation using the stored predictor data (`SVMModel.X`) and the class labels (`SVMModel.Y`). The transformation function computes the posterior probability that an observation is classified into the positive class (`SVMModel.Classnames(2)`).

- If the classes are inseparable, then the transformation function is the sigmoid function.
- If the classes are perfectly separable, the transformation function is the step function.
- In two-class learning, if one of the two classes has a relative frequency of 0, then the transformation function is the constant function. `fitSVMPosterior` is not appropriate for one-class learning.
- If `SVMModel` is a `ClassificationSVM` classifier, then the software estimates the optimal transformation function by 10-fold cross validation as outlined in [1]. Otherwise, `SVMModel` must be a `ClassificationPartitionedModel` classifier. `SVMModel` specifies the cross-validation method.
- The software stores the optimal transformation function in `ScoreSVMModel.ScoreTransform`.

`ScoreSVMModel = fitSVMPosterior(SVMModel,Name,Value)` uses additional options specified by one or more Name,Value pair arguments provided SVMModel is a `ClassificationSVM` classifier.

For example, you can specify the number of folds to use in *k*-fold cross validation.

`ScoreSVMModel = fitSVMPosterior(SVMModel,X,Y)` returns a trained, support vector classifier containing the transformation function from the trained, compact SVM classifier SVMModel. The software estimates the score transformation function using predictor data X and class labels Y.

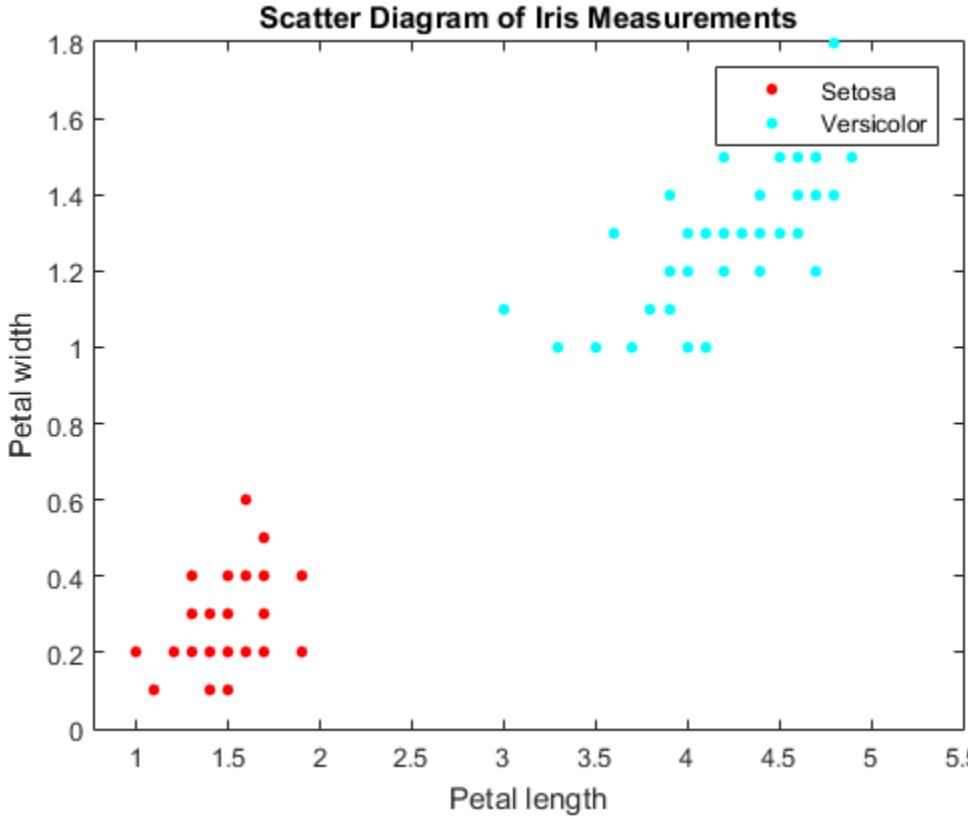
`[ScoreSVMModel,ScoreTransform] = fitSVMPosterior(___)` additionally returns the transformation function parameters (ScoreTransform) using any of the input arguments in the previous syntaxes.

Examples

Fit the Score-to-Posterior Probability Function for Separable Classes

Load Fisher's iris data set. Train the classifier using the petal lengths and widths, and remove the virginica species from the data.

```
load fisheriris
classKeep = ~strcmp(species,'virginica');
X = meas(classKeep,3:4);
y = species(classKeep);

gscatter(X(:,1),X(:,2),y);
title('Scatter Diagram of Iris Measurements')
xlabel('Petal length')
ylabel('Petal width')
legend('Setosa','Versicolor')
```



The classes are perfectly separable. Therefore, the score transformation function is a step function.

Train an SVM classifier using the data. Cross validate the classifer using 10-fold cross validation (the default).

```
rng(1);
CVSVMModel = fitcsvm(X,y,'CrossVal','on');
```

`CVSVMModel` is a trained `ClassificationPartitionedModel` SVM classifier.

Estimate the step function that transforms scores to posterior probabilities.

```
[ScoreCVSVMModel,ScoreParameters] = fitSVMPosterior(CVSVMModel);
```

```
Warning: Classes are perfectly separated. The optimal score-to-posterior
transformation is a step function.
```

`fitSVMPosterior` does the following:

- Uses the data that the software stored in `CVSVMModel` to fit the transformation function
- Warns whenever the classes are separable
- Stores the step function in `ScoreCSVMModel.ScoreTransform`

Display the score function type and its parameter values.

```
ScoreParameters
```

```
ScoreParameters =

                        Type: 'step'
                  LowerBound: -0.8431
                  UpperBound: 0.6897
    PositiveClassProbability: 0.5000
```

`ScoreParameters` is a structure array with four fields:

- The score transformation function type (`Type`)
- The score corresponding to the negative class boundary (`LowerBound`)
- The score corresponding to the positive class boundary (`UpperBound`)
- The positive class probability (`PositiveClassProbability`)

Since the classes are separable, the step function transforms the score to either `0` or `1`, which is the posterior probability that an observation is a versicolor iris.

Fit the Score-to-Posterior Probability Function for Inseparable Classes

Load the `ionosphere` data set.

```
load ionosphere
```

The classes of this data set are not separable.

Train an SVM classifier. Cross validate using 10-fold cross validation (the default). It is good practice to standardize the predictors and specify the class order.

```
rng(1) % For reproducibility
CVSVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true,...
    'CrossVal','on');
ScoreTransform = CVSVMModel.ScoreTransform
```

```
ScoreTransform =

none
```

`CVSVMModel` is a trained `ClassificationPartitionedModel` SVM classifier. The positive class is `'g'`. The `ScoreTransform` property is `none`.

Estimate the optimal score function for mapping observation scores to posterior probabilities of an observation being classified as `'g'`.

```
[ScoreCVSVMModel,ScoreParameters] = fitSVMPosterior(CVSVMModel);
ScoreTransform = ScoreCVSVMModel.ScoreTransform
ScoreParameters
```

```
ScoreTransform =

@(S)sigmoid(S,-9.481576e-01,-1.218300e-01)


ScoreParameters =

         Type: 'sigmoid'
        Slope: -0.9482
    Intercept: -0.1218
```

`ScoreTransform` is the optimal score transform function. `ScoreParameters` contains the score transformation function, slope estimate, and the intercept estimate.

You can estimate test-sample, posterior probabilities by passing `ScoreCVSVMModel` to `kfoldPredict`.

Estimate Posterior Probabilities for Test Samples

Estimate positive class posterior probabilities for the test set of an SVM algorithm.

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. Specify a 20% holdout sample. It is good practice to standardize the predictors and specify the class order.

```
rng(1) % For reproducibility
CVSVMModel = fitcsvm(X,Y,'Holdout',0.2,'Standardize',true,...
    'ClassNames',{'b','g'});
```

`CVSVMModel` is a trained `ClassificationPartitionedModel` cross-validated classifier.

Estimate the optimal score function for mapping observation scores to posterior probabilities of an observation being classified as `'g'`.

```
ScoreCVSVMModel = fitSVMPosterior(CVSVMModel);
```

`ScoreSVMModel` is a trained `ClassificationPartitionedModel` cross-validated classifier containing the optimal score transformation function estimated from the training data.

Estimate the out-of-sample positive class posterior probabilities. Display the results for the first 10 out-of-sample observations.

```
[~,OOSPostProbs] = kfoldPredict(ScoreCVSVMModel);
indx = ~isnan(OOSPostProbs(:,2));
hoObs = find(indx); % Holdout observation numbers
OOSPostProbs = [hoObs, OOSPostProbs(indx,2)];
table(OOSPostProbs(1:10,1),OOSPostProbs(1:10,2),...
    'VariableNames',{'ObservationIndex','PosteriorProbability'})
```

```
ans =

    ObservationIndex    PosteriorProbability
    ________________    ____________________

     6                     0.17378
     7                     0.89637
     8                   0.0076609
     9                     0.91602
    16                     0.026718
```

```
22                  4.6081e-06
23                      0.9024
24                  2.4129e-06
38                  0.00042697
41                     0.86427
```

Input Arguments

`SVMModel` — Trained SVM classifier

`ClassificationSVM` classifier | `CompactClassificationSVM` classifier | `ClassificationPartitionedModel` classifier

Trained SVM classifier, specified as a `ClassificationSVM`, `CompactClassificationSVM`, or `ClassificationPartitionedModel` classifier.

If `SVMModel` is a `ClassificationSVM` classifier, then you can set optional name-value pair arguments.

If `SVMModel` is a `CompactClassificationSVM` classifier, then you must input predictor data `X` and class labels `Y`.

`X` — Predictor data

matrix

Predictor data used to estimate the score-to-posterior-probability transformation function, specified as a matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature).

The length of `Y` and the number of rows of `X` must be equal.

If you set `'Standardize',true` in `fitcsvm` to train `SVMModel`, then the software standardizes the columns of `X` using the corresponding means in `SVMModel.Mu` and standard deviations in `SVMModel.Sigma`. If the software fits the transformation-function parameter estimates using standardized data, then the estimates might differ from estimation without standardized data.

Data Types: `double` | `single`

Y — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels used to estimate the score-to-posterior-probability transformation function, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `Y` is a character array, then each element must correspond to one class label.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'KFold',8` performs 8-fold cross validation when `SVMModel` is a `ClassificationSVM` classifier.

'CVPartition' — Cross-validation partition

`[]` (default) | `cvpartition` partition

Cross-validation partition used to compute the transformation function, specified as the comma-separated pair consisting of `'CVPartition'` and a `cvpartition` partition as created by `cvpartition`. You can use only one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

`crossval` splits the data into subsets using `cvpartition`.

'Holdout' — Fraction of data for holdout validation

scalar value in the range (0,1)

Fraction of data for holdout validation used to compute the transformation function, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range (0,1). Holdout validation tests the specified fraction of the data, and uses the remaining data for training.

You can use only one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'Holdout',0.1`

Data Types: `double` | `single`

`'KFold'` — Number of folds

`10` (default) | positive integer value

Number of folds to use when computing the transformation function, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

You can use only one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag

`'off'` (default) | `'on'`

Leave-one-out cross-validation flag indicating whether to use leave-one-out cross validation to compute the transformation function, specified as the comma-separated pair consisting of `'Leaveout'` and `'on'` or `'off'`. Use leave-one-out cross validation by using `'on'`.

You can use only one of these four options at a time for creating a cross-validated model: `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`.

Example: `'Leaveout','on'`

Output Arguments

`ScoreSVMModel` — Trained SVM classifier

`ClassificationSVM` classifier | `CompactClassificationSVM` classifier | `ClassificationPartitionedModel` classifier

Trained SVM classifier containing the estimated score transformation function, returned as a `ClassificationSVM`, `CompactClassificationSVM`, or `ClassificationPartitionedModel` classifier.

The `ScoreSVMModel` classifier type is the same as the `SVMModel` classifier type.

To estimate posterior probabilities, pass `ScoreSVMModel` and predictor data to `predict`. If you set `'Standardize',true` in `fitcsvm` to train `SVMModel`, then `predict` standardizes the columns of `X` using the corresponding means in `SVMModel.Mu` and standard deviations in `SVMModel.Sigma`.

`ScoreTransform` — Optimal score-to-posterior-probability transformation function parameters

structure array

Optimal score-to-posterior-probability transformation function parameters, specified as a structure array. If field `Type` is:

- `sigmoid`, then `ScoreTransform` has these fields:
  - `Slope` — The value of A in the sigmoid function
  - `Intercept` — The value of `B` in the sigmoid function
- `step`, then `ScoreTransform` has these fields:
  - `PositiveClassProbability`: the value of π in the step function. π represents:
    - The probability that an observation is in the positive class.
    - The posterior probability that a score is in the interval (`LowerBound`,`UpperBound`).
  - `LowerBound`: the value $\max_{y_n=-1} s_n$ in the step function. It represents the lower bound of the interval that assigns the posterior probability of being in the positive class `PositiveClassProbability` to scores. Any observation with a score less than `LowerBound` has posterior probability of being the positive class `0`.
  - `UpperBound`: the value $\min_{y_n=+1} s_n$ in the step function. It represents the upper bound of the interval that assigns the posterior probability of being in the positive class `PositiveClassProbability`. Any observation with a score greater than `UpperBound` has posterior probability of being the positive class `1`.
- `constant`, then `ScoreTransform.PredictedClass` contains the name of the class prediction.

  This result is the same as `SVMModel.ClassNames`. The posterior probability of an observation being in `ScoreTransform.PredictedClass` is always `1`.

More About

Sigmoid Function

The sigmoid function that maps score s_j corresponding to observation j to the positive class posterior probability is

$$P(s_j) = \frac{1}{1+\exp(As_j + B)}.$$

If the output argument `ScoreTransform.Type` is `sigmoid`, then parameters A and B correspond to the fields `Scale` and `Intercept` of `ScoreTransform`, respectively.

Step Function

The step function that maps score s_j corresponding to observation j to the positive class posterior probability is

$$P\left(s_j\right) = \begin{cases} 0; & s < \max\limits_{y_k=-1} s_k \\ \pi; & \max\limits_{y_k=-1} s_k \le s_j \le \min\limits_{y_k=+1} s_k \\ 1; & s_j > \min\limits_{y_k=+1} s_k \end{cases},$$

where:

- s_j the score of observation j.
- +1 and –1 denote the positive and negative classes, respectively.
- π is the prior probability that an observation is in the positive class.

If the output argument `ScoreTransform.Type` is `step`, then the quantities $\max\limits_{y_k=-1} s_k$ and $\min\limits_{y_k=+1} s_k$ correspond to the fields `LowerBound` and `UpperBound` of `ScoreTransform`, respectively.

Constant Function

The constant function maps all scores in a sample to posterior probabilities 1 or 0.

If all observations have posterior probability 1, then they are expected to come from the positive class.

If all observations have posterior probability 0, then they are not expected to come from the positive class.

Tips

Here is one way to predict positive class posterior probabilities.

1. Train an SVM classifier by passing the data to `fitcsvm`. The result is a trained SVM classifier, such as, `SVMModel`, that stores the data. The software sets the score transformation function property (`SVMModel.ScoreTransformation`) to `none`.
2. Pass the trained SVM classifier `SVMModel` to `fitSVMPosterior` or `fitPosterior`. The result, for example, `ScoreSVMModel`, is the same, trained SVM classifier as `SVMModel`, except the software sets `ScoreSVMModel.ScoreTransformation` to the optimal score transformation function.

   If you skip step 2, then `predict` returns the positive class score rather than the positive class posterior probability.
3. Pass the trained SVM classifier containing the optimal score transformation function (`ScoreSVMModel`) and predictor data matrix to `predict`. The second column of the second output argument stores the positive class posterior probabilities corresponding to each row of the predictor data matrix.

Algorithms

If you reestimate the score-to-posterior-probability transformation function, that is, if you pass an SVM classifier to `fitPosterior` or `fitSVMPosterior` and its `ScoreTransform` property is not `none`, then the software:

- Displays a warning
- Resets the original transformation function to `'none'` before estimating the new one

References

[1] Platt, J. “Probabilistic outputs for support vector machines and comparisons to regularized likelihood methods”. In: *Advances in Large Margin Classifiers*. Cambridge, MA: The MIT Press, 2000, pp. 61–74.

See Also

`ClassificationPartitionedModel` | `ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm` | `fitPosterior` | `fitPosterior` | `kfoldPredict` | `predict`

fitted

Class: GeneralizedLinearMixedModel

Fitted responses from generalized linear mixed-effects model

Syntax

```
mufit = fitted(glme)
mufit = fitted(glme,Name,Value)
```

Description

`mufit = fitted(glme)` returns the fitted conditional response of the generalized linear mixed-effects model glme.

`mufit = fitted(glme,Name,Value)` returns the fitted response with additional options specified by one or more name-value pair arguments. For example, you can specify to compute the marginal fitted response.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Conditional'` — Indicator for conditional response

`true` (default) | `false`

Indicator for conditional response, specified as the comma-separated pair consisting of `'Conditional'` and one of the following.

`true`	Contributions from both fixed effects and random effects (conditional)
`false`	Contribution from only fixed effects (marginal)

To obtain fitted marginal response values, `fitted` computes the conditional mean of the response with the empirical Bayes predictor vector of random effects b set equal to 0. For more information, see "Conditional and Marginal Response" on page 22-1915

Example: `'Conditional',false`

Output Arguments

`mufit` — Fitted response values

n-by-1 vector

Fitted response values, returned as an n-by-1 vector, where n is the number of observations.

Definitions

Conditional and Marginal Response

A *conditional response* includes contributions from both fixed- and random-effects predictors. A *marginal response* includes contribution from only fixed effects.

Suppose the generalized linear mixed-effects model `glme` has an n-by-p fixed-effects design matrix `X` and an n-by-q random-effects design matrix `Z`. Also, suppose the estimated p-by-1 fixed-effects vector is $\hat{\beta}$, and the q-by-1 empirical Bayes predictor vector of random effects is $\hat{b}$.

The fitted conditional response corresponds to the `'Conditional',true` name-value pair argument, and is defined as

$$\hat{\mu}_{cond} = g^{-1}(\hat{\eta}_{ME}),$$

where $\hat{\eta}_{ME}$ is the linear predictor including the fixed- and random-effects of the generalized linear mixed-effects model

$$\hat{\eta}_{ME} = X\hat{\beta} + Z\hat{b} + \delta .$$

The fitted marginal response corresponds to the `'Conditional',false` name-value pair argument, and is defined as

$$\hat{\mu}_{mar} = g^{-1}(\hat{\eta}_{FE}),$$

where $\hat{\eta}_{FE}$ is the linear predictor including only the fixed-effects portion of the generalized linear mixed-effects model

$$\hat{\eta}_{FE} = X\hat{\beta} + \delta .$$

Examples

Plot Observed Versus Fitted Values

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The

company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where $i = 1, 2, ..., 20$) during batch j (where $j = 1, 2, ..., 5$).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

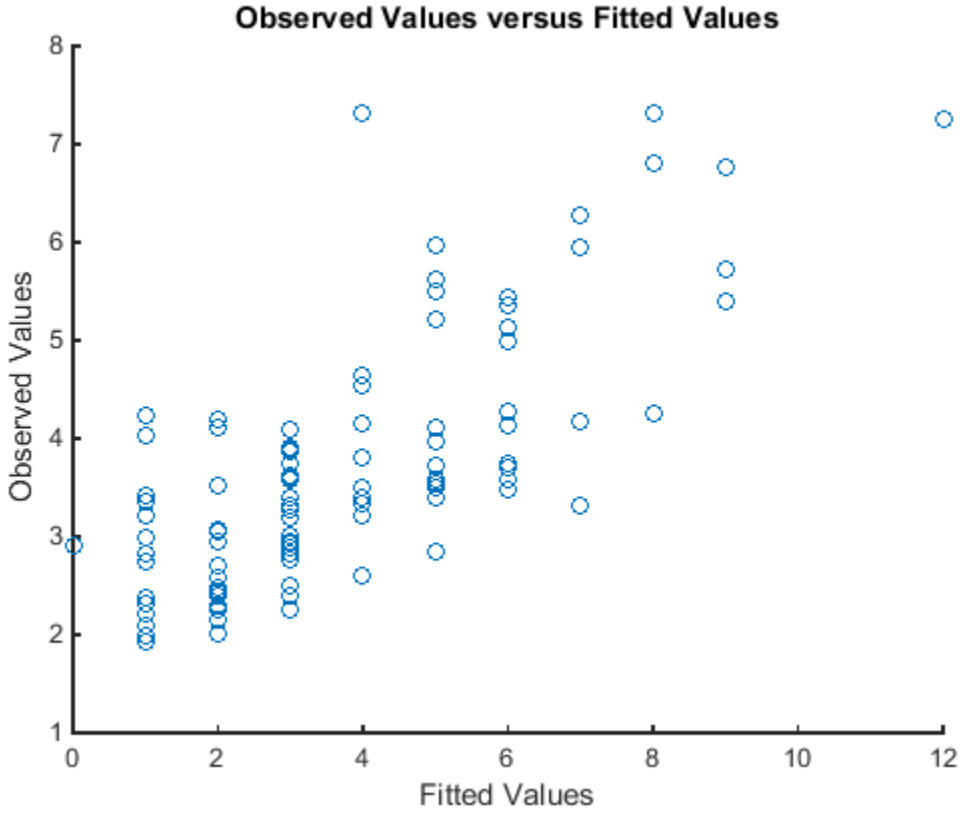
```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Generate the fitted conditional mean values for the model.

```
mufit = fitted(glme);
```

Create a scatterplot of the observed values versus fitted values.

```
figure
scatter(mfr.defects,mufit)
title('Residuals versus Fitted Values')
xlabel('Fitted Values')
ylabel('Residuals')
```



See Also

`GeneralizedLinearMixedModel` | `designMatrix` | `fitglme` | `residuals` | `response`

fitted

Class: LinearMixedModel

Fitted responses from a linear mixed-effects model

Syntax

```
yfit = fitted(lme)
yfit = fitted(lme,Name,Value)
```

Description

`yfit = fitted(lme)` returns the fitted conditional response from the linear mixed-effects model `lme`.

`yfit = fitted(lme,Name,Value)` returns the fitted response from the linear mixed-effects model `lme` with additional options specified by one or more Name,Value pair arguments.

For example, you can specify if you want to compute the fitted marginal response.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Conditional'` — Indicator for conditional response

True (default) | False

Indicator for conditional response, specified as the comma-separated pair consisting of `'Conditional'` and either of the following.

`True`	Contribution from both fixed effects and random effects (conditional)
`False`	Contribution from only fixed effects (marginal)

Example: `'Conditional','False'`

Output Arguments

`yfit` — Fitted response values

n-by-1 vector

Fitted response values, returned as an *n*-by-1 vector, where *n* is the number of observations.

Examples

Compute Fitted Conditional and Marginal Responses

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables containing estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the Center for Disease Control and Prevention, CDC).

To fit a linear-mixed effects model, your data must be in a properly formatted dataset array. To fit a linear mixed-effects model with the influenza rates as the responses and region as the predictor variable, combine the nine columns corresponding to the regions into a tall array. The new dataset array, `flu2`, must have the response variable, `FluRate`, the nominal variable, `Region`, that shows which region each estimate is from, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Fit a linear mixed-effects model with fixed effects for region and a random intercept that varies by `Date`.

Region is a categorical variable. You can specify the contrasts for categorical variables using the `DummyVarCoding` name-value pair argument when fitting the model. When you do not specify the contrasts, `fitlme` uses the `'reference'` contrast by default. Because the model has an intercept, `fitlme` takes the first region, `NE`, as the reference and creates eight dummy variables representing the other eight regions. For example, $I[MidAtl]$ is the dummy variable representing the region `MidAtl`. For details, see "Dummy Indicator Variables" on page 2-55.

The corresponding model is

$$y_{im} = \beta_0 + \beta_1 I[MidAtl]_i + \beta_2 I[ENCentral]_i + \beta_3 I[WNCentral]_i + \beta_4 I[SAtl]_i + \beta_5 I[ESCentral]_i + \beta_6 I[WSCentral]_i + \beta_7 I[Mtn]_i + \beta_8 I[Pac]_i + b_{0m} + \varepsilon_{im}, \quad m = 1,2,\ldots,52,$$

where y_{im} is the observation i for level m of grouping variable `Date`, β_j, j = 0, 1, ..., 8, are the fixed-effects coefficients, with β_0 being the coefficient for region `NE`. b_{0m} is the random effect for level m of the grouping variable `Date`, and ε_{im} is the observation error for observation i. The random effect has the prior distribution, $b_{0m} \sim N(0,\sigma_b^2)$ and the error term has the distribution, $\varepsilon_{im} \sim N(0,\sigma^2)$.

```
lme = fitlme(flu2,'FluRate ~ 1 + Region + (1|Date)')
```

```
Linear mixed-effects model fit by ML

Model information:
```

```
    Number of observations             468
    Fixed effects coefficients           9
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    FluRate ~ 1 + Region + (1|Date)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    318.71    364.35    -148.36          296.71

Fixed effects coefficients (95% CIs):
    Name                      Estimate    SE          tStat      DF     pValue        L
    '(Intercept)'               1.2233    0.096678     12.654    459     1.085e-31
    'Region_MidAtl'            0.010192    0.052221    0.19518    459       0.84534
    'Region_ENCentral'         0.051923    0.052221     0.9943    459        0.3206
    'Region_WNCentral'          0.23687    0.052221     4.5359    459    7.3324e-06
    'Region_SAtl'              0.075481    0.052221     1.4454    459       0.14902
    'Region_ESCentral'          0.33917    0.052221      6.495    459    2.1623e-10
    'Region_WSCentral'            0.069    0.052221     1.3213    459       0.18705
    'Region_Mtn'               0.046673    0.052221    0.89377    459       0.37191
    'Region_Pac'               -0.16013    0.052221    -3.0665    459     0.0022936

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1               Name2                Type         Estimate    Lower     Upper
    '(Intercept)'       '(Intercept)'        'std'        0.6443      0.5297    0.7836

Group: Error
    Name             Estimate    Lower      Upper
    'Res Std'        0.26627     0.24878    0.285
```

The p-values 7.3324e-06 and 2.1623e-10 respectively show that the fixed effects of the flu rates in regions `WNCentral` and `ESCentral` are significantly different relative to the flu rates in region `NE`.

The confidence limits for the standard deviation of the random-effects term, σ^2_b, do not include 0 (0.5297, 0.78368), which indicates that the random-effects term is significant. You can also test the significance of the random-effects terms using the `compare` method.

The conditional fitted response from the model at a given observation includes contributions from fixed and random effects. For example, the estimated best linear unbiased predictor (BLUP) of the flu rate for region `WNCentral` in week 10/9/2005 is

$$\begin{aligned}\hat{y}_{WNCentral,10/9/2005} &= \hat{\beta}_0 + \hat{\beta}_3 I[WNCentral] + \hat{b}_{10/9/2005} \\ &= 1.2233 + 0.23687 - 0.1718 \\ &= 1.28837.\end{aligned}$$

This is the fitted conditional response, since it includes contributions to the estimate from both the fixed and random effects. You can compute this value as follows.

```
beta = fixedEffects(lme);
[~,~,STATS] = randomEffects(lme); % Compute the random-effects statistics (STATS)
STATS.Level = nominal(STATS.Level);
y_hat = beta(1) + beta(4) + STATS.Estimate(STATS.Level=='10/9/2005')
```

```
y_hat =

    1.2884
```

In the previous calculation, `beta(1)` corresponds to the estimate for β_0 and `beta(4)` corresponds to the estimate for β_3 You can simply display the fitted value using the `fitted` method.

```
F = fitted(lme);
F(flu2.Date == '10/9/2005' & flu2.Region == 'WNCentral')
```

```
ans =

    1.2884
```

The estimated marginal response for region `WNCentral` in week 10/9/2005 is

$$\begin{aligned}\hat{y}^{(\text{marginal})}_{WNCentral,10/9/2005} &= \hat{\beta}_0 + \hat{\beta}_3 I[WNCentral] \\ &= 1.2233 + 0.23687 \\ &= 1.46017.\end{aligned}$$

Compute the fitted marginal response.

```
F = fitted(lme,'Conditional',false);
F(flu2.Date == '10/9/2005' & flu2.Region == 'WNCentral')
```

```
ans =

    1.4602
```

Plot Residuals vs. Fitted Values

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

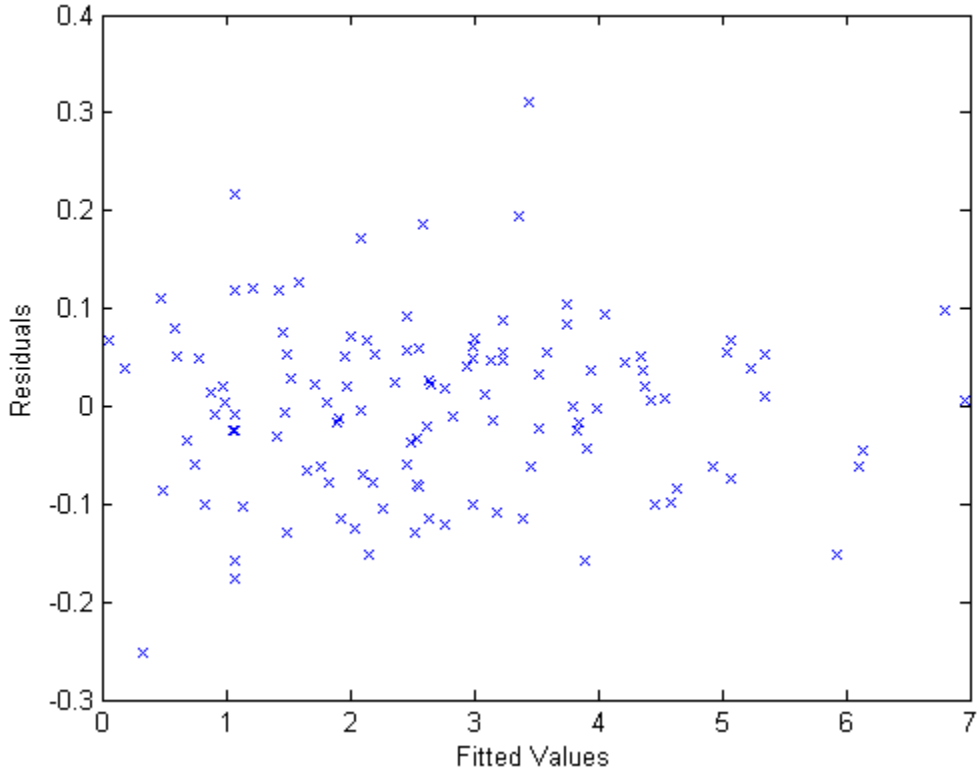
```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)');
```

Compute the fitted values and raw residuals.

```
F = fitted(lme);
R = residuals(lme);
```

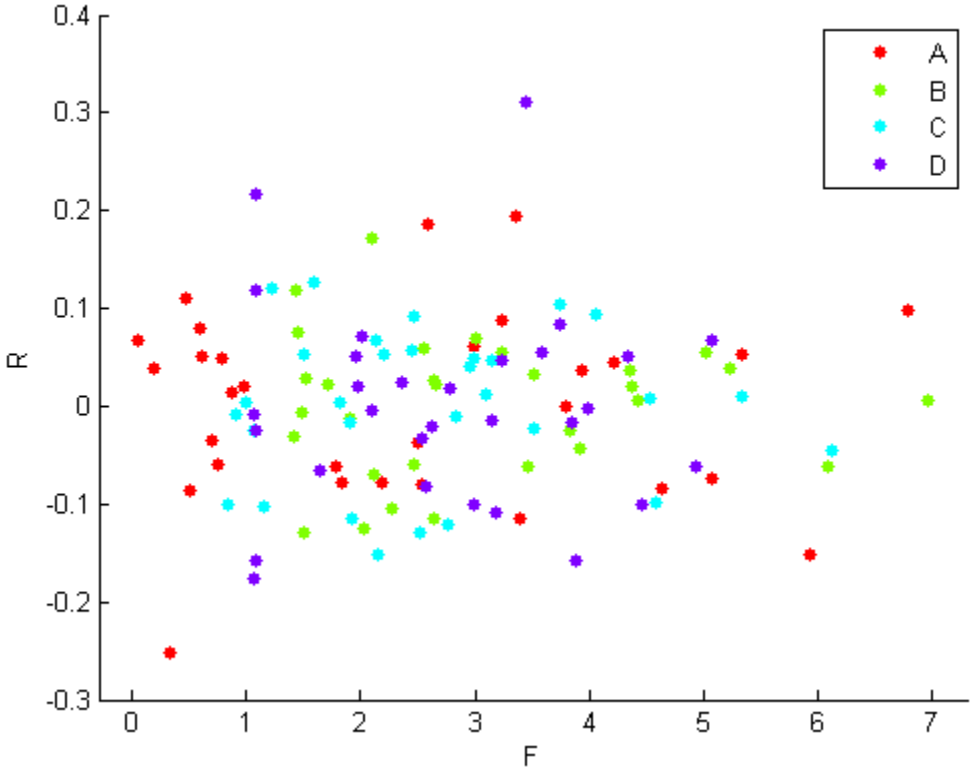
Plot the residuals versus the fitted values.

```
plot(F,R,'bx')
xlabel('Fitted Values')
ylabel('Residuals')
```



Now, plot the residuals versus the fitted values, grouped by program.

```
figure();
gscatter(F,R,Program)
```



Definitions

Fitted Conditional and Marginal Response

A conditional response includes contributions from both fixed and random effects, whereas a marginal response includes contribution from only fixed effects.

Suppose the linear mixed-effects model, `lme`, has an n-by-p fixed-effects design matrix X and an n-by-q random-effects design matrix Z. Also, suppose the p-by-1 estimated

fixed-effects vector is $\hat{\beta}$, and the q-by-1 estimated best linear unbiased predictor (BLUP) vector of random effects is $\hat{b}$. The fitted conditional response is

$$\hat{y}_{Cond} = X\hat{\beta} + Z\hat{b},$$

and the fitted marginal response is

$$\hat{y}_{Mar} = X\hat{\beta},$$

See Also

`LinearMixedModel` | `residuals` | `response`

fixedEffects

Class: GeneralizedLinearMixedModel

Estimates of fixed effects and related statistics

Syntax

```
beta = fixedEffects(glme)
[beta,betanames] = fixedEffects(glme)
[beta,betanames,stats] = fixedEffects(glme)
[___] = fixedEffects(glme,Name,Value)
```

Description

`beta = fixedEffects(glme)` returns the estimated fixed-effects coefficients, beta, of the generalized linear mixed-effects model glme.

`[beta,betanames] = fixedEffects(glme)` also returns the names of estimated fixed-effects coefficients in betanames. Each name corresponds to a fixed-effects coefficient in beta.

`[beta,betanames,stats] = fixedEffects(glme)` also returns a table of statistics, stats, related to the estimated fixed-effects coefficients of glme.

`[___] = fixedEffects(glme,Name,Value)` returns any of the output arguments in previous syntaxes using additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the confidence level, or the method for computing the approximate degrees of freedom for the *t*-statistic.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range [0,1]

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range [0,1]. For a value α, the confidence level is $100 \times (1 - \alpha)\%$.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single | double`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'residual'` (default) | `'none'`

Method for computing approximate degrees of freedom, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'residual'`	The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'none'`	All degrees of freedom are set to infinity.

Example: `'DFMethod','none'`

Output Arguments

`beta` — Estimated fixed-effects coefficients

vector

Estimated fixed-effects coefficients of the fitted generalized linear mixed-effects model `glme`, returned as a vector.

`betanames` — Names of fixed-effects coefficients

table

Names of fixed-effects coefficients in beta, returned as a table.

`stats` — Fixed-effects estimates and related statistics

dataset array

Fixed-effects estimates and related statistics, returned as a dataset array that has one row for each of the fixed effects and one column for each of the following statistics.

`Name`	Name of the fixed-effects coefficient
`Estimate`	Estimated coefficient value
`SE`	Standard error of the estimate
`tStat`	*t*-statistic for a test that the coefficient is 0
`DF`	Estimated degrees of freedom for the *t*-statistic
`pValue`	*p*-value for the *t*-statistic
`Lower`	Lower limit of a 95% confidence interval for the fixed-effects coefficient
`Upper`	Upper limit of a 95% confidence interval for the fixed-effects coefficient

When fitting a model using `fitglme` and one of the maximum likelihood fit methods (`'Laplace'` or `'ApproximateLaplace'`), if you specify the `'CovarianceMethod'` name-value pair argument as `'conditional'`, then `SE` does not account for the uncertainty in estimating the covariance parameters. To account for this uncertainty, specify `'CovarianceMethod'` as `'JointHessian'`.

When fitting a GLME model using `fitglme` and one of the pseudo likelihood fit methods (`'MPL'` or `'REMPL'`), `fixedEffects` bases the fixed effects estimates and related statistics on the fitted linear mixed-effects model from the final pseudo likelihood iteration.

Examples

Estimate Fixed-Effects Coefficients

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Compute and display the estimated fixed-effects coefficient values and related statistics.

```
[beta,betanames,stats] = fixedEffects(glme);
stats
```

```
stats =


    Fixed effect coefficients: DFMethod = 'residual', Alpha = 0.05

    Name                 Estimate     SE          tStat       DF
    '(Intercept)'           1.4689     0.15988      9.1875    94
    'newprocess'          -0.36766     0.17755     -2.0708    94
    'time_dev'            -0.094521    0.82849    -0.11409    94
    'temp_dev'            -0.28317      0.9617    -0.29444    94
    'supplier_C'          -0.071868    0.078024    -0.9211    94
    'supplier_B'           0.071072     0.07739     0.91836    94


    pValue        Lower        Upper
    9.8194e-15       1.1515       1.7864
```

```
    0.041122      -0.72019     -0.015134
     0.90941       -1.7395        1.5505
     0.76907       -2.1926        1.6263
     0.35936      -0.22679      0.083051
     0.36078     -0.082588       0.22473
```

The returned results indicate, for example, that the estimated coefficient for `temp_dev` is –0.28317. Its large *p*-value, 0.76907, indicates that it is not a statistically significant predictor at the 5% significance level. Additionally, the confidence interval boundaries `Lower` and `Upper` indicate that the 95% confidence interval for the coefficient for `temp_dev` is [-0.2.1926 , 1.6263]. This interval contains 0, which supports the conclusion that `temp_dev` is not statistically significant at the 5% significance level.

See Also

`coefCI` | `coefTest` | `fitglme` | `GeneralizedLinearMixedModel` | `randomEffects`

fixedEffects

Class: LinearMixedModel

Estimates of fixed effects and related statistics

Syntax

```
beta = fixedEffects(lme)
[beta,betanames] = fixedEffects(lme)
[beta,betanames,stats] = fixedEffects(lme)
[beta,betanames,stats] = fixedEffects(lme,Name,Value)
```

Description

`beta = fixedEffects(lme)` returns the estimated fixed-effects coefficients, `beta`, of the linear mixed-effects model `lme`.

`[beta,betanames] = fixedEffects(lme)` also returns the names of estimated fixed-effects coefficients in `betanames`. Each name corresponds to a fixed-effects coefficient in `beta`.

`[beta,betanames,stats] = fixedEffects(lme)` also returns the estimated fixed-effects coefficients of the linear mixed-effects model `lme` and related statistics in `stats`.

`[beta,betanames,stats] = fixedEffects(lme,Name,Value)` also returns the estimated fixed-effects coefficients of the linear mixed-effects model `lme` and related statistics with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 to 1

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range 0 to 1. For a value α, the confidence level is 100*(1–α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'Residual'` (default) | `'Satterthwaite'` | `'None'`

Method for computing approximate degrees of freedom for the *t*-statistic that tests the fixed-effects coefficients against 0, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'Residual'`	Default. The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'Satterthwaite'`	Satterthwaite approximation.
`'None'`	All degrees of freedom are set to infinity.

For example, you can specify the Satterthwaite approximation as follows.

Example: `'DFMethod','Satterthwaite'`

Output Arguments

`beta` — Fixed-effects coefficients estimates

vector

Fixed-effects coefficients estimates of the fitted linear mixed-effects model `lme`, returned as a vector.

`betanames` — Names of fixed-effects coefficients

table

Names of fixed-effects coefficients in beta, returned as a table.

`stats` — Fixed-effects estimates and related statistics

dataset array

Fixed-effects estimates and related statistics, returned as a dataset array that has one row for each of the fixed effects and one column for each of the following statistics.

`Name`	Name of the fixed effect coefficient
`Estimate`	Estimated coefficient value
`SE`	Standard error of the estimate
`tStat`	*t*-statistic for a test that the coefficient is zero
`DF`	Estimated degrees of freedom for the *t*-statistic
`pValue`	*p*-value for the *t*-statistic
`Lower`	Lower limit of a 95% confidence interval for the fixed-effect coefficient
`Upper`	Upper limit of a 95% confidence interval for the fixed-effect coefficient

Examples

Display Fixed-Effects Coefficient Estimates and Names

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

The data set `weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = tbl(InitWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between week and program are the fixed effects. The intercept and week vary by subject.

```
lme = fitlme(tbl,'y ~ InitWeight + Program*Week + (Week|Subject)');
```

Display the fixed-effects coefficient estimates and corresponding fixed-effects names.

```
[beta,betanames] = fixedEffects(lme);
```

```
beta =

    0.6610
    0.0032
    0.3608
   -0.0333
    0.1132
    0.1732
    0.0388
    0.0305
    0.0331


betanames =

    Name
    '(Intercept)'
    'InitWeight'
    'Program_B'
    'Program_C'
    'Program_D'
    'Week'
    'Program_B:Week'
```

```
    'Program_C:Week'
    'Program_D:Week'
```

Compute Coefficient Estimates and Related Statistics

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration and horsepower, and potentially correlated random effects for intercept and acceleration grouped by model year. First, store the data in a table.

```
tbl = table(Acceleration,Horsepower,Model_Year,MPG);
```

Fit the model.

```
lme = fitlme(tbl, 'MPG ~ Acceleration + Horsepower + (Acceleration|Model_Year)');
```

Compute the fixed-effects coefficients estimates and related statistics.

```
[~,~,stats] = fixedEffects(lme)
```

```
stats =

    Fixed effect coefficients: DFMethod = 'Residual', Alpha = 0.05

    Name                  Estimate    SE           tStat      DF     pValue        Lowe
    '(Intercept)'           50.133       2.2652     22.132    389    7.7727e-71      45
    'Acceleration'        -0.58327      0.13394    -4.3545    389    1.7075e-05    -0.8
    'Horsepower'          -0.16954    0.0072609     -23.35    389     5.188e-76    -0.1
```

The small p-values (under `pValue`) indicate that all fixed-effects coefficients are significant.

Compute Confidence Intervals with Specified Options

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load shift
```

The data shows the deviations from the target quality characteristic measured from the products that five operators manufacture during three shifts: morning, evening, and night. This is a randomized block design, where the operators are the blocks. The experiment is designed to study the impact of the time of shift on the performance. The performance measure is the deviation of the quality characteristics from the target value. This is simulated data.

`Shift` and `Operator` are nominal variables.

```
shift.Shift = nominal(shift.Shift);
shift.Operator = nominal(shift.Operator);
```

Fit a linear mixed-effects model with a random intercept grouped by operator to assess if performance significantly differs according to the time of the shift.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)');
```

Compute the 99% confidence intervals for fixed-effects coefficients, using the residual method to compute the degrees of freedom. This is the default method.

```
[~,~,stats] = fixedEffects(lme,'alpha',0.01)
```

```
stats =


    Fixed effect coefficients: DFMethod = 'Residual', Alpha = 0.01

    Name                  Estimate    SE         tStat       DF    pValue       Lower
    '(Intercept)'          3.1196     0.88681      3.5178    12    0.0042407    0.410
    'Shift_Morning'       -0.3868     0.48344     -0.80009   12      0.43921    -1.86
    'Shift_Night'          1.9856     0.48344      4.1072    12    0.0014535     0.50
```

Compute the 99% confidence intervals for fixed-effects coefficients, using the Satterthwaite approximation to compute the degrees of freedom.

```
[~,~,stats] = fixedEffects(lme,'DFMethod','Satterthwaite','alpha',0.01)
```

```
stats =


    Fixed effect coefficients: DFMethod = 'Satterthwaite', Alpha = 0.01

    Name                  Estimate    SE         tStat       DF       pValue     Lowe
    '(Intercept)'          3.1196     0.88681      3.5178    6.123    0.01214    -0.1
    'Shift_Morning'       -0.3868     0.48344     -0.80009      10    0.44225      -1
```

```
    'Shift_Night'           1.9856     0.48344      4.1072       10     0.00212      0.45
```

The Satterthwaite approximation usually produces smaller `DF` values than the residual method. That is why it produces larger *p*-values (`pValue`) and larger confidence intervals (see `Lower` and `Upper`).

See Also

`coefCI` | `coefTest` | `fitlme` | `LinearMixedModel` | `randomEffects`

fpdf

F probability density function

Syntax

```
Y = fpdf(X,V1,V2)
```

Description

`Y = fpdf(X,V1,V2)` computes the *F* pdf at each of the values in `X` using the corresponding numerator degrees of freedom `V1` and denominator degrees of freedom `V2`. `X`, `V1`, and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. `V1` and `V2` parameters must contain real positive values, and the values in `X` must lie on the interval [0 ∞).

The probability density function for the *F* distribution is

$$y = f(x \mid \nu_1,\nu_2) = \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{x^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)x\right]^{\frac{\nu_1+\nu_2}{2}}}$$

Examples

```
y = fpdf(1:6,2,2)
y =
  0.2500  0.1111  0.0625  0.0400  0.0278  0.0204

z = fpdf(3,5:10,5:10)
z =
  0.0689  0.0659  0.0620  0.0577  0.0532  0.0487
```

More About

- "F Distribution" on page B-45

See Also

`pdf` | `fcdf` | `finv` | `fstat` | `frnd`

fracfact

Fractional factorial design

Syntax

```
X = fracfact(gen)
[X,conf] = fracfact(gen)
[X,conf] = fracfact(gen,Name,Value)
```

Description

`X = fracfact(gen)` creates the two-level fractional factorial design defined by the generator string `gen`.

`[X,conf] = fracfact(gen)` returns a cell array of strings containing the confounding pattern for the design.

`[X,conf] = fracfact(gen,Name,Value)` creates a fractional factorial designs with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`gen`

Either a cell array of strings where each cell contains one "word," or a string consisting of "words" separated by spaces. "Words" consist of case-sensitive letters or groups of letters, where `'a'` represents string `1`, `'b'` represents string `2`, ..., `'A'` represents string `27`, ..., `'Z'` represents string `52`.

Each word defines how the corresponding factor's levels are defined as products of generators from a `2^K` full-factorial design. `K` is the number of letters of the alphabet in `gen`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'FactorNames'`

Cell array specifying the name for each factor.

Default: `{'X1','X2',...}`

`'MaxInt'`

Positive integer setting the maximum level of interaction to include in the confounding output.

Default: `2`

Output Arguments

`X`

The two-level fractional factorial design. `X` is a matrix of size `N`-by-`P`, where

- `N = 2^K`, where `K` is the number of letters of the alphabet in gen.
- `P` is the number of words in `gen`.

Because `X` is a two-level design, the components of `X` are `±1`. For the meaning of `X`, see "Fractional Factorial Designs" on page 19-5.

`conf`

Cell array of strings containing the confounding pattern for the design.

Examples

Generate a fractional factorial design for four variables, where the fourth variable is the product of the first three:

```
x = fracfact('a b c abc')

x =
    -1    -1    -1    -1
    -1    -1     1     1
```

```
    -1     1    -1     1
    -1     1     1    -1
     1    -1    -1     1
     1    -1     1    -1
     1     1    -1    -1
     1     1     1     1
```

Find generators for a six-factor design that uses four factors and achieves resolution IV using `fracfactgen`. Use the result to specify the design:

```
generators = fracfactgen('a b c d e f',4, ... % 4 factors
    4) % resolution 4

generators =
    'a'
    'b'
    'c'
    'd'
    'bcd'
    'acd'

x = fracfact(generators)

x =
    -1    -1    -1    -1    -1    -1
    -1    -1    -1     1     1     1
    -1    -1     1    -1     1     1
    -1    -1     1     1    -1    -1
    -1     1    -1    -1     1    -1
    -1     1    -1     1    -1     1
    -1     1     1    -1    -1     1
    -1     1     1     1     1    -1
     1    -1    -1    -1    -1     1
     1    -1    -1     1     1    -1
     1    -1     1    -1     1    -1
     1    -1     1     1    -1     1
     1     1    -1    -1     1     1
     1     1    -1     1    -1    -1
     1     1     1    -1    -1    -1
     1     1     1     1     1     1
```

More About

- “Fractional Factorial Designs” on page 19-5

References

[1] Box, G. E. P., W. G. Hunter, and J. S. Hunter. *Statistics for Experimenters*. Hoboken, NJ: Wiley-Interscience, 1978.

See Also

`ff2n` | `fracfactgen` | `fullfact` | `hadamard`

fracfactgen

Fractional factorial design generators

Syntax

```
generators = fracfactgen(terms)
generators = fracfactgen(terms,k)
generators = fracfactgen(terms,k,R)
generators = fracfactgen(terms,k,R,basic)
```

Description

`generators = fracfactgen(terms)` uses the Franklin-Bailey algorithm to find generators for the smallest two-level fractional-factorial design for estimating linear model terms specified by `terms`. `terms` is a string consisting of words formed from the `52` case-sensitive letters `a`-`Z`, separated by spaces. Use `'a'-'z'` for the first 26 factors, and, if necessary, `'A'-'Z'` for the remaining factors. For example, `terms = 'a b c ab ac'`. Single-character words indicate main effects to be estimated; multiple-character words indicate interactions. Alternatively, `terms` is an m-by-n matrix of `0`s and `1`s where m is the number of model terms to be estimated and n is the number of factors. For example, if `terms` contains rows `[0 1 0 0]` and `[1 0 0 1]`, then the factor `b` and the interaction between factors `a` and `d` are included in the model. `generators` is a cell array of strings with one generator per cell. Pass `generators` to `fracfact` to produce the fractional-factorial design and corresponding confounding pattern.

`generators = fracfactgen(terms,k)` returns generators for a two-level fractional-factorial design with 2^k-runs, if possible. If `k` is `[]`, `fracfactgen` finds the smallest design.

`generators = fracfactgen(terms,k,R)` finds a design with resolution `R`, if possible. The default resolution is `3`.

A design of *resolution* R is one in which no n-factor interaction is confounded with any other effect containing less than $R - n$ factors. Thus a resolution III design does not confound main effects with one another but may confound them with two-way interactions, while a resolution IV design does not confound either main effects or two-way interactions but may confound two-way interactions with each other.

If `fracfactgen` is unable to find a design at the requested resolution, it tries to find a lower-resolution design sufficient to calibrate the model. If it is successful, it returns the generators for the lower-resolution design along with a warning. If it fails, it returns an error.

`generators = fracfactgen(terms,k,R,basic)` also accepts a vector `basic` specifying the indices of factors that are to be treated as basic. These factors receive full-factorial treatments in the design. The default includes factors that are part of the highest-order interaction in `terms`.

Examples

Suppose you wish to determine the effects of four two-level factors, for which there may be two-way interactions. A full-factorial design would require $2^4 = 16$ runs. The `fracfactgen` function finds generators for a resolution IV (separating main effects) fractional-factorial design that requires only $2^3 = 8$ runs:

```
generators = fracfactgen('a b c d',3,4)
generators =
    'a'
    'b'
    'c'
    'abc'
```

The more economical design and the corresponding confounding pattern are returned by `fracfact`:

```
[dfF,confounding] = fracfact(generators)
dfF =
    -1    -1    -1    -1
    -1    -1     1     1
    -1     1    -1     1
    -1     1     1    -1
     1    -1    -1     1
     1    -1     1    -1
     1     1    -1    -1
     1     1     1     1
confounding =
    'Term'     'Generator'    'Confounding'
    'X1'       'a'            'X1'
    'X2'       'b'            'X2'
```

```
'X3'       'c'            'X3'
'X4'       'abc'          'X4'
'X1*X2'    'ab'           'X1*X2 + X3*X4'
'X1*X3'    'ac'           'X1*X3 + X2*X4'
'X1*X4'    'bc'           'X1*X4 + X2*X3'
'X2*X3'    'bc'           'X1*X4 + X2*X3'
'X2*X4'    'ac'           'X1*X3 + X2*X4'
'X3*X4'    'ab'           'X1*X2 + X3*X4'
```

The confounding pattern shows, for example, that the two-way interaction between `X1` and `X2` is confounded by the two-way interaction between `X3` and `X4`.

More About

- "Fractional Factorial Designs" on page 19-5

References

[1] Box, G. E. P., W. G. Hunter, and J. S. Hunter. *Statistics for Experimenters*. Hoboken, NJ: Wiley-Interscience, 1978.

See Also

`fracfact` | `hadamard`

friedman

Friedman's test

Syntax

```
p = friedman(x,reps)
p = friedman(x,reps,displayopt)
[p,tbl] = friedman( ___ )
[p,tbl,stats] = friedman( ___ )
```

Description

`p = friedman(x,reps)` returns the *p*-value for the nonparametric Friedman's test to compare column effects in a two-way layout. `friedman` tests the null hypothesis that the column effects are all the same against the alternative that they are not all the same.

`p = friedman(x,reps,displayopt)` enables the ANOVA table display when displayopt is `'on'` (default) and suppresses the display when displayopt is `'off'`.

`[p,tbl] = friedman( ___ )` returns the ANOVA table (including column and row labels) in cell array `tbl`.

`[p,tbl,stats] = friedman( ___ )` also returns a structure stats that you can use to perform a follow-up multiple comparison test.

Examples

Test For Column Effects Using Friedman's Test

This example shows how to test for column effects in a two-way layout using Friedman's test.

Load the sample data.

```
load popcorn
```

```
popcorn
```

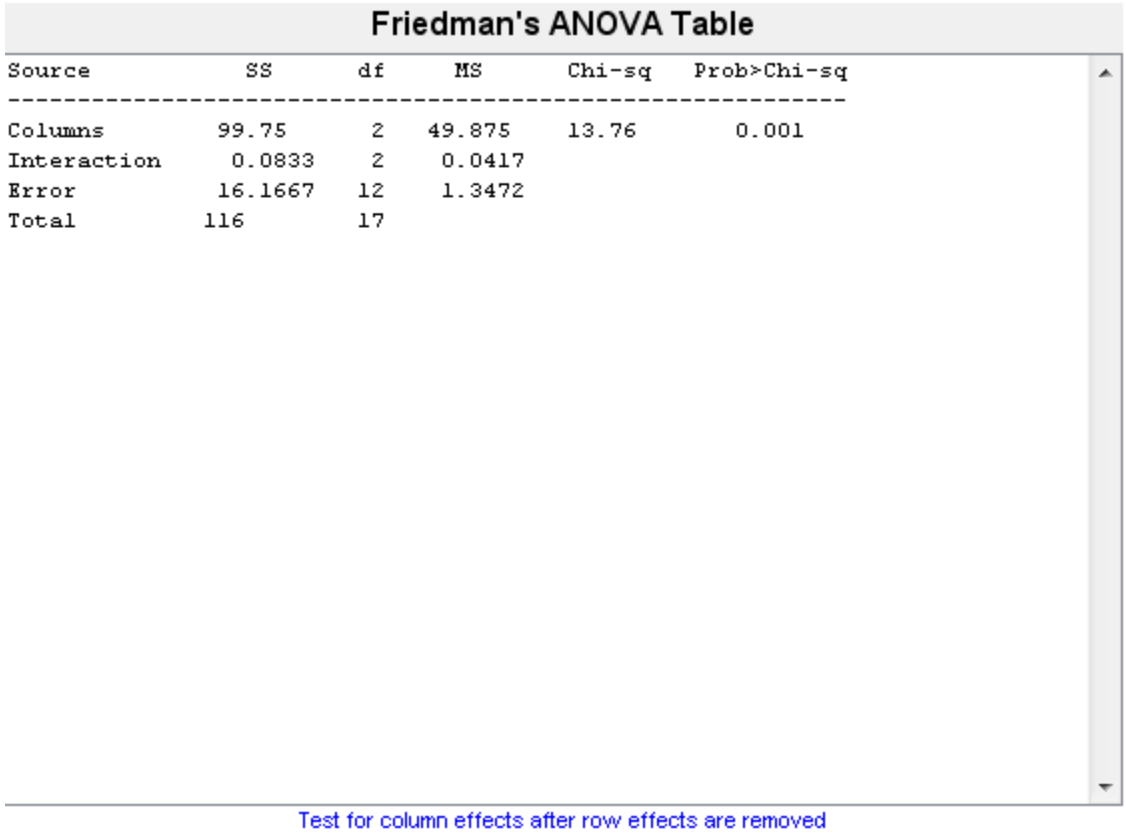
```
popcorn =

    5.5000    4.5000    3.5000
    5.5000    4.5000    4.0000
    6.0000    4.0000    3.0000
    6.5000    5.0000    4.0000
    7.0000    5.5000    5.0000
    7.0000    5.0000    4.5000
```

This data comes from a study of popcorn brands and popper type (Hogg 1987). The columns of the matrix `popcorn` are brands (Gourmet, National, and Generic). The rows are popper type (Oil and Air). The study popped a batch of each brand three times with each popper. The values are the yield in cups of popped popcorn.

Use Friedman's test to determine whether the popcorn brand affects the yield of popcorn.

```
p = friedman(popcorn,3)
```

```
p =

    0.0010
```



The small value of `p = 0.001` indicates the popcorn brand affects the yield of popcorn.

Input Arguments

x — Sample data

matrix

Sample data for the hypothesis test, specified as a matrix. The columns of x represent changes in a factor A. The rows represent changes in a blocking factor B. If there is more than one observation for each combination of factors, input reps indicates the number of replicates in each "cell," which must be constant.

Data Types: `single` | `double`

`reps` — Number of replicates per cell

1 (default) | positive integer value

Number of replicates per cell, specified as a positive integer value.

Data Types: `single` | `double`

`displayopt` — ANOVA table display option

`'off'` (default) | `'on'`

ANOVA table display option, specified as `'off'` or `'on'`.

If displayopt is `'on'`, then `friedman` displays a figure showing an ANOVA table, which divides the variability of the ranks into two or three parts:

- The variability due to the differences among the column effects
- The variability due to the interaction between rows and columns (if reps is greater than its default value of 1)
- The remaining variability not explained by any systematic source

The ANOVA table has six columns:

- The first shows the source of the variability.
- The second shows the Sum of Squares (SS) due to each source.
- The third shows the degrees of freedom (df) associated with each source.
- The fourth shows the Mean Squares (MS), which is the ratio SS/df.
- The fifth shows Friedman's chi-square statistic.
- The sixth shows the *p* value for the chi-square statistic.

You can copy a text version of the ANOVA table to the clipboard by selecting `Copy Text` from the **Edit** menu.

Output Arguments

`p` — *p*-value

scalar value in the range `[0,1]`

p-value of the test, returned as a scalar value in the range `[0,1]`. `p` is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of `p` cast doubt on the validity of the null hypothesis.

`tbl` — ANOVA table

cell array

ANOVA table, including column and row labels, returned as a cell array. The ANOVA table has six columns:

- The first shows the source of the variability.
- The second shows the Sum of Squares (SS) due to each source.
- The third shows the degrees of freedom (df) associated with each source.
- The fourth shows the Mean Squares (MS), which is the ratio SS/df.
- The fifth shows Friedman's chi-square statistic.
- The sixth shows the *p* value for the chi-square statistic.

You can copy a text version of the ANOVA table to the clipboard by selecting `Copy Text` from the **Edit** menu.

`stats` — Test data

structure

Test data, returned as a structure. `friedman` evaluates the hypothesis that the column effects are all the same against the alternative that they are not all the same. However, sometimes it is preferable to perform a test to determine which pairs of column effects are significantly different, and which are not. You can use the `multcompare` function to perform such tests by supplying stats as the input value.

More About

Friedman's Test

Friedman's test is similar to classical balanced two-way ANOVA, but it tests only for column effects after adjusting for possible row effects. It does not test for row effects or interaction effects. Friedman's test is appropriate when columns represent treatments that are under study, and rows represent nuisance effects (blocks) that need to be taken into account but are not of any interest.

The different columns of `X` represent changes in a factor A. The different rows represent changes in a blocking factor B. If there is more than one observation for each combination of factors, input `reps` indicates the number of replicates in each "cell," which must be constant.

The matrix below illustrates the format for a set-up where column factor A has three levels, row factor B has two levels, and there are two replicates (`reps=2`). The subscripts indicate row, column, and replicate, respectively.

$$\begin{bmatrix} x_{111} & x_{121} & x_{131} \\ x_{112} & x_{122} & x_{132} \\ x_{211} & x_{221} & x_{231} \\ x_{212} & x_{222} & x_{232} \end{bmatrix}$$

Friedman's test assumes a model of the form

$$x_{ijk} = \mu + \alpha_i + \beta_j + \varepsilon_{ijk}$$

where μ is an overall location parameter, α_i represents the column effect, β_j represents the row effect, and ε_{ijk} represents the error. This test ranks the data within each level of B, and tests for a difference across levels of A. The `p` that `friedman` returns is the p value for the null hypothesis that $\alpha_i = 0$. If the p value is near zero, this casts doubt on the null hypothesis. A sufficiently small p value suggests that at least one column-sample median is significantly different than the others; i.e., there is a main effect due to factor A. The choice of a critical p value to determine whether a result is "statistically significant" is left to the researcher. It is common to declare a result significant if the p value is less than 0.05 or 0.01.

Friedman's test makes the following assumptions about the data in `X`:

- All data come from populations having the same continuous distribution, apart from possibly different locations due to column and row effects.
- All observations are mutually independent.

The classical two-way ANOVA replaces the first assumption with the stronger assumption that data come from normal distributions.

References

[1] Hogg, R. V., and J. Ledolter. *Engineering Statistics*. New York: MacMillan, 1987.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`anova2` | `kruskalwallis` | `multcompare`

frnd

F random numbers

Syntax

```
R = frnd(V1,V2)
R = frnd(V1,V2,m,n,...)
R = frnd(V1,V2,[m,n,...])
```

Description

`R = frnd(V1,V2)` generates random numbers from the *F* distribution with numerator degrees of freedom `V1` and denominator degrees of freedom `V2`. `V1` and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `V1` or `V2` is expanded to a constant array with the same dimensions as the other input.

`R = frnd(V1,V2,m,n,...)` or `R = frnd(V1,V2,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the *F* distribution with parameters `V1` and `V2`. `V1` and `V2` can each be scalars or arrays of the same size as `R`.

Examples

```
n1 = frnd(1:6,1:6)
n1 =
  0.0022  0.3121  3.0528  0.3189  0.2715  0.9539

n2 = frnd(2,2,[2 3])
n2 =
  0.3186  0.9727  3.0268
  0.2052 148.5816  0.2191

n3 = frnd([1 2 3;4 5 6],1,2,3)
n3 =
  0.6233  0.2322  31.5458
  2.5848  0.2121  4.4955
```

More About

- “F Distribution” on page B-45

See Also

`random` | `fpdf` | `fcdf` | `finv` | `fstat`

fstat

F mean and variance

Syntax

```
[M,V] = fstat(V1,V2)
```

Description

`[M,V] = fstat(V1,V2)` returns the mean of and variance for the *F* distribution with numerator degrees of freedom `V1` and denominator degrees of freedom `V2`. `V1` and `V2` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `V1` or `V2` is expanded to a constant arrays with the same dimensions as the other input.

The mean of the *F* distribution for values of ν_2 greater than 2 is

$$\frac{\nu_2}{\nu_2 - 2}$$

The variance of the *F* distribution for values of ν_2 greater than 4 is

$$\frac{2\nu_2^2(\nu_1 + \nu_2 - 2)}{\nu_1(\nu_2 - 2)^2(\nu_2 - 4)}$$

The mean of the *F* distribution is undefined if ν_2 is less than 3. The variance is undefined for ν_2 less than 5.

Examples

`fstat` returns `NaN` when the mean and variance are undefined.

```
[m,v] = fstat(1:5,1:5)
```

```
m =
    NaN  NaN  3.0000  2.0000  1.6667
v =
    NaN  NaN  NaN  NaN  8.8889
```

More About

- "F Distribution" on page B-45

See Also

`fpdf` | `fcdf` | `finv` | `frnd`

fsurfht

Interactive contour plot

Syntax

```
fsurfht(fun,xlims,ylims)
fsurfht(fun,xlims,ylims,p1,p2,p3,p4,p5)
```

Description

`fsurfht(fun,xlims,ylims)` is an interactive contour plot of the function specified by the text variable `fun`. The *x*-axis limits are specified by `xlims` in the form `[xmin xmax]`, and the *y*-axis limits are specified by `ylims` in the form `[ymin ymax]`.

`fsurfht(fun,xlims,ylims,p1,p2,p3,p4,p5)` allows for five optional parameters that you can supply to the function `fun`.

The intersection of the vertical and horizontal reference lines on the plot defines the current *x* value and *y* value. You can drag these reference lines and watch the calculated *z*-values (at the top of the plot) update simultaneously. Alternatively, you can type the *x* value and *y* value into editable text fields on the *x*-axis and *y*-axis.

Examples

Plot the Gaussian likelihood function for the `gas.mat` data.

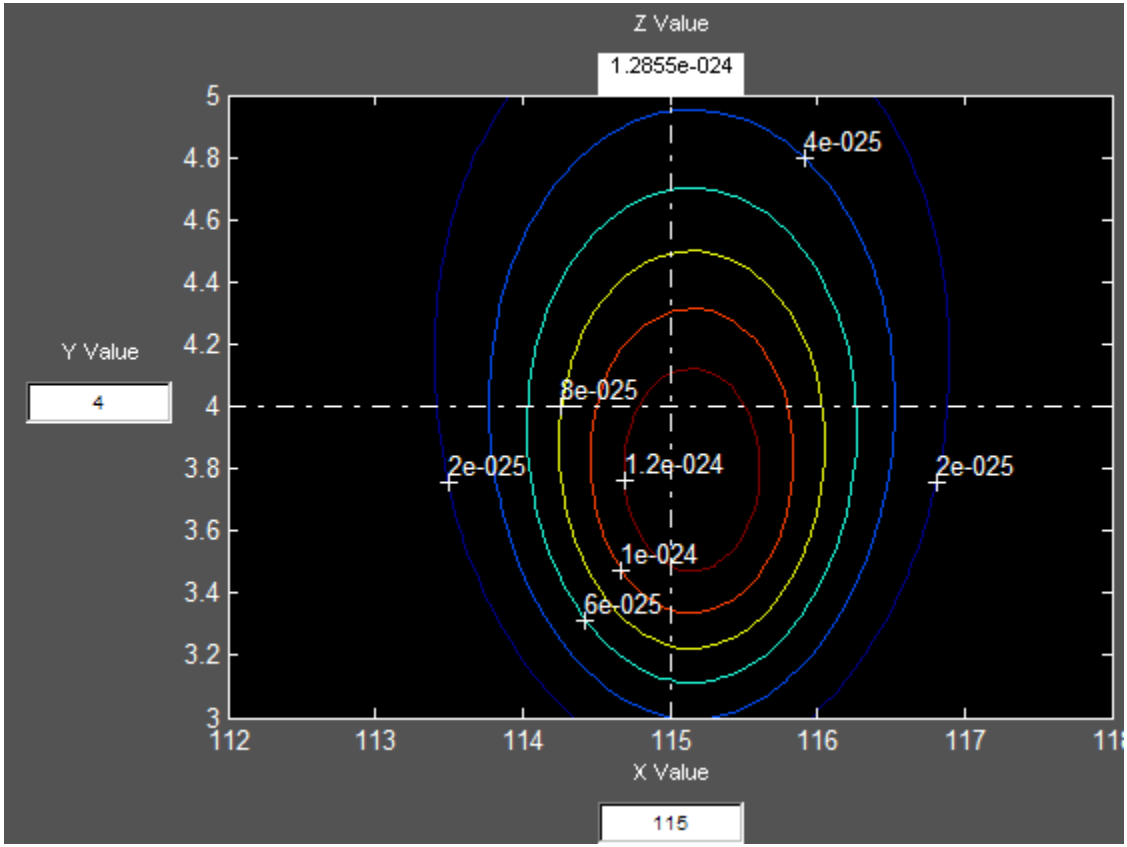
```
load gas
```

Create a function containing the following commands, and name it `gauslike.m`.

```
function z = gauslike(mu,sigma,p1)
n = length(p1);
z = ones(size(mu));
for i = 1:n
z = z .* (normpdf(p1(i),mu,sigma));
end
```

The `gauslike` function calls `normpdf`, treating the data sample as fixed and the parameters μ and σ as variables. Assume that the gas prices are normally distributed, and plot the likelihood surface of the sample.

```
fsurfht('gauslike',[112 118],[3 5],price1)
```



The sample mean is the *x* value at the maximum, but the sample standard deviation is *not* the *y* value at the maximum.

```
mumax = mean(price1)
mumax =
 115.1500
sigmamax = std(price1)*sqrt(19/20)
sigmamax =
```

```
3.7719
```

fullfact

Full factorial design

Syntax

```
dFF = fullfact(levels)
```

Description

`dFF = fullfact(levels)` gives factor settings `dFF` for a full factorial design with n factors, where the number of levels for each factor is given by the vector `levels` of length n. `dFF` is m-by-n, where m is the number of treatments in the full-factorial design. Each row of `dFF` corresponds to a single treatment. Each column contains the settings for a single factor, with integer values from one to the number of levels.

Examples

The following generates an eight-run full-factorial design with two levels in the first factor and four levels in the second factor:

```
dFF = fullfact([2 4])
dFF =
   1   1
   2   1
   1   2
   2   2
   1   3
   2   3
   1   4
   2   4
```

See Also

`ff2n`

gagerr

Gage repeatability and reproducibility study

Syntax

```
gagerr(y,{part,operator})
gagerr(y,GROUP)
gagerr(y,part)
gagerr(...,param1,val1,param2,val2,...)
[TABLE, stats] = gagerr(...)
```

Description

`gagerr(y,{part,operator})` performs a gage repeatability and reproducibility study on measurements in `y` collected by `operator` on `part`. `y` is a column vector containing the measurements on different parts. `part` and `operator` are categorical variables, numeric vectors, character matrices, or cell arrays of strings. The number of elements in `part` and `operator` should be the same as in `y`.

`gagerr` prints a table in the command window in which the decomposition of variance, standard deviation, study var (5.15 `x` standard deviation) are listed with respective percentages for different sources. Summary statistics are printed below the table giving the number of distinct categories (NDC) and the percentage of Gage R&R of total variations (PRR).

`gagerr` also plots a bar graph showing the percentage of different components of variations. Gage R&R, repeatability, reproducibility, and part-to-part variations are plotted as four vertical bars. Variance and study var are plotted as two groups.

To determine the capability of a measurement system using NDC, use the following guidelines:

- If NDC > 5, the measurement system is capable.
- If NDC < 2, the measurement system is not capable.
- Otherwise, the measurement system may be acceptable.

To determine the capability of a measurement system using PRR, use the following guidelines:

- If PRR < 10%, the measurement system is capable.
- If PRR > 30%, the measurement system is not capable.
- Otherwise, the measurement system may be acceptable.

`gagerr(y,GROUP)` performs a gage R&R study on measurements in `y` with `part` and `operator` represented in `GROUP`. `GROUP` is a numeric matrix whose first and second columns specify different parts and operators, respectively. The number of rows in `GROUP` should be the same as the number of elements in `y`.

`gagerr(y,part)` performs a gage R&R study on measurements in `y` without operator information. The assumption is that all variability is contributed by `part`.

`gagerr(...,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` performs a gage R&R study using one or more of the following parameter name/value pairs:

- `'spec'` — A two-element vector that defines the lower and upper limit of the process, respectively. In this case, summary statistics printed in the command window include Precision-to-Tolerance Ratio (PTR). Also, the bar graph includes an additional group, the percentage of tolerance.

  To determine the capability of a measurement system using PTR, use the following guidelines:

  - If PTR < 0.1, the measurement system is capable.
  - If PTR > 0.3, the measurement system is not capable.
  - Otherwise, the measurement system may be acceptable.
- `'printtable'` — A string with a value `'on'` or `'off'` that indicates whether the tabular output should be printed in the command window or not. The default value is `'on'`.
- `'printgraph'` — A string with a value `'on'` or `'off'` that indicates whether the bar graph should be plotted or not. The default value is `'on'`.
- `'randomoperator'` — A logical value, `true` or `false`, that indicates whether the effect of `operator` is random or not. The default value is `true`.
- `'model'` — The model to use, specified by one of:

  - `'linear'` — Main effects only (default)
  - `'interaction'` — Main effects plus two-factor interactions
  - `'nested'` — Nest `operator` in `part`

The default value is `'linear'`.

`[TABLE, stats] = gagerr(...)` returns a 6-by-5 matrix `TABLE` and a structure `stats`. The columns of `TABLE`, from left to right, represent variance, percentage of variance, standard deviations, study var, and percentage of study var. The rows of `TABLE`, from top to bottom, represent different sources of variations: gage R&R, repeatability, reproducibility, operator, operator and part interactions, and part. `stats` is a structure containing summary statistics for the performance of the measurement system. The fields of `stats` are:

- `ndc` — Number of distinct categories
- `prr` — Percentage of gage R&R of total variations
- `ptr` — Precision-to-tolerance ratio. The value is `NaN` if the parameter `'spec'` is not given.

Examples

Gage R&R Study

Simulate a measurement system by randomly generating the operators, parts, and the measurements, `y` , operators do on the parts.

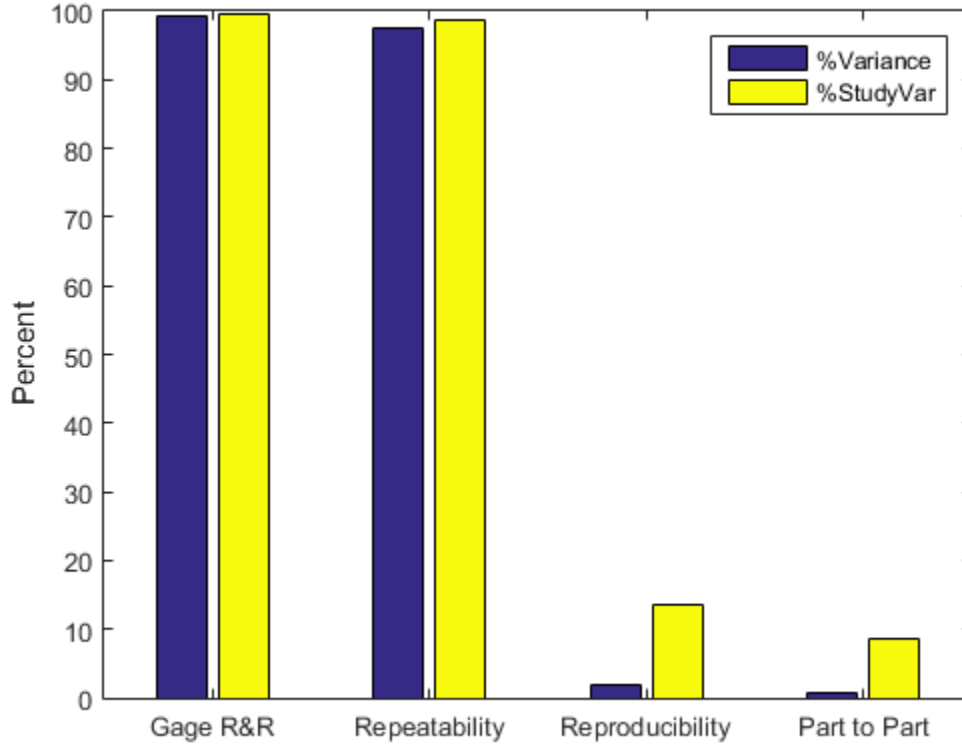
```
rng(1234,'twister')              % for reproducibility
y = randn(100,1);                % measurements
part = ceil(3*rand(100,1));      % parts
operator = ceil(4*rand(100,1));  % operators
```

Conduct a gage R&R study for this system using a mixed ANOVA model without interactions.

```
gagerr(y,{part, operator},'randomoperator',true)
```

```
  Columns 1 through 4

    'Source'               'Variance'     '% Variance'     'sigma'
    'Gage R&R'             [  0.9715]     [   99.2653]     [0.9857]
    '  Repeatability'      [  0.9535]     [   97.4201]     [0.9765]
    '  Reproducibility'    [  0.0181]     [    1.8452]     [0.1344]
    '   Operator'          [  0.0181]     [    1.8452]     [0.1344]
    'Part'                 [  0.0072]     [    0.7347]     [0.0848]
    'Total'                [  0.9787]     [       100]     [0.9893]
```

```
  Columns 5 through 6

    '5.15*sigma'    '% 5.15*sigma'
    [    5.0762]    [     99.6320]
    [    5.0288]    [     98.7016]
    [    0.6921]    [     13.5838]
    [    0.6921]    [     13.5838]
    [    0.4367]    [      8.5716]
    [    5.0949]    ''

Number of distinct categories (NDC):0
% of Gage R&R of total variations (PRR): 99.63
Note: The last column of the above table does not have to sum to 100%
```



More About

- "Grouping Variables" on page 2-52

gamcdf

Gamma cumulative distribution function

Syntax

```
gamcdf(x,a,b)
[p,plo,pup] = gamcdf(x,a,b,pcov,alpha)
[p,plo,pup] = gamcdf(___,'upper')
```

Description

`gamcdf(x,a,b)` returns the gamma cdf at each of the values in `x` using the corresponding shape parameters in `a` and scale parameters in `b`. `x`, `a`, and `b` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `a` and `b` must be positive.

`[p,plo,pup] = gamcdf(x,a,b,pcov,alpha)` produces confidence bounds for `p` when the input parameters `a` and `b` are estimates. `pcov` is a 2-by-2 matrix containing the covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies `100(1-alpha)`% confidence bounds. `plo` and `pup` are arrays of the same size as `p` containing the lower and upper confidence bounds.

`[p,plo,pup] = gamcdf(___,'upper')` returns the complement of the gamma cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities. You can use the `'upper'` argument with any of the previous syntaxes.

The gamma cdf is

$$p = F(x \mid a,b) = \frac{1}{b^a \Gamma(a)} \int_0^x t^{a-1} e^{\frac{-t}{b}} dt$$

The result, p, is the probability that a single observation from a gamma distribution with parameters a and b will fall in the interval $[0\ x]$.

`gammainc` is the gamma distribution with b fixed at 1.

Examples

Compute Gamma Distribution CDF

The mean of the gamma distribution is the product of the parameters, *ab*. In this example, the mean approaches the median as it increases (i.e., the distribution becomes more symmetric).

```
a = 1:6;
b = 5:10;
prob = gamcdf(a.*b,a,b)
```

```
prob =
  0.6321  0.5940  0.5768  0.5665  0.5595  0.5543
```

More About

- "Gamma Distribution" on page B-48

See Also

`cdf` | `gampdf` | `gaminv` | `gamstat` | `gamfit` | `gamlike` | `gamrnd` | `gamma`

gamfit

Gamma parameter estimates

Syntax

```
phat = gamfit(data)
[phat,pci] = gamfit(data)
[phat,pci] = gamfit(data,alpha)
[...] = gamfit(data,alpha,censoring,freq,options)
```

Description

`phat = gamfit(data)` returns the maximum likelihood estimates (MLEs) for the parameters of the gamma distribution given the data in vector `data`.

`[phat,pci] = gamfit(data)` returns MLEs and 95% percent confidence intervals. The first row of `pci` is the lower bound of the confidence intervals; the last row is the upper bound.

`[phat,pci] = gamfit(data,alpha)` returns `100(1 - alpha)`% confidence intervals. For example, `alpha` = `0.01` yields 99% confidence intervals.

`[...] = gamfit(data,alpha,censoring)` accepts a Boolean vector of the same size as `data` that is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = gamfit(data,alpha,censoring,freq)` accepts a frequency vector of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but may contain any nonnegative values.

`[...] = gamfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. The gamma fit function accepts an `options` structure which can be created using the function `statset`. Enter `statset('gamfit')` to see the names and default values of the parameters that `gamfit` accepts in the `options` structure.

Examples

Fit a gamma distribution to random data generated from a specified gamma distribution:

```
a = 2; b = 4;
data = gamrnd(a,b,100,1);

[p,ci] = gamfit(data)
p =
  2.1990  3.7426
ci =
  1.6840  2.8298
  2.7141  4.6554
```

More About

- "Gamma Distribution" on page B-48

References

[1] Hahn, Gerald J., and S. S. Shapiro. *Statistical Models in Engineering*. Hoboken, NJ: John Wiley & Sons, Inc., 1994, p. 88.

See Also

`mle` | `gamlike` | `gampdf` | `gamcdf` | `gaminv` | `gamstat` | `gamrnd`

prob.GammaDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Gamma probability distribution object

Description

`prob.GammaDistribution` is an object consisting of parameters, a model description, and sample data for a gamma probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Gamma')` creates a gamma probability distribution object using the default parameter values.

`pd = makedist('Gamma','a',a,'b',b)` creates a gamma probability distribution object using the specified parameter values.

Input Arguments

a — Shape parameter

1 (default) | positive scalar value

Shape parameter for the gamma distribution, specified as a positive scalar value.

Data Types: `single` | `double`

b — Scale parameter

1 (default) | nonnegative scalar value

Scale parameter for the gamma distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

Properties

a — Shape parameter

positive scalar value

Shape parameter for the gamma distribution, stored as a positive scalar value.

Data Types: `single | double`

b — Scale parameter

nonnegative scalar value

Scale parameter for the gamma distribution, stored as a nonnegative scalar value.

Data Types: `single | double`

DistributionName — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

InputData — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

IsTruncated — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Gamma Distribution

The gamma distribution is a two-parameter family of distributions used to model sums of exponentially distributed random variables. The chi-square and the exponential distributions, which are children of the gamma distribution, are one-parameter distributions that fix one of the two gamma parameters.

The gamma distribution uses the following parameters.

Parameter	Description	Support
a	Shape parameter	$a > 0$
b	Scale parameter	$b \geq 0$

The probability density function (pdf) is

$$f(x \mid a,b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{-x}{b}} \quad ; \quad x > 0,$$

where $\Gamma(\cdot)$ is the Gamma function.

Examples

Create a Gamma Distribution Object Using Default Parameters

Create a gamma distribution object using the default parameter values.

```
pd = makedist('Gamma')
```

```
pd =

  GammaDistribution

  Gamma distribution
    a = 1
    b = 1
```

Create a Gamma Distribution Object Using Specified Parameters

Create a gamma distribution object by specifying the parameter values.

```
pd = makedist('Gamma', 'a',2,'b',4)
```

```
pd =

  GammaDistribution

  Gamma distribution
    a = 2
    b = 4
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

     8
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Gamma Distribution"
- Class Attributes
- Property Attributes

gaminv

Gamma inverse cumulative distribution function

Syntax

```
X = gaminv(P,A,B)
[X,XLO,XUP] = gamcdf(P,A,B,pcov,alpha)
```

Description

`X = gaminv(P,A,B)` computes the inverse of the gamma cdf with shape parameters in `A` and scale parameters in `B` for the corresponding probabilities in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must all be positive, and the values in `P` must lie on the interval [0 1].

The gamma inverse function in terms of the gamma cdf is

$$x = F^{-1}(p \mid a,b) = \{x : F(x \mid a,b) = p\}$$

where

$$p = F(x \mid a,b) = \frac{1}{b^a \Gamma(a)} \int_0^x t^{a-1} e^{\frac{-t}{b}} dt$$

`[X,XLO,XUP] = gamcdf(P,A,B,pcov,alpha)` produces confidence bounds for `P` when the input parameters `A` and `B` are estimates. `pcov` is a 2-by-2 matrix containing the covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies `100(1-alpha)`% confidence bounds. `PLO` and `PUP` are arrays of the same size as `P` containing the lower and upper confidence bounds.

Examples

This example shows the relationship between the gamma cdf and its inverse function.

```
a = 1:5;
b = 6:10;
x = gaminv(gamcdf(1:5,a,b),a,b)
x =
  1.0000  2.0000  3.0000  4.0000  5.0000
```

More About

Algorithms

There is no known analytical solution to the integral equation above. `gaminv` uses an iterative approach (Newton's method) to converge on the solution.

- "Gamma Distribution" on page B-48

See Also

`icdf` | `gamcdf` | `gampdf` | `gamstat` | `gamfit` | `gamlike` | `gamrnd`

gamlike

Gamma negative log-likelihood

Syntax

```
nlogL = gamlike(params,data)
[nlogL,AVAR] = gamlike(params,data)
```

Description

`nlogL = gamlike(params,data)` returns the negative of the gamma log-likelihood of the parameters, `params`, given `data`. `params(1)=A`, shape parameters, and `params(2)=B`, scale parameters.

`[nlogL,AVAR] = gamlike(params,data)` also returns `AVAR`, which is the asymptotic variance-covariance matrix of the parameter estimates when the values in `params` are the maximum likelihood estimates. `AVAR` is the inverse of Fisher's information matrix. The diagonal elements of `AVAR` are the asymptotic variances of their respective parameters.

`[...] = gamlike(params,data,censoring)` accepts a Boolean vector of the same size as `data` that is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = gamfit(params,data,censoring,freq)` accepts a frequency vector of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but may contain any non-negative values.

`gamlike` is a utility function for maximum likelihood estimation of the gamma distribution. Since `gamlike` returns the negative gamma log-likelihood function, minimizing `gamlike` using `fminsearch` is the same as maximizing the likelihood.

Examples

Compute the negative log-likelihood of parameter estimates computed by the `gamfit` function:

```
a = 2; b = 3;
r = gamrnd(a,b,100,1);

[nlogL,AVAR] = gamlike(gamfit(r),r)
nlogL =
  267.5648
AVAR =
  0.0788  -0.1104
 -0.1104  0.1955
```

More About

- "Gamma Distribution" on page B-48

See Also

gamfit | gampdf | gamcdf | gaminv | gamstat | gamrnd

gampdf

Gamma probability density function

Syntax

```
Y = gampdf(X,A,B)
```

Description

`Y = gampdf(X,A,B)` computes the gamma pdf at each of the values in `X` using the corresponding shape parameters in `A` and scale parameters in `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `A` and `B` must all be positive, and the values in `X` must lie on the interval $[0\ \infty)$.

The gamma pdf is

$$y = f(x \mid a,b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{-x}{b}}$$

The gamma probability density function is useful in reliability models of lifetimes. The gamma distribution is more flexible than the exponential distribution in that the probability of a product surviving an additional period may depend on its current age. The exponential and χ^2 functions are special cases of the gamma function.

Examples

The exponential distribution is a special case of the gamma distribution.

```
mu = 1:5;

y = gampdf(1,1,mu)
y =
```

```
  0.3679  0.3033  0.2388  0.1947  0.1637

y1 = exppdf(1,mu)
y1 =
  0.3679  0.3033  0.2388  0.1947  0.1637
```

More About

- "Gamma Distribution" on page B-48

See Also

pdf | gamcdf | gaminv | gamstat | gamfit | gamlike | gamrnd

gamrnd

Gamma random numbers

Syntax

```
R = gamrnd(A,B)
R = gamrnd(A,B,m,n,...)
R = gamrnd(A,B,[m,n,...])
```

Description

`R = gamrnd(A,B)` generates random numbers from the gamma distribution with shape parameters in `A` and scale parameters in `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

`R = gamrnd(A,B,m,n,...)` or `R = gamrnd(A,B,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the gamma distribution with parameters `A` and `B`. `A` and `B` can each be scalars or arrays of the same size as `R`.

Examples

```
n1 = gamrnd(1:5,6:10)
n1 =
  9.1132  12.8431  24.8025  38.5960 106.4164

n2 = gamrnd(5,10,[1 5])
n2 =
  30.9486  33.5667  33.6837  55.2014  46.8265

n3 = gamrnd(2:6,3,1,5)
n3 =
  12.8715  11.3068  3.0982  15.6012  21.6739
```

More About

- "Gamma Distribution" on page B-48

See Also

randg | random | gampdf | gamcdf | gaminv | gamstat | gamfit | gamlike

gamstat

Gamma mean and variance

Syntax

```
[M,V] = gamstat(A,B)
```

Description

`[M,V] = gamstat(A,B)` returns the mean of and variance for the gamma distribution with shape parameters in `A` and scale parameters in `B`. `A` and `B` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant array with the same dimensions as the other input.

The mean of the gamma distribution with parameters a and b is ab. The variance is ab^2.

Examples

```
[m,v] = gamstat(1:5,1:5)
m =
   1   4   9  16  25
v =
   1   8  27  64  125

[m,v] = gamstat(1:5,1./(1:5))
m =
   1   1   1   1   1
v =
  1.0000  0.5000  0.3333  0.2500  0.2000
```

More About

- “Gamma Distribution” on page B-48

See Also

gampdf | gamcdf | gaminv | gamfit | gamlike | gamrnd

ge

Class: qrandstream

Greater than or equal relation for handles

Syntax

```
h1 >= h2
```

Description

`h1 >= h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise `>=` result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = ge(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `gt` | `le` | `ne` | `eq` | `lt`

prob.GeneralizedExtremeValueDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Generalized extreme value probability distribution object

Description

`prob.GeneralizedExtremeValueDistribution` is an object consisting of parameters, a model description, and sample data for a generalized extreme value probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('GeneralizedExtremeValue')` creates a generalized extreme value probability distribution object using the default parameter values.

`pd = makedist('GeneralizedExtremeValue','k',k,'sigma',sigma,'mu',mu)` creates a generalized extreme value probability distribution object using the specified parameter values.

Input Arguments

`k` — Shape parameter

0 (default) | scalar value

Shape parameter for the generalized extreme value distribution, specified as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

1 (default) | nonnegative scalar value

Scale parameter for the generalized extreme value distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

`mu` — Location parameter
`0` (default) | scalar value

Location parameter for the generalized extreme value distribution, specified as a scalar value.

Data Types: `single` | `double`

Properties

`k` — Shape parameter
scalar value

Shape parameter of the generalized extreme value distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter
nonnegative scalar value

Scale parameter of the generalized extreme value distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`mu` — Location parameter
scalar value

Location parameter of the generalized extreme value distribution, stored as a scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object

icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Generalized Extreme Value Distribution

The generalized extreme value distribution is often used to model the smallest or largest value among a large set of independent, identically distributed random values representing measurements or observations. It combines three simpler distributions into a single form, allowing a continuous range of possible shapes that include all three of the simpler distributions.

The three distribution types correspond to the limiting distribution of block maxima from different classes of underlying distributions:

- Type 1 — Distributions whose tails decrease exponentially, such as the normal distribution
- Type 2 — Distributions whose tails decrease as a polynomial, such as Student's t distribution
- Type 3 — Distributions whose tails are finite, such as the beta distribution

The generalized extreme value distribution uses the following parameters.

Parameter	Description	Support
`k`	Shape parameter	$-\infty \le k \le \infty$
`sigma`	Scale parameter	$\sigma \ge 0$
`mu`	Location parameter	$-\infty \le \mu \le \infty$

The probability density function (pdf) for a Type 1 distribution, where shape parameter $k = 0$, is

$$f(x \mid 0,\mu,\sigma) = \left(\frac{1}{\sigma}\right)\exp\left(-\exp\left(-\frac{(x-\mu)}{\sigma}\right)-\frac{(x-\mu)}{\sigma}\right) \quad ; \quad -\infty < x < \infty.$$

When $k \neq 0$, the pdf is

$$f(x \mid k,\mu,\sigma) = \left(\frac{1}{\sigma}\right)\exp\left(-\left(1+k\frac{(x-\mu)}{\sigma}\right)^{-\frac{1}{k}}\right)\left(1+k\frac{(x-\mu)}{\sigma}\right)^{-1-\frac{1}{k}}$$

for

$$1+k\frac{(x-\mu)}{\sigma} > 0.$$

For the Type 2 case, $k > 0$ and $x \geq \mu - \frac{\sigma}{k}$. For the Type 3 case, $k < 0$ and $x < \mu - \frac{\sigma}{k}$.

Examples

Create a Generalized Extreme Value Distribution Object Using Default Parameters

Create a generalized extreme value distribution object using the default parameter values.

```
pd = makedist('GeneralizedExtremeValue')
```

```
pd =

  GeneralizedExtremeValueDistribution

  Generalized Extreme Value distribution
        k = 0
    sigma = 1
       mu = 0
```

Create a Generalized Extreme Value Distribution Object Using Specified Parameters

Create a generalized extreme value distribution object by specifying values for the parameters.

```
pd = makedist('GeneralizedExtremeValue','k',0,'sigma',2,'mu',1)
```

```
pd =
```

```
  GeneralizedExtremeValueDistribution

  Generalized Extreme Value distribution
        k = 0
    sigma = 2
       mu = 1
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    2.1544
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Generalized Extreme Value Distribution"
- Class Attributes
- Property Attributes

GeneralizedLinearMixedModel class

Generalized linear mixed-effects model class

Description

A `GeneralizedLinearMixedModel` object represents a regression model of a response variable that contains both fixed and random effects. The object comprises data, a model description, fitted coefficients, covariance parameters, design matrices, residuals, residual plots, and other diagnostic information for a generalized linear mixed-effects (GLME) model. You can predict model responses with the `predict` function and generate random data at new design points using the `random` function.

Construction

You can fit a generalized linear mixed-effects (GLME) model to sample data using `fitglme(tbl,formula)`. For more information, see `fitglme`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or dataset array. The predictor variables can be continuous or grouping variables (see “Grouping Variables” on page 2-52). You must specify the model for the variables using formula.

Data Types: `table`

`formula` — Formula for model specification

string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`

Formula for model specification, specified as a string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`. For a full description, see Formula.

Example: `'y ~ treatment +(1|block)'`

Properties

`Coefficients` — Estimates of fixed-effects coefficients

dataset array

Estimates of fixed-effects coefficients and related statistics, stored as a dataset array that has one row for each coefficient and the following columns:

- `Name` — Name of the coefficient
- `Estimate` — Estimated coefficient value
- `SE` — Standard error of the estimate
- `tStat` — t-statistic for a test that the coefficient is equal to 0
- `DF` — Degrees of freedom associated with the t statistic
- `pValue` — p-value for the t-statistic
- `Lower` — Lower confidence limit
- `Upper` — Upper confidence limit

To obtain any of these columns as a vector, index into the property using dot notation.

Use the `coefTest` method to perform other tests on the coefficients.

`CoefficientCovariance` — Covariance of estimated fixed-effects vector

matrix

Covariance of estimated fixed-effects vector, stored as a matrix.

Data Types: `single | double`

`CoefficientNames` — Names of fixed-effects coefficients

cell array of strings

Names of fixed-effects coefficients, stored as a cell array of strings. The label for the coefficient of the constant term is `(Intercept)`. The labels for other coefficients indicate the terms that they multiply. When the term includes a categorical predictor, the label also indicates the level of that predictor.

Data Types: `cell`

`DFE` — Degrees of freedom for error

positive integer value

Degrees of freedom for error, stored as a positive integer value. `DFE` is the number of observations minus the number of estimated coefficients.

`DFE` contains the degrees of freedom corresponding to the `'Residual'` method of calculating denominator degrees of freedom for hypothesis tests on fixed-effects coefficients. If n is the number of observations and p is the number of fixed-effects coefficients, then `DFE` is equal to $n - p$.

Data Types: `double`

`Dispersion` — Model dispersion parameter

scalar value

Model dispersion parameter, stored as a scalar value. The dispersion parameter defines the conditional variance of the response.

For observation i, the conditional variance of the response y_i, given the conditional mean μ_i and the dispersion parameter σ^2, in a generalized linear mixed-effects model is

$$\mathrm{var}\left(y_i \mid \mu_i, \sigma^2\right) = \frac{\sigma^2}{w_i} v\left(\mu_i\right),$$

where w_i is the ith observation weight and v is the variance function for the specified conditional distribution of the response. The `Dispersion` property contains an estimate of σ^2 for the specified GLME model. The value of `Dispersion` depends on the specified conditional distribution of the response. For binomial and Poisson distributions, the theoretical value of `Dispersion` is equal to $\sigma^2 = 1.0$.

- If `FitMethod` is `MPL` or `REMPL` and the `'DispersionFlag'` name-value pair argument in `fitglme` is `true`, then a dispersion parameter is estimated from data for all distributions, including binomial and Poisson distributions.
- If `FitMethod` is `ApproximateLaplace` or `Laplace`, then the `'DispersionFlag'` name-value pair argument in `fitglme` does not apply, and the dispersion parameter is fixed at 1.0 for binomial and Poisson distributions. For all other distributions, `Dispersion` is estimated from data.

Data Types: `double`

`DispersionEstimated` — Flag indicating if dispersion parameter was estimated

`true` | `false`

Flag indicating estimated dispersion parameter, stored as a logical value.

- If `FitMethod` is `ApproximateLaplace` or `Laplace`, then the dispersion parameter is fixed at its theoretical value of 1.0 for binomial and Poisson distributions, and `DispersionEstimated` is `false`. For other distributions, the dispersion parameter is estimated from the data, and `DispersionEstimated` is `true`.
- If `FitMethod` is `MPL` or `REMPL`, and the `'DispersionFlag'` name-value pair argument in `fitglme` is specified as `true`, then the dispersion parameter is estimated for all distributions, including binomial and Poisson distributions, and `DispersionEstimated` is `true`.
- If `FitMethod` is `MPL` or `REMPL`, and the `'DispersionFlag'` name-value pair argument in `fitglme` is specified as `false`, then the dispersion parameter is fixed at its theoretical value for binomial and Poisson distributions, and `DispersionEstimated` is `false`. For distributions other than binomial and Poisson, the dispersion parameter is estimated from the data, and `DispersionEstimated` is `true`.

Data Types: `logical`

`Distribution` — Response distribution name

`'Normal'` | `'Binomial'` | `'Poisson'` | `'Gamma'` | `'InverseGaussian'`

Response distribution name, stored as one of the following:

- `'Normal'` — Normal distribution
- `'Binomial'` — Binomial distribution
- `'Poisson'` — Poisson distribution
- `'Gamma'` — Gamma distribution
- `'InverseGaussian'` — Inverse Gaussian distribution

`FitMethod` — Method used to fit the model

`'MPL'` | `'REMPL'` | `'ApproximateLaplace'` | `'Laplace'`

Method used to fit the model, stored as one of the following.

- `'MPL'` — Maximum pseudo likelihood
- `'REMPL'` — Restricted maximum pseudo likelihood
- `'ApproximateLaplace'` — Maximum likelihood using the approximate Laplace method, with fixed effects profiled out
- `'Laplace'` — Maximum likelihood using the Laplace method

`Formula` — Model specification formula

object

Model specification formula, stored as an object. The model specification formula uses Wilkinson's notation to describe the relationship between the fixed-effects terms, random-effects terms, and grouping variables in the GLME model. For more information see Formula.

`Link` — Link function characteristics

structure

Link function characteristics, stored as a structure containing the following fields. The link is a function `G` that links the distribution parameter `MU` to the linear predictor `ETA` as follows: `G(MU) = ETA`.

`Name`	Name of the link function
`Link`	Function that defines `G`
`Derivative`	Derivative of `G`
`SecondDerivative`	Second derivative of `G`
`Inverse`	Inverse of `G`

Data Types: `struct`

`LogLikelihood` — Log of likelihood function

scalar value

Log of likelihood function evaluated at the estimated coefficient values, stored as a scalar value. `LogLikelihood` depends on the method used to fit the model.

- If you use `'Laplace'` or `'ApproximateLaplace'`, then `LogLikelihood` is the maximized log likelihood.

- If you use 'MPL', then LogLikelihood is the maximized log likelihood of the pseudo data from the final pseudo likelihood iteration.
- If you use 'REMPL', then LogLikelihood is the maximized restricted log likelihood of the pseudo data from the final pseudo likelihood iteration.

Data Types: double

ModelCriterion — Model criterion

table

Model criterion to compare fitted generalized linear mixed-effects models, stored as a table with the following fields.

AIC	Akaike information criterion
BIC	Bayesian information criterion
LogLikelihood	• For a model fit using 'Laplace' or 'ApproximateLaplace', LogLikelihood is the maximized log likelihood. • For a model fit using 'MPL', LogLikelihood is the maximized log likelihood of the pseudo data from the final pseudo likelihood iteration. • For a model fit using 'REMPL', LogLikelihood is the maximized restricted log likelihood of the pseudo data from the final pseudo likelihood iteration.
Deviance	–2 times LogLikelihood

NumCoefficients — Number of fixed-effects coefficients

positive integer value

Number of fixed-effects coefficients in the fitted generalized linear mixed-effects model, stored as a positive integer value.

Data Types: double

NumEstimatedCoefficients — Number of estimated fixed-effects coefficients

positive integer value

Number of estimated fixed-effects coefficients in the fitted generalized linear mixed-effects model, stored as a positive integer value.

Data Types: `double`

`NumObservations` — Number of observations

positive integer value

Number of observations used in the fit, stored as a positive integer value. `NumObservations` is the number of rows in the table or dataset array `tbl`, minus rows excluded using the `'Exclude'` name-value pair of `fitglme` or rows containing `NaN` values.

Data Types: `double`

`NumPredictors` — Number of predictors

positive integer value

Number of variables used as predictors in the generalized linear mixed-effects model, stored as a positive integer value.

Data Types: `double`

`NumVariables` — Total number of variables

positive integer value

Total number of variables, including the response and predictors, stored as a positive integer value. If the sample data is in a table or dataset array `tbl`, then `NumVariables` is the total number of variables in `tbl`, including the response variable. `NumVariables` includes variables, if any, that are not used as predictors or as the response.

Data Types: `double`

`ObservationInfo` — Information about the observations

table

Information about the observations used in the fit, stored as a table.

`ObservationInfo` has one row for each observation and the following columns.

`Weights`	The weight value for the observation. The default value is 1.

`Excluded`	If the observation was excluded from the fit using the `'Exclude'` name-value pair argument in `fitglme`, then `Excluded` is `true`, or `1`. Otherwise, `Excluded` is `false`, or `0`.
`Missing`	If the observation was excluded from the fit because any response or predictor value is missing, then `Missing` is `true`. Otherwise, `Missing` is `false`. Missing values include `NaN` for numeric variables, empty cells for cell arrays, blank rows for character arrays, and the `<undefined>` value for categorical arrays.
`Subset`	If the observation was used in the fit, then `Subset` is `true`. If the observation was not used in the fit because it is missing or excluded, then `Subset` is `false`.
`BinomSize`	Binomial size for each observation. This column only applies when fitting a binomial distribution.

Data Types: `table`

`ObservationNames` — Names of observations

cell array of strings

Names of observations used in the fit, stored as a cell array of strings.

- If the data is in a table or dataset array `tbl` that contains observation names, then `ObservationNames` uses those names.
- If the data is provided in matrices, or in a table or dataset array without observation names, then `ObservationNames` is an empty cell array.

Data Types: `cell`

`PredictorNames` — Names of predictors

cell array of strings

Names of the variables used as predictors in the fit, stored as a cell array of strings that has the same length as `NumPredictors`.

Data Types: `cell`

`ResponseName` — Name of response variable

character string

Name of the variable used as the response variable in the fit, stored as a character string.

Data Types: `char`

`Rsquared` — Proportion of variability in the response explained by the fitted model

structure

Proportion of variability in the response explained by the fitted model, stored as a structure. `Rsquared` contains the R-squared value of the fitted model, also known as the multiple correlation coefficient. `Rsquared` contains the following fields.

`Ordinary`	R-squared value, stored as a scalar value in a structure. `Rsquared.Ordinary = 1 – SSE./SST`
`Adjusted`	R-squared value adjusted for the number of fixed-effects coefficients, stored as a scalar value in a structure. `Rsquared.Adjusted = 1 – (SSE./SST)*(DFT./DFE)`, where `DFE = n – p`, `DFT = n – 1`, `n` is the total number of observations, and `p` is the number of fixed-effects coefficients.

Data Types: `struct`

`SSE` — Error sum of squares

positive scalar value

Error sum of squares, stored as a positive scalar value. `SSE` is the weighted sum of the squared conditional residuals, and is calculated as

$$SSE = \sum_{i=1}^{n} w_i^{eff} \left(y_i - f_i \right)^2 ,$$

where n is the number of observations, w_i^{eff} is the ith effective weight, y_i is the ith response, and f_i is the ith fitted value.

The ith effective weight is calculated as

$$w_i^{eff} = \left\{ \frac{w_i}{v_i\left(\mu_i\left(\hat{\beta},\hat{b}\right)\right)} \right\},$$

where v_i is the variance term for the ith observation, $\hat{\beta}$ and $\hat{b}$ are estimated values of β and b, respectively.

The ith fitted value is calculated as

$$f_i = g^{-1}\left(x_i^T\hat{\beta} + z_i^T\hat{b} + \delta_i\right),$$

where x_i^{T} is the ith row of the fixed-effects design matrix X, and z_i^{T} is the ith row of the random-effects design matrix Z. δ_i is the ith offset value.

Data Types: `double`

SSR — Regression sum of squares
positive scalar value

Regression sum of squares, stored as a positive scalar value. SSR is the sum of squares explained by the generalized linear mixed-effects regression, or equivalently the weighted sum of the squared deviations of the conditional fitted values from their weighted mean. SSR is calculated as

$$SSR = \sum_{i=1}^{N} w_i^{eff}\left(f_i - \bar{f}\right)^2,$$

where n is the number of observations, w_i^{eff} is the ith effective weight, f_i is the ith fitted value, and $\bar{f}$ is a weighted average of the fitted values.

The ith effective weight is calculated as

$$w_i^{eff} = \left\{ \frac{w_i}{v_i\left(\mu_i\left(\hat{\beta},\hat{b}\right)\right)} \right\},$$

where $\hat{\beta}$ and $\hat{b}$ are estimated values of β and b, respectively.

The ith fitted value is calculated as

$$f_i = g^{-1}\left(x_i^T\hat{\beta} + z_i^T\hat{b} + \delta_i\right),$$

where x_i^{T} is the ith row of the fixed-effects design matrix X, and z_i^{T} is the ith row of the random-effects design matrix Z. δ_i is the ith offset value.

The weighted average of fitted values is calculated as

$$\bar{f} = \frac{\left[\sum_{i=1}^{n} w_i^{eff} f_i\right]}{\sum_{i=1}^{n} w_i^{eff}}.$$

Data Types: `double`

SST — Total sum of squares

positive scalar value

Total sum of squares, stored as a positive scalar value. For a GLME model, `SST` is defined as `SST = SSE + SSR`.

Data Types: `double`

`VariableInfo` — Information about the variables

table

Information about the variables used in the fit, stored as a table. `VariableInfo` has one row for each variable and contains the following columns.

`Class`	Class of the variable (`'double'`, `'cell'`, `'nominal'`, and so on).
`Range`	Value range of the variable. • For a numerical variable, `Range` is a two-element vector of the form `[min,max]`. • For a cell or categorical variable, `Range` is a cell or categorical array containing all unique values of the variable.
`InModel`	If the variable is a predictor in the fitted model, `InModel` is `true`. If the variable is not in the fitted model, `InModel` is `false`.
`IsCategorical`	If the variable type is treated as a categorical predictor (such as cell, logical, or categorical), then `IsCategorical` is `true`. If the variable is a continuous predictor, then `IsCategorical` is `false`

Data Types: `table`

`VariableNames` — Names of the variables

cell array of strings

Names of all the variables contained in the table or dataset array `tbl`, stored as a cell array of strings.

Data Types: `cell`

`Variables` — Variables

table

Variables, stored as a table. If the fit is based on a table or dataset array `tbl`, then `Variables` is identical to `tbl`.

Data Types: `table`

Methods

anova	Analysis of variance for generalized linear mixed-effects model
coefCI	Confidence intervals for coefficients of generalized linear mixed-effects model
coefTest	Hypothesis test on fixed and random effects of generalized linear mixed-effects model
compare	Compare generalized linear mixed-effects models
covarianceParameters	Extract covariance parameters of generalized linear mixed-effects model
designMatrix	Fixed- and random-effects design matrices
fitted	Fitted responses from generalized linear mixed-effects model
fixedEffects	Estimates of fixed effects and related statistics
plotResiduals	Plot residuals of generalized linear mixed-effects model
predict	Predict response of generalized linear mixed-effects model

random	Generate random responses from fitted generalized linear mixed-effects model
randomEffects	Estimates of random effects and related statistics
refit	Refit generalized linear mixed-effects model
residuals	Residuals of fitted generalized linear mixed-effects model
response	Response vector of generalized linear mixed-effects model

Definitions

Formula

In general, a formula for model specification is a string of the form `'y ~ terms'`. For generalized linear mixed-effects models, this formula is in the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` and `random` contain the fixed-effects and the random-effects terms, respectively, and R is the number of grouping variables in the model.

Suppose a table `tbl` contains the following:

- A response variable, `y`
- Predictor variables, X_j, which can be continuous or grouping variables
- Grouping variables, g_1, g_2, ..., g_R,

where the grouping variables in X_j and g_r can be categorical, logical, character arrays, or cell arrays of strings.

Then, in a formula of the form, `'y ~ fixed + (random`$_1$`|g`$_1$`) + ... + (random`$_R$`|g`$_R$`)'`, the term `fixed` corresponds to a specification of the fixed-effects design matrix

X, $\texttt{random}_1$ is a specification of the random-effects design matrix Z_1 corresponding to grouping variable g_1, and similarly $\texttt{random}_R$ is a specification of the random-effects design matrix Z_R corresponding to grouping variable g_R. You can express the `fixed` and `random` terms using Wilkinson notation.

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	X, X^2, ..., X^k
`X1 + X2`	X1, X2
`X1*X2`	X1, X2, `X1.*X2` (elementwise multiplication of X1 and X2)
`X1:X2`	`X1.*X2` only
`- X2`	Do not include X2
`X1*X2 + X3`	X1, X2, X3, X1*X2
`X1 + X2 + X3 + X1:X2`	X1, X2, X3, X1*X2
`X1*X2*X3 - X1:X2:X3`	X1, X2, X3, X1*X2, X1*X3, X2*X3
`X1*(X2 + X3)`	X1, X2, X3, X1*X2, X1*X3

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`. Here are some examples for linear mixed-effects model specification.

Examples:

Formula	Description
`'y ~ X1 + X2'`	Fixed effects for the intercept, X1 and X2. This is equivalent to `'y ~ 1 + X1 + X2'`.
`'y ~ -1 + X1 + X2'`	No intercept and fixed effects for X1 and X2. The implicit intercept term is suppressed by including `-1`.
`'y ~ 1 + (1 | g1)'`	Fixed effects for the intercept plus random effect for the intercept for each level of the grouping variable g1.

Formula	Description
`'y ~ X1 + (1 | g1)'`	Random intercept model with a fixed slope.
`'y ~ X1 + (X1 | g1)'`	Random intercept and slope, with possible correlation between them. This is equivalent to `'y ~ 1 + X1 + (1 + X1| g1)'`.
`'y ~ X1 + (1 | g1) + (-1 + X1 | g1)'`	Independent random effects terms for intercept and slope.
`'y ~ 1 + (1 | g1) + (1 | g2) + (1 | g1:g2)'`	Random intercept model with independent main effects for `g1` and `g2`, plus an independent interaction effect.

Examples

Fit a Generalized Linear Mixed-Effects Model

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier of the chemical used in the batch (`supplier`)

- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Display the model.

```
disp(glme)
```

```
glme =


Generalized linear mixed-effects model fit by ML

Model information:
    Number of observations             100
    Fixed effects coefficients           6
    Random effects coefficients         20
    Covariance parameters                1
    Distribution                   Poisson
    Link                           Log
    FitMethod                      Laplace

Formula:
    defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1 | factory)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    416.35    434.58    -201.17          402.35

Fixed effects coefficients (95% CIs):
    Name                 Estimate     SE          tStat       DF    pValue
    '(Intercept)'           1.4689     0.15988      9.1875    94    9.8194e-15
    'newprocess'          -0.36766     0.17755     -2.0708    94      0.041122
    'time_dev'            -0.094521    0.82849     -0.11409   94      0.90941
    'temp_dev'             -0.28317     0.9617     -0.29444   94      0.76907
    'supplier_C'          -0.071868    0.078024     -0.9211   94      0.35936
    'supplier_B'           0.071072     0.07739     0.91836    94      0.36078


    Lower        Upper
       1.1515       1.7864
     -0.72019    -0.015134
      -1.7395       1.5505
      -2.1926       1.6263
     -0.22679     0.083051
    -0.082588      0.22473
```

```
Random effects covariance parameters:
Group: factory (20 Levels)
    Name1               Name2               Type         Estimate
    '(Intercept)'       '(Intercept)'       'std'        0.31381

Group: Error
    Name                      Estimate
    'sqrt(Dispersion)'        1
```

The `Model information` table displays the total number of observations in the sample data (100), the number of fixed- and random-effects coefficients (6 and 20, respectively), and the number of covariance parameters (1). It also indicates that the response variable has a `Poisson` distribution, the link function is `Log`, and the fit method is `Laplace`.

`Formula` indicates the model specification using Wilkinson's notation.

The `Model fit statistics` table displays statistics used to assess the goodness of fit of the model. This includes the Akaike information criterion (`AIC`), Bayesian information criterion (`BIC`) values, log likelihood (`LogLikelihood`), and deviance (`Deviance`) values.

The `Fixed effects coefficients` table indicates that `fitglme` returned 95% confidence intervals. It contains one row for each fixed-effects predictor, and each column contains statistics corresponding to that predictor. Column 1 (`Name`) contains the name of each fixed-effects coefficient, column 2 (`Estimate`) contains its estimated value, and column 3 (`SE`) contains the standard error of the coefficient. Column 4 (`tStat`) contains the *t*-statistic for a hypothesis test that the coefficient is equal to 0. Column 5 (`DF`) and column 6 (`pValue`) contain the degrees of freedom and *p*-value that correspond to the *t*-statistic, respectively. The last two columns (`Lower` and `Upper`) display the lower and upper limits, respectively, of the 95% confidence interval for each fixed-effects coefficient.

`Random effects covariance parameters` displays a table for each grouping variable (here, only `factory`), including its total number of levels (20), and the type and estimate of the covariance parameter. Here, `std` indicates that `fitglme` returns the standard deviation of the random effect associated with the factory predictor, which has an estimated value of 0.31381. It also displays a table containing the error parameter type (here, the square root of the dispersion parameter), and its estimated value of 1.

The standard display generated by `fitglme` does not provide confidence intervals for the random-effects parameters. To compute and display these values, use `covarianceParameters`.

- "Fit a Generalized Linear Mixed-Effects Model" on page 10-79

See Also

`fitglme`

More About

- “Generalized Linear Mixed-Effects Models” on page 10-64

GeneralizedLinearModel class

Generalized linear regression model class

Description

An object comprising training data, model description, diagnostic information, and fitted coefficients for a generalized linear regression. Predict model responses with the `predict` or `feval` methods.

Construction

`mdl = fitglm(tbl)` or `mdl = fitglm(X,y)` creates a generalized linear model of a table or dataset array `tbl`, or of the responses `y` to a data matrix `X`. For details, see `fitglm`.

`mdl = stepwiseglm(tbl)` or `mdl = stepwiseglm(X,y)` creates a generalized linear model of a table or dataset array `tbl`, or of the responses `y` to a data matrix `X`, with unimportant predictors excluded. For details, see `stepwiseglm`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see “Grouping Variables” on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

X — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single | double | logical`

y — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single | double`

Properties

CoefficientCovariance

Covariance matrix of coefficient estimates.

CoefficientNames

Cell array of strings containing a label for each coefficient.

Coefficients

Coefficient values stored as a table. `Coefficients` has one row for each coefficient and these columns:

- `Estimate` — Estimated coefficient value
- `SE` — Standard error of the estimate
- `tStat` — t statistic for a test that the coefficient is zero
- `pValue` — p-value for the t statistic

To obtain any of these columns as a vector, index into the property using dot notation. For example, in `mdl` the estimated coefficient vector is

```
beta = mdl.Coefficients.Estimate
```

Use `coefTest` to perform other tests on the coefficients.

`Deviance`

Deviance of the fit. It is useful for comparing two models when one is a special case of the other. The difference between the deviance of the two models has a chi-square distribution with degrees of freedom equal to the difference in the number of estimated parameters between the two models. For more information on deviance, see "Deviance" on page 22-2035.

`DFE`

Degrees of freedom for error (residuals), equal to the number of observations minus the number of estimated coefficients.

`Diagnostics`

Table with diagnostics helpful in finding outliers and influential observations. The table contains the following fields:

Field	Meaning	Utility
`Leverage`	Diagonal elements of `HatMatrix`	Leverage indicates to what extent the predicted value for an observation is determined by the observed value for that observation. A value close to `1` indicates that the prediction is largely determined by that observation, with little contribution from the other observations. A value close to `0` indicates the fit is largely determined by the other observations. For a model with p coefficients and n observations, the average value of `Leverage` is p/n. An observation with `Leverage` larger than $2*p/n$ can be an outlier.
`CooksDistance`	Cook's measure of scaled change in fitted values	`CooksDistance` is a measure of scaled change in fitted values. An observation with `CooksDistance` larger than three times the mean Cook's distance can be an outlier.
`HatMatrix`	Projection matrix to compute fitted from observed responses	`HatMatrix` is an n-by-n matrix such that `Fitted = HatMatrix*Y`, where `Y` is the response vector and `Fitted` is the vector of fitted response values.

All of these quantities are computed on the scale of the linear predictor. So, for example, in the equation that defines the hat matrix,

```
Yfit = glm.Fitted.LinearPredictor
Y = glm.Fitted.LinearPredictor + glm.Residuals.LinearPredictor
```

`Dispersion`

Scale factor of the variance of the response. `Dispersion` multiplies the variance function for the distribution.

For example, the variance function for the binomial distribution is $p(1–p)/n$, where p is the probability parameter and n is the sample size parameter. If `Dispersion` is near `1`, the variance of the data appears to agree with the theoretical variance of the binomial distribution. If `Dispersion` is larger than `1`, the data are "overdispersed" relative to the binomial distribution.

`DispersionEstimated`

Logical value indicating whether `fitglm` used the `Dispersion` property to compute standard errors for the coefficients in `Coefficients.SE`. If `DispersionEstimated` is `false`, `fitglm` used the theoretical value of the variance.

- `DispersionEstimated` can be `false` only for `'binomial'` or `'poisson'` distributions.
- Set `DispersionEstimated` by setting the `DispersionFlag` name-value pair in `fitglm`.

`Distribution`

Structure with the following fields relating to the generalized distribution:

Field	Description
`Name`	Name of the distribution, one of `'normal'`, `'binomial'`, `'poisson'`, `'gamma'`, or `'inverse gamma'`.
`DevianceFunction`	Function that computes the components of the deviance as a function of the fitted parameter values and the response values.
`VarianceFunction`	Function that computes the theoretical variance for the distribution as a function of the fitted parameter values. When `DispersionEstimated` is `true`, `Dispersion` multiplies the variance function in the computation of the coefficient standard errors.

Fitted

Table of predicted (fitted) values based on the training data, a table with one row for each observation and the following columns.

Field	Description
`Response`	Predicted values on the scale of the response.
`LinearPredictor`	Predicted values on the scale of the linear predictor. These are the same as the link function applied to the `Response` fitted values.
`Probability`	Fitted probabilities (this column is included only with the binomial distribution).

To obtain any of the columns as a vector, index into the property using dot notation. For example, in the model `mdl`, the vector `f` of fitted values on the response scale is

```
f = mdl.Fitted.Response
```

Use `predict` to compute predictions for other predictor values, or to compute confidence bounds on `Fitted`.

Formula

Object containing information about the model.

Link

Structure with fields relating to the link function. The link is a function f that links the distribution parameter μ to the fitted linear combination Xb of the predictors: $f(\mu) = Xb$.

The structure has the following fields.

Field	Description
`Name`	Name of the link function, or `''` if you specified the link as a function handle rather than a string.
`LinkFunction`	The function that defines f, a function handle.
`DevianceFunction`	Derivative of f, a function handle.

Field	Description
`VarianceFunction`	Inverse of *f*, a function handle.

`LogLikelihood`

Log likelihood of the model distribution at the response values, with mean fitted from the model, and other parameters estimated as part of the model fit.

`ModelCriterion`

`AIC` and other information criteria for comparing models. A structure with fields:

- `AIC` — Akaike information criterion
- `AICc` — Akaike information criterion corrected for sample size
- `BIC` — Bayesian information criterion
- `CAIC` — Consistent Akaike information criterion

To obtain any of these values as a scalar, index into the property using dot notation. For example, in a model `mdl`, the AIC value `aic` is:

```
aic = mdl.ModelCriterion.AIC
```

`NumCoefficients`

Number of coefficients in the model, a positive integer. `NumCoefficients` includes coefficients that are set to zero when the model terms are rank deficient.

`NumEstimatedCoefficients`

Number of estimated coefficients in the model, a positive integer. `NumEstimatedCoefficients` does not include coefficients that are set to zero when the model terms are rank deficient. `NumEstimatedCoefficients` is the degrees of freedom for regression.

`NumObservations`

Number of observations the fitting function used in fitting. This is the number of observations supplied in the original table, dataset, or matrix, minus any excluded rows (set with the `Excluded` name-value pair) or rows with missing values.

NumPredictors

Number of variables `fitlm` used as predictors for fitting.

NumVariables

Number of variables in the data. `NumVariables` is the number of variables in the original table or dataset, or the total number of columns in the predictor matrix and response vector when the fit is based on those arrays. It includes variables, if any, that are not used as predictors or as the response.

ObservationInfo

Table with the same number of rows as the input data (`tbl` or `X`).

Field	Description
`Weights`	Observation weights. Default is all `1`.
`Excluded`	Logical value, `1` indicates an observation that you excluded from the fit with the `Exclude` name-value pair.
`Missing`	Logical value, `1` indicates a missing value in the input. Missing values are not used in the fit.
`Subset`	Logical value, `1` indicates the observation is not excluded or missing, so is used in the fit.

ObservationNames

Cell array of strings containing the names of the observations used in the fit.

- If the fit is based on a table or dataset containing observation names, `ObservationNames` uses those names.
- Otherwise, `ObservationNames` is an empty cell array

Offset

Vector with the same length as the number of rows in the data, passed from `fitglm` or `stepwiseglm` in the `Offset` name-value pair. The fitting function used `Offset` as a predictor variable, but with the coefficient set to exactly `1`. In other words, the formula for fitting was

μ ~ `Offset + (terms involving real predictors)`

with the `Offset` predictor having coefficient `1`.

For example, consider a Poisson regression model. Suppose the number of counts is known for theoretical reasons to be proportional to a predictor `A`. By using the log link function and by specifying `log(A)` as an offset, you can force the model to satisfy this theoretical constraint.

`PredictorNames`

Cell array of strings, the names of the predictors used in fitting the model.

`Residuals`

Table containing residuals, with one row for each observation and these variables.

Field	Description
`Raw`	Observed minus fitted values.
`LinearPredictor`	Residuals on the linear predictor scale, equal to the adjusted response value minus the fitted linear combination of the predictors.
`Pearson`	Raw residuals divided by the estimated standard deviation of the response.
`Anscombe`	Residuals defined on transformed data with the transformation chosen to remove skewness.
`Deviance`	Residuals based on the contribution of each observation to the deviance.

To obtain any of these columns as a vector, index into the property using dot notation. For example, in a model `mdl`, the ordinary raw residual vector `r` is:

```
r = mdl.Residuals.Raw
```

Rows not used in the fit because of missing values (in `ObservationInfo.Missing`) contain `NaN` values.

Rows not used in the fit because of excluded values (in `ObservationInfo.Excluded`) contain `NaN` values, with the following exceptions:

- `raw` contains the difference between the observed and predicted values.
- `standardized` is the residual, standardized in the usual way.
- `studentized` matches the standardized values because this residual is not used in the estimate of the residual standard deviation.

`ResponseName`

String giving naming the response variable.

`Rsquared`

Proportion of total sum of squares explained by the model. The ordinary R-squared value relates to the `SSR` and `SST` properties:
`Rsquared = SSR/SST = 1 - SSE/SST`.

For a linear or nonlinear model, `Rsquared` is a structure with two fields:

- `Ordinary` — Ordinary (unadjusted) R-squared
- `Adjusted` — R-squared adjusted for the number of coefficients

For a generalized linear model, `Rsquared` is a structure with five fields:

- `Ordinary` — Ordinary (unadjusted) R-squared
- `Adjusted` — R-squared adjusted for the number of coefficients
- `LLR` — Log-likelihood ratio
- `Deviance` — Deviance
- `AdjGeneralized` — Adjusted generalized R-squared

To obtain any of these values as a scalar, index into the property using dot notation. For example, the adjusted R-squared value in `mdl` is

```
r2 = mdl.Rsquared.Adjusted
```

`SSE`

Sum of squared errors (residuals).

The Pythagorean theorem implies

`SST = SSE + SSR`.

`SSR`

Regression sum of squares, the sum of squared deviations of the fitted values from their mean.

The Pythagorean theorem implies
`SST = SSE + SSR`.

`SST`

Total sum of squares, the sum of squared deviations of `y` from `mean(y)`.

The Pythagorean theorem implies
`SST = SSE + SSR`.

`Steps`

Structure that is empty unless `stepwiselm` constructed the model.

Field	Description
`Start`	Formula representing the starting model
`Lower`	Formula representing the lower bound model, these terms that must remain in the model
`Upper`	Formula representing the upper bound model, model cannot contain more terms than `Upper`
`Criterion`	Criterion used for the stepwise algorithm, such as `'sse'`
`PEnter`	Value of the parameter, such as `0.05`
`PRemove`	Value of the parameter, such as `0.10`
`History`	Table representing the steps taken in the fit

The `History` table has one row for each step including the initial fit, and the following variables (columns).

Field	Description
`Action`	Action taken during this step, one of: • `'Start'` — First step

Field	Description
	• `'Add'` — A term is added • `'Remove'` — A term is removed
`TermName`	• `'Start'` step: The starting model specification • `'Add'` or `'Remove'` steps: The term moved in that step
`Terms`	Terms matrix (see `modelspec` of `fitlm`)
`DF`	Regression degrees of freedom after this step
`delDF`	Change in regression degrees of freedom from previous step (negative for steps that remove a term)
`Deviance`	Deviance (residual sum of squares) at that step
`FStat`	*F* statistic that led to this step
`PValue`	*p*-value of the *F* statistic

`VariableInfo`

Table containing metadata about `Variables`. There is one row for each term in the model, and the following columns.

Field	Description
`Class`	String giving variable class, such as `'double'`
`Range`	Cell array giving variable range: • Continuous variable — Two-element vector `[min,max]`, the minimum and maximum values • Categorical variable — Cell array of distinct variable values
`InModel`	Logical vector, where `true` indicates the variable is in the model
`IsCategorical`	Logical vector, where `true` indicates a categorical variable

`VariableNames`

Cell array of strings containing names of the variables in the fit.

- If the fit is based on a table or dataset, this property provides the names of the variables in that table or dataset.

- If the fit is based on a predictor matrix and response vector, `VariableNames` is the values in the `VarNames` name-value pair of the fitting method.
- Otherwise the variables have the default fitting names.

`Variables`

Table containing the data, both observations and responses, that the fitting function used to construct the fit. If the fit is based on a table or dataset array, `Variables` contains all of the data from that table or dataset array. Otherwise, `Variables` is a table created from the input data matrix `X` and response vector `y`.

Methods

addTerms	Add terms to generalized linear model
coefCI	Confidence intervals of coefficient estimates of generalized linear model
coefTest	Linear hypothesis test on generalized linear regression model coefficients
devianceTest	Analysis of deviance
disp	Display generalized linear regression model
feval	Evaluate generalized linear regression model prediction
fit	Create generalized linear regression model
plotDiagnostics	Plot diagnostics of generalized linear regression model
plotResiduals	Plot residuals of generalized linear regression model

plotSlice	Plot of slices through fitted generalized linear regression surface
predict	Predict response of generalized linear regression model
random	Simulate responses for generalized linear regression model
removeTerms	Remove terms from generalized linear model
step	Improve generalized linear regression model by adding or removing terms
stepwise	Create generalized linear regression model by stepwise regression

Definitions

Canonical Link Function

The default link function for a generalized linear model is the *canonical link function*.

Canonical Link Functions for Generalized Linear Models

Distribution	Link Function Name	Link Function	Mean (Inverse) Function
`'normal'`	`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'binomial'`	`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'poisson'`	`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'gamma'`	`-1`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`'inverse gaussian'`	`-2`	$f(\mu) = 1/\mu^2$	$\mu = (Xb)^{-1/2}$

Hat Matrix

The *hat matrix H* is defined in terms of the data matrix X and a diagonal weight matrix W:
$H = X(X^TWX)^{-1}X^TW^T$.

W has diagonal elements w_i:

$$w_i = \frac{g'(\mu_i)}{\sqrt{V(\mu_i)}},$$

where

- g is the link function mapping y_i to x_ib.
- g' is the derivative of the link function g.
- V is the variance function.
- μ_i is the ith mean.

The diagonal elements H_{ii} satisfy

$$0 \le h_{ii} \le 1$$

$$\sum_{i=1}^{n} h_{ii} = p,$$

where n is the number of observations (rows of X), and p is the number of coefficients in the regression model.

Leverage

The *leverage* of observation i is the value of the ith diagonal term, h_{ii}, of the hat matrix H. Because the sum of the leverage values is p (the number of coefficients in the regression model), an observation i can be considered to be an outlier if its leverage substantially exceeds p/n, where n is the number of observations.

Cook's Distance

The Cook's distance D_i of observation i is

$$D_i = w_i \frac{e_i^2}{p\hat{\varphi}} \frac{h_{ii}}{(1-h_{ii})^2},$$

where

- $\hat{\varphi}$ is the dispersion parameter (estimated or theoretical).
- e_i is the linear predictor residual, $g(y_i) - x_i\hat{\beta}$, where
  - g is the link function.
  - y_i is the observed response.
  - x_i is the observation.
  - $\hat{\beta}$ is the estimated coefficient vector.
- p is the number of coefficients in the regression model.
- h_{ii} is the ith diagonal element of the Hat Matrix H.

Deviance

Deviance of a model M_1 is twice the difference between the loglikelihood of that model and the saturated model, M_S. The saturated model is the model with the maximum number of parameters that can be estimated. For example, if there are n observations y_i, $i = 1, 2, ..., n$, with potentially different values for $X_i^T\beta$, then you can define a saturated model with n parameters. Let $L(b,y)$ denote the maximum value of the likelihood function for a model. Then the deviance of model M_1 is

$$-2\left(\log L(b_1, y) - \log L(b_S, y)\right),$$

where b_1 are the estimated parameters for model M_1 and b_S are the estimated parameters for the saturated model. The deviance has a chi-square distribution with $n - p$ degrees of freedom, where n is the number of parameters in the saturated model and p is the number of parameters in model M_1.

If M_1 and M_2 are two different generalized linear models, then the fit of the models can be assessed by comparing the deviances D_1 and D_2 of these models. The difference of the deviances is

$$D = D_2 - D_1 = -2\left(\log L(b_2, y) - \log L(b_S, y)\right) + 2\left(\log L(b_1, y) - \log L(b_S, y)\right)$$
$$= -2\left(\log L(b_2, y) - \log L(b_1, y)\right).$$

Asymptotically, this difference has a chi-square distribution with degrees of freedom v equal to the number of parameters that are estimated in one model but fixed (typically at 0) in the other. That is, it is equal to the difference in the number of parameters estimated in M_1 and M_2. You can get the p-value for this test using `1 - chi2cdf(D,V)`, where $D = D_2 - D_1$.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Fit a Generalized Linear Model

Fit a logistic regression model of probability of smoking as a function of age, weight, and sex, using a two-way interactions model.

Load the `hospital` dataset array.

```
load hospital
ds = hospital; % just to use the ds name
```

Specify the model using a formula that allows up to two-way interactions.

```
modelspec = 'Smoker ~ Age*Weight*Sex - Age:Weight:Sex';
```

Create the generalized linear model.

```
mdl = fitglm(ds,modelspec,'Distribution','binomial')
```

```
mdl =


Generalized Linear regression model:
    logit(Smoker) ~ 1 + Sex*Age + Sex*Weight + Age*Weight
    Distribution = Binomial
```

```
Estimated Coefficients:
                       Estimate       SE           tStat       pValue
    (Intercept)            -6.0492       19.749     -0.3063    0.75938
    Sex_Male               -2.2859       12.424    -0.18399    0.85402
    Age                    0.11691      0.50977     0.22934    0.81861
    Weight                0.031109      0.15208     0.20455    0.83792
    Sex_Male:Age          0.020734      0.20681     0.10025    0.92014
    Sex_Male:Weight        0.01216     0.053168     0.22871     0.8191
    Age:Weight         -0.00071959    0.0038964    -0.18468    0.85348


100 observations, 93 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 5.07, p-value = 0.535
```

The large *p*-value indicates the model might not differ statistically from a constant.

Create a Generalized Linear Model Stepwise

Create response data using just three of 20 predictors, and create a generalized linear model stepwise to see if it uses just the correct predictors.

Create data with 20 predictors, and Poisson response using just three of the predictors, plus a constant.

```
rng('default') % for reproducibility
X = randn(100,20);
mu = exp(X(:,[5 10 15])*[.4;.2;.3] + 1);
y = poissrnd(mu);
```

Fit a generalized linear model using the Poisson distribution.

```
mdl =  stepwiseglm(X,y,...
    'constant','upper','linear','Distribution','poisson')
```

```
1. Adding x5, Deviance = 134.439, Chi2Stat = 52.24814, PValue = 4.891229e-13
2. Adding x15, Deviance = 106.285, Chi2Stat = 28.15393, PValue = 1.1204e-07
3. Adding x10, Deviance = 95.0207, Chi2Stat = 11.2644, PValue = 0.000790094

mdl =


Generalized Linear regression model:
    log(y) ~ 1 + x5 + x10 + x15
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)     1.0115     0.064275    15.737    8.4217e-56
    x5             0.39508     0.066665    5.9263    3.0977e-09
    x10            0.18863      0.05534    3.4085     0.0006532
    x15            0.29295     0.053269    5.4995    3.8089e-08


100 observations, 96 error degrees of freedom
```

```
Dispersion: 1
Chi^2-statistic vs. constant model: 91.7, p-value = 9.61e-20
```

- “Generalized Linear Model Workflow” on page 10-39

See Also

`fitglm` | `LinearModel` | `NonLinearModel` | `stepwiseglm`

More About

- “Generalized Linear Models” on page 10-12

prob.GeneralizedParetoDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Generalized Pareto probability distribution object

Description

`prob.GeneralizedParetoDistribution` is an object consisting of parameters, a model description, and sample data for a generalized Pareto probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('GeneralizedPareto')` creates a generalized Pareto probability distribution object using default parameter values.

`pd = makedist('GeneralizedPareto','k',k,'sigma',sigma,'theta',theta)` creates a generalized Pareto probability distribution object using the specified parameter values.

Input Arguments

`k` — Shape parameter

1 (default) | scalar value

Shape parameter for the generalized Pareto distribution, specified as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

1 (default) | nonnegative scalar value

Scale parameter for the generalized Pareto distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

`theta` — Location parameter

1 (default) | scalar value

Location parameter for the generalized Pareto distribution, specified as a scalar value.

Data Types: `single` | `double`

Properties

`k` — Shape parameter

scalar value

Shape parameter for the generalized Pareto distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

nonnegative scalar value

Scale parameter for the generalized Pareto distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`theta` — Location parameter

scalar value

Location parameter for the generalized Pareto distribution, stored as a scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object

icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Generalized Pareto Distribution

The generalized Pareto distribution is used to model the tails of another distribution. It allows a continuous range of possible shapes that include both the exponential and Pareto distributions as special cases. It has three basic forms, each corresponding to a limiting distribution of exceedence data from a different class of underlying distributions.

- Distributions whose tails decrease exponentially, such as the normal, lead to a generalized Pareto shape parameter of zero.
- Distributions whose tails decrease polynomially, such as the Student's *t*, lead to a positive shape parameter.
- Distributions whose tails are finite, such as the beta, lead to a negative shape parameter.

The generalized Pareto distribution uses the following parameters.

Parameter	Description	Support
`k`	Shape parameter	$-\infty < k < \infty$
`sigma`	Scale parameter	$\sigma \geq 0$
`theta`	Location parameter	$-\infty < \theta < \infty$

The probability density function (pdf) of the generalized Pareto distribution with shape parameter $k \neq 0$ is

$$f\left(x \mid k,\sigma,\theta\right) = \left(\frac{1}{\sigma}\right)\left(1 + k\frac{\left(x-\theta\right)}{\sigma}\right)^{-1-\frac{1}{k}}$$

for $x > \theta$, when $k > 0$, or for $\theta < x < -\frac{\sigma}{k}$, when $k < 0$.

For $k = 0$, the pdf is

$$y = f\left(x \mid 0,\sigma,\theta\right) = \left(\frac{1}{\sigma}\right)\exp\left(-\frac{\left(x-\theta\right)}{\sigma}\right)$$

for $x > \theta$.

If $k = 0$ and $\theta = 0$, the generalized Pareto distribution is equivalent to the exponential distribution. If $k > 0$ and $\theta = \frac{\sigma}{k}$, the generalized Pareto distribution is equivalent to the Pareto distribution.

Examples

Create a Generalized Pareto Distribution Object Using Default Parameters

Create a generalized Pareto distribution object using the default parameter values.

```
pd = makedist('GeneralizedPareto')
```

```
pd =

  GeneralizedParetoDistribution

  Generalized Pareto distribution
        k = 1
    sigma = 1
    theta = 1
```

Create a Generalized Pareto Distribution Object Using Specified Parameters

Create a generalized Pareto distribution object by specifying parameter values.

```
pd = makedist('GeneralizedPareto','k',0,'sigma',2,'theta',1)
```

```
pd =

  GeneralizedParetoDistribution

  Generalized Pareto distribution
        k = 0
    sigma = 2
```

```
    theta = 1
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    2.1544
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Generalized Pareto Distribution"
- Class Attributes
- Property Attributes

geocdf

Geometric cumulative distribution function

Syntax

```
y = geocdf(x,p)
y = geocdf(x,p,'upper')
```

Description

`y = geocdf(x,p)` returns the cumulative distribution function (cdf) of the geometric distribution at each value in `x` using the corresponding probabilities in `p`. `x` and `p` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `p` must lie on the interval `[0,1]`.

`y = geocdf(x,p,'upper')` returns the complement of the geometric distribution cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

Examples

Compute Geometric Distribution cdf

Suppose you toss a fair coin repeatedly, and a "success" occurs when the coin lands with heads facing up. What is the probability of observing three or fewer tails ("failures") before tossing a heads?

To solve, determine the value of the cumulative distribution function (cdf) for the geometric distribution at x equal to 3. The probability of success (tossing a heads) p in any given trial is 0.5.

```
x = 3;
p = 0.5;
y = geocdf(x,p)
```

```
y =

    0.9375
```

The returned value of y indicates that the probability of observing three or fewer tails before tossing a heads is 0.9375.

More About

Geometric Distribution cdf

The cumulative distribution function (cdf) of the geometric distribution is

$$y = F(x \mid p) = 1 - (1-p)^{x+1}\ ;\ x = 0, 1, 2, \ldots,$$

where p is the probability of success, and x is the number of failures before the first success. The result y is the probability of observing up to x trials before a success, when the probability of success in any given trial is p.

- "Geometric Distribution" on page B-65

See Also

`geopdf` | `geoinv` | `geostat` | `geornd` | `cdf` | `mle`

geoinv

Geometric inverse cumulative distribution function

Syntax

```
x = geoinv(y,p)
```

Description

`x = geoinv(y,p)` returns the inverse cumulative distribution function (icdf) of the geometric distribution at each value in `y` using the corresponding probabilities in `p`.

`geoinv` returns the smallest positive integer `x` such that the geometric cdf evaluated at `x` is equal to or exceeds `y`. You can think of `y` as the probability of observing `x` successes in a row in independent trials, where `p` is the probability of success in each trial.

`y` and `p` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `p` or `y` is expanded to a constant array with the same dimensions as the other input. The values in `p` and `y` must lie on the interval `[0,1]`.

Examples

Compute Geometric Distribution icdf

Suppose the probability of a five-year-old car battery not starting in cold weather is 0.03. If we want no more than a ten percent chance that the car does not start, what is the maximum number of days in a row that we should try to start the car?

To solve, compute the inverse cdf of the geometric distribution. In this example, a "success" means the car does not start, while a "failure" means the car does start. The probability of success for each trial p equals 0.03, while the probability of observing x failures in a row before observing a success y equals 0.1.

```
y = 0.1;
p = 0.03;
x = geoinv(y,p)
```

```
x =

     3
```

The returned result indicates that if we start the car three times, there is at least a ten percent chance that it will not start on one of those tries. Therefore, if we want no greater than a ten percent chance that the car will not start, we should only attempt to start it for a maximum of two days in a row.

We can confirm this result by evaluating the cdf at values of x equal to 2 and 3, given the probability of success for each trial p equal to 0.03.

```
y2 = geocdf(2,p)  % cdf for x = 2
y3 = geocdf(3,p)  % cdf for x = 3
```

```
y2 =

    0.0873


y3 =

    0.1147
```

The returned results indicate an 8.7% chance of the car not starting if we try two days in a row, and an 11.5% chance of not starting if we try three days in a row.

More About

- “Geometric Distribution” on page B-65

See Also

`geocdf` | `geopdf` | `geostat` | `geornd` | `icdf`

geomean

Geometric mean

Syntax

```
m = geomean(x)
geomean(X,dim)
```

Description

`m = geomean(x)` calculates the geometric mean of a sample. For vectors, `geomean(x)` is the geometric mean of the elements in `x`. For matrices, `geomean(X)` is a row vector containing the geometric means of each column. For N-dimensional arrays, `geomean` operates along the first nonsingleton dimension of `X`.

`geomean(X,dim)` takes the geometric mean along the dimension `dim` of `X`.

The geometric mean is

$$m = \left[\prod_{i=1}^{n} x_i \right]^{\frac{1}{n}}$$

Examples

The arithmetic mean is greater than or equal to the geometric mean.

```
x = exprnd(1,10,6);

geometric = geomean(x)
geometric =
  0.7466  0.6061  0.6038  0.2569  0.7539  0.3478

average = mean(x)
average =
```

```
  1.3509   1.1583   0.9741   0.5319   1.0088   0.8122
```

More About

- "Geometric Distribution" on page B-65

See Also

`mean` | `median` | `harmmean` | `trimmean`

geopdf

Geometric probability density function

Syntax

```
y = geopdf(x,p)
```

Description

`y = geopdf(x,p)` returns the probability density function (pdf) of the geometric distribution at each value in `x` using the corresponding probabilities in `p`. `x` and `p` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `p` must lie on the interval `[0,1]`.

Examples

Compute Geometric Distribution pdf

Suppose you toss a fair coin repeatedly, and a "success" occurs when the coin lands with heads facing up. What is the probability of observing exactly three tails ("failures") before tossing a heads?

To solve, determine the value of the probability density function (pdf) for the geometric distributon at x equal to 3. The probability of success (tossing a heads) p in any given trial is 0.5.

```
x = 3;
p = 0.5;
y = geopdf(x,p)
```

```
y =

    0.0625
```

The returned value of y indicates that the probability of observing exactly three tails before tossing a heads is 0.0625.

More About

Geometric Distribution pdf

The probability distribution function (pdf) of the geometric distribution is

$$y = f(x \mid p) = p(1-p)^x \quad ; \quad x = 0,1,2,\ldots,$$

where p is the probability of success, and x is the number of failures before the first success. The result y is the probability of observing exactly x trials before a success, when the probability of success in any given trial is p. For discrete distributions, the probability distribution function is also known as the probability mass function (pmf).

- "Geometric Distribution" on page B-65

See Also

`geocdf` | `geoinv` | `geostat` | `geornd` | `pdf` | `mle`

geornd

Geometric random numbers

Syntax

```
r = geornd(p)
r = geornd(p,m,n,...)
r = geornd(p,[m,n,...])
```

Description

`r = geornd(p)` generates random numbers from a geometric distribution with probability parameter `p`. `p` can be a vector, a matrix, or a multidimensional array. The size of `r` is equal to the size of `p`. The parameters in `p` must lie in the interval `[0,1]`.

`r = geornd(p,m,n,...)` or `r = geornd(p,[m,n,...])` generates a multidimensional `m`-by-`n`-by-`...` array containing random numbers from the geometric distribution with probability parameter `p`. `p` can be a scalar or an array of the same size as `r`.

The geometric distribution is useful to model the number of failures before one success in a series of independent trials, where each trial results in either success or failure, and the probability of success in any individual trial is the constant `p`.

Examples

Generate Random Numbers from Geometric Distribution

Generate a single random number from a geometric distribution with probability parameter p equal to 0.01.

```
rng default  % For reproducibility
p = 0.01;
r1 = geornd(0.01)
```

```
r1 =

    20
```

The returned random number represents a single experiment in which 20 failures were observed before a success, where each independent trial has a probability of success p equal to 0.01.

Generate a 1-by-5 array of random numbers from a geometric distribution with probability parameter p equal to 0.01.

```
r2 = geornd(p,1,5)
```

```
r2 =

     9   205     9    45   231
```

Each random number in the returned array represents the result of an experiment to determine the number of failures observed before a success, where each independent trial has a probability of success p equal to 0.01.

Generate a 1-by-3 array containing one random number from each of the three geometric distributions corresponding to the parameters in the 1-by-3 array of probabilities p.

```
p = [0.01 0.1 0.5];
r3 = geornd(p,[1 3])
```

```
r3 =

   127     5     0
```

Each element of the returned 1-by-3 array `r3` contains one random number generated from the geometric distribution described by the corresponding parameter in `P`. For example, the first element in `r3` represents an experiment in which 127 failures were observed before a success, where each independent trial has a probability of success p equal to 0.01. The second element in `r3` represents an experiment in which 5 failures were observed before a success, where each independent trial has a probability of success p equal to 0.1. The third element in `r3` represents an experiment in which zero failures

were observed before a success - in other words, the first attempt was a success - where each independent trial has a probability of success p equal to 0.5.

More About

- "Geometric Distribution" on page B-65

See Also

`geopdf` | `geocdf` | `geoinv` | `geostat` | `random`

geostat

Geometric mean and variance

Syntax

```
[m,v] = geostat(p)
```

Description

`[m,v] = geostat(p)` returns the mean `m` and variance `v` of a geometric distribution with corresponding probability parameters in `p`. `p` can be a vector, a matrix, or a multidimensional array. The parameters in `p` must lie in the interval `[0,1]`.

Examples

Compute Mean and Variance of Geometric Distribution

Define a probability vector that contains six different parameter values.

```
p = 1./(1:6)
```

```
p =

    1.0000    0.5000    0.3333    0.2500    0.2000    0.1667
```

Compute the mean and variance of the geometric distribution that corresponds to each value contained in probability vector.

```
[m,v] = geostat(1./(1:6))
```

```
m =

         0    1.0000    2.0000    3.0000    4.0000    5.0000
```

```
v =

         0    2.0000    6.0000   12.0000   20.0000   30.0000
```

The returned values indicate that, for example, the mean of a geometric distribution with probability parameter p equal to 1/3 is 2, and its variance is 6.

More About

Geometric Distribution Mean and Variance

The mean of the geometric distribution is

$$\text{mean} = \frac{1-p}{p},$$

and the variance of the geometric distribution is

$$\text{var} = \frac{1-p}{p^2},$$

where p is the probability of success.

- "Geometric Distribution" on page B-65

See Also

`geopdf` | `geocdf` | `geoinv` | `geornd`

clustering.evaluation.GapEvaluation class

Package: clustering.evaluation
Superclasses: clustering.evaluation.ClusterCriterion

Gap criterion clustering evaluation object

Description

`clustering.evaluation.GapEvaluation` is an object consisting of sample data, clustering data, and gap criterion values used to evaluate the optimal number of clusters. Create a gap criterion clustering evaluation object using `evalclusters`.

Construction

`eva = evalclusters(x,clust,'Gap')` creates a gap criterion clustering evaluation object.

`eva = evalclusters(x,clust,'Gap',Name,Value)` creates a gap criterion clustering evaluation object using additional options specified by one or more name-value pair arguments.

Input Arguments

x — Input data

matrix

Input data, specified as an *N*-by-*P* matrix. *N* is the number of observations, and *P* is the number of variables.

Data Types: `single` | `double`

clust — Clustering algorithm

`'kmeans'` | `'linkage'` | `'gmdistribution'` | matrix of clustering solutions | function handle

Clustering algorithm, specified as one of the following.

`'kmeans'`	Cluster the data in x using the `kmeans` clustering algorithm, with `'EmptyAction'` set to `'singleton'` and `'Replicates'` set to `5`.
`'linkage'`	Cluster the data in x using the `clusterdata` agglomerative clustering algorithm, with `'Linkage'` set to `'ward'`.
`'gmdistribution'`	Cluster the data in x using the `gmdistribution` Gaussian mixture distribution algorithm, with `'SharedCov'` set to `true` and `'Replicates'` set to `5`.

If `Criterion` is `'CalinskHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can specify a clustering algorithm using the `function_handle` (`@`) operator. The function must be of the form `C = clustfun(DATA,K)`, where `DATA` is the data to be clustered, and `K` is the number of clusters. The output of `clustfun` must be one of the following:

- A vector of integers representing the cluster index for each observation in `DATA`. There must be `K` unique values in this vector.
- A numeric n-by-K matrix of score for n observations and K classes. In this case, the cluster index for each observation is determined by taking the largest score value in each row.

If `Criterion` is `'CalinskHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can also specify `clust` as a n-by-K matrix containing the proposed clustering solutions. n is the number of observations in the sample data, and K is the number of proposed clustering solutions. Column j contains the cluster indices for each of the N points in the jth clustering solution.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'KList',[1:5],'Distance','cityblock'` specifies to test 1, 2, 3, 4, and 5 clusters using the sum of absolute differences distance measure.

`'B'` — Number of reference data sets

`100` (default) | positive integer value

Number of reference data sets generated from the reference distribution ReferenceDistribution, specified as the comma-separated pair consisting of `'B'` and a positive integer value.

Example: `'B',150`

`'Distance'` — Distance metric

`'sqEuclidean'` (default) | `'Euclidean'` | `'cityblock'` | function | ...

Distance metric used for computing the criterion values, specified as the comma-separated pair consisting of `'Distance'` and one of the following.

`'sqEuclidean'`	Squared Euclidean distance
`'Euclidean'`	Euclidean distance
`'cityblock'`	Sum of absolute differences
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors)
`'correlation'`	One minus the sample correlation between points (treated as sequences of values)
`'Hamming'`	Percentage of coordinates that differ
`'Jaccard'`	Percentage of nonzero coordinates that differ

For detailed information about each distance metric, see `pdist`.

You can also specify a function for the distance metric by using the `function_handle` (`@`) operator. The distance function must be of the form

```
d2 = distfun(XI,XJ),
```

where `XI` is a 1-by-n vector corresponding to a single row of the input matrix `X`, and `XJ` is an m_2-by-n matrix corresponding to multiple rows of `X`. `distfun` must return an m_2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

If `Criterion` is `'silhouette'`, you can also specify `Distance` as the output vector output created by the function `pdist`.

When `Clust` a string representing a built-in clustering algorithm, `evalclusters` uses the distance metric specified for `Distance` to cluster the data, except for the following:

- If `Clust` is `'linkage'`, and `Distance` is either `'sqEuclidean'` or `'Euclidean'`, then the clustering algorithm uses Euclidean distance and Ward linkage.

- If `Clust` is `'linkage'` and `Distance` is any other metric, then the clustering algorithm uses the specified distance metric and average linkage.

In all other cases, the distance metric specified for Distance must match the distance metric used in the clustering algorithm to obtain meaningful results.

Example: `'Distance','Euclidean'`

`'KList'` — List of number of clusters to evaluate

vector

List of number of clusters to evaluate, specified as the comma-separated pair consisting of `'KList'` and a vector of positive integer values. You must specify `KList` when clust is a clustering algorithm name string or a function handle. When criterion is `'gap'`, clust must be a string or a function handle, and you must specify KList.

Example: `'KList',[1:6]`

`'ReferenceDistribution'` — Reference data generation method

`'PCA'` (default) | `'uniform'`

Reference data generation method, specified as the comma-separated pair consisting of `'ReferenceDistributions'` and one of the following.

`'PCA'`	Generate reference data from a uniform distribution over a box aligned with the principal components of the data matrix `x`.
`'uniform'`	Generate reference data uniformly over the range of each feature in the data matrix `x`.

Example: `'ReferenceDistribution','uniform'`

`'SearchMethod'` — Method for selecting optimal number of clusters

`'globalMaxSE'` (default) | `'firstMaxSE'`

Method for selecting the optimal number of clusters, specified as the comma-separated pair consisting of `'SearchMethod'` and one of the following.

`'globalMaxSE'`	Evaluate each proposed number of clusters in KList and select the smallest number of clusters satisfying $$\mathrm{Gap}(K) \geq GAPMAX - \mathrm{SE}(GAPMAX),$$

where K is the number of clusters, Gap(K) is the gap value for the clustering solution with K clusters, *GAPMAX* is the largest gap value, and SE(*GAPMAX*) is the standard error corresponding to the largest gap value.

`'firstMaxSE'` Evaluate each proposed number of clusters in KList and select the smallest number of clusters satisfying

$$\mathrm{Gap}(K) \geq \mathrm{Gap}(K+1) - \mathrm{SE}(K+1),$$

where K is the number of clusters, Gap(K) is the gap value for the clustering solution with K clusters, and SE(K + 1) is the standard error of the clustering solution with K + 1 clusters.

Example: `'SearchMethod','globalMaxSE'`

Properties

B

Number of data sets generated from the reference distribution, stored as a positive integer value.

ClusteringFunction

Clustering algorithm used to cluster the input data, stored as a valid clustering algorithm name string or function handle. If the clustering solutions are provided in the input, `ClusteringFunction` is empty.

CriterionName

Name of the criterion used for clustering evaluation, stored as a valid criterion name string.

CriterionValues

Criterion values corresponding to each proposed number of clusters in `InspectedK`, stored as a vector of numerical values.

`Distance`

Distance measure used for clustering data, stored as a valid distance measure name string.

`ExpectedLogW`

Expectation of the natural logarithm of *W* based on the generated reference data, stored as a vector of scalar values. *W* is the within-cluster dispersion computed using the distance measurement `Distance`.

`InspectedK`

List of the number of proposed clusters for which to compute criterion values, stored as a vector of positive integer values.

`LogW`

Natural logarithm of *W* based on the input data, stored as a vector of scalar values. *W* is the within-cluster dispersion computed using the distance measurement `Distance`.

`Missing`

Logical flag for excluded data, stored as a column vector of logical values. If `Missing` equals `true`, then the corresponding value in the data matrix `x` is not used in the clustering solution.

`NumObservations`

Number of observations in the data matrix `X`, minus the number of missing (`NaN`) values in `X`, stored as a positive integer value.

`OptimalK`

Optimal number of clusters, stored as a positive integer value.

`OptimalY`

Optimal clustering solution corresponding to `OptimalK`, stored as a column vector of positive integer values. If the clustering solutions are provided in the input, `OptimalY` is empty.

`ReferenceDistribution`

Reference data generation method, stored as a valid reference distribution name string.

`SE`

Standard error of the natural logarithm of *W* with respect to the reference data for each number of clusters in `InspectedK`, stored as a vector of scalar values. *W* is the within-cluster dispersion computed using the distance measurement `Distance`.

`SearchMethod`

Method for determining the optimal number of clusters, stored as a valid search method name string.

`StdLogW`

Standard deviation of the natural logarithm of *W* with respect to the reference data for each number of clusters in `InspectedK`. *W* is the within-cluster dispersion computed using the distance measurement `Distance`.

`X`

Data used for clustering, stored as a matrix of numerical values.

Methods

increaseB	Increase reference data sets

Inherited Methods

addK	Evaluate additional numbers of clusters
plot	Plot clustering evaluation object criterion values

compact

Compact clustering evaluation object

Definitions

Gap Value

A common graphical approach to cluster evaluation involves plotting an error measurement versus several proposed numbers of clusters, and locating the “elbow” of this plot. The “elbow” occurs at the most dramatic decrease in error measurement. The gap criterion formalizes this approach by estimating the “elbow” location as the number of clusters with the largest gap value. Therefore, under the gap criterion, the optimal number of clusters occurs at the solution with the largest local or global gap value within a tolerance range.

The gap value is defined as

$$Gap_n(k) = E_n^*\{\log(W_k)\} - \log(W_k),$$

where n is the sample size, k is the number of clusters being evaluated, and W_k is the pooled within-cluster dispersion measurement

$$W_k = \sum_{r=1}^{k} \frac{1}{2n_r} D_r,$$

where n_r is the number of data points in cluster r, and D_r is the sum of the pairwise distances for all points in cluster r.

The expected value $E_n^*\{\log(W_k)\}$ is determined by Monte Carlo sampling from a reference distribution, and `log(`W_k`)` is computed from the sample data.

The gap value is defined even for clustering solutions that contain only one cluster, and can be used with any distance metric. However, the gap criterion is more computationally

expensive than other cluster evaluation criteria, because the clustering algorithm must be applied to the reference data for each proposed clustering solution.

Examples

Evaluate the Clustering Solution Using Gap Criterion

Evaluate the optimal number of clusters using the gap clustering evaluation criterion.

Load the sample data.

```
load fisheriris;
```

The data contains sepal and petal measurements from three species of iris flowers.

Evaluate the number of clusters based on the gap criterion values. Cluster the data using `kmeans`.

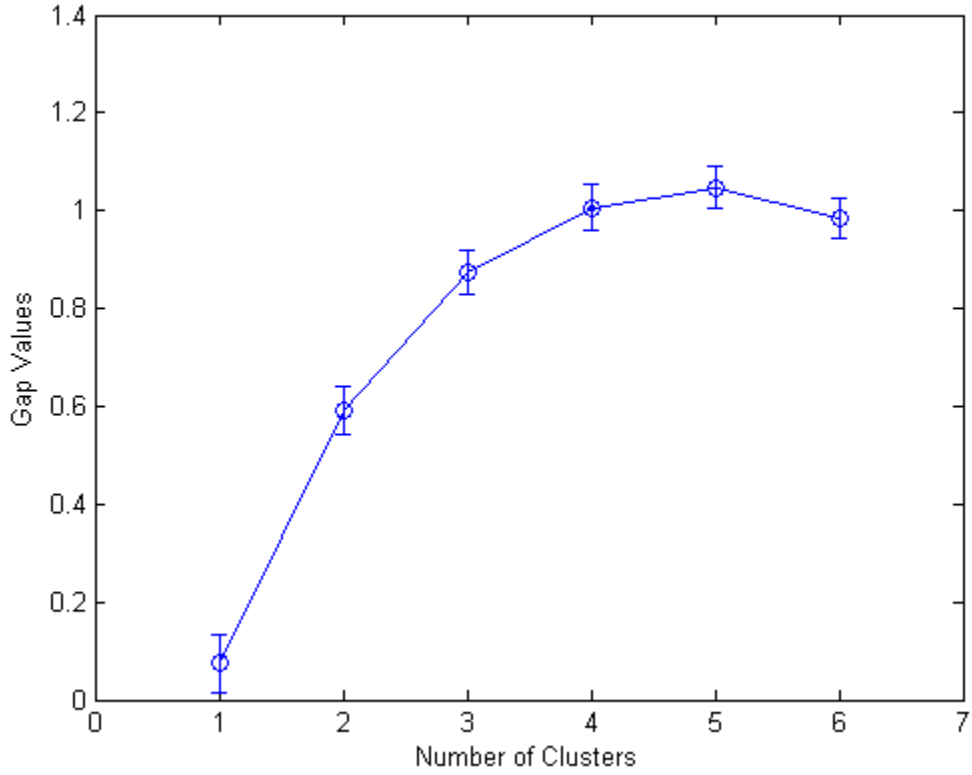
```
rng('default');  % For reproducibility
eva = evalclusters(meas,'kmeans','gap','KList',[1:6])
```

```
eva =

  GapEvaluation with properties:

    NumObservations: 150
       InspectecedK: [1 2 3 4 5 6]
    CriterionValues: [1x6 double]
           OptimalK: 4
```

The `OptimalK` value indicates that, based on the gap criterion, the optimal number of clusters is four.

Plot the gap criterion values for each number of clusters tested.

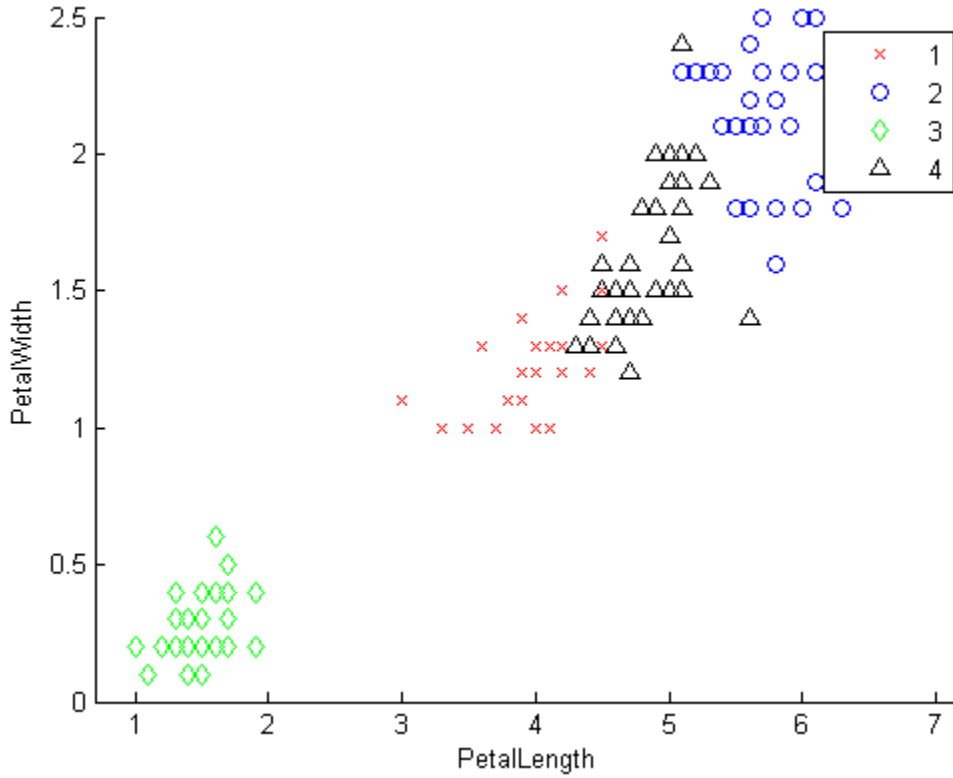
```
figure;
plot(eva);
```



Based on the plot, the maximum value of the gap criterion occurs at five clusters. However, the value at four clusters is within one standard error of the maximum, so the suggested optimal number of clusters is four.

Create a grouped scatter plot to examine the relationship between petal length and width. Group the data by suggested clusters.

```
figure;
PetalLength = meas(:,3);
PetalWidth = meas(:,4);
ClusterGroup = eva.OptimalY;
figure;
gscatter(PetalLength,PetalWidth,ClusterGroup,'rbgk','xod^');
```



The plot shows cluster 1 in the lower-left corner, completely separated from the other three clusters. Cluster 1 contains flowers with the smallest petal widths and lengths. Cluster 4 is in the upper-right corner, and contains flowers with the largest petal widths and lengths. Clusters 2 and 3 are near the center of the plot, and contain flowers with measurements between the two extremes.

References

[1] Tibshirani, R., G. Walther, and T. Hastie. "Estimating the number of clusters in a data set via the gap statistic." *Journal of the Royal Statistical Society: Series B.* Vol. 63, Part 2, 2001, pp. 411–423.

See Also

`clustering.evaluation.CalinskiHarabaszEvaluation` | `clustering.evaluation.DaviesBouldinEvaluation` | `clustering.evaluation.SilhouetteEvaluation` | `evalclusters` | `evalclusters`

More About

- Class Attributes
- Property Attributes

get

Class: dataset

Access dataset array properties

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
get(A)
s = get(A)
p = get(A,PropertyName)
p = get(A,{PropertyName1,PropertyName2,...})
```

Description

`get(A)` displays a list of property/value pairs for the dataset array `A`.

`s = get(A)` returns the values in a scalar structure `s` with field names given by the properties.

`p = get(A,PropertyName)` returns the value of the property specified by the string *`PropertyName`*.

`p = get(A,{PropertyName1,PropertyName2,...})` allows multiple property names to be specified and returns their values in a cell array.

Examples

Create a dataset array from Fisher's iris data and access the information.

```
load fisheriris
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);

get(iris)
   Description: ''
   Units: {}
   DimNames: {'Observations' 'Variables'}
   UserData: []
   ObsNames: {150x1 cell}
   VarNames: {'species' 'SL' 'SW' 'PL' 'PW'}

ON = get(iris,'ObsNames');
ON(1:3)
ans =
    'Obs1'
    'Obs2'
    'Obs3'
```

See Also

set | summary

getlabels

Access categorical array labels

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
labels = getlabels(A)
```

Description

`labels = getlabels(A)` returns the labels of the levels in the nominal or ordinal array A as a cell array of strings, labels. If A is an ordinal array, `getlabels` returns the labels in the order of the levels.

Examples

- “Change Category Labels” on page 2-9

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

More About

- Using nominal Objects

- Using ordinal Objects

See Also

`getlevels` | `nominal` | `ordinal`

getlevels

Access categorical array levels

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
L = getlevels(A)
```

Description

`L = getlevels(A)` returns the levels in the nominal or ordinal array A in L, a vector with the same type as A.

Examples

- “Add and Drop Category Levels” on page 2-21
- “Merge Category Levels” on page 2-19
- “Reorder Category Levels” on page 2-11

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`getlabels` | `nominal` | `ordinal`

gevcdf

Generalized extreme value cumulative distribution function

Syntax

```
p = gevcdf(x,k,sigma,mu)
p = gevcdf(x,k,sigma,mu,'upper')
```

Description

`p = gevcdf(x,k,sigma,mu)` returns the cdf of the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`, evaluated at the values in `x`. The size of `p` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

`p = gevcdf(x,k,sigma,mu,'upper')` returns the complement of the cdf of the GEV distribution, using an algorithm that more accurately computes the extreme upper tail probabilities.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblcdf` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evcdf` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

More About

- “Generalized Extreme Value Distribution” on page B-54

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`cdf` | `gevpdf` | `gevinv` | `gevstat` | `gevfit` | `gevlike` | `gevrnd`

gevfit

Generalized extreme value parameter estimates

Syntax

```
parmhat = gevfit(X)
[parmhat,parmci] = gevfit(X)
[parmhat,parmci] = gevfit(X,alpha)
[...] = gevfit(X,alpha,options)
```

Description

`parmhat = gevfit(X)` returns maximum likelihood estimates of the parameters for the generalized extreme value (GEV) distribution given the data in X. `parmhat(1)` is the shape parameter, `k`, `parmhat(2)` is the scale parameter, `sigma`, and `parmhat(3)` is the location parameter, `mu`.

`[parmhat,parmci] = gevfit(X)` returns 95% confidence intervals for the parameter estimates.

`[parmhat,parmci] = gevfit(X,alpha)` returns `100(1-alpha)`% confidence intervals for the parameter estimates.

`[...] = gevfit(X,alpha,options)` specifies control parameters for the iterative algorithm used to compute ML estimates. This argument can be created by a call to `statset`. See `statset('gevfit')` for parameter names and default values. Pass in `[]` for `alpha` to use the default values.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblfit` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evfit` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution is defined for `k*(X-mu)/sigma > -1`.

More About

- "Generalized Extreme Value Distribution" on page B-54

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`mle` | `gevlike` | `gevpdf` | `gevcdf` | `gevinv` | `gevstat` | `gevrnd`

gevinv

Generalized extreme value inverse cumulative distribution function

Syntax

```
X = gevinv(P,k,sigma,mu)
```

Description

`X = gevinv(P,k,sigma,mu)` returns the inverse cdf of the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter `mu`, evaluated at the values in `P`. The size of `X` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblinv` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evinv` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

More About

- “Generalized Extreme Value Distribution” on page B-54

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`icdf` | `gevcdf` | `gevpdf` | `gevstat` | `gevfit` | `gevlike` | `gevrnd`

gevlike

Generalized extreme value negative log-likelihood

Syntax

```
nlogL = gevlike(params,data)
[nlogL,ACOV] = gevlike(params,data)
```

Description

`nlogL = gevlike(params,data)` returns the negative of the log-likelihood `nlogL` for the generalized extreme value (GEV) distribution, evaluated at parameters `params`. `params(1)` is the shape parameter, `k`, `params(2)` is the scale parameter, `sigma`, and `params(3)` is the location parameter, `mu`.

`[nlogL,ACOV] = gevlike(params,data)` returns the inverse of Fisher's information matrix, `ACOV`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `ACOV` are their asymptotic variances. `ACOV` is based on the observed Fisher's information, not the expected information.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wbllike` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evlike` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

More About

- “Generalized Extreme Value Distribution” on page B-54

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah.*Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`gevfit` | `gevpdf` | `gevcdf` | `gevinv` | `gevstat` | `gevrnd`

gevpdf

Generalized extreme value probability density function

Syntax

```
Y = gevpdf(X,k,sigma,mu)
```

Description

`Y = gevpdf(X,k,sigma,mu)` returns the pdf of the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`, evaluated at the values in `X`. The size of `Y` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblpdf` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evcdf` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

More About

- “Generalized Extreme Value Distribution” on page B-54

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`pdf` | `gevcdf` | `gevinv` | `gevstat` | `gevfit` | `gevlike` | `gevrnd`

gevrnd

Generalized extreme value random numbers

Syntax

```
R = gevrnd(k,sigma,mu)
R = gevrnd(k,sigma,mu,m,n,...)
R = gevrnd(k,sigma,mu,[m,n,...])
```

Description

`R = gevrnd(k,sigma,mu)` returns an array of random numbers chosen from the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`. The size of `R` is the common size of the input arguments if all are arrays. If any parameter is a scalar, the size of `R` is the size of the other parameters.

`R = gevrnd(k,sigma,mu,m,n,...)` or `R = gevrnd(k,sigma,mu,[m,n,...])` generates an `m`-by-`n`-by-... array containing random numbers from the GEV distribution with parameters `k`, `sigma`, and `mu`. The `k`, `sigma`, `mu` parameters can each be scalars or arrays of the same size as `R`.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblrnd` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evrnd` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

More About

- “Generalized Extreme Value Distribution” on page B-54

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`random` | `gevpdf` | `gevcdf` | `gevinv` | `gevstat` | `gevfit` | `gevlike`

gevstat

Generalized extreme value mean and variance

Syntax

```
[M,V] = gevstat(k,sigma,mu)
```

Description

`[M,V] = gevstat(k,sigma,mu)` returns the mean of and variance for the generalized extreme value (GEV) distribution with shape parameter `k`, scale parameter `sigma`, and location parameter, `mu`. The sizes of `M` and `V` are the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `mu` are 0, 1, and 0, respectively.

When `k < 0`, the GEV is the type III extreme value distribution. When `k > 0`, the GEV distribution is the type II, or Frechet, extreme value distribution. If `w` has a Weibull distribution as computed by the `wblstat` function, then `-w` has a type III extreme value distribution and `1/w` has a type II extreme value distribution. In the limit as `k` approaches 0, the GEV is the mirror image of the type I extreme value distribution as computed by the `evstat` function.

The mean of the GEV distribution is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. The GEV distribution has positive density only for values of `X` such that `k*(X-mu)/sigma > -1`.

More About

- “Generalized Extreme Value Distribution” on page B-54

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`gevpdf` | `gevcdf` | `gevinv` | `gevfit` | `gevlike` | `gevrnd`

gline

Interactively add line to plot

Syntax

```
gline(h)
gline
hline = gline(...)
```

Description

`gline(h)` allows you to draw a line segment in the figure with handle `h` by clicking the pointer at the two endpoints. A rubber-band line tracks the pointer movement.

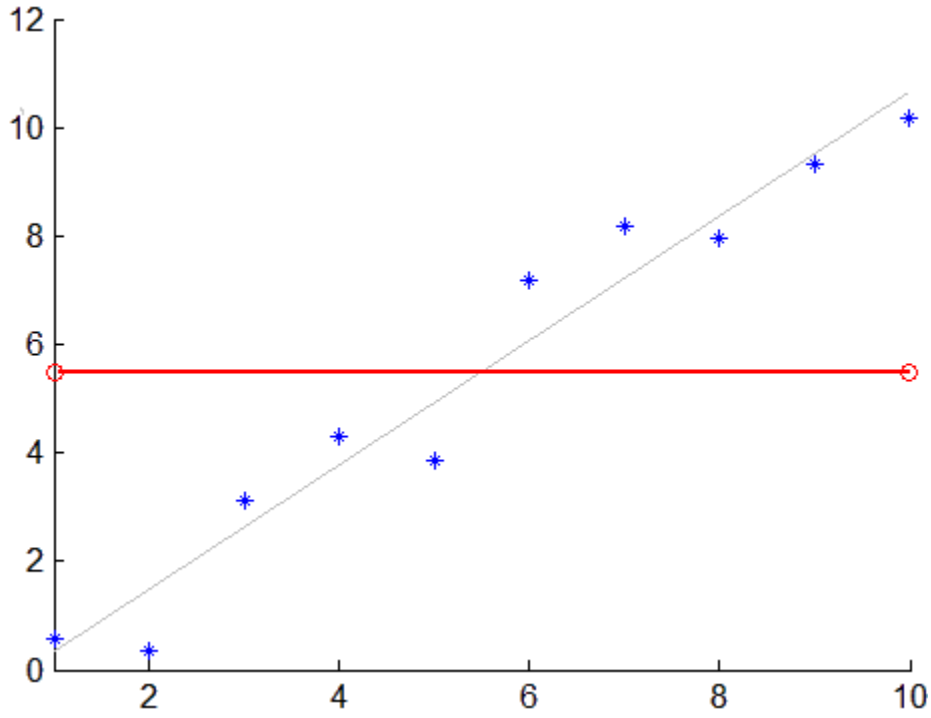
`gline` with no input arguments defaults to `h = gcf` and draws in the current figure.

`hline = gline(...)` returns the handle `hline` to the line.

Examples

Use `gline` to connect two points in a plot:

```
x = 1:10;

y = x + randn(1,10);
scatter(x,y,25,'b','*')

lsline

mu = mean(y);
hold on
plot([1 10],[mu mu],'ro')

hline = gline; % Connect circles
set(hline,'Color','r')
```



See Also

`refline` | `refcurve` | `lsline`

glmfit

Generalized linear model regression

Syntax

```
b = glmfit(X,y,distr)
b = glmfit(X,y,distr,param1,val1,param2,val2,...)
[b,dev] = glmfit(...)
[b,dev,stats] = glmfit(...)
```

Description

`b = glmfit(X,y,distr)` returns a (p + 1)-by-1 vector `b` of coefficient estimates for a generalized linear regression of the responses in `y` on the predictors in `X`, using the distribution `distr`. `X` is an n-by-p matrix of p predictors at each of n observations. `distr` can be any of the following strings: `'binomial'`, `'gamma'`, `'inverse gaussian'`, `'normal'` (the default), and `'poisson'`.

In most cases, `y` is an n-by-1 vector of observed responses. For the binomial distribution, `y` can be a binary vector indicating success or failure at each observation, or a two column matrix with the first column indicating the number of successes for each observation and the second column indicating the number of trials for each observation.

This syntax uses the canonical link (see below) to relate the distribution to the predictors.

Note: By default, `glmfit` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`. You can change the default behavior of `glmfit` using the `'constant'` parameter, below.

`glmfit` treats `NaN`s in either `X` or `y` as missing values, and ignores them.

`b = glmfit(X,y,distr,param1,val1,param2,val2,...)` additionally allows you to specify optional parameter name/value pairs to control the model fit. Acceptable parameters are as follows.

Parameter	Value	Description
`'link'`	`'identity'`, default for the distribution `'normal'`	$\mu = Xb$
	`'log'`, default for the distribution `'poisson'`	$\log(\mu) = Xb$
	`'logit'`, default for the distribution `'binomial'`	$\log(\mu/(1-\mu)) = Xb$
	`'probit'`	$\text{norminv}(\mu) = Xb$
	`'comploglog'`	$\log(-\log(1-\mu)) = Xb$
	`'reciprocal'`, default for the distribution `'gamma'`	$1/\mu = Xb$
	`'loglog'`	$\log(-\log(\mu)) = Xb$
	`p` (a number), default for the distribution `'inverse gaussian'` (with $p = -2$)	$\mu^p = Xb$
	cell array of the form `{FL FD FI}`, containing three function handles, created using `@`, that define the link (`FL`), the derivative of the link (`FD`), and the inverse link (`FI`).	Custom-defined link function. You must provide • `FL(mu)` • `FD = dFL(mu)/dmu` • `FI = FL^(-1)`
`'estdisp'`	`'on'`	Estimates a dispersion parameter for the binomial or Poisson distribution.
	`'off'` (Default for binomial or Poisson distribution)	Uses the theoretical value of 1.0 for those distributions.
`'offset'`	Vector	Used as an additional predictor variable, but with a coefficient value fixed at 1.0.
`'weights'`	Vector of prior weights, such as the inverses of the relative variance of each observation	

Parameter	Value	Description
`'constant'`	`'on'` (default)	Includes a constant term in the model. The coefficient of the constant term is the first element of `b`.
	`'off'`	Omit the constant term.

`[b,dev] = glmfit(...)` returns `dev`, the deviance of the fit at the solution vector. The deviance is a generalization of the residual sum of squares. It is possible to perform an analysis of deviance to compare several models, each a subset of the other, and to test whether the model with more terms is significantly better than the model with fewer terms.

`[b,dev,stats] = glmfit(...)` returns `dev` and `stats`.

`stats` is a structure with the following fields:

- `beta` — Coefficient estimates `b`
- `dfe` — Degrees of freedom for error
- `sfit` — Estimated dispersion parameter
- `s` — Theoretical or estimated dispersion parameter
- `estdisp` — 0 when the `'estdisp'` name-value pair argument value is `'off'` and 1 when the `'estdisp'` name-value pair argument value is `'on'`.
- `covb` — Estimated covariance matrix for B
- `se` — Vector of standard errors of the coefficient estimates `b`
- `coeffcorr` — Correlation matrix for `b`
- `t` — *t* statistics for `b`
- `p` — *p*-values for `b`
- `resid` — Vector of residuals
- `residp` — Vector of Pearson residuals
- `residd` — Vector of deviance residuals
- `resida` — Vector of Anscombe residuals

If you estimate a dispersion parameter for the binomial or Poisson distribution, then `stats.s` is set equal to `stats.sfit`. Also, the elements of `stats.se` differ by the factor `stats.s` from their theoretical values.

Examples

Fit Generalized Linear Model with Probit Link

Enter sample data.

```
x = [2100 2300 2500 2700 2900 3100 ...
     3300 3500 3700 3900 4100 4300]';
n = [48 42 31 34 31 21 23 23 21 16 17 21]';
y = [1 2 0 3 8 8 14 17 19 15 17 21]';
```

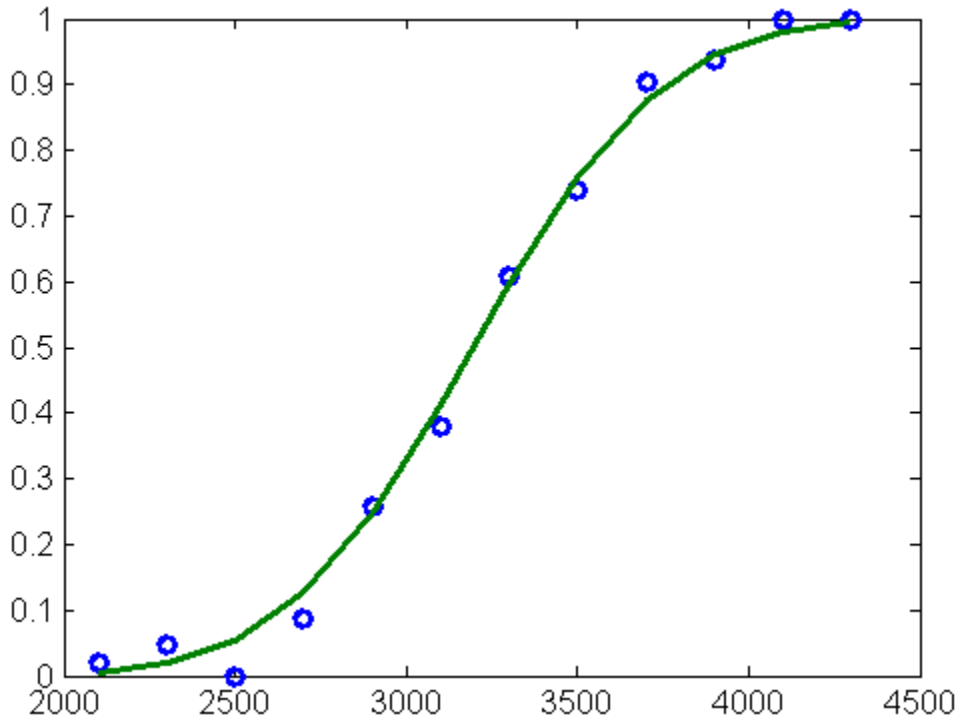
Each `y` value is the number of successes in corresponding number of trials in`n`, and `x` contains the predictor variable values.

Fit a probit regression model for `y` on `x`.

```
b = glmfit(x,[y n],'binomial','link','probit');
```

Compute the estimated number of successes and plot the percent observed and estimated percent success versus the `x` values.

```
yfit = glmval(b,x,'probit','size',n);
plot(x, y./n,'o',x,yfit./n,'-','LineWidth',2)
```



Use Custom-defined Link Function

Load the sample data.

```
load fisheriris
```

The column vector, `species`, consists of iris flowers of three different species, setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers, the length and width of sepals and petals in centimeters, respectively.

Define the response and predictor variables.

```
X = meas(51:end,:);
y = strcmp('versicolor',species(51:end));
```

Define three function handles, created using `@`, that define the link, the derivative of the link, and the inverse link for a logit link function, and store them in a cell array.

```
link = @(mu) log(mu ./ (1-mu));
```

```
derlink = @(mu) 1 ./ (mu .* (1-mu));
invlink = @(resp) 1 ./ (1 + exp(-resp));
F = {link, derlink, invlink};
```

Fit a logistic regression using `glmfit` with the link function you defined.

```
b = glmfit(X,y,'binomial','link',F)
```

```
b =

   42.6378
    2.4652
    6.6809
   -9.4294
  -18.2861
```

Now, fit a generalized linear model using the `logit` link function and compare the results.

```
b = glmfit(X,y,'binomial','link','logit')
```

```
b =

   42.6378
    2.4652
    6.6809
   -9.4294
  -18.2861
```

References

[1] Dobson, A. J. *An Introduction to Generalized Linear Models*. New York: Chapman & Hall, 1990.

[2] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

[3] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

See Also

`glmval` | `regress` | `regstats` | `GeneralizedLinearModel` | `fitglm` | `stepwiseglm`

glmval

Generalized linear model values

Syntax

```
yhat = glmval(b,X,link)
[yhat,dylo,dyhi] = glmval(b,X,link,stats)
[...] = glmval(...,param1,val1,param2,val2,...)
```

Description

`yhat = glmval(b,X,link)` computes predicted values for the generalized linear model with link function `link` and predictors `X`. Distinct predictor variables should appear in different columns of `X`. `b` is a vector of coefficient estimates as returned by the `glmfit` function. `link` can be any of the strings or the custom-defined link functions used as values for the `'link'` name-value pair argument in the `glmfit` function.

Note: By default, `glmval` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`. You can change the default behavior of `glmval` using the `'constant'` parameter, below.

`[yhat,dylo,dyhi] = glmval(b,X,link,stats)` also computes 95% confidence bounds for the predicted values. When the `stats` structure output of the `glmfit` function is specified, `dylo` and `dyhi` are also returned. `dylo` and `dyhi` define a lower confidence bound of `yhat-dylo`, and an upper confidence bound of `yhat+dyhi`. Confidence bounds are nonsimultaneous, and apply to the fitted curve, not to a new observation.

`[...] = glmval(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs to control the predicted values. Acceptable parameters are:

Parameter	Value
`'confidence'` — the confidence level for the confidence bounds	A scalar between 0 and 1

Parameter	Value
`'size'` — the size parameter (N) for a binomial model	A scalar, or a vector with one value for each row of X
`'offset'` — used as an additional predictor variable, but with a coefficient value fixed at 1.0	A vector
`'constant'`	• `'on'` — Includes a constant term in the model. The coefficient of the constant term is the first element of `b`. • `'off'` — Omit the constant term
`'simultaneous'` — Compute simultaneous confidence intervals (`true`), or compute non-simultaneous confidence intervals (default `false`)	`true` or `false`

Examples

Fit Generalized Linear Model with Probit Link

Enter sample data.

```
x = [2100 2300 2500 2700 2900 3100 ...
     3300 3500 3700 3900 4100 4300]';
n = [48 42 31 34 31 21 23 23 21 16 17 21]';
y = [1 2 0 3 8 8 14 17 19 15 17 21]';
```

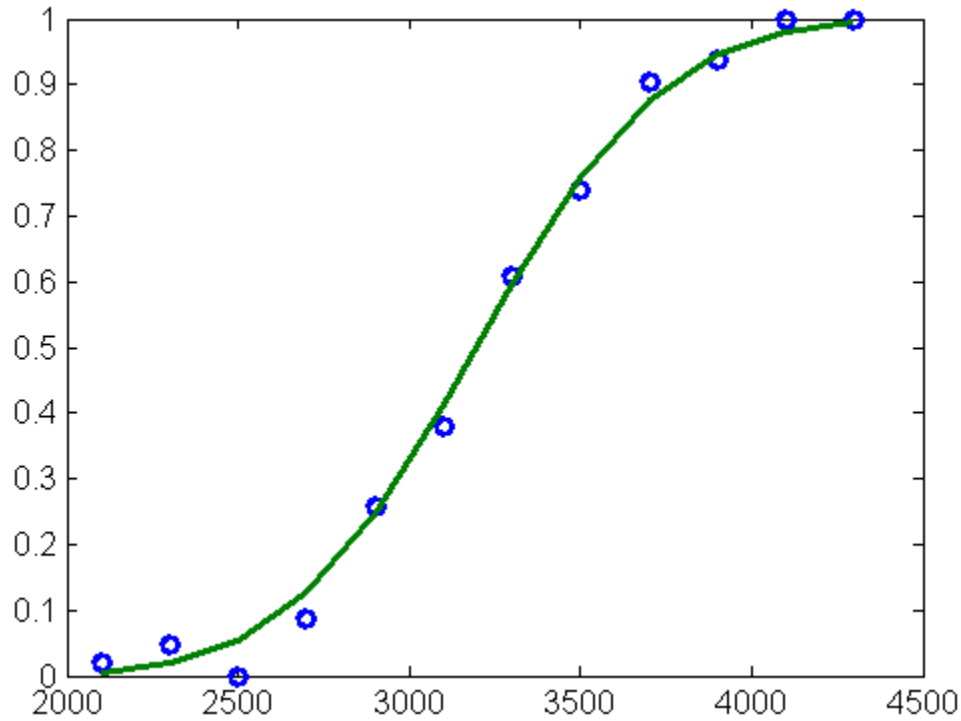
Each `y` value is the number of successes in corresponding number of trials in`n`, and `x` contains the predictor variable values.

Fit a generalized linear model for `y` on `x` using a probit link function.

```
b = glmfit(x,[y n],'binomial','link','probit');
```

Compute the estimated number of successes and plot the observed and estimated percent success versus the `x` values.

```
yfit = glmval(b,x,'probit','size',n);
plot(x, y./n,'o',x,yfit./n,'-','LineWidth',2)
```



Use Custom-defined Link Function

Enter sample data.

```
x = [2100 2300 2500 2700 2900 3100 ...
     3300 3500 3700 3900 4100 4300]';
n = [48 42 31 34 31 21 23 23 21 16 17 21]';
y = [1 2 0 3 8 8 14 17 19 15 17 21]';
```

Each `y` value is the number of successes in corresponding number of trials in `n`, and `x` contains the predictor variable values.

Now define three function handles, created using @, that define the link, the derivative of the link, and the inverse link for a probit link function, and store them in a cell array.

```
link = @(mu) norminv(mu);
derlink = @(mu) 1 ./ normpdf(norminv(mu));
invlink = @(resp) normcdf(resp);
```

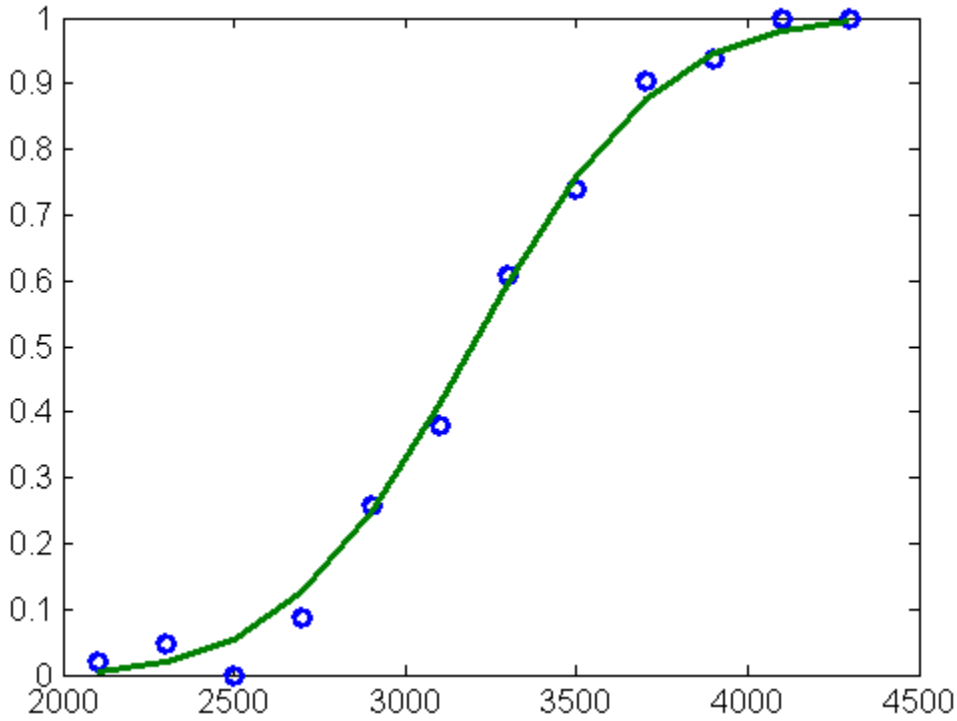
```
F = {link, derlink, invlink};
```

Fit a generalized linear model for `y` on `x` using the link function you defined.

```
b = glmfit(x,[y n],'binomial','link',F);
```

Compute the estimated number of successes and plot the observed and estimated percent success versus the `x` values.

```
yfit = glmval(b,x,F,'size',n);
plot(x, y./n,'o',x,yfit./n,'-','LineWidth',2)
```



References

[1] Dobson, A. J. *An Introduction to Generalized Linear Models*. New York: Chapman & Hall, 1990.

[2] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

[3] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

See Also

`glmfit` | `GeneralizedLinearModel` | `fitglm` | `stepwiseglm`

glyphplot

Glyph plot

Syntax

```
glyphplot(X)
glyphplot(X,'glyph','face')
glyphplot(X,'glyph','face','features',f)
glyphplot(X,...,'grid',[rows,cols])
glyphplot(X,...,'grid',[rows,cols],'page',p)
glyphplot(X,...,'centers',C)
glyphplot(X,...,'centers',C,'radius',r)
glyphplot(X,...,'obslabels',labels)
glyphplot(X,...,'standardize',method)
glyphplot(X,...,prop1,val1,...)
h = glyphplot(X,...)
```

Description

`glyphplot(X)` creates a star plot from the multivariate data in the n-by-p matrix `X`. Rows of `X` correspond to observations, columns to variables. A star plot represents each observation as a "star" whose ith spoke is proportional in length to the ith coordinate of that observation. `glyphplot` standardizes `X` by shifting and scaling each column separately onto the interval `[0,1]` before making the plot, and centers the glyphs on a rectangular grid that is as close to square as possible. `glyphplot` treats `NaN`s in `X` as missing values, and does not plot the corresponding rows of `X`. `glyphplot(X,'glyph','star')` is a synonym for `glyphplot(X)`.

`glyphplot(X,'glyph','face')` creates a face plot from `X`. A face plot represents each observation as a "face," whose ith facial feature is drawn with a characteristic proportional to the ith coordinate of that observation. The features are described in "Face Features" on page 22-2107.

`glyphplot(X,'glyph','face','features',f)` creates a face plot where the ith element of the index vector `f` defines which facial feature will represent the ith column of

`X`. `f` must contain integers from `0` to `17`, where `0` indicate that the corresponding column of `X` should not be plotted. See "Face Features" on page 22-2107 for more information.

`glyphplot(X,...,'grid',[rows,cols])` organizes the glyphs into a `rows`-by-`cols` grid.

`glyphplot(X,...,'grid',[rows,cols],'page',p)` organizes the glyph into one or more pages of a `rows`-by-`cols` grid, and displays the page `p`. If `p` is a vector, `glyphplot` displays multiple pages in succession. If `p` is `'all'`, `glyphplot` displays all pages. If `p` is `'scroll'`, `glyphplot` displays a single plot with a scrollbar.

`glyphplot(X,...,'centers',C)` creates a plot with each glyph centered at the locations in the *n*-by-2 matrix `C`.

`glyphplot(X,...,'centers',C,'radius',r)` creates a plot with glyphs positioned using `C`, and scale the glyphs so the largest has radius `r`.

`glyphplot(X,...,'obslabels',labels)` labels each glyph with the text in the character array or cell array of strings `labels`. By default, the glyphs are labelled `1:N`. Use `''` for blank labels.

`glyphplot(X,...,'standardize',`*`method`*`)` standardizes `X` before making the plot. Choices for *`method`* are

- `'column'` — Maps each column of `X` separately onto the interval [0,1]. This is the default.
- `'matrix'` — Maps the entire matrix `X` onto the interval `[0,1]`.
- `'PCA'` — Transforms `X` to its principal component scores, in order of decreasing eigenvalue, and maps each one onto the interval `[0,1]`.
- `'off'` — No standardization. Negative values in `X` may make a star plot uninterpretable.

`glyphplot(X,...,`*`prop1`*`,`*`val1`*`,...)` sets properties to the specified property values for all line graphics objects created by `glyphplot`.

`h = glyphplot(X,...)` returns a matrix of handles to the graphics objects created by `glyphplot`. For a star plot, `h(:,1)` and `h(:,2)` contain handles to the line objects for each star's perimeter and spokes, respectively. For a face plot, `h(:,1)` and `h(:,2)` contain object handles to the lines making up each face and to the pupils, respectively. `h(:,3)` contains handles to the text objects for the labels, if present.

Face Features

The following table describes the correspondence between the columns of the vector `f`, the value of the `'Features'` input parameter, and the facial features of the glyph plot. If `X` has fewer than 17 columns, unused features are displayed at their default value.

Column	Facial Feature
1	Size of face
2	Forehead/jaw relative arc length
3	Shape of forehead
4	Shape of jaw
5	Width between eyes
6	Vertical position of eyes
7	Height of eyes
8	Width of eyes (this also affects eyebrow width)
9	Angle of eyes (this also affects eyebrow angle)
10	Vertical position of eyebrows
11	Width of eyebrows (relative to eyes)
12	Angle of eyebrows (relative to eyes)
13	Direction of pupils
14	Length of nose
15	Vertical position of mouth
16	Shape of mouth
17	Mouth arc length

Examples

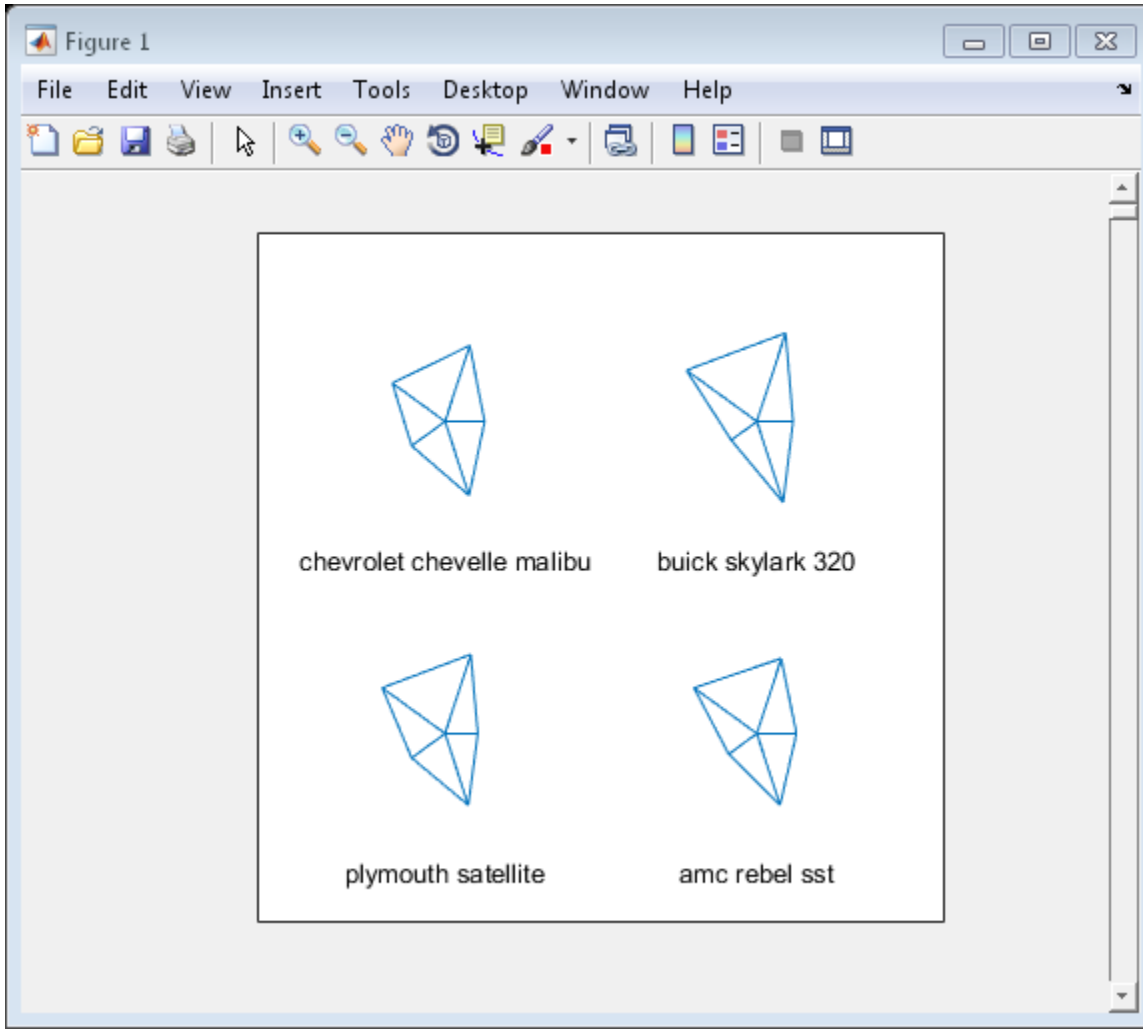
Star and Face Plots of Multivariate Data

Load the sample data.

```
load carsmall
X = [Acceleration Displacement Horsepower MPG Weight];
```

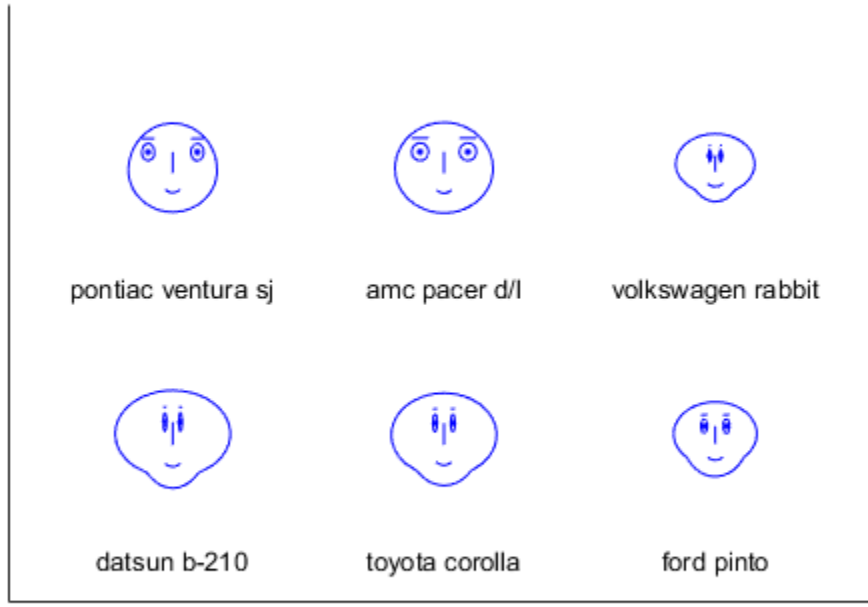
Create a star plot of the data in `X` . Standardize the data before plotting.

```
glyphplot(X,'standardize','column','obslabels',Model,'grid',[2 2],...
            'page','scroll');
```



Create a faceplot of the data in `X` .

```
glyphplot(X,'glyph','face','obslabels',Model,'grid',[2 3],'page',9);
```



See Also

`andrewsplot` | `parallelcoords`

gmdistribution class

Gaussian mixture models

Description

An object of the `gmdistribution` class defines a Gaussian mixture distribution, which is a multivariate distribution that consists of a mixture of one or more multivariate Gaussian distribution components. The number of components for a given `gmdistribution` object is fixed. Each multivariate Gaussian component is defined by its mean and covariance, and the mixture is defined by a vector of mixing proportions.

Construction

To create a Gaussian mixture distribution by specifying the distribution parameters, use the `gmdistribution` constructor. To fit a Gaussian mixture distribution model to data, use `fitgmdist`.

fit	Gaussian mixture parameter estimates
.gmdistribution	Construct Gaussian mixture distribution

Properties

All objects of the class have the properties listed in the following table.

CovarianceType	Type of covariance matrices
DistributionName	Type of distribution
mu	Input matrix of means `mu`
NumComponents	Number k of mixture components

NumVariables	Dimension d of multivariate Gaussian distributions
ComponentProportion	Input vector of mixing proportions
SharedCovariance	`true` if all covariance matrices are restricted to be the same
Sigma	Input array of covariances

Objects constructed with `fitgmdist` have the additional properties listed in the following table.

AIC	Akaike Information Criterion
BIC	Bayes Information Criterion
Converged	Determine if algorithm converged
NumIterations	Number of iterations
NegativeLogLikelihood	Negative of log-likelihood
RegularizationValue	Value of `'Regularize'` parameter

Methods

cdf	Cumulative distribution function for Gaussian mixture distribution
cluster	Construct clusters from Gaussian mixture distribution

disp	Display Gaussian mixture distribution object
display	Display Gaussian mixture distribution object
fit	Gaussian mixture parameter estimates
mahal	Mahalanobis distance to component means
pdf	Probability density function for Gaussian mixture distribution
posterior	Posterior probabilities of components
random	Random numbers from Gaussian mixture distribution
subsasgn	Subscripted reference for Gaussian mixture distribution object
subsref	Subscripted reference for Gaussian mixture distribution object

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

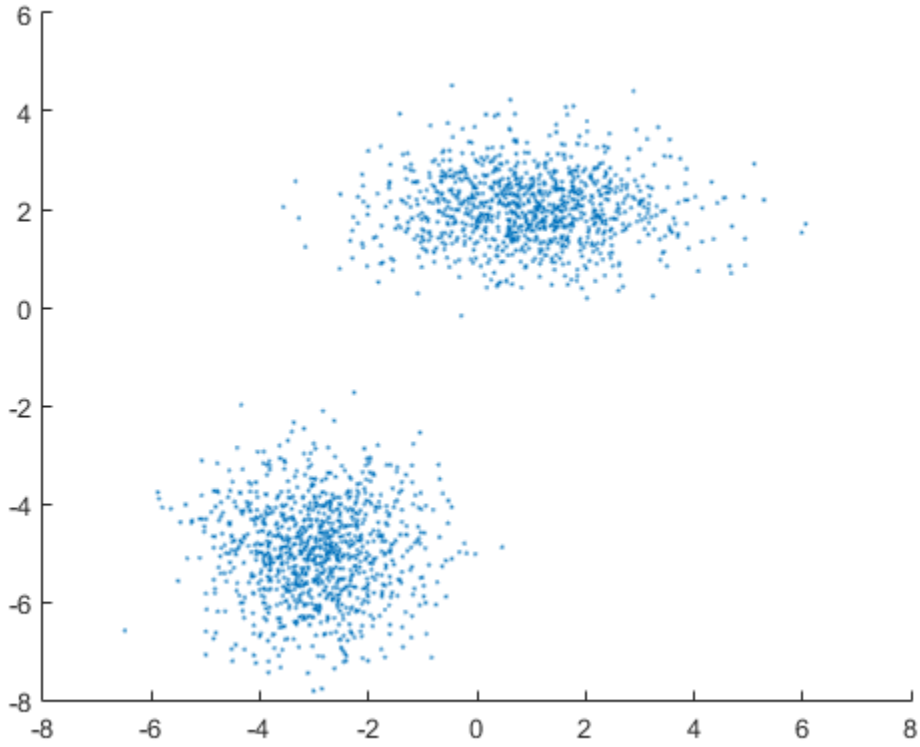
Examples

Fit a Gaussian Mixture Model

Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function. Fit the resulting data.

Generate the data using 1000 points from each distribution.

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



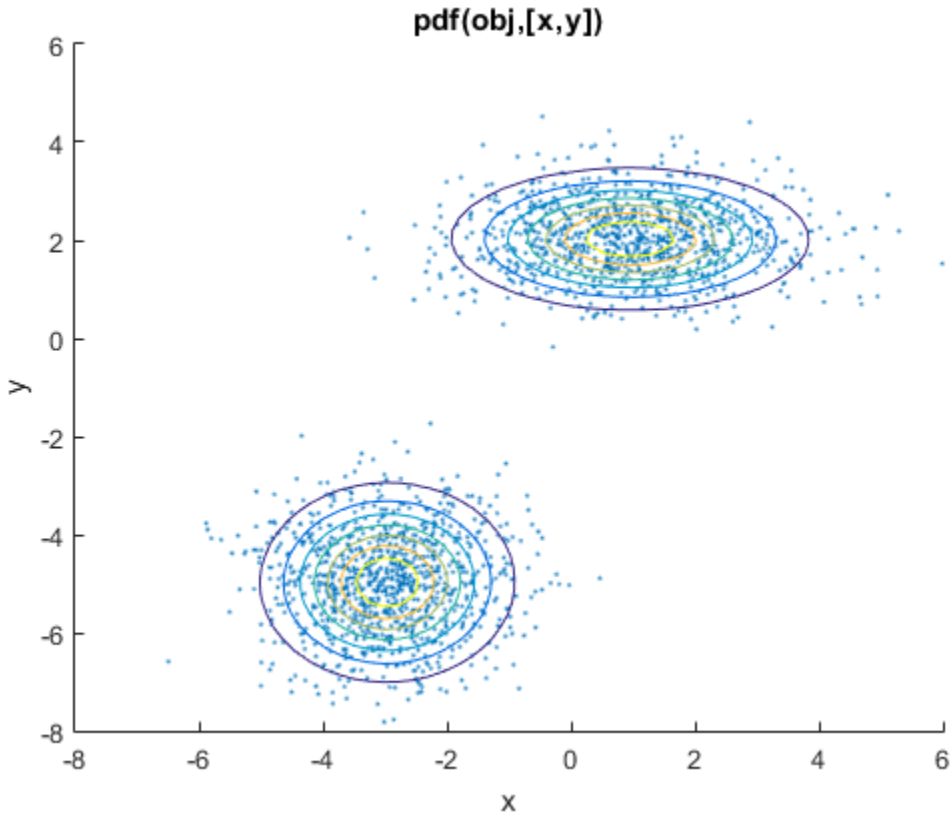
Fit a two-component Gaussian mixture model.

```
options = statset('Display','final');
obj = fitgmdist(X,2,'Options',options);
```

```
18 iterations, log-likelihood = -7058.35
```

Plot the fit.

```
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



- "Normal Distribution"

References

[1] McLachlan, G., and D. Peel. *Finite Mixture Models*. Hoboken, NJ: John Wiley & Sons, Inc., 2000.

See Also

`fitgmdist`

gmdistribution

Class: gmdistribution

Construct Gaussian mixture distribution

Syntax

```
obj = gmdistribution(mu,sigma,p)
```

Description

`obj = gmdistribution(mu,sigma,p)` constructs an object `obj` of the `gmdistribution` class defining a Gaussian mixture distribution.

`mu` is a k-by-d matrix specifying the d-dimensional mean of each of the k components.

`sigma` specifies the covariance of each component. The size of `sigma` is:

- d-by-d-by-k if there are no restrictions on the form of the covariance. In this case, `sigma(:,:,I)` is the covariance of component `I`.
- 1-by-d-by-k if the covariance matrices are restricted to be diagonal, but not restricted to be same across components. In this case, `sigma(:,:,I)` contains the diagonal elements of the covariance of component I.
- d-by-d matrix if the covariance matrices are restricted to be the same across components, but not restricted to be diagonal. In this case, `sigma` is the pooled estimate of covariance.
- 1-by-d if the covariance matrices are restricted to be diagonal and the same across components. In this case, `sigma` contains the diagonal elements of the pooled estimate of covariance.

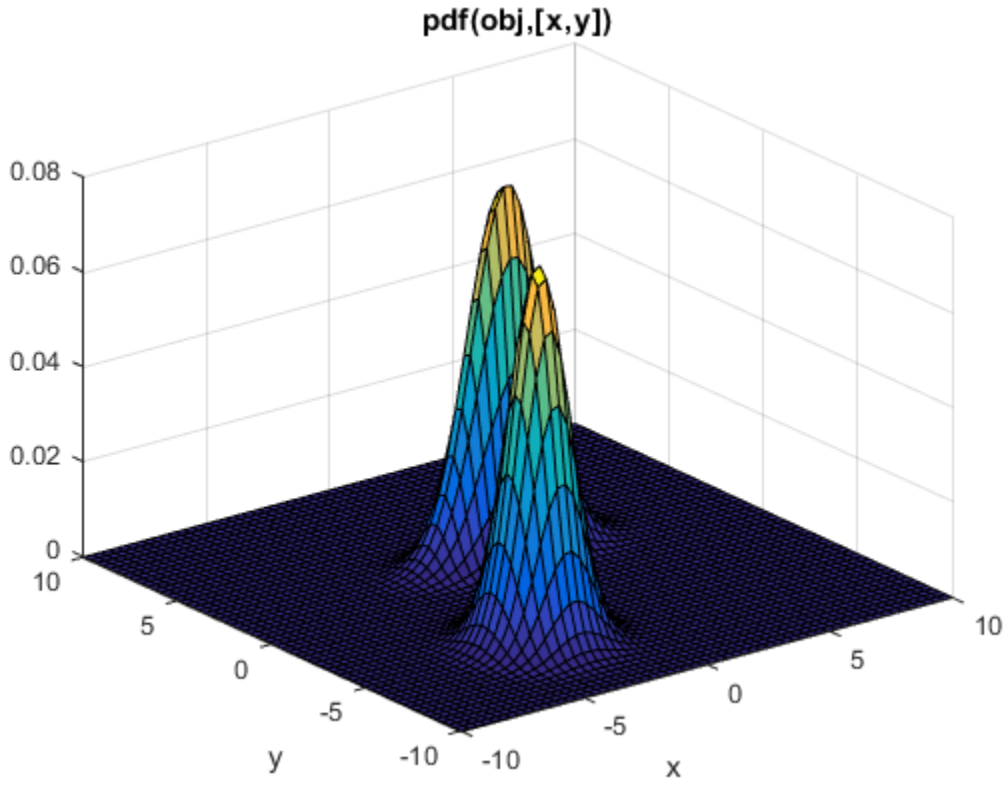
`p` is an optional 1-by-k vector specifying the mixing proportions of each component. If `p` does not sum to `1`, `gmdistribution` normalizes it. The default is equal proportions.

Examples

Construct a Gaussian Mixture Distribution

Create a `gmdistribution` distribution defining a two-component mixture of bivariate Gaussian distributions.

```
mu = [1 2;-3 -5];
sigma = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(mu,sigma,p);

ezsurf(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
```



References

[1] McLachlan, G., and D. Peel. *Finite Mixture Models*. Hoboken, NJ: John Wiley & Sons, Inc., 2000.

See Also

`fitgmdist` | `cdf` | `cluster` | `mahal` | `pdf` | `random` | `posterior`

gname

Add case names to plot

Syntax

```
gname(cases)
gname
h = gname(cases,line_handle)
```

Description

`gname(cases)` displays a figure window and waits for you to press a mouse button or a keyboard key. The input argument `cases` is a character array or a cell array of strings, in which each row of the character array or each element of the cell array contains the case name of a point. Moving the mouse over the graph displays a pair of cross-hairs. If you position the cross-hairs near a point with the mouse and click once, the graph displays the label corresponding to that point. Alternatively, you can click and drag the mouse to create a rectangle around several points. When you release the mouse button, the graph displays the labels for all points in the rectangle. Right-click a point to remove its label. When you are done labelling points, press the **Enter** or **Escape** key to stop labeling.

`gname` with no arguments labels each case with its case number.

`cases` typically contains unique case names for each point, and is a cell array of strings or a character matrix with each row representing a name. `cases` can also be any grouping variable, which `gname` converts to labels.

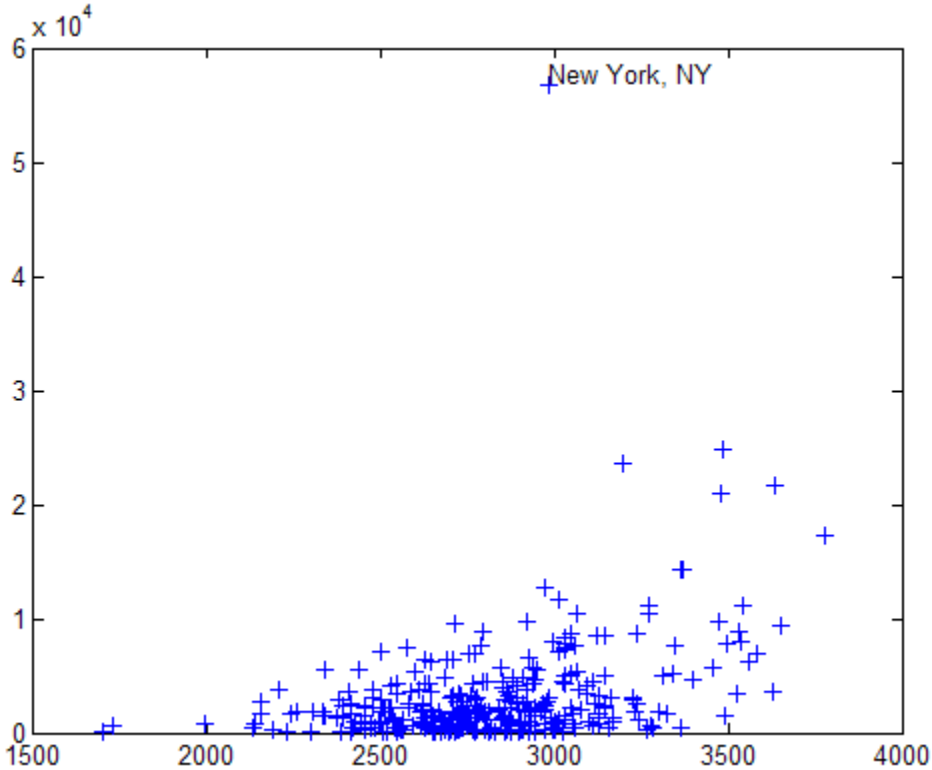
`h = gname(cases,line_handle)` returns a vector of handles to the text objects on the plot. Use the scalar `line_handle` to identify the correct line if there is more than one line object on the plot.

You can use `gname` to label plots created by the `plot`, `scatter`, `gscatter`, `plotmatrix`, and `gplotmatrix` functions.

Examples

This example uses the city ratings data sets to find out which cities are the best and worst for education and the arts.

```
load cities
education = ratings(:,6);
arts = ratings(:,7);
plot(education,arts,'+')
gname(names)
```



Click the point at the top of the graph to display its label, “New York.”

See Also

gtext | gscatter | gplotmatrix

gpcdf

Generalized Pareto cumulative distribution function

Syntax

```
p = gpcdf(x,k,sigma,theta)
p = gpcdf(x,k,sigma,theta,'upper')
```

Description

`p = gpcdf(x,k,sigma,theta)` returns the cdf of the generalized Pareto (GP) distribution with the tail index (shape) parameter `k`, scale parameter `sigma`, and threshold (location) parameter, `theta`, evaluated at the values in `x`. The size of `p` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

`p = gpcdf(x,k,sigma,theta,'upper')` returns the complement of the cdf of the generalized Pareto (GP) distribution, using an algorithm that more accurately computes the extreme upper tail probabilities.

Default values for `k`, `sigma`, and `theta` are 0, 1, and 0, respectively.

When `k = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `k > 0` and `theta = sigma/k`, the GP is equivalent to a Pareto distribution with a scale parameter equal to `sigma/k` and a shape parameter equal to `1/k`. The mean of the GP is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. When $k \geq 0$, the GP has positive density for

`x > theta`, or, when

`k < 0`, $0 \leq \frac{x-\theta}{\sigma} \leq -\frac{1}{k}$.

More About

- “Generalized Pareto Distribution” on page B-60

- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61
- "Supported Distributions" on page 5-17

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`cdf` | `gppdf` | `gpinv` | `gpstat` | `gpfit` | `gplike` | `gprnd`

gpfit

Generalized Pareto parameter estimates

Syntax

```
parmhat = gpfit(x)
[parmhat,parmci] = gpfit(x)
[parmhat,parmci] = gpfit(x,alpha)
[...] = gpfit(x,alpha,options)
```

Description

`parmhat = gpfit(x)` returns maximum likelihood estimates of the parameters for the two-parameter generalized Pareto (GP) distribution given the data in `x`. `parmhat(1)` is the tail index (shape) parameter, `k` and `parmhat(2)` is the scale parameter, `sigma`. `gpfit` does not fit a threshold (location) parameter.

`[parmhat,parmci] = gpfit(x)` returns 95% confidence intervals for the parameter estimates.

`[parmhat,parmci] = gpfit(x,alpha)` returns `100(1-alpha)`% confidence intervals for the parameter estimates.

`[...] = gpfit(x,alpha,options)` specifies control parameters for the iterative algorithm used to compute ML estimates. This argument can be created by a call to `statset`. See `statset('gpfit')` for parameter names and default values.

Other functions for the generalized Pareto, such as `gpcdf` allow a threshold parameter, `theta`. However, `gpfit` does not estimate theta. It is assumed to be known, and subtracted from `x` before calling `gpfit`.

When `k = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `k > 0` and `theta = sigma/k`, the GP is equivalent to a Pareto distribution with a scale parameter equal to `sigma/k` and a shape parameter equal to `1/k`. The mean of the GP is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. When $k \geq 0$, the GP has positive density for

`k > theta`, or, when `k < 0`, for

$$0 \le \frac{x-\theta}{\sigma} \le -\frac{1}{k}$$

More About

- "Generalized Pareto Distribution" on page B-60
- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61
- "Supported Distributions" on page 5-17

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`mle` | `gplike` | `gppdf` | `gpcdf` | `gpinv` | `gpstat` | `gprnd`

gpinv

Generalized Pareto inverse cumulative distribution function

Syntax

```
x = gpinv(p,k,sigma,theta)
```

Description

`x = gpinv(p,k,sigma,theta)` returns the inverse cdf for a generalized Pareto (GP) distribution with tail index (shape) parameter `k`, scale parameter `sigma`, and threshold (location) parameter `theta`, evaluated at the values in `p`. The size of `x` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `theta` are 0, 1, and 0, respectively.

When `k = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `k > 0` and `theta = sigma/k`, the GP is equivalent to a Pareto distribution with a scale parameter equal to `sigma/k` and a shape parameter equal to `1/k`. The mean of the GP is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. When $k \geq 0$, the GP has positive density for

`x > theta`, or, when

`k < 0`, $0 \leq \frac{x-\theta}{\sigma} \leq -\frac{1}{k}$.

More About

- "Generalized Pareto Distribution" on page B-60
- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61

- "Supported Distributions" on page 5-17

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`icdf` | `gpcdf` | `gppdf` | `gpstat` | `gpfit` | `gplike` | `gprnd`

gplike

Generalized Pareto negative log-likelihood

Syntax

```
nlogL = gplike(params,data)
[nlogL,acov] = gplike(params,data)
```

Description

`nlogL = gplike(params,data)` returns the negative of the log-likelihood `nlogL` for the two-parameter generalized Pareto (GP) distribution, evaluated at parameters `params`. `params(1)` is the tail index (shape) parameter, `k`, and `params(2)` is the scale parameter. `gplike` does not allow a threshold (location) parameter.

`[nlogL,acov] = gplike(params,data)` returns the inverse of Fisher's information matrix, `acov`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `acov` are their asymptotic variances. `acov` is based on the observed Fisher's information, not the expected information.

When `k = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `k > 0` and `theta = sigma/k`, the GP is equivalent to a Pareto distribution with a scale parameter equal to `sigma/k` and a shape parameter equal to `1/k`. The mean of the GP is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. When $k \geq 0$, the GP has positive density for

`x > theta`, or, when

`k < 0`, $0 \leq \frac{x-\theta}{\sigma} \leq -\frac{1}{k}$.

More About

- "Generalized Pareto Distribution" on page B-60
- "Working with Probability Distributions" on page 5-3

- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61
- "Supported Distributions" on page 5-17

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`gpfit` | `gppdf` | `gpcdf` | `gpinv` | `gpstat` | `gprnd`

gppdf

Generalized Pareto probability density function

Syntax

```
p = gppdf(x,k,sigma,theta)
```

Description

`p = gppdf(x,k,sigma,theta)` returns the pdf of the generalized Pareto (GP) distribution with the tail index (shape) parameter `k`, scale parameter `sigma`, and threshold (location) parameter, `theta`, evaluated at the values in `x`. The size of `p` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Default values for `k`, `sigma`, and `theta` are 0, 1, and 0, respectively.

When `k = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `k > 0` and `theta = sigma/k`, the GP is equivalent to a Pareto distribution with a scale parameter equal to `sigma/k` and a shape parameter equal to `1/k`. The mean of the GP is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. When $k \geq 0$, the GP has positive density for

`x > theta`, or, when

`k < 0`, $0 \leq \frac{x-\theta}{\sigma} \leq -\frac{1}{k}$.

More About

- "Generalized Pareto Distribution" on page B-60
- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61

- “Supported Distributions” on page 5-17

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`pdf` | `gpcdf` | `gpinv` | `gpstat` | `gpfit` | `gplike` | `gprnd`

gplotmatrix

Matrix of scatter plots by group

Syntax

```
gplotmatrix(x,y,group)
gplotmatrix(x,y,group,clr,sym,siz)
gplotmatrix(x,y,group,clr,sym,siz,doleg)
gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt)
gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt,xnam,ynam)
[h,ax,bigax] = gplotmatrix(...)
```

Description

`gplotmatrix(x,y,group)` creates a matrix of scatter plots. Each individual set of axes in the resulting figure contains a scatter plot of a column of `x` against a column of `y`. All plots are grouped by the grouping variable `group`.

`x` and `y` are matrices with the same number of rows. If `x` has p columns and `y` has q columns, the figure contains a p-by-q matrix of scatter plots. If you omit `y` or specify it as the empty matrix, `[]`, `gplotmatrix` creates a square matrix of scatter plots of columns of `x` against each other.

`group` is a grouping variable that can be a categorical variable, vector, string array, or cell array of strings. `group` must have the same number of rows as `x` and `y`. Points with the same value of `group` are placed in the same group, and appear on the graph with the same marker and color. Alternatively, `group` can be a cell array containing several grouping variables (such as `{g1 g2 g3}`); in that case, observations are in the same group if they have common values of all grouping variables.

`gplotmatrix(x,y,group,clr,sym,siz)` specifies the color, marker type, and size for each group. *`clr`* is a string array of colors recognized by the `plot` function. *`sym`* is a string array of symbols recognized by the `plot` command, with the default value `'.'`. `siz` is a vector of sizes, with the default determined by the `DefaultLineMarkerSize` property. If you do not specify enough values for all groups, `gplotmatrix` cycles through the specified values as needed.

`gplotmatrix(x,y,group,clr,sym,siz,doleg)` controls whether a legend is displayed on the graph (*`doleg`* is `'on'`, the default) or not (*`doleg`* is `'off'`).

`gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt)` controls what appears along the diagonal of a plot matrix of `y` versus `x`. Allowable values are `'none'`, to leave the diagonals blank, `'hist'`, to plot histograms, `'stairs'` to display the outlines of grouped histograms (default if there is more than one group), `'grpbars'` to plot grouped histogram bars. or `'variable'`, to write the variable names. `gplotmatrix` displays histograms along the diagonal only when there is only one variable (i.e., `gplotmatrix(x,[],[],[],[],[],[],'hist')`.

`gplotmatrix(x,y,group,clr,sym,siz,doleg,dispopt,xnam,ynam)` specifies the names of the columns in the `x` and `y` arrays. These names are used to label the *x*- and *y*-axes. `xnam` and `ynam` must be character arrays or cell arrays of strings, with one name for each column of `x` and `y`, respectively.

`[h,ax,bigax] = gplotmatrix(...)` returns three arrays of handles. `h` is an array of handles to the lines on the graphs. The array's third dimension corresponds to groups in the input argument `group`. `ax` is a matrix of handles to the axes of the individual plots. If *`dispopt`* is `'hist'`, `'stairs'`, or `'grpbars'`, `ax` contains one extra row of handles to invisible axes in which the histograms are plotted. `bigax` is a handle to big (invisible) axes framing the entire plot matrix. `bigax` is fixed to point to the current axes, so a subsequent `title`, `xlabel`, or `ylabel` command will produce labels that are centered with respect to the entire plot matrix.

Examples

Create Grouped Data Scatter Plot Matrix

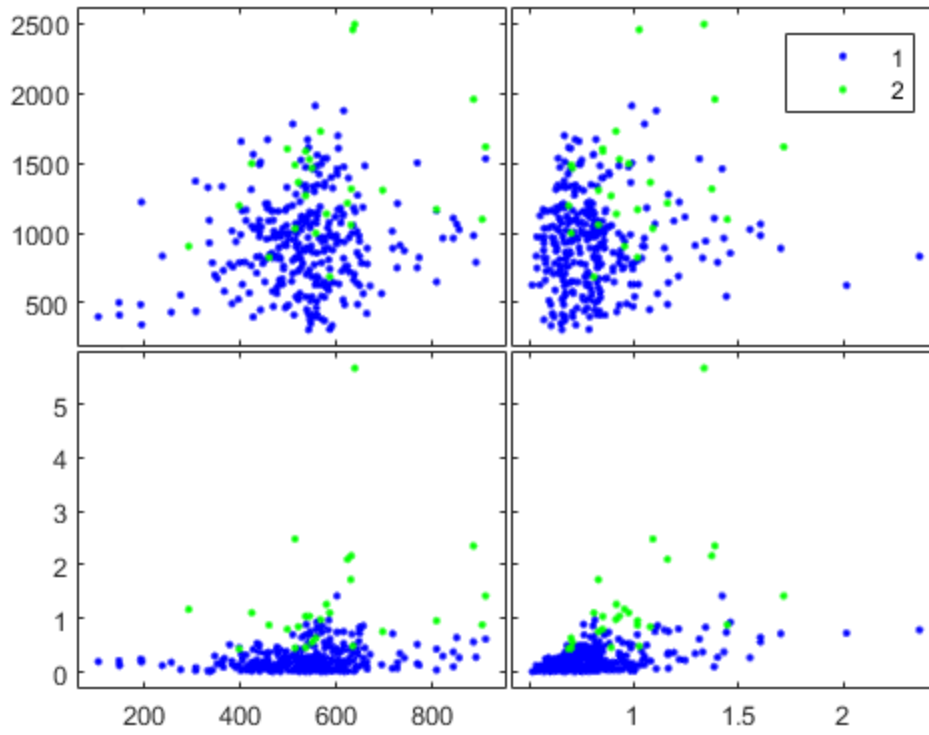
Load the sample data.

```
load discrim;
```

The `ratings` array contains rating values for 329 U.S. cities in the nine different categories listed in the `categories` array. The `group` array contains a city size code that is equal to `2` for the 26 largest cities, and `1` otherwise.

Create a matrix of scatter plots to compare the first two categories, `climate` and `housing`, with categories 4 (`crime`) and 7 (`arts`). Specify `group` as the grouping variable to visually distinguish the data for large and small cities.

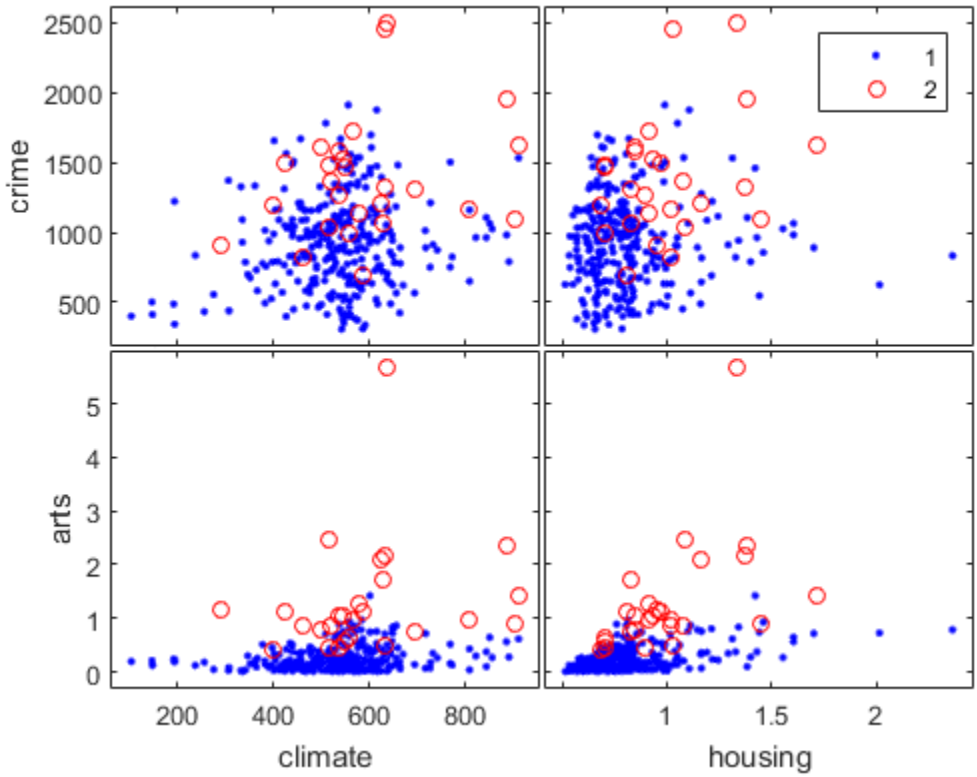
```
figure;
gplotmatrix(ratings(:,1:2),ratings(:,[4 7]),group);
```



The figure displays a matrix of scatter plots for the specified comparisons, with each city size group represented by a different color.

For better clarity, you can adjust the appearance of the graphs by specifying colors and plotting symbols, and labeling the axes with the rating categories.

```
figure;
gplotmatrix(ratings(:,1:2),ratings(:,[4 7]),group,...
    'br','.o',[],'on','',categories(1:2,:),...
    categories([4 7],:));
```



More About

- "Grouping Variables" on page 2-52

See Also

`grpstats` | `gscatter` | `plotmatrix`

gprnd

Generalized Pareto random numbers

Syntax

```
r = gprnd(k,sigma,theta)
r = gprnd(k,sigma,theta,m,n,...)
R = gprnd(K,sigma,theta,[m,n,...])
```

Description

`r = gprnd(k,sigma,theta)` returns an array of random numbers chosen from the generalized Pareto (GP) distribution with tail index (shape) parameter `k`, scale parameter `sigma`, and threshold (location) parameter, `theta`. The size of `r` is the common size of the input arguments if all are arrays. If any parameter is a scalar, the size of `r` is the size of the other parameters.

`r = gprnd(k,sigma,theta,m,n,...)` or `R = gprnd(K,sigma,theta,[m,n,...])` generates an `m`-by-`n`-by-... array. The `k`, `sigma`, `theta` parameters can each be scalars or arrays of the same size as `r`.

When `k = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `k > 0` and `theta = sigma/k`, the GP is equivalent to a Pareto distribution with a scale parameter equal to `sigma/k` and a shape parameter equal to `1/k`. The mean of the GP is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. When $k \geq 0$, the GP has positive density for

`x > theta`, or, when

$$0 \leq \frac{x-\theta}{\sigma} \leq -\frac{1}{k}$$

More About

- “Generalized Pareto Distribution” on page B-60

- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61
- "Supported Distributions" on page 5-17

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`random` | `gppdf` | `gpcdf` | `gpinv` | `gpstat` | `gpfit` | `gplike`

gpstat

Generalized Pareto mean and variance

Syntax

```
[m,v] = gpstat(k,sigma,theta)
```

Description

`[m,v] = gpstat(k,sigma,theta)` returns the mean of and variance for the generalized Pareto (GP) distribution with the tail index (shape) parameter `k`, scale parameter `sigma`, and threshold (location) parameter, `theta`.

The default value for `theta` is 0.

When `k = 0` and `theta = 0`, the GP is equivalent to the exponential distribution. When `k > 0` and `theta = sigma/k`, the GP is equivalent to a Pareto distribution with a scale parameter equal to `sigma/k` and a shape parameter equal to `1/k`. The mean of the GP is not finite when $k \geq 1$, and the variance is not finite when $k \geq 1/2$. When $k \geq 0$, the GP has positive density for `x > theta`, or when

`k < 0`, $0 \leq \frac{x-\theta}{\sigma} \leq -\frac{1}{k}$.

More About

- "Generalized Pareto Distribution" on page B-60
- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61
- "Supported Distributions" on page 5-17

References

[1] Embrechts, P., C. Klüppelberg, and T. Mikosch. *Modelling Extremal Events for Insurance and Finance*. New York: Springer, 1997.

[2] Kotz, S., and S. Nadarajah. *Extreme Value Distributions: Theory and Applications*. London: Imperial College Press, 2000.

See Also

`gppdf` | `gpcdf` | `gpinv` | `gpfit` | `gplike` | `gprnd`

growTrees

Class: TreeBagger

Train additional trees and add to ensemble

Syntax

```
B = growTrees(B,ntrees)
B = growTrees(B,ntrees,'param1',val1,'param2',val2,...)
```

Description

`B = growTrees(B,ntrees)` grows `ntrees` new trees and appends them to those trees already stored in the ensemble `B`.

`B = growTrees(B,ntrees,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'nprint'`	Specifies that a diagnostic message showing training progress should display after every `value` training cycles (grown trees). Default is no diagnostic messages.
`'options'`	A `struct` that specifies options that govern computation when growing the ensemble of decision trees. One option requests that the computation of decision trees on multiple bootstrap replicates uses multiple processors, if the Parallel Computing Toolbox is available. Two options specify the random number streams to use in selecting bootstrap replicates. You can create this argument with a call to `statset`. You can retrieve values of the individual fields with a call to `statget`. Applicable `statset` parameters are: • `'UseParallel'` — If `true` and if a `parpool` of the Parallel Computing Toolbox is open, compute decision trees drawn on separate boostrap replicates in parallel. If the Parallel Computing Toolbox is not installed, or a `parpool`

is not open, computation occurs in serial mode. Default is `false`, or serial computation.

- `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
- `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `growTrees` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case

  - You have an open Parallel pool
  - `UseParallel` is `true`
  - `UseSubstreams` is `false`

  In that case, use a cell array the same size as the Parallel pool.

See Also

`TreeBagger` | `TreeBagger` | `fitctree` | `fitrtree` | `statset` | `statget`

grp2idx

Create index vector from grouping variable

Syntax

```
[G,GN]=grp2idx(S)
[G,GN,GL] = grp2idx(S)
```

Description

`[G,GN]=grp2idx(S)` creates an index vector `G` from the grouping variable `S`. `S` can be a categorical, numeric, logical, datetime, or duration vector; a cell vector of strings; or a character matrix with each row representing a group label. The result `G` is a vector taking integer values from 1 up to the number `K` of distinct groups. `GN` is a cell array of strings representing group labels. `GN(G)` reproduces `S` (aside from any differences in type).

The order of `GN` depends on the grouping variable:

- For numeric and logical grouping variables, the order is the sorted order of `S`.
- For categorical grouping variables, the order is the order of `getlabels(S)`.
- For string grouping variables, the order is the order of first appearance in `S`.

`[G,GN,GL] = grp2idx(S)` returns a column vector `GL` representing the group levels. The set of groups and their order in `GL` and `GN` are the same, except that `GL` has the same type as `S`. If `S` is a character matrix, `GL(G,:)` reproduces `S`, otherwise `GL(G)` reproduces `S`.

`grp2idx` treats `NaN`s (numeric, duration, or logical), empty strings (char or cell array of strings), or `<undefined>` values (categorical) or `NaT`s (datetime) in `S` as missing values and returns `NaN`s in the corresponding rows of `G`. `GN` and `GL` don't include entries for missing values.

Examples

Load the data in `hospital.mat` and create a categorical grouping variable:

```
load hospital
edges = 0:10:100;
labels = strcat(num2str((0:10:90)','%d'),{'s'});
AgeGroup = ordinal(hospital.Age,labels,[],edges);

ages = hospital.Age(1:5)

ages =
    38
    43
    38
    40
    49

group = AgeGroup(1:5)

group =
     30s
     40s
     30s
     40s
     40s

indices = grp2idx(group)

indices =
     4
     5
     4
     5
     5
```

More About

- "Grouping Variables" on page 2-52

See Also

gscatter | grpstats | crosstab | getlabels

grpstats

Summary statistics organized by group

Syntax

```
statarray = grpstats(tbl,groupvar)
statarray = grpstats(tbl,groupvar,whichstats)
statarray = grpstats(tbl,groupvar,whichstats,Name,Value)

means = grpstats(X,group)
[stats1,...,statsN] = grpstats(X,group,whichstats)
[stats1,...,statsN] = grpstats(X,group,whichstats,'Alpha',alpha)

grpstats(X,group,alpha)
```

Description

`statarray = grpstats(tbl,groupvar)` returns a table or dataset array with the means for the data groups specified in tbl determined by the values of the grouping variable or variables specified in groupvar.

- If there is a single grouping variable, then there is a row in `statarray` for each value of the grouping variable. `grpstats` sorts the groups by order of appearance (if the grouping variable is a character array), in ascending numeric order (if the grouping variable is numeric), or in order of the levels (if the grouping variable is categorical).
- If groupvar is a cell array of strings containing multiple grouping variable names, or a vector of column numbers, then there is a row in `statarray` for each observed unique combination of values of the grouping variables. `grpstats` sorts the groups by the values of the first grouping variable, then the second grouping variable, and so on.
- If any variables in tbl (other than those specified in `groupvar`) are not numeric or logical arrays, then you must specify the names or column numbers of the numeric and logical variables for which you want to calculate means using the name-value pair argument, DataVars.

`statarray = grpstats(tbl,groupvar,whichstats)` returns the group values for the summary statistics types specified in whichstats.

`statarray = grpstats(tbl,groupvar,whichstats,Name,Value)` uses additional options specified by one or more Name,Value pair arguments.

`means = grpstats(X,group)` returns a column vector or matrix with the means of the groups of the data in the matrix or vector X determined by the values of the grouping variable or variables, group. The rows of `means` correspond to the grouping variable values.

- If there is a single grouping variable, then there is a row in `means` for each value of the grouping variable. `grpstats` sorts the groups by order of appearance (if the grouping variable is a character array), in ascending numeric order (if the grouping variable is numeric), or in order of the levels (if the grouping variable is categorical).
- If group is a cell array of grouping variables, then there is a row in `means` for each observed unique combination of values of the grouping variables. `grpstats` sorts the groups by the values of the first grouping variable, then the second grouping variable, and so on.
- If X is a matrix, then means is a matrix with the same number of columns as `X`. Each column of `means` has the group means for the corresponding column of `X`.

`[stats1,...,statsN] = grpstats(X,group,whichstats)` returns column vectors or arrays with group values for the summary statistic types specified in whichstats.

`[stats1,...,statsN] = grpstats(X,group,whichstats,'Alpha',alpha)` specifies the significance level for confidence and prediction intervals.

`grpstats(X,group,alpha)` plots the means of the groups of data in the vector or matrix X determined by the values of the grouping variable, group. The grouping variable values are on the horizontal plot axis. Each group mean has 100×(1 – alpha)% confidence intervals.

- If X is a matrix, then `grpstats` plots the means and confidence intervals for each column of `X`.
- If group is a cell array of grouping variables, then `grpstats` plots the means and confidence intervals for the groups of data in `X` determined by the unique combinations of values of the grouping variables. For example, if there are two grouping variables, each with two values, there are four possible combinations of grouping variable values. The plot includes only the combinations of values that exist in the input grouping variables (not all possible combinations).

Examples

Dataset Array Summary Statistics Organized by Group

Load the sample data.

```
load('hospital')
```

The dataset array `hospital` has 100 observations and 7 variables.

Create a dataset array with only the variables `Sex`, `Age`, `Weight`, and `Smoker`.

```
ds = hospital(:,{'Sex','Age','Weight','Smoker'});
```

`Sex` is a nominal array, with levels `Male` and `Female`. The variables `Age` and `Weight` have numeric values, and `Smoker` has logical values.

Compute the mean for the numeric and logical arrays, `Age`, `Weight`, and `Smoker`, grouped by the levels in `Sex`.

```
statarray = grpstats(ds,'Sex')
```

```
statarray =

              Sex       GroupCount    mean_Age    mean_Weight    mean_Smoker
    Female    Female    53            37.717      130.47         0.24528
    Male      Male      47            38.915      180.53         0.44681
```

`statarray` is a dataset array with two rows, corresponding to the levels in `Sex`. `GroupCount` is the number of observations in each group. The means of `Age`, `Weight`, and `Smoker`, grouped by `Sex`, are given in `mean_Age`, `mean_Weight`, and `mean_Smoker`.

Compute the mean for `Age` and `Weight`, grouped by the values in `Smoker`.

```
statarray = grpstats(ds,'Smoker','mean','DataVars',{'Age','Weight'})
```

```
statarray =

          Smoker    GroupCount    mean_Age    mean_Weight
    0     false     66             37.97      149.91
    1     true      34            38.882      161.94
```

In this case, not all variables in `ds` (excluding the grouping variable, `Smoker`) are numeric or logical arrays; the variable `Sex` is a nominal array. When not all variables in

the input dataset array are numeric or logical arrays, you must specify the variables for which you want to calculate summary statistics using `DataVars`.

Compute the minimum and maximum weight, grouped by the combinations of values in `Sex` and `Smoker`.

```
statarray = grpstats(ds,{'Sex','Smoker'},{'min','max'},...
                     'DataVars','Weight')
```

```
statarray =

                Sex       Smoker    GroupCount    min_Weight    max_Weight
    Female_0    Female    false     40            111           147
    Female_1    Female    true      13            115           146
    Male_0      Male      false     26            158           194
    Male_1      Male      true      21            164           202
```

There are two unique values in `Smoker` and two levels in `Sex`, for a total of four possible combinations of values: Female Nonsmoker (`Female_0`), Female Smoker (`Female_1`), Male Nonsmoker (`Male_0`), and Male Smoker (`Male_1`).

Specify the names for the columns in the output.

```
statarray = grpstats(ds,{'Sex','Smoker'},{'min','max'},...
          'DataVars','Weight','VarNames',{'Gender','Smoker',...
     'GroupCount','LowestWeight','HighestWeight'})
```

```
statarray =

                Gender    Smoker    GroupCount    LowestWeight    HighestWeight
    Female_0    Female    false     40            111             147
    Female_1    Female    true      13            115             146
    Male_0      Male      false     26            158             194
    Male_1      Male      true      21            164             202
```

Summary Statistics for a Dataset Array Without Grouping

Load the sample data.

```
load('hospital')
```

The dataset array `hospital` has 100 observations and 7 variables.

Create a dataset array with only the variables `Age`, `Weight`, and `Smoker`.

```
ds = hospital(:,{'Age','Weight','Smoker'});
```

The variables `Age` and `Weight` have numeric values, and `Smoker` has logical values.

Compute the mean, minimum, and maximum for the numeric and logical arrays, `Age`, `Weight`, and `Smoker`, with no grouping.

```
statarray = grpstats(ds,[],{'mean','min','max'})
```

```
statarray =

           GroupCount    mean_Age    min_Age    max_Age    mean_Weight
    All    100           38.28       25         50         154


           min_Weight    max_Weight    mean_Smoker    min_Smoker    max_Smoker
    All    111           202           0.34           false         true
```

The observation name `All` indicates that all observations in `ds` were used to compute the summary statistics.

Group Means for a Matrix Using One or More Grouping Variables

Load the sample data.

```
load('carsmall')
```

All variables are measured for 100 cars. `Origin` is the country of origin for each car (France, Germany, Italy, Japan, Sweden, or USA). `Cylinders` has three unique values, `4`, `6`, and `8`, indicating the number of cylinders in each car.

Calculate the mean acceleration, grouped by country of origin.

```
means = grpstats(Acceleration,Origin)
```

```
means =

   14.4377
   18.0500
   15.8867
   16.3778
   16.6000
   15.5000
```

`means` is a 6-by-1 vector of mean accelerations, where each value corresponds to a country of origin.

Calculate the mean acceleration, grouped by both country of origin and number of cylinders.

```
means = grpstats(Acceleration,{Origin,Cylinders})
```

```
means =

   17.0818
   16.5267
   11.6406
   18.0500
   15.9143
   15.5000
   16.3375
   16.7000
   16.6000
   15.5000
```

There are 18 possible combinations of grouping variable values because `Origin` has 6 unique values and `Cylinders` has 3 unique values. Only 10 of the possible combinations appear in the data, so `means` is a 10-by-1 vector of group means corresponding to the observed combinations of values.

Return the group names along with the mean acceleration for each group.

```
[means,grps] = grpstats(Acceleration,{Origin,Cylinders},...
                        {'mean','gname'})
```

```
means =

   17.0818
   16.5267
   11.6406
   18.0500
   15.9143
   15.5000
   16.3375
   16.7000
   16.6000
   15.5000


grps =

    'USA'        '4'
```

```
    'USA'        '6'
    'USA'        '8'
    'France'     '4'
    'Japan'      '4'
    'Japan'      '6'
    'Germany'    '4'
    'Germany'    '6'
    'Sweden'     '4'
    'Italy'      '4'
```

The output `grps` shows the 10 observed combinations of grouping variable values. For example, the mean acceleration of 4-cylinder cars made in France is 18.05.

Multiple Summary Statistics for a Matrix Organized by Group

Load the sample data.

```
load('carsmall')
```

The variable `Acceleration` was measured for 100 cars. The variable `Origin` is the country of origin for each car (France, Germany, Italy, Japan, Sweden, or USA).

Return the minimum, median, and maximum acceleration, grouped by country of origin.

```
[grpMin,grpMed,grpMax,grp] = grpstats(Acceleration,Origin,...
                                {'min','median','max','gname'})
```

```
grpMin =

    8.0000
   15.3000
   13.9000
   12.2000
   15.7000
   15.5000


grpMed =

   14.7000
   17.5000
   15.7000
   15.3000
   16.6000
```

```
   15.5000


grpMax =

   22.2000
   21.9000
   18.2000
   24.6000
   17.5000
   15.5000


grp =

    'USA'
    'France'
    'Japan'
    'Germany'
    'Sweden'
    'Italy'
```

The sample car with the lowest acceleration is made in the USA, and the sample car with the highest acceleration is made in Germany.

Plot Prediction Intervals for a New Observation in Each Group

Load the sample data.

```
load('carsmall')
```

The variable `Weight` was measured for 100 cars. The variable `Model_Year` has three unique values, `70`, `76`, and `82`, which correspond to model years 1970, 1976, and 1982.

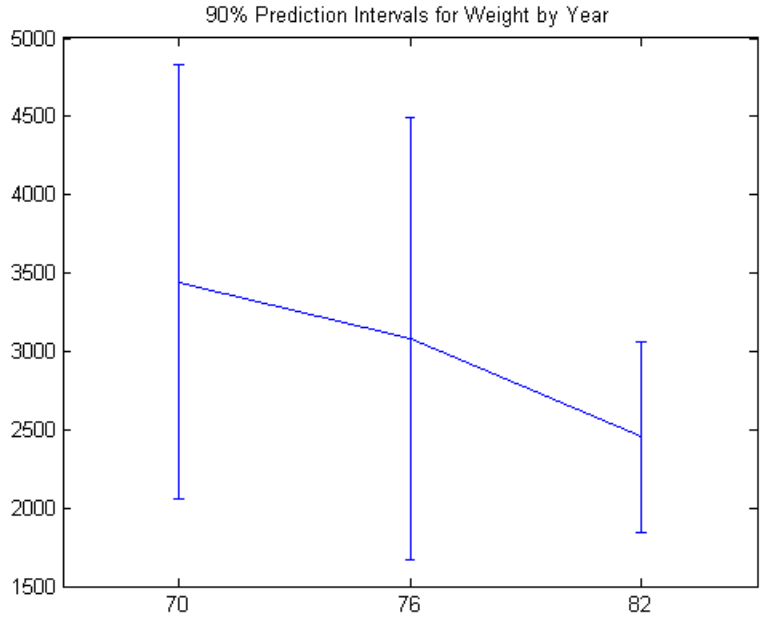
Calculate the mean weight and 90% prediction intervals for each model year.

```
[means,pred,grp] = grpstats(Weight,Model_Year,...
                      {'mean','predci','gname'},'Alpha',0.1);
```

Plot error bars showing the mean weight and 90% prediction intervals, grouped by model year. Label the horizontal axis with the group names.

```
ngrps = length(grp); % Number of groups
```

```
figure()
errorbar((1:ngrps)',means,pred(:,2)-means)
set(gca,'xtick',1:ngrps,'xticklabel',grp)
title('90% Prediction Intervals for Weight by Year')
```



Plot Group Means and Confidence Intervals

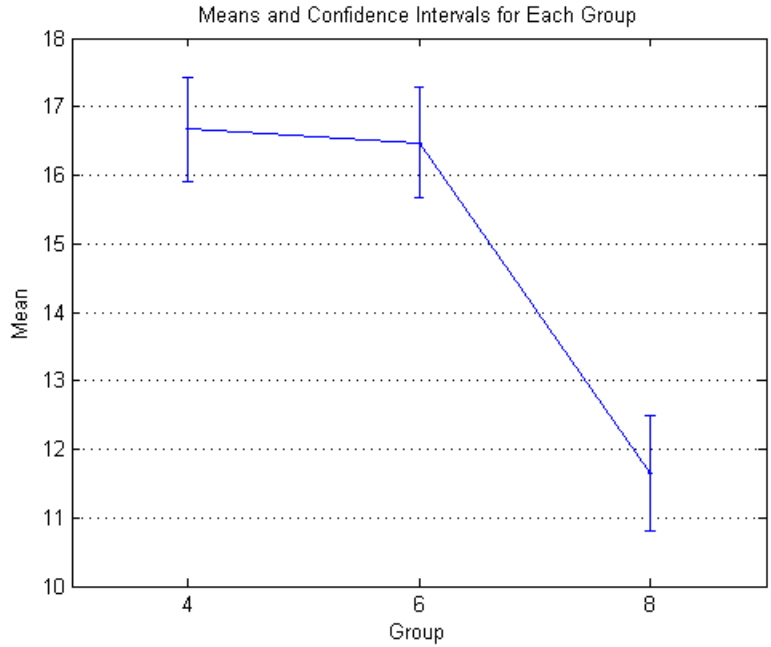
Load the sample data.

```
load('carsmall')
```

The variables `Acceleration` and `Weight` are the acceleration and weight values measured for 100 cars. The variable `Cylinders` is the number of cylinders in each car. The variable `Model_Year` has three unique values, `70`, `76`, and `82`, which correspond to model years 1970, 1976, and 1982.

Plot mean acceleration, grouped by `Cylinders`, with 95% confidence intervals.

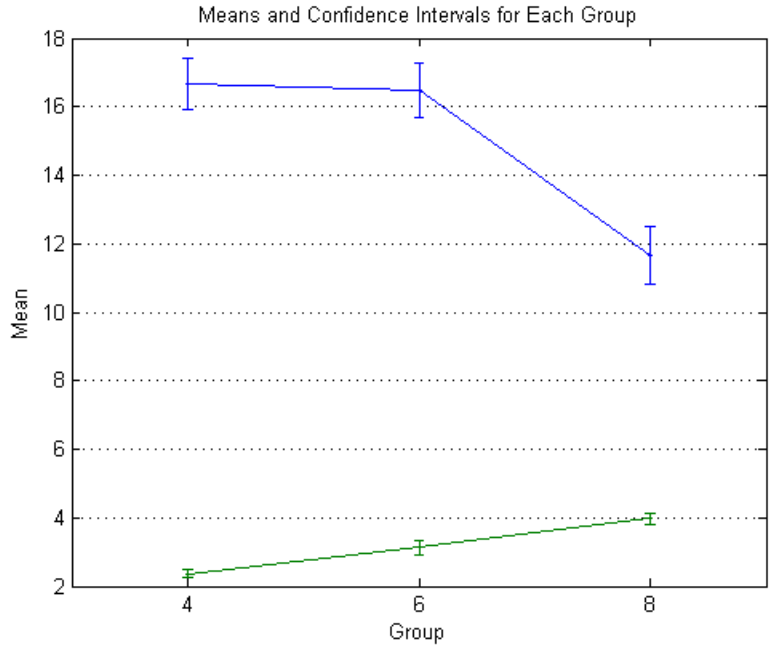
```
grpstats(Acceleration,Cylinders,0.05)
```



The mean acceleration for cars with 8 cylinders is significantly lower than for cars with 4 or 6 cylinders.

Plot mean acceleration and weight, grouped by `Cylinders`, and 95% confidence intervals. Scale the `Weight` values by 1000 so the means of `Weight` and `Acceleration` are the same order of magnitude.

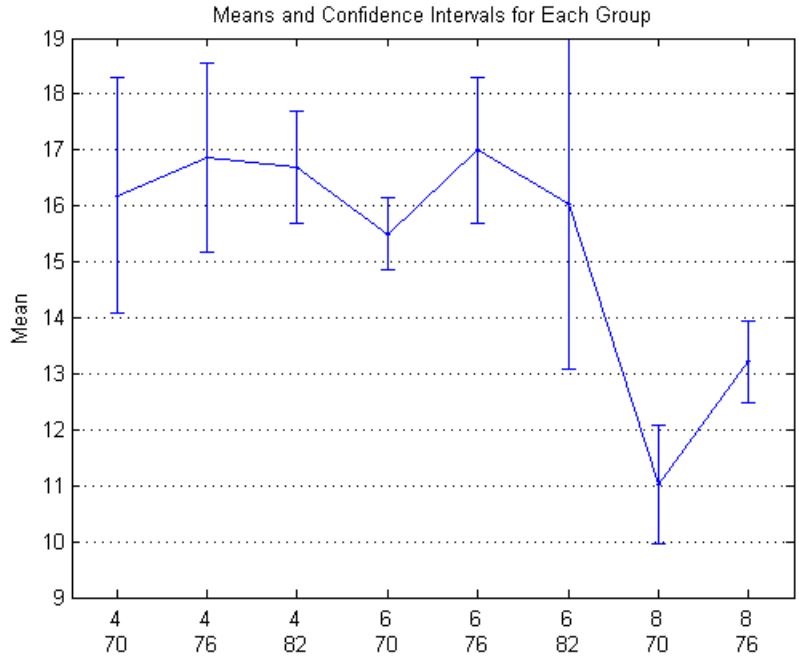
```
grpstats([Acceleration,Weight/1000],Cylinders,0.05)
```



The average weight of cars increases with the number of cylinders, and the average acceleration decreases with the number of cylinders.

Plot mean acceleration, grouped by both `Cylinders` and `Model_Year`. Specify 95% confidence intervals.

```
grpstats(Acceleration,{Cylinders,Model_Year},0.05)
```



There are nine possible combinations of grouping variable values because there are three unique values in `Cylinders` and three unique values in `Model_Year`. The plot does not show 8-cylinder cars with model year 1982 because the data did not include this combination.

The mean acceleration of 8-cylinder cars made in 1976 is significantly larger than the mean acceleration of 8-cylinder cars made in 1970.

- “Summary Statistics Grouped by Category” on page 2-38
- “Test Differences Between Category Means” on page 2-29
- “Plot Data Grouped by Category” on page 2-25
- “Calculations on Dataset Arrays” on page 2-108

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. tbl must include at least one variable that is a grouping variable.

Summary statistics can only be calculated for variables that have a numeric or logical data type. If any variables in tbl (other than the grouping variables) are not numeric or logical arrays, then use the name-value pair argument DataVars to specify the names or column numbers of the numeric and logical variables for which to calculate summary statistics.

`groupvar` — Identifiers for the grouping variables

cell array of strings | vector of positive integers | logical vector | `[]`

Identifiers for the grouping variables in the input data, tbl, specified as one of the following:

String or cell array of strings	Names of the grouping variables
Positive integer or vector of positive integers	Variable numbers of the grouping variables
Vector of logical values with number of elements equal to the number of variables in tbl	Logical indicator with value `true` for grouping variables and `false` otherwise
`[]`	No groups (returns summary statistics for all data)

Any variable that is identified by `groupvar` as a grouping variable must have a valid grouping variable data type: categorical array, logical or numeric vector, datetime or duration vector, or cell array of strings.

For example, consider an input table, `tbl`, with six variables. The fourth variable is named `Gender`. To be a valid grouping variable, the data type of `Gender` might be a cell array of strings or a nominal array, with the unique values `Male` and `Female`. To specify the variable `Gender` as the grouping variable, you can use any of these syntaxes:

- `statarray = grpstats(tbl,'Gender')`
- `statarray = grpstats(tbl,4)`
- `statarray = grpstats(tbl,logical([0 0 0 1 0 0]))`

Data Types: `double` | `logical` | `cell` | `char`

`whichstats` — Types of summary statistics

string | function handle

Types of summary statistics to compute, specified as a string or function handle, or a cell array of strings and function handles. Use a cell array to specify multiple types of summary statistics.

Possible string values are:

`'mean'`	Mean
`'sem'`	Standard error of the mean
`'numel'`	Count, or number, of non-`NaN` elements
`'gname'`	Group name
`'std'`	Standard deviation
`'var'`	Variance
`'min'`	Minimum
`'max'`	Maximum
`'range'`	Range
`'meanci'`	95% confidence interval for the mean
`'predci'`	95% prediction interval for a new observation

Example: `[stat1,stat2] = grpstats(X,group,{'mean','sem'})`

You can specify different significance levels for the `'meanci'` and `'predci'` options using the name-value pair argument, Alpha.

To specify other types of summary statistics, you can use function handles. You can use the handle to any function that accepts a column or matrix of data, and returns the same size output each time `grpstats` calls it (even if the output for some groups is empty).

If the function accepts a column of data, then the function can return either a scalar value, or an *nvals*-by-1 column vector for descriptive statistics of length *nvals* (for example, confidence intervals have length two). If the function accepts a matrix, it must either return a 1-by-*ncols* row vector, or an *nvals*-by-*ncols* matrix, where *ncols* is the number of columns in the input data matrix.

Example:
```
[stat1,stat2,stat3] = grpstats(X,group,
{'mean','std',@skewness})
```

For functions that do not compute column-wise statistics, specify the computation direction while specifying the function.

Example: `stat1 = grpstats(X,group,@(x)sum(x,1))`

Data Types: `char` | `function_handle`

`alpha` — Significance level

scalar value in the range (0,1)

Significance level, specified as a scalar value in the range (0,1).

- When you specify `'meanci'` or `'predci'` in whichstats, you can use `alpha` to specify the significance level for the confidence or prediction intervals. If you specify `alpha`, then `grpstats` returns 100×(1 – `alpha`)% confidence or prediction intervals. If you do not specify `alpha`, then `grpstats` returns 95% intervals (`alpha = 0.05`).
- Use `alpha` with the grpstats(X,group,alpha) syntax to plot group means and corresponding 100×(1 – alpha)% confidence intervals.

Data Types: `double`

`X` — Input data

vector | matrix

Input data, specified as a vector or a matrix. If `X` is a matrix, then `grpstats` returns summary statistics for each column of `X`.

Data Types: `double` | `single`

`group` — Grouping variable

categorical array | logical or numeric vector | datetime or duration vector | cell array of strings | `[]`

Grouping variable, specified as a categorical array, logical or numeric vector, or cell array of strings. Each unique value in a grouping variable defines a group. `grpstats` groups data for summary statistics using the grouping variable values.

There must be a grouping variable value for each row of the input data X. Observations (rows) with the same value of the grouping variable are in the same group. Use `[]` to compute summary statistics for all data, without using groups.

For example, if `Gender` is a cell array of strings with values `'Male'` and `'Female'`, you can use `Gender` as a grouping variable to summarize your data by gender.

You can also use more than one grouping variable to group data for summary statistics. In this case, specify a cell array of grouping variables.

For example, if `Smoker` is a logical vector with values `0` for nonsmokers and `1` for smokers, then specifying the cell array `{Gender,Smoker}` divides observations into four groups: Male Smoker, Male Nonsmoker, Female Smoker, and Female Nonsmoker. `grpstats` returns summary statistics only for the combinations of values that exist in the input grouping variables (not all possible combinations).

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'DataVars',[1,3,4],'Alpha',0.01` specifies that summary statistics be calculated for the 1st, 3rd, and 4th variables in a dataset array, with 99% confidence intervals.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level for confidence and prediction intervals, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

When you include `'meanci'` or `'predci'` in whichstats, you can use `Alpha` to specify the significance level for confidence or prediction intervals. If you specify the value α, then `grpstats` returns $100\times(1-\alpha)\%$ confidence or prediction intervals.

If you do not specify a value for `Alpha`, then `grpstats` returns 95% intervals ($\alpha = 0.05$).

Example: `'Alpha',0.1`

Data Types: `double`

`'DataVars'` — Variable names or columns

cell array of strings | vector of positive integers | logical vector

Variable names or columns indicating which variables in the input data tbl you want to compute summary statistics for, specified as the comma-separated pair consisting of `'DataVars'` and a cell array of strings, vector of positive integers, or a logical vector. Use a string to specify a variable name, a positive integer to specify a variable column

number, or logical values to indicate which variables to include (`true` if you want to compute summary statistics, `false` otherwise).

You must specify `DataVars` if there are any variables in tbl (other than the grouping variables specified in groupvar) that are not numeric or logical arrays. Summary statistics can only be calculated for variables that have a numeric or logical data type.

Example: `'DataVars',{'Height','Weight'}`

Data Types: `double | cell | char`

`'VarNames'` — Variable names for output

cell array of strings

Variable names for the output statarray, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings. By default, `grpstats` constructs output variable names by appending a prefix to the variable names from the input data tbl. This prefix corresponds to the summary statistic name.

Example: `'VarNames',{'Gender','GroupCount','MaleMean','FemaleMean'}`

Data Types: `cell`

Output Arguments

`statarray` — Group summary statistics

table | dataset array

Group summary statistics, returned as a table or a dataset array. If tbl is a table, `grpstats` returns statarray as a table. If tbl is a dataset array, `grpstats` returns statarray as a dataset array.

`statarray` contains summary statistic values for the groups of data in tbl determined by the levels of the grouping variables specified by groupvar. There is a row in `statarray` for each observed value or combination of values in the variables specified by `groupvar`. The output `statarray` contains:

- All grouping variables specified by `groupvar`.
- The variable `GroupCount`, containing the number of observations in each group.
- Group summary statistic values for all variables in tbl (other than those specified by groupvar), or for only the variables specified using DataVars.

The total number of variables in `statarray` is *ngroupvars* + 1 + *ndatavars*×*nstats*, where *ngroupvars* is the number of variables in `groupvar`, *ndatavars* is the number of variables for which summary statistics are computed, and *nstats* is the number of summary statistic types specified in whichstats.

`grpstats` assigns default names to the variables in `statarray`, unless you specify variable names using the name-value pair argument VarNames.

`means` — Group means
column vector | array

Group means for the groups of data in the vector or matrix X determined by the levels of group, returned as an *ngroups*-by-*ncols* array. Here, *ngroups* is the number of unique values in the grouping variable, and *ncols* is the number of columns in X. If `X` is a vector, then `means` is a column vector.

`stats1,...,statsN` — Group summary statistics
column vectors | arrays

Group summary statistics for the groups of data in the vector or matrix X determined by the levels of group, returned as *ngroups*-by-*ncols* arrays. Here, *ngroups* is the number of unique values in the grouping variable, and *ncols* is the number of columns in X. You must specify an output argument for each type of summary statistic specified in whichstats.

If a summary statistic type in `whichstats` returns a value of length *nvals* (for example, a confidence interval is a descriptive statistic of length two), then the corresponding output argument is an *ngroups*-by-*ncols*-by-*nvals* array.

More About

Algorithms

- `grpstats` treats `NaN`s as missing values, and removes them from the input data before calculating summary statistics.
- `grpstats` ignores empty group names.

- "Dataset Arrays" on page 2-132
- "Grouping Variables" on page 2-52

- “Categorical Arrays” on page 2-42

See Also

`dataset` | `table`

grpstats

Class: RepeatedMeasuresModel

Compute descriptive statistics of repeated measures data by group

Syntax

```
statstbl = grpstats(rm,g)
statstbl = grpstats(rm,g,stats)
```

Description

`statstbl = grpstats(rm,g)` returns the count, mean, and variance for the data used to fit the repeated measures model rm, grouped by the factors, g.

`statstbl = grpstats(rm,g,stats)` returns the statistics specified by stats for the data used to fit the repeated measures model rm, grouped by the factors, g.

Tips

- `grpstats` computes results separately for each group. The results do not depend on the fitted repeated measures model. It computes the results on all available data, without omitting entire rows that contain `NaN`s.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

g — Name of grouping factor or factors

string | cell array of strings

Name of grouping factor or factors, specified as a string or cell array of strings.

Example: `'Drug'`

Example: `{'Drug','Sex'}`

Data Types: `char`

stats — Statistics to compute

string | function handle | cell array of multiple strings and function handles

Statistics to compute, specified as one of the following:

- String specifying the name of the statistics to compute. Names can be one of the following.

Name	Description
`'mean'`	Mean
`'sem'`	Standard error of the mean
`'numel'`	Count or number of elements
`'gname'`	Group name
`'std'`	Standard deviation
`'var'`	Variance
`'min'`	Minimum
`'max'`	Maximum
`'range'`	Maximum minus minimum
`'meanci'`	95% confidence interval for the mean
`'predci'`	95% prediction interval for a new observation

- Function handle — The function you specify must accept a vector of response values for a single group, and compute descriptive statistics for it. A function should typically return a value that has one row. A function must return the same size output each time `grpstats` calls it, even if the input for some groups is empty.
- A cell array of strings and function handles.

Example: `@median`

Example: `@skewness`

Example: `'gname'`

Example: `{'gname','range','predci'}`

Data Types: `char` | `function_handle` | `cell`

Output Arguments

`statstbl` — Statistics values for each group

table

Statistics values for each group, returned as a table.

Examples

Compute Group Statistics

Load the sample data.

```
load fisheriris
```

The column vector, `species` consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Compute group counts, mean, and standard deviation with respect to species.

```
grpstats(rm,'species')
```

```
ans =

    species       GroupCount     mean      std
    ___________    __________    ______    ______

    'setosa'        200          2.5355    1.8483
    'versicolor'    200           3.573    1.7624
    'virginica'     200           4.285    1.9154
```

Now, compute the range of data and 95% confidence intervals for the group means for the factor species. Also display the group name.

```
grpstats(rm,'species',{'gname','range','predci'})
```

```
ans =

    species          gname        GroupCount    range          predci
    ___________    ___________    __________    _____    ____________________

    'setosa'        'setosa'        200           5.7       -1.1185      6.1895
    'versicolor'    'versicolor'    200             6      0.088976       7.057
    'virginica'     'virginica'     200           6.5        0.4985      8.0715
```

Statistics for Data Grouped by Two Factors

Load the sample data.

```
load repeatedmeas
```

The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ through $y8$ as responses. The table `within` includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ through $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Compute group counts, mean, standard deviation, skewness, and kurtosis of data grouped by the factors `Group` and `Gender`.

```
GS = grpstats(rm,{'Group','Gender'},{'mean','std',@skewness,@kurtosis})
```

```
GS =
```

Group	Gender	GroupCount	mean	std	skewness	kurtosis
A	Female	40	16.554	21.498	0.35324	3.7807
A	Male	40	9.8335	20.602	-0.38722	2.7834
B	Female	40	11.261	25.779	-0.49177	4.1484
B	Male	40	3.6078	24.646	0.55447	2.7966
C	Female	40	-11.335	27.186	1.7499	6.1429
C	Male	40	-14.028	31.984	1.7362	5.141

See Also

`fitrm` | `plot`

gscatter

Scatter plot by group

Syntax

```
gscatter(x,y,group)
gscatter(x,y,group,clr,sym,siz)
gscatter(x,y,group,clr,sym,siz,doleg)
gscatter(x,y,group,clr,sym,siz,doleg,xnam,ynam)
h = gscatter(...)
```

Description

`gscatter(x,y,group)` creates a scatter plot of `x` and `y`, grouped by `group`. `x` and `y` are vectors of the same size. `group` is a grouping variable in the form of a categorical variable, vector, string array, or cell array of strings. Alternatively, `group` can be a cell array containing several grouping variables (such as `{g1 g2 g3}`), in which case observations are in the same group if they have common values of all grouping variables. Points in the same group and appear on the graph with the same marker and color.

`gscatter(x,y,group,clr,sym,siz)` specifies the color, marker type, and size for each group. *`clr`* is a string array of colors recognized by the `plot` function. *`sym`* is a string array of symbols recognized by the `plot` command, with the default value `'.'`. `siz` is a vector of sizes, with the default determined by the `'DefaultLineMarkerSize'` property. If you do not specify enough values for all groups, `gscatter` cycles through the specified values as needed.

`gscatter(x,y,group,clr,sym,siz,doleg)` controls whether a legend is displayed on the graph (*`doleg`* is `'on'`, the default) or not (*`doleg`* is `'off'`).

`gscatter(x,y,group,clr,sym,siz,doleg,xnam,ynam)` specifies the name to use for the *x*-axis and *y*-axis labels. If the `x` and `y` inputs are simple variable names and `xnam` and `ynam` are omitted, `gscatter` labels the axes with the variable names.

`h = gscatter(...)` returns an array of handles to the lines on the graph.

Examples

Scatter Plot of Climate and Housing Ratings

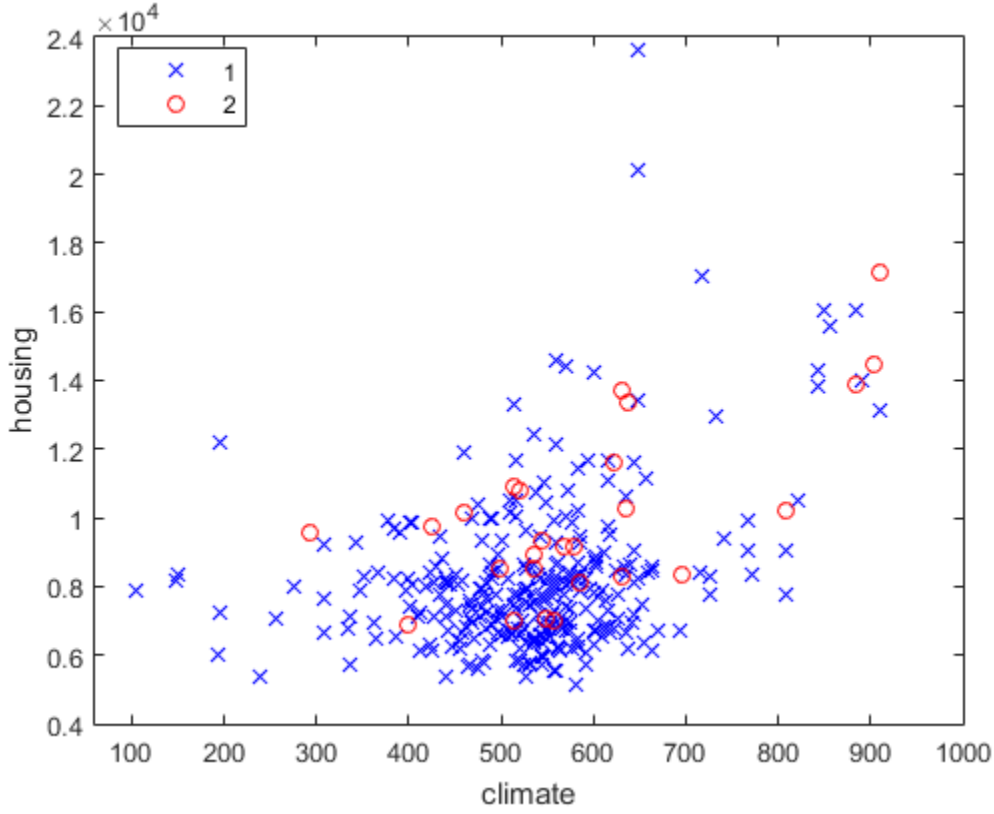
Load the sample data.

```
load discrim
```

The sample data contains ratings of cities according to nine factors such as climate, housing, education, and health in the matrix `ratings` .

Plot the relationship between the ratings for climate (first column) and housing (second column) grouped by city size in the matrix `group`. Choose different colors and plotting symbols for each group.

```
figure;
gscatter(ratings(:,1),ratings(:,2),group,'br','xo')
xlabel('climate');
ylabel('housing');
```



More About

- "Grouping Variables" on page 2-52

See Also

`gplotmatrix` | `grpstats` | `scatter`

gt

Class: qrandstream

Greater than relation for handles

Syntax

```
h1 > h2
```

Description

`h1 > h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise > result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = gt(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `ge` | `le` | `ne` | `eq` | `lt`

haltonset class

Superclasses: qrandset

Halton quasi-random point sets

Description

`haltonset` is a quasi-random point set class that produces points from the Halton sequence.

Construction

.haltonset	Construct Halton quasi-random point set

Methods

Inherited Methods

Methods in the following table are inherited from `qrandset`.

disp	Display qrandset object
end	Last index in indexing expression for point set
length	Length of point set
ndims	Number of dimensions in matrix
net	Generate quasi-random point set
scramble	Scramble quasi-random point set

size	Number of dimensions in matrix
subsref	Subscripted reference for qrandset

Properties

Inherited Properties

Properties in the following table are inherited from `qrandset`.

Dimensions	Number of dimensions
Leap	Interval between points
ScrambleMethod	Settings that control scrambling
Skip	Number of initial points to omit from sequence
Type	Name of sequence on which point set `P` is based

Copy Semantics

Handle. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

References

[1] Kocis, L., and W. J. Whiten, "Computational Investigations of Low-Discrepancy Sequences," ACM Transactions on Mathematical Software, Vol. 23, No. 2, pp. 266-294, 1997.

See Also

`sobolset`

How To

- "Quasi-Random Point Sets" on page 6-17

haltonset

Class: haltonset

Construct Halton quasi-random point set

Syntax

```
p = haltonset(d)
p = haltonset(d,prop1,val1,prop2,val2,...)
```

Description

`p = haltonset(d)` constructs a `d`-dimensional point set `p` of the `haltonset` class, with default property settings.

`p = haltonset(d,prop1,val1,prop2,val2,...)` specifies property name/value pairs used to construct `p`.

The object `p` returned by `haltonset` encapsulates properties of a specified quasi-random sequence. The point set is finite, with a length determined by the `Skip` and `Leap` properties and by limits on the size of point set indices (maximum value of 2^{53}). Values of the point set are not generated and stored in memory until you access `p` using `net` or parenthesis indexing.

Examples

Generate a 3-D Halton point set, skip the first 1000 values, and then retain every 101st point:

```
p = haltonset(3,'Skip',1e3,'Leap',1e2)
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

Use `scramble` to apply reverse-radix scrambling:

```
p = scramble(p,'RR2')
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.0928    0.6950    0.0029
    0.6958    0.2958    0.8269
    0.3013    0.6497    0.4141
    0.9087    0.7883    0.2166
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.0928    0.6950    0.0029
    0.9087    0.7883    0.2166
    0.3843    0.9840    0.9878
    0.6831    0.7357    0.7923
```

References

[1] Kocis, L., and W. J. Whiten. "Computational Investigations of Low-Discrepancy Sequences." *ACM Transactions on Mathematical Software*. Vol. 23, No. 2, 1997, pp. 266–294.

See Also

`net` | `scramble` | `sobolset`

harmmean

Harmonic mean

Syntax

```
m = harmmean(X)
harmmean(X,dim)
```

Description

`m = harmmean(X)` calculates the harmonic mean of a sample. For vectors, `harmmean(x)` is the harmonic mean of the elements in `x`. For matrices, `harmmean(X)` is a row vector containing the harmonic means of each column. For *N*-dimensional arrays, `harmmean` operates along the first nonsingleton dimension of `X`.

`harmmean(X,dim)` takes the harmonic mean along dimension `dim` of `X`.

The harmonic mean is

$$m = \frac{n}{\sum_{i=1}^{n} \frac{1}{x_i}}$$

Examples

The arithmetic mean is greater than or equal to the harmonic mean.

```
x = exprnd(1,10,6);

harmonic = harmmean(x)
harmonic =
  0.3382  0.3200  0.3710  0.0540  0.4936  0.0907

average = mean(x)
average =
```

```
  1.3509   1.1583   0.9741   0.5319   1.0088   0.8122
```

See Also

`mean` | `median` | `geomean` | `trimmean`

hist3

Bivariate histogram

Syntax

```
hist3(X)
hist3(X,nbins)
hist3(X,ctrs)
hist3(X,'Edges',edges)
N = hist3(X,...)
[N,C] = hist3(X,...)
hist3(...,param1,val1,param2,val2,...)
```

Description

`hist3(X)` bins the elements of the *m*-by-2 matrix `X` into a 10-by-10 grid of equally spaced containers, and plots a histogram. Each column of **`X`** corresponds to one dimension in the bin grid.

`hist3(X,nbins)` plots a histogram using an `nbins(1)`-by-`nbins(2)` grid of bins. `hist3(X,'Nbins',nbins)` is equivalent to `hist3(X,nbins)`.

`hist3(X,ctrs)`, where `ctrs` is a two-element cell array of numeric vectors with monotonically non-decreasing values, uses a 2-D grid of bins centered on `ctrs{1}` in the first dimension and on `ctrs{2}` in the second. `hist3` assigns rows of `X` falling outside the range of that grid to the bins along the outer edges of the grid, and ignores rows of `X` containing `NaN`s. `hist3(X,'Ctrs',ctrs)` is equivalent to `hist3(X,ctrs)`.

`hist3(X,'Edges',edges)`, where `edges` is a two-element cell array of numeric vectors with monotonically non-decreasing values, uses a 2-D grid of bins with edges at `edges{1}` in the first dimension and at `edges{2}` in the second. The (*i*, *j*)th bin includes the value `X(k,:)` if

```
edges{1}(i) <= X(k,1) < edges{1}(i+1)
edges{2}(j) <= X(k,2) < edges{2}(j+1)
```

Rows of `X` that fall on the upper edges of the grid, `edges{1}(end)` or `edges{2}(end)`, are counted in the `(I,j)`th or `(i,J)`th bins, where `I` and `J` are the lengths of `edges{1}` and `edges{2}`. `hist3` does not count rows of `X` falling outside the range of the grid. Use `-Inf` and `Inf` in `edges` to include all non-`NaN` values.

`N = hist3(X,...)` returns a matrix containing the number of elements of `X` that fall in each bin of the grid, and does not plot the histogram.

`[N,C] = hist3(X,...)` returns the positions of the bin centers in a 1-by-2 cell array of numeric vectors, and does not plot the histogram. `hist3(ax,X,...)` plots onto an `axes` with handle `ax` instead of the current `axes`. See the `axes` reference page for more information about handles to plots.

`hist3(...,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` allows you to specify graphics parameter name/value pairs to fine-tune the plot.

Examples

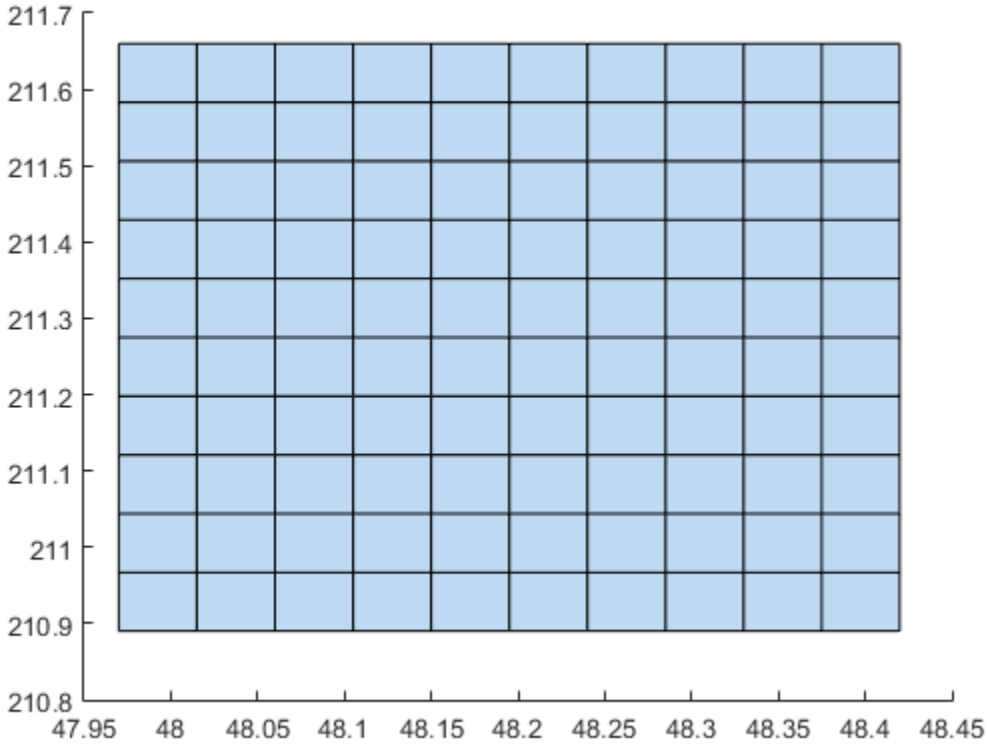
Plot Density Histogram with Intensity Map

Load the sample data.

```
load seamount
```

Correct grid for negative y-values and draw histogram in 2D.

```
hold on
dat = [-y,x];
hist3(dat)
```



Extract histogram data.

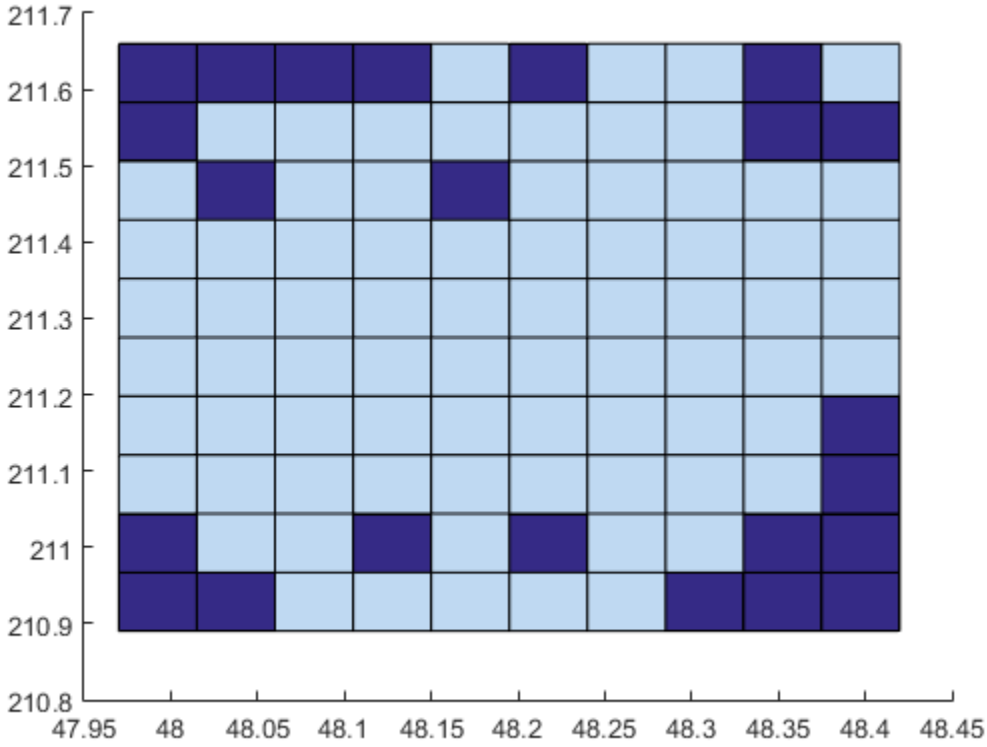
```
n = hist3(dat); % default is to 10x10 bins
n1 = n';
n1(size(n,1) + 1, size(n,2) + 1) = 0;
```

Generate grid for 2-D projected view of intensities.

```
xb = linspace(min(dat(:,1)),max(dat(:,1)),size(n,1)+1);
yb = linspace(min(dat(:,2)),max(dat(:,2)),size(n,1)+1);
```

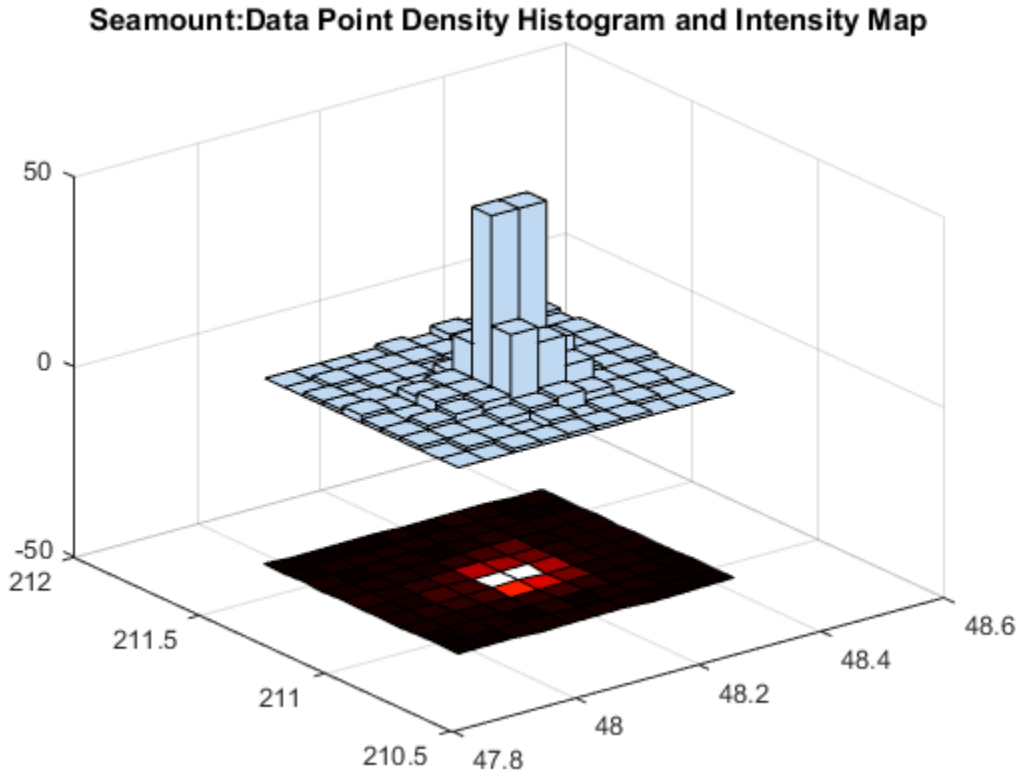
Make a pseudocolor plot.

```
h = pcolor(xb,yb,n1);
```



Set the z-level and colormap of the displayed grid, and display the default 3-D perspective view.

```
h.ZData = ones(size(n1)) * -max(max(n));
colormap(hot) % heat map
title('Seamount:Data Point Density Histogram and Intensity Map');
grid on
view(3);
```



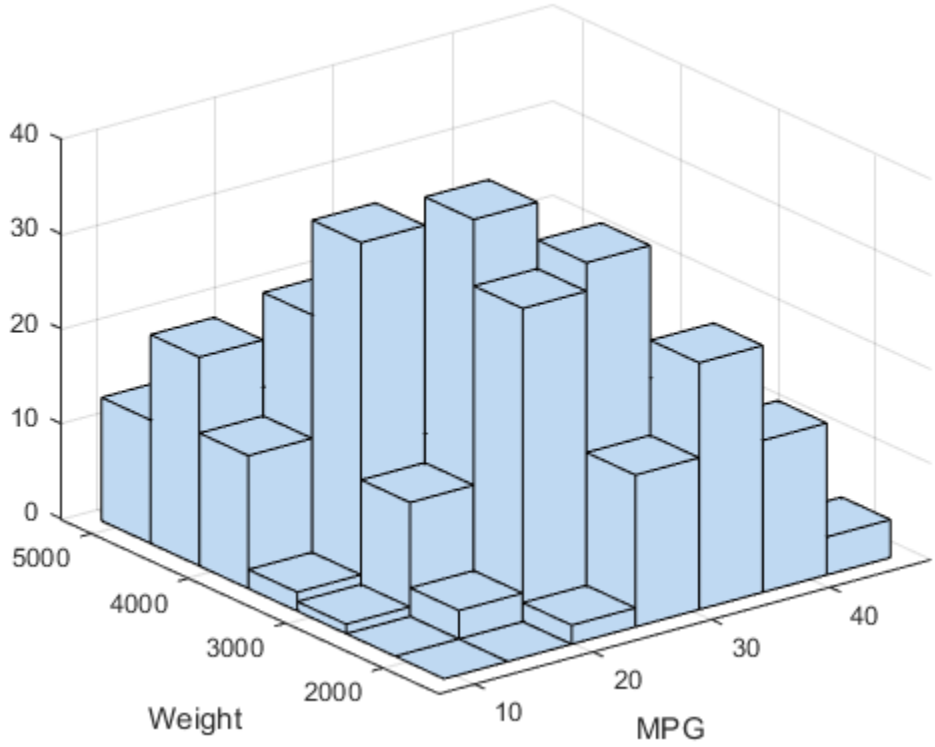
Histogram with Semi-Transparent Bars

Load the sample data.

```
load carbig
```

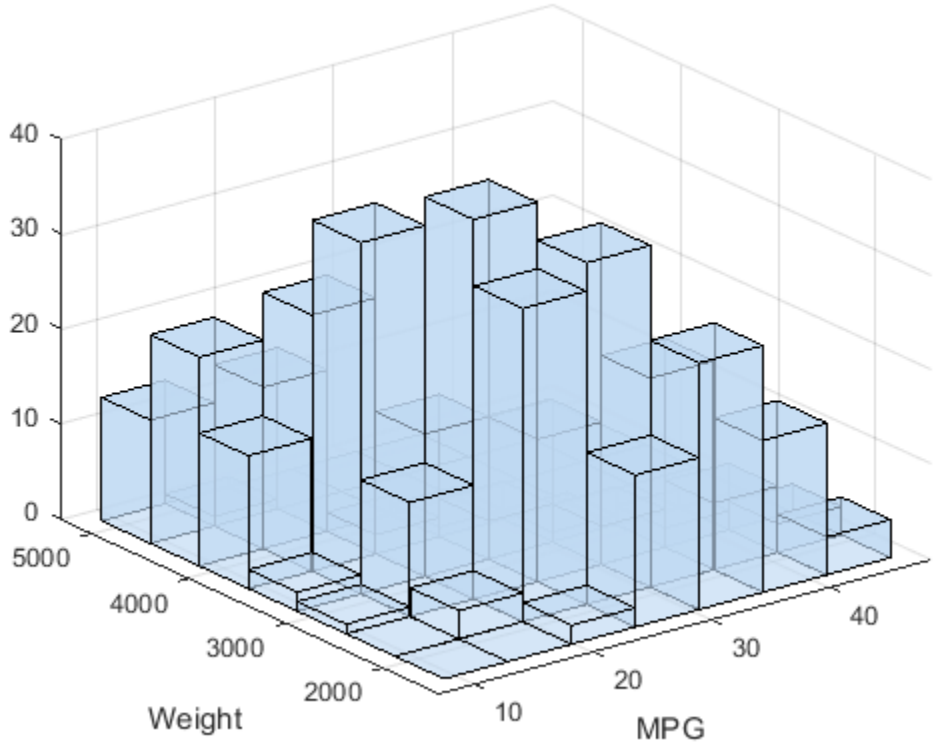
Use the data to make histogram on a 7-by-7 grid of bins.

```
X = [MPG,Weight];
hist3(X,[7 7]);
xlabel('MPG'); ylabel('Weight');
```



Make a histogram with semi-transparent bars.

```
hist3(X,[7 7],'FaceAlpha',.65);
xlabel('MPG'); ylabel('Weight');
set(gcf,'renderer','opengl');
```



Specify bin centers, different in each direction; get back counts, but don't make the plot.

```
cnt = hist3(X, {0:10:50 2000:500:5000});
```

Histogram Bars Colored According to Height

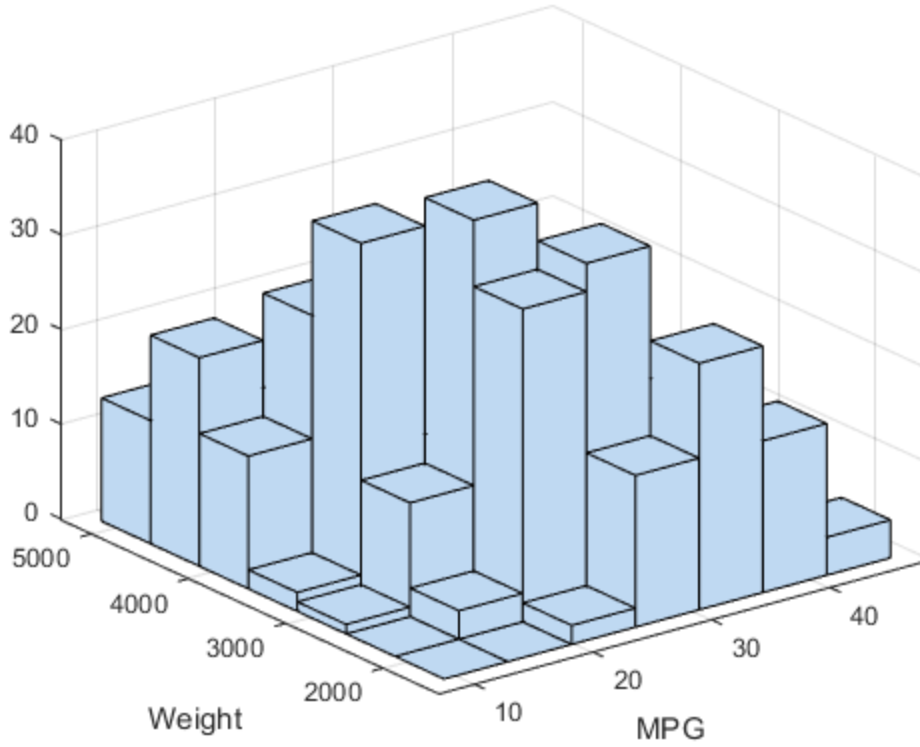
Load the sample data.

```
load carbig
```

Make a histogram on a 7-by-7 grid of bins.

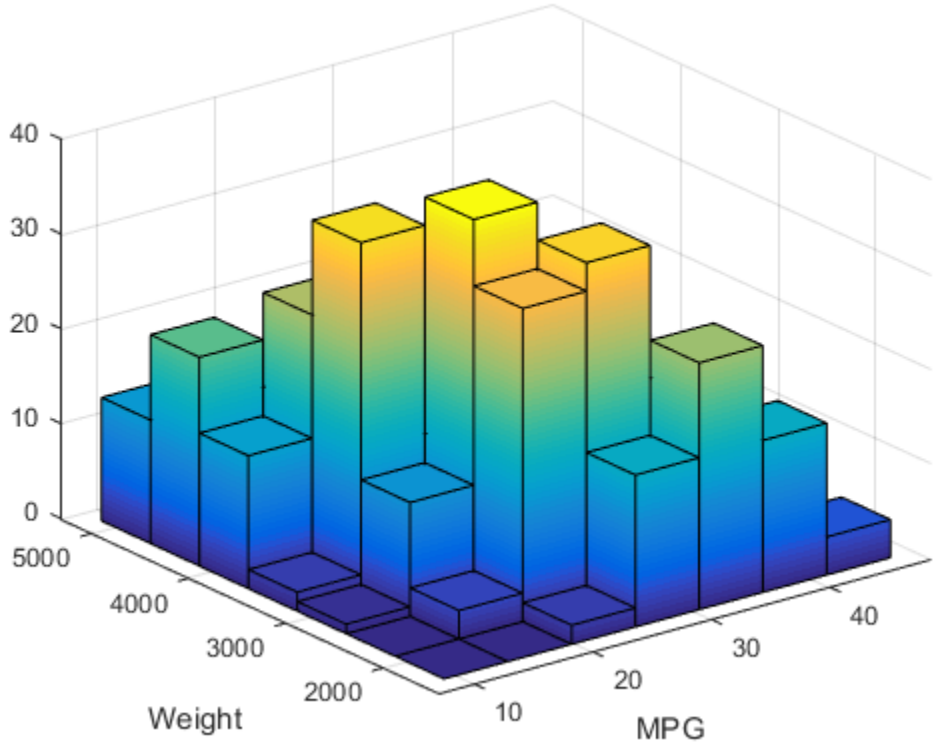
```
X = [MPG,Weight];
hist3(X,[7 7]);
```

```
xlabel('MPG'); ylabel('Weight');
set(gcf,'renderer','opengl');
```



Color the bars based on the frequency of the observations, i.e. according to the height of the bars.

```
set(get(gca,'child'),'FaceColor','interp','CDataMode','auto');
```



See Also

`accumarray` | `histc` | `bar` | `bar3` | `histogram`

histfit

Histogram with a distribution fit

Syntax

```
histfit(data)
histfit(data,nbins)
histfit(data,nbins,dist)

h = histfit( ___ )
```

Description

`histfit(data)` plots a histogram of values in `data` using the number of bins equal to the square root of the number of elements in `data` and fits a normal density function.

`histfit(data,nbins)` plots a histogram using `nbins` bins and fits a normal density function.

`histfit(data,nbins,dist)` plots a histogram with `nbins` bins and fits a density function from the distribution specified by `dist`.

`h = histfit( ___ )` returns a vector of handles `h`, where `h(1)` is the handle to the histogram and `h(2)` is the handle to the density curve. It can include any of the input arguments in previous syntaxes.

Examples

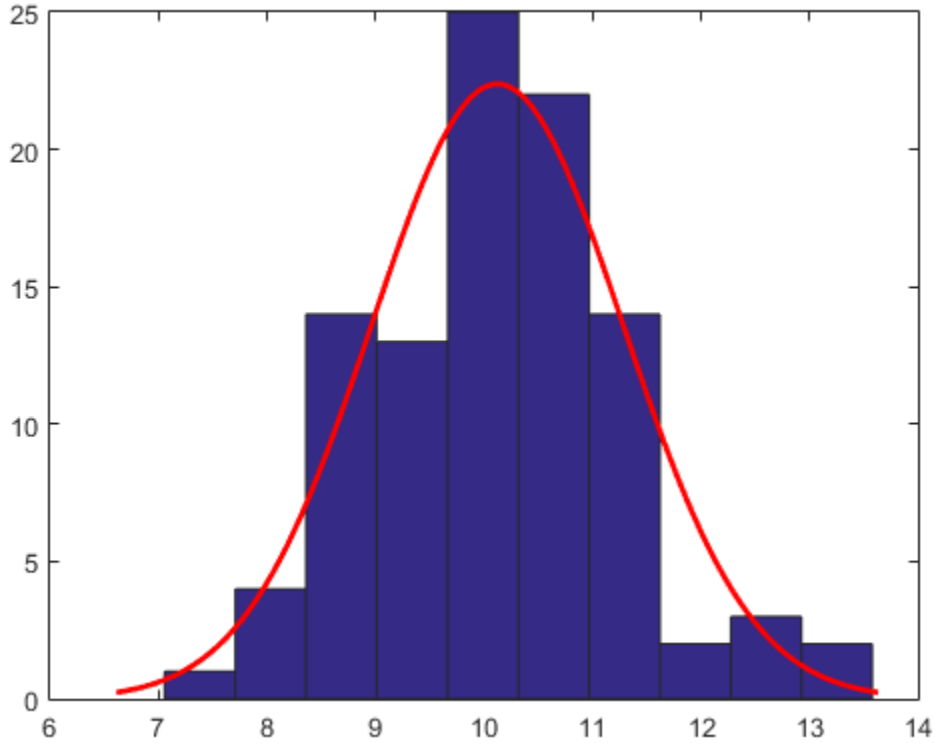
Histogram with a Normal Distribution Fit

Generate a sample of size 100 from a normal distribution with mean 10 and variance 1.

```
rng default; % For reproducibility
r = normrnd(10,1,100,1);
```

Construct a histogram with a normal distribution fit.

```
histfit(r)
```



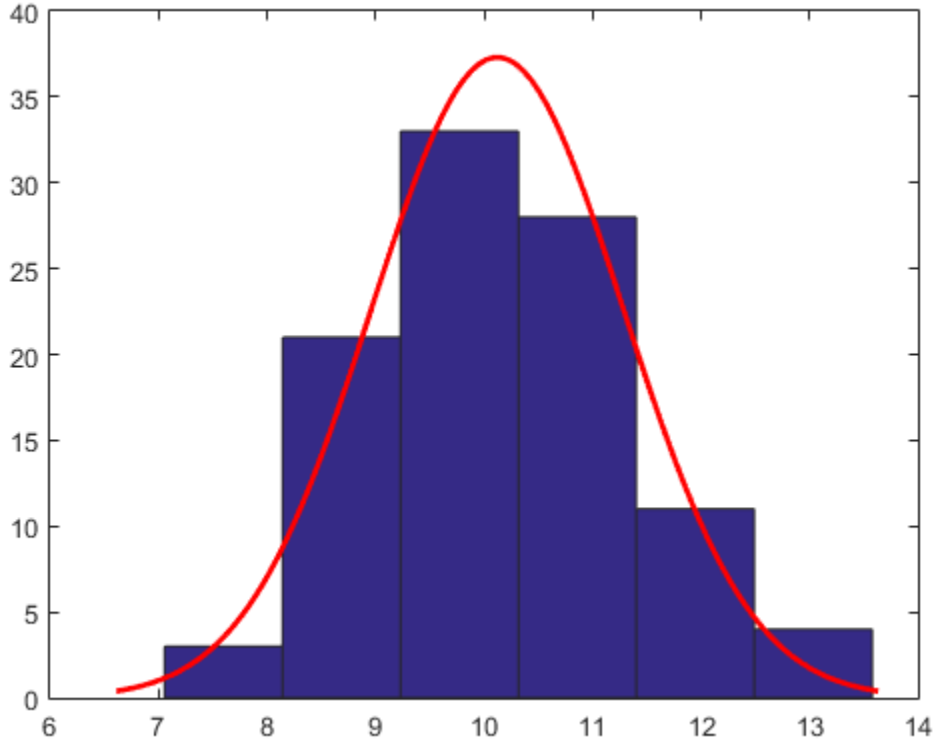
Histogram for a Given Number of Bins

Generate a sample of size 100 from a normal distribution with mean 10 and variance 1.

```
rng default; % For reproducibility
r = normrnd(10,1,100,1);
```

Construct a histogram using six bins with a normal distribution fit.

```
histfit(r,6)
```



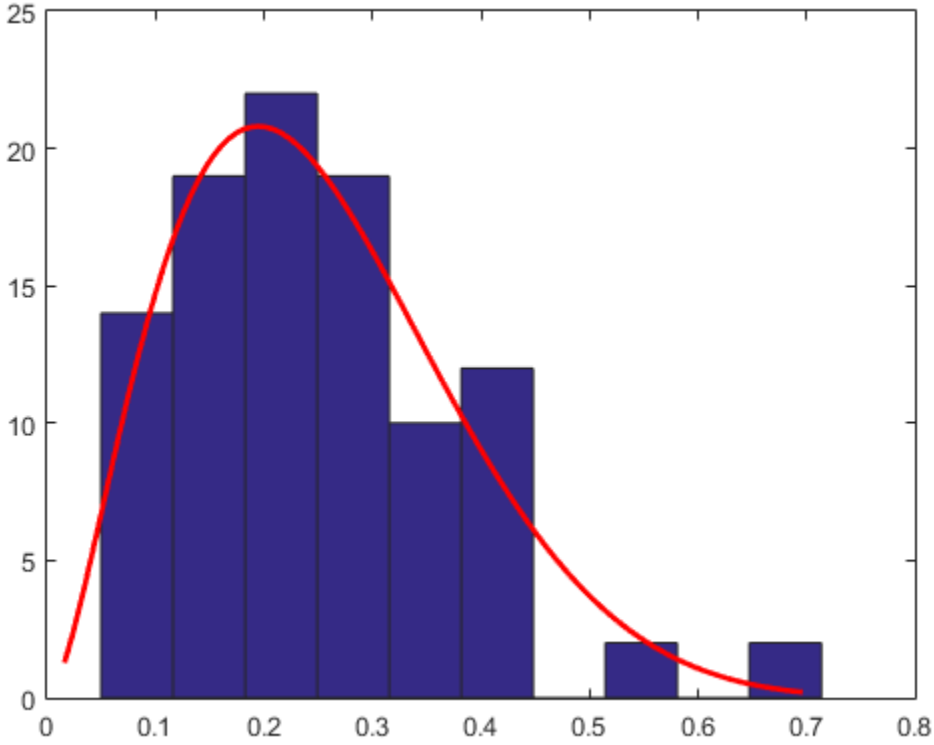
Histogram with a Specified Distribution Fit

Generate a sample of size 100 from a beta distribution with parameters (3,10).

```
rng default;  % For reproducibility
b = betarnd(3,10,100,1);
```

Construct a histogram using 10 bins with a beta distribution fit.

```
histfit(b,10,'beta')
```



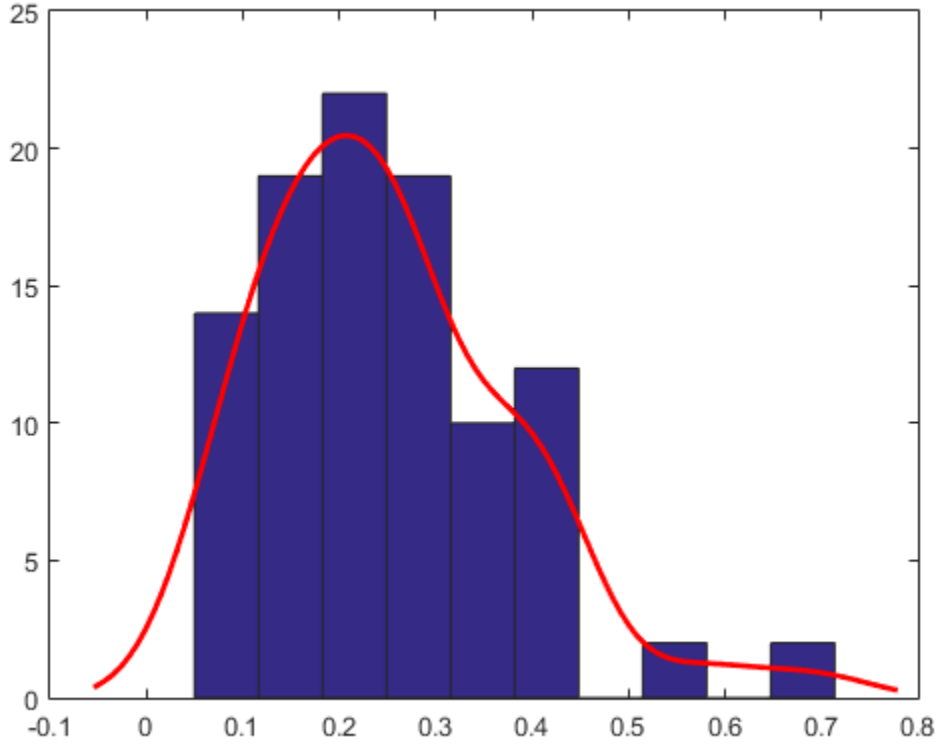
Histogram with a Kernel Smoothing Function Fit

Generate a sample of size 100 from a beta distribution with parameters (3,10).

```
rng default;  % For reproducibility
b = betarnd(3,10,[100,1]);
```

Construct a histogram using 10 bins with a smoothing function fit.

```
histfit(b,10,'kernel')
```



Handle for a Histogram with a Distribution Fit

Generate a sample of size 100 from a normal distribution with mean 10 and variance 1.

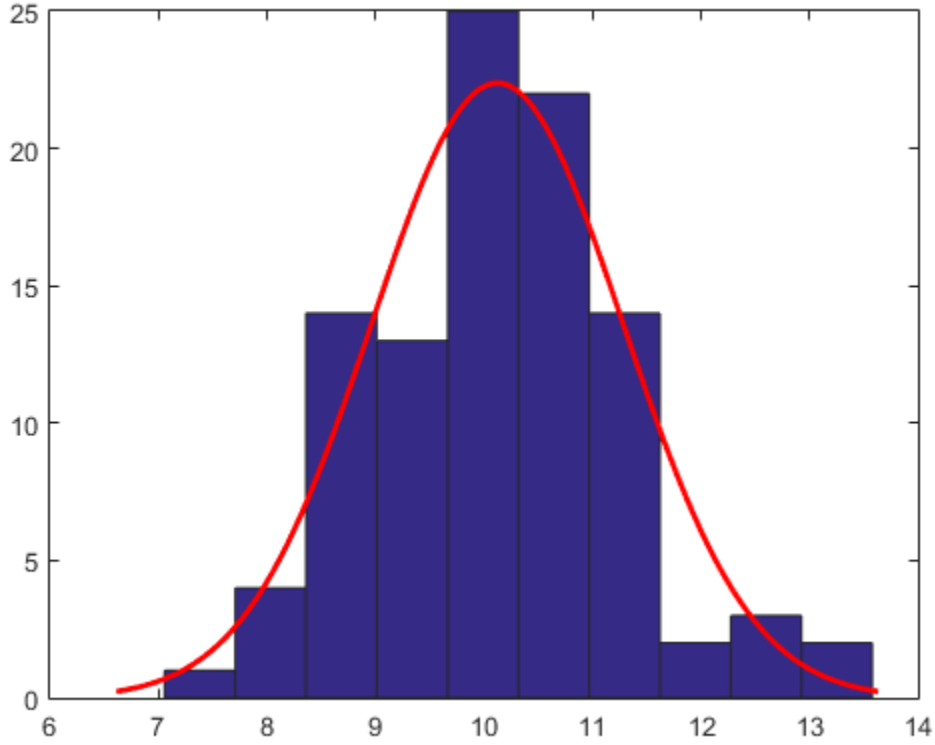
```
rng default % for reproducibility
r = normrnd(10,1,100,1);
```

Construct a histogram with a normal distribution fit.

```
h = histfit(r,10,'normal')
```

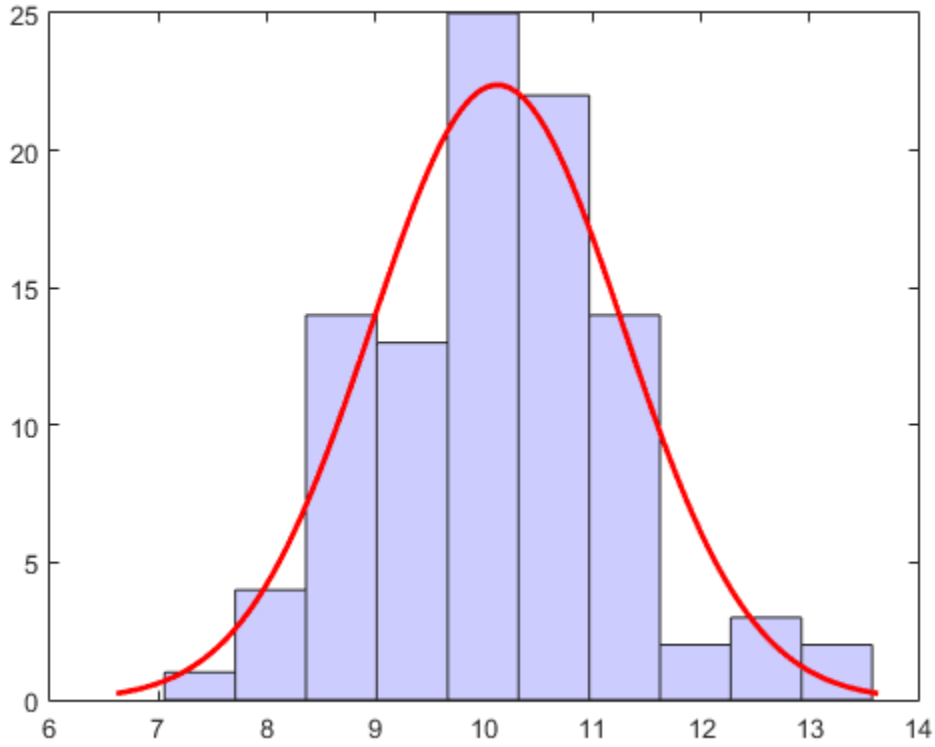
```
h =
```

```
2x1 graphics array:

Patch
Line
```



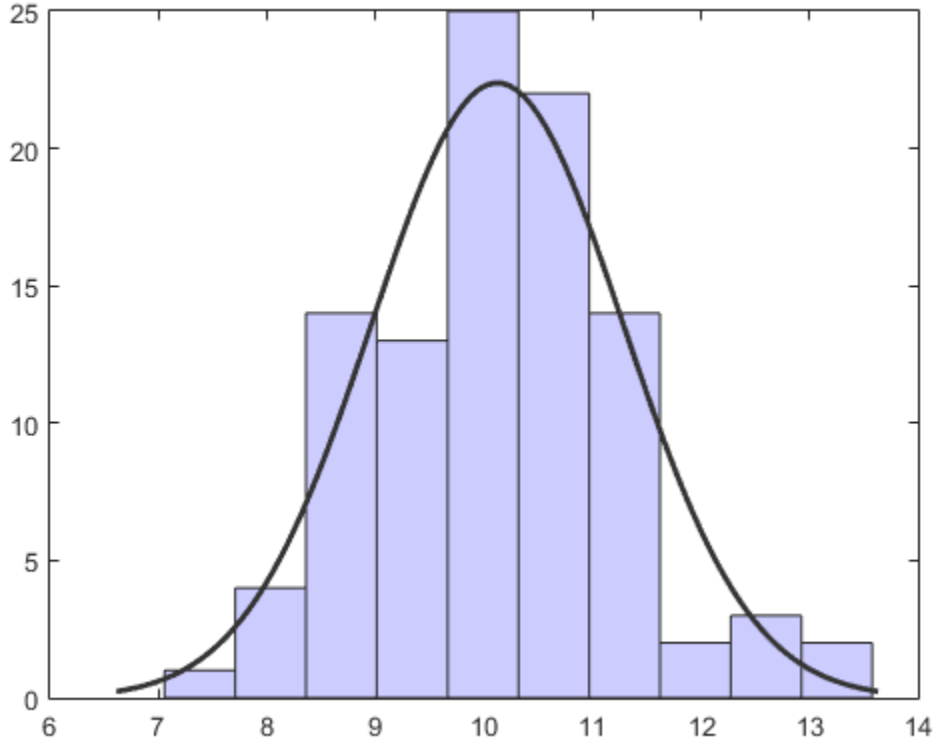
Change the bar colors of the histogram.

```
h(1).FaceColor = [.8 .8 1];
```



Change the color of the density curve.

```
h(2).Color = [.2 .2 .2];
```



Input Arguments

`data` — Input data

vector

Input data, specified as a vector.

Example: `data = [1.5 2.5 4.6 1.2 3.4]`

Example: `data = [1.5 2.5 4.6 1.2 3.4]'`

Data Types: `double` | `single`

`nbins` — Number of bins

positive integer | [ ]

Number of bins for the histogram, specified as a positive integer. Default value is the square root of the number of elements in `data`, rounded up. Use [ ] for the default number of bins when fitting a distribution.

Example: y = histfit(x,8)

Example: y = histfit(x,10,'gamma')

Example: y = histfit(x,[ ],'weibull')

Data Types: `double | single`

`dist` — Distribution to fit

`'normal'` (default) | string

Distribution to fit to the histogram, specified as a string. The following table shows the supported distributions.

`dist`	Description
`'beta'`	Beta
`'birnbaumsaunders'`	Birnbaum-Saunders
`'burr'`	Burr Type XII
`'exponential'`	Exponential
`'extreme value'` or `'ev'`	Extreme value
`'gamma'`	Gamma
`'generalized extreme value'` or `'gev'`	Generalized extreme value
`'generalized pareto'` or `'gp'`	Generalized Pareto (threshold 0)
`'inversegaussian'`	Inverse Gaussian
`'logistic'`	Logistic
`'loglogistic'`	Loglogistic
`'lognormal'`	Lognormal
`'nakagami'`	Nakagami
`'negative binomial'` or `'nbin'`	Negative binomial

dist	Description
'normal'	Normal
'poisson'	Poisson
'rayleigh'	Rayleigh
'rician'	Rician
'tlocationscale'	t location-scale
'weibull' or 'wbl'	Weibull
'kernel'	Nonparametric kernel-smoothing distribution. The density is evaluated at 100 equally spaced points that cover the range of the data in data. It works best with continuously distributed samples.

Data Types: char

Output Arguments

h — Handles for the plot
plot handle

Handles for the plot, returned as a vector, where h(1) is the handle to the histogram, and h(2) is the handle to the density curve.

See Also
dfittool | histogram | normfit

hmmdecode

Hidden Markov model posterior state probabilities

Syntax

```
PSTATES = hmmdecode(seq,TRANS,EMIS)
[PSTATES,logpseq] = hmmdecode(...)
[PSTATES,logpseq,FORWARD,BACKWARD,S] = hmmdecode(...)
hmmdecode(...,'Symbols',SYMBOLS)
```

Description

`PSTATES = hmmdecode(seq,TRANS,EMIS)` calculates the posterior state probabilities, `PSTATES`, of the sequence `seq`, from a hidden Markov model. The posterior state probabilities are the conditional probabilities of being at state k at step i, given the observed sequence of symbols, `sym`. You specify the model by a transition probability matrix, `TRANS`, and an emissions probability matrix, `EMIS`. `TRANS(i,j)` is the probability of transition from state `i` to state `j`. `EMIS(k,seq)` is the probability that symbol `seq` is emitted from state `k`.

`PSTATES` is an array with the same length as `seq` and one row for each state in the model. The (i, j)th element of `PSTATES` gives the probability that the model is in state i at the jth step, given the sequence `seq`.

Note The function `hmmdecode` begins with the model in state 1 at step 0, prior to the first emission. `hmmdecode` computes the probabilities in `PSTATES` based on the fact that the model begins in state 1.

`[PSTATES,logpseq] = hmmdecode(...)` returns `logpseq`, the logarithm of the probability of sequence `seq`, given transition matrix `TRANS` and emission matrix `EMIS`.

`[PSTATES,logpseq,FORWARD,BACKWARD,S] = hmmdecode(...)` returns the forward and backward probabilities of the sequence scaled by `S`.

`hmmdecode(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

Examples

```
trans = [0.95,0.05;
         0.10,0.90];
emis = [1/6 1/6 1/6 1/6 1/6 1/6;
   1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(100,trans,emis);
pStates = hmmdecode(seq,trans,emis);
[seq,states] = hmmgenerate(100,trans,emis,...
   'Symbols',{'one','two','three','four','five','six'})
pStates = hmmdecode(seq,trans,emis,...
   'Symbols',{'one','two','three','four','five','six'});
```

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

See Also

`hmmgenerate` | `hmmestimate` | `hmmviterbi` | `hmmtrain`

hmmestimate

Hidden Markov model parameter estimates from emissions and states

Syntax

```
[TRANS,EMIS] = hmmestimate(seq,states)
hmmestimate(...,'Symbols',SYMBOLS)
hmmestimate(...,'Statenames',STATENAMES)
hmmestimate(...,'Pseudoemissions',PSEUDOE)
hmmestimate(...,'Pseudotransitions',PSEUDOTR)
```

Description

`[TRANS,EMIS] = hmmestimate(seq,states)` calculates the maximum likelihood estimate of the transition, `TRANS`, and emission, `EMIS`, probabilities of a hidden Markov model for sequence, `seq`, with known states, `states`.

`hmmestimate(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers 1 through N, where N is the number of possible emissions.

`hmmestimate(...,'Statenames',STATENAMES)` specifies the names of the states. `STATENAMES` can be a numeric array or a cell array of the names of the states. The default state names are 1 through `M`, where `M` is the number of states.

`hmmestimate(...,'Pseudoemissions',PSEUDOE)` specifies pseudocount emission values in the matrix `PSEUDO`. Use this argument to avoid zero probability estimates for emissions with very low probability that might not be represented in the sample sequence. `PSEUDOE` should be a matrix of size m-by-n, where m is the number of states in the hidden Markov model and n is the number of possible emissions. If the $i \to k$ emission does not occur in `seq`, you can set `PSEUDOE(i,k)` to be a positive number representing an estimate of the expected number of such emissions in the sequence `seq`.

`hmmestimate(...,'Pseudotransitions',PSEUDOTR)` specifies pseudocount transition values. You can use this argument to avoid zero probability estimates for transitions with very low probability that might not be represented in the sample sequence. `PSEUDOTR` should be a matrix of size m-by-m, where m is the number of states

in the hidden Markov model. If the $i \to j$ transition does not occur in `states`, you can set `PSEUDOTR(i,j)` to be a positive number representing an estimate of the expected number of such transitions in the sequence `states`.

Pseudotransitions and Pseudoemissions

If the probability of a specific transition or emission is very low, the transition might never occur in the sequence `states`, or the emission might never occur in the sequence `seq`. In either case, the algorithm returns a probability of 0 for the given transition or emission in `TRANS` or `EMIS`. You can compensate for the absence of transition with the `'Pseudotransitions'` and `'Pseudoemissions'` arguments. The simplest way to do this is to set the corresponding entry of `PSEUDO` or `PSEUDOTR` to `1`. For example, if the transition $i \to j$ does not occur in `states`, set `PSEUOTR(i,j) = 1`. This forces `TRANS(i,j)` to be positive. If you have an estimate for the expected number of transitions $i \to j$ in a sequence of the same length as `states`, and the actual number of transitions $i \to j$ that occur in `seq` is substantially less than what you expect, you can set `PSEUOTR(i,j)` to the expected number. This increases the value of `TRANS(i,j)`. For transitions that do occur in states with the frequency you expect, set the corresponding entry of `PSEUDOTR` to `0`, which does not increase the corresponding entry of `TRANS`.

If you do not know the sequence of states, use `hmmtrain` to estimate the model parameters.

Examples

```
trans = [0.95,0.05; 0.10,0.90];
emis = [1/6 1/6 1/6 1/6 1/6 1/6;
   1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(1000,trans,emis);
[estimateTR,estimateE] = hmmestimate(seq,states);
```

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

See Also

`hmmgenerate` | `hmmdecode` | `hmmviterbi` | `hmmtrain`

hmmgenerate

Hidden Markov model states and emissions

Syntax

```
[seq,states] = hmmgenerate(len,TRANS,EMIS)
hmmgenerate(...,'Symbols',SYMBOLS)
hmmgenerate(...,'Statenames',STATENAMES)
```

Description

`[seq,states] = hmmgenerate(len,TRANS,EMIS)` takes a known Markov model, specified by transition probability matrix `TRANS` and emission probability matrix `EMIS`, and uses it to generate

- A random sequence `seq` of emission symbols
- A random sequence `states` of states

The length of both `seq` and `states` is `len`. `TRANS(i,j)` is the probability of transition from state `i` to state `j`. `EMIS(k,l)` is the probability that symbol `l` is emitted from state `k`.

Note The function `hmmgenerate` begins with the model in state 1 at step 0, prior to the first emission. The model then makes a transition to state i_1, with probability T_{1i_1}, and generates an emission a_{k_1} with probability $E_{i_1k_1}$. `hmmgenerate` returns i_1 as the first entry of `states`, and a_{k_1} as the first entry of `seq`.

`hmmgenerate(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

`hmmgenerate(...,'Statenames',STATENAMES)` specifies the names of the states. `STATENAMES` can be a numeric array or a cell array of the names of the states. The default state names are `1` through `M`, where `M` is the number of states.

Since the model always begins at state 1, whose transition probabilities are in the first row of TRANS, in the following example, the first entry of the output `states` is be 1 with probability 0.95 and 2 with probability 0.05.

Examples

```
 trans = [0.95,0.05;
          0.10,0.90];
 emis = [1/6 1/6 1/6 1/6 1/6 1/6;
    1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(100,trans,emis)
[seq,states] = hmmgenerate(100,trans,emis,...
    'Symbols',{'one','two','three','four','five','six'},...
    'Statenames',{'fair';'loaded'})
```

See Also

`hmmviterbi` | `hmmdecode` | `hmmestimate` | `hmmtrain`

hmmtrain

Hidden Markov model parameter estimates from emissions

Syntax

```
[ESTTR,ESTEMIT] = hmmtrain(seq,TRGUESS,EMITGUESS)
hmmtrain(...,'Algorithm',algorithm)
hmmtrain(...,'Symbols',SYMBOLS)
hmmtrain(...,'Tolerance',tol)
hmmtrain(...,'Maxiterations',maxiter)
hmmtrain(...,'Verbose',true)
hmmtrain(...,'Pseudoemissions',PSEUDOE)
hmmtrain(...,'Pseudotransitions',PSEUDOTR)
```

Description

`[ESTTR,ESTEMIT] = hmmtrain(seq,TRGUESS,EMITGUESS)` estimates the transition and emission probabilities for a hidden Markov model using the Baum-Welch algorithm. `seq` can be a row vector containing a single sequence, a matrix with one row per sequence, or a cell array with each cell containing a sequence. `TRGUESS` and `EMITGUESS` are initial estimates of the transition and emission probability matrices. `TRGUESS(i,j)` is the estimated probability of transition from state `i` to state `j`. `EMITGUESS(i,k)` is the estimated probability that symbol `k` is emitted from state `i`.

`hmmtrain(...,'Algorithm',algorithm)` specifies the training algorithm. *`algorithm`* can be either `'BaumWelch'` or `'Viterbi'`. The default algorithm is `'BaumWelch'`.

`hmmtrain(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

`hmmtrain(...,'Tolerance',tol)` specifies the tolerance used for testing convergence of the iterative estimation process. The default tolerance is `1e-4`.

`hmmtrain(...,'Maxiterations',maxiter)` specifies the maximum number of iterations for the estimation process. The default maximum is `100`.

`hmmtrain(...,'Verbose',true)` returns the status of the algorithm at each iteration.

`hmmtrain(...,'Pseudoemissions',PSEUDOE)` specifies pseudocount emission values for the Viterbi training algorithm. Use this argument to avoid zero probability estimates for emissions with very low probability that might not be represented in the sample sequence. `PSEUDOE` should be a matrix of size m-by-n, where m is the number of states in the hidden Markov model and n is the number of possible emissions. If the $i \rightarrow k$ emission does not occur in `seq`, you can set `PSEUDOE(i,k)` to be a positive number representing an estimate of the expected number of such emissions in the sequence `seq`.

`hmmtrain(...,'Pseudotransitions',PSEUDOTR)` specifies pseudocount transition values for the Viterbi training algorithm. Use this argument to avoid zero probability estimates for transitions with very low probability that might not be represented in the sample sequence. `PSEUDOTR` should be a matrix of size m-by-m, where m is the number of states in the hidden Markov model. If the $i \rightarrow j$ transition does not occur in `states`, you can set `PSEUDOTR(i,j)` to be a positive number representing an estimate of the expected number of such transitions in the sequence `states`.

If you know the states corresponding to the sequences, use `hmmestimate` to estimate the model parameters.

Tolerance

The input argument `'tolerance'` controls how many steps the `hmmtrain` algorithm executes before the function returns an answer. The algorithm terminates when all of the following three quantities are less than the value that you specify for `tolerance`:

- The log likelihood that the input sequence `seq` is generated by the currently estimated values of the transition and emission matrices
- The change in the norm of the transition matrix, normalized by the size of the matrix
- The change in the norm of the emission matrix, normalized by the size of the matrix

The default value of `'tolerance'` is `.0001`. Increasing the tolerance decreases the number of steps the `hmmtrain` algorithm executes before it terminates.

maxiterations

The maximum number of iterations, `'maxiterations'`, controls the maximum number of steps the algorithm executes before it terminates. If the algorithm

executes `maxiter` iterations before reaching the specified tolerance, the algorithm terminates and the function returns a warning. If this occurs, you can increase the value of `'maxiterations'` to make the algorithm reach the desired tolerance before terminating.

Examples

```
trans = [0.95,0.05;
      0.10,0.90];
emis = [1/6, 1/6, 1/6, 1/6, 1/6, 1/6;
   1/10, 1/10, 1/10, 1/10, 1/10, 1/2];

seq1 = hmmgenerate(100,trans,emis);
seq2 = hmmgenerate(200,trans,emis);
seqs = {seq1,seq2};
[estTR,estE] = hmmtrain(seqs,trans,emis);
```

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

See Also

`hmmgenerate` | `hmmdecode` | `hmmestimate` | `hmmviterbi`

hmmviterbi

Hidden Markov model most probable state path

Syntax

```
STATES = hmmviterbi(seq,TRANS,EMIS)
hmmviterbi(...,'Symbols',SYMBOLS)
hmmviterbi(...,'Statenames',STATENAMES)
```

Description

`STATES = hmmviterbi(seq,TRANS,EMIS)` given a sequence, `seq`, calculates the most likely path through the hidden Markov model specified by transition probability matrix, `TRANS`, and emission probability matrix `EMIS`. `TRANS(i,j)` is the probability of transition from state `i` to state `j`. `EMIS(i,k)` is the probability that symbol `k` is emitted from state `i`.

Note The function `hmmviterbi` begins with the model in state 1 at step 0, prior to the first emission. `hmmviterbi` computes the most likely path based on the fact that the model begins in state 1.

`hmmviterbi(...,'Symbols',SYMBOLS)` specifies the symbols that are emitted. `SYMBOLS` can be a numeric array or a cell array of the names of the symbols. The default symbols are integers `1` through `N`, where `N` is the number of possible emissions.

`hmmviterbi(...,'Statenames',STATENAMES)` specifies the names of the states. `STATENAMES` can be a numeric array or a cell array of the names of the states. The default state names are 1 through `M`, where `M` is the number of states.

Examples

```
trans = [0.95,0.05;
         0.10,0.90];
```

```
emis = [1/6 1/6 1/6 1/6 1/6 1/6;
   1/10 1/10 1/10 1/10 1/10 1/2];

[seq,states] = hmmgenerate(100,trans,emis);
estimatedStates = hmmviterbi(seq,trans,emis);

[seq,states] = ...
   hmmgenerate(100,trans,emis,...
               'Statenames',{'fair';'loaded'});
estimatesStates = ...
   hmmviterbi(seq,trans,emis,...
              'Statenames',{'fair';'loaded'});
```

References

[1] Durbin, R., S. Eddy, A. Krogh, and G. Mitchison. *Biological Sequence Analysis*. Cambridge, UK: Cambridge University Press, 1998.

See Also

`hmmgenerate` | `hmmdecode` | `hmmestimate` | `hmmtrain`

horzcat

Class: dataset

Horizontal concatenation for dataset arrays

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds = horzcat(ds1, ds2, ...)
```

Description

`ds = horzcat(ds1, ds2, ...)` horizontally concatenates the dataset arrays `ds1, ds2, ...` . You may concatenate dataset arrays that have duplicate variable names, however, the variables must contain identical data, and `horzcat` includes only one copy of the variable in the output dataset.

Observation names for all dataset arrays that have them must be identical except for order. `horzcat` concatenates by matching observation names when present, or by position for datasets that do not have observation names.

See Also

`cat` | `vertcat`

hougen

Hougen-Watson model

Syntax

```
yhat = hougen(beta,x)
```

Description

`yhat = hougen(beta,x)` returns the predicted values of the reaction rate, `yhat`, as a function of the vector of parameters, `beta`, and the matrix of data, `X`. `beta` must have 5 elements and `X` must have three columns.

`hougen` is a utility function for `rsmdemo`.

The model form is:

$$\hat{y} = \frac{\beta_1 x_2 - x_3 \,/\, \beta_5}{1 + \beta_2 x_1 + \beta_3 x_2 + \beta_4 x_3}$$

References

[1] Bates, D. M., and D. G. Watts. *Nonlinear Regression Analysis and Its Applications*. Hoboken, NJ: John Wiley & Sons, Inc., 1988.

See Also

`rsmdemo`

hygecdf

Hypergeometric cumulative distribution function

Syntax

```
hygecdf(x,M,K,N)
hygecdf(x,M,K,N,'upper')
```

Description

`hygecdf(x,M,K,N)` computes the hypergeometric cdf at each of the values in `x` using the corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. Vector or matrix inputs for `x`, `M`, `K`, and `N` must all have the same size. A scalar input is expanded to a constant matrix with the same dimensions as the other inputs.

`hygecdf(x,M,K,N,'upper')` returns the complement of the hypergeometric cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The hypergeometric cdf is

$$p = F(x \mid M,K,N) = \sum_{i=0}^{x} \frac{\binom{K}{i}\binom{M-K}{N-i}}{\binom{M}{N}}$$

The result, p, is the probability of drawing up to x of a possible K items in N drawings without replacement from a group of M objects.

Examples

Compute Hypergeometric Distribution CDF

Suppose you have a lot of 100 floppy disks and you know that 20 of them are defective. What is the probability of drawing zero to two defective floppies if you select 10 at random?

```
p = hygecdf(2,100,20,10)
```

```
p =
  0.6812
```

See Also

`cdf` | `hygepdf` | `hygeinv` | `hygestat` | `hygernd`

hygeinv

Hypergeometric inverse cumulative distribution function

Syntax

```
hygeinv(P,M,K,N)
```

Description

`hygeinv(P,M,K,N)` returns the smallest integer `X` such that the hypergeometric cdf evaluated at `X` equals or exceeds `P`. You can think of `P` as the probability of observing `X` defective items in `N` drawings without replacement from a group of `M` items where `K` are defective.

Examples

Suppose you are the Quality Assurance manager for a floppy disk manufacturer. The production line turns out floppy disks in batches of 1,000. You want to sample 50 disks from each batch to see if they have defects. You want to accept 99% of the batches if there are no more than 10 defective disks in the batch. What is the maximum number of defective disks should you allow in your sample of 50?

```
x = hygeinv(0.99,1000,10,50)
x =
   3
```

What is the median number of defective floppy disks in samples of 50 disks from batches with 10 defective disks?

```
x = hygeinv(0.50,1000,10,50)
x =
   0
```

See Also

`icdf` | `hygecdf` | `hygepdf` | `hygestat` | `hygernd`

hygepdf

Hypergeometric probability density function

Syntax

```
Y = hygepdf(X,M,K,N)
```

Description

`Y = hygepdf(X,M,K,N)` computes the hypergeometric pdf at each of the values in `X` using the corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. `X`, `M`, `K`, and `N` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

The parameters in `M`, `K`, and `N` must all be positive integers, with $N \le M$. The values in `X` must be less than or equal to all the parameter values.

The hypergeometric pdf is

$$y = f(x \mid M,K,N) = \frac{\binom{K}{x}\binom{M-K}{N-x}}{\binom{M}{N}}$$

The result, y, is the probability of drawing exactly x of a possible K items in n drawings without replacement from a group of M objects.

Examples

Suppose you have a lot of 100 floppy disks and you know that 20 of them are defective. What is the probability of drawing 0 through 5 defective floppy disks if you select 10 at random?

```
p = hygepdf(0:5,100,20,10)
p =
  0.0951   0.2679   0.3182   0.2092   0.0841   0.0215
```

See Also

pdf | hygecdf | hygeinv | hygestat | hygernd

hygernd

Hypergeometric random numbers

Syntax

```
R = hygernd(M,K,N)
R = hygernd(M,K,N,m,n,...)
R = hygernd(M,K,N,[m,n,...])
```

Description

`R = hygernd(M,K,N)` generates random numbers from the hypergeometric distribution with corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. `M`, `K`, and `N` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `R`. A scalar input for `M`, `K`, or `N` is expanded to a constant array with the same dimensions as the other inputs.

`R = hygernd(M,K,N,m,n,...)` or `R = hygernd(M,K,N,[m,n,...])` generates an `m`-by-`n`-by-... array. The `M`, `K`, `N` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
numbers = hygernd(1000,40,50)
numbers =
   1
```

See Also

`random` | `hygepdf` | `hygecdf` | `hygeinv` | `hygestat`

hygestat

Hypergeometric mean and variance

Syntax

```
[MN,V] = hygestat(M,K,N)
```

Description

`[MN,V] = hygestat(M,K,N)` returns the mean of and variance for the hypergeometric distribution with corresponding size of the population, `M`, number of items with the desired characteristic in the population, `K`, and number of samples drawn, `N`. Vector or matrix inputs for `M`, `K`, and `N` must have the same size, which is also the size of `MN` and `V`. A scalar input for `M`, `K`, or `N` is expanded to a constant matrix with the same dimensions as the other inputs.

The mean of the hypergeometric distribution with parameters `M`, `K`, and `N` is `NK/M`, and the variance is `NK(M-K)(M-N)/[M^2(M-1)]`.

Examples

The hypergeometric distribution approaches the binomial distribution, where `p = K/M`, as `M` goes to infinity.

```
[m,v] = hygestat(10.^(1:4),10.^(0:3),9)
m =
  0.9000  0.9000  0.9000  0.9000
v =
  0.0900  0.7445  0.8035  0.8094

[m,v] = binostat(9,0.1)
m =
  0.9000
v =
  0.8100
```

See Also

`hygepdf` | `hygecdf` | `hygeinv` | `hygernd`

icdf

Inverse cumulative distribution functions

Syntax

```
x = icdf('name',y,A)
x = icdf('name',y,A,B)
x = icdf('name',y,A,B,C)

x = icdf(pd,y)
```

Description

`x = icdf('name',y,A)` returns the inverse cumulative distribution function (icdf) for the one-parameter distribution family specified by 'name', evaluated at the probability values in y. A contains the parameter value for the distribution.

`x = icdf('name',y,A,B)` returns the icdf for the two-parameter distribution family specified by 'name', evaluated at the probability values in y. A and B contain the parameter values for the distribution.

`x = icdf('name',y,A,B,C)` returns the icdf for the three-parameter distribution family specified by 'name', evaluated at the probability values in y. A, B, and C contain the parameter values for the distribution.

`x = icdf(pd,y)` returns the inverse cumulative distribution function of the probability distribution object, pd, evaluated at the probability values in y.

Examples

Compute the Normal Distribution icdf

Create a standard normal distribution object with the mean, μ, equal to 0 and the standard deviation, σ, equal to 1.

```
mu = 0;
sigma = 1;
```

```
pd = makedist('Normal',mu,sigma);
```

Define the input vector y to contain the probability values at which to calculate the icdf.

```
y = [0.1,0.25,0.5,0.75,0.9];
```

Compute the icdf values for the standard normal distribution at the values in y.

```
x = icdf(pd,y)
```

```
x =

   -1.2816   -0.6745         0    0.6745    1.2816
```

Each value in x corresponds to a value in the input vector y. For example, at the value y equal to 0.9, the corresponding icdf value x is equal to 1.2816.

Alternatively, you can compute the same icdf values without creating a probability distribution object. Use the `icdf` function and specify a standard normal distribution using the same parameter values for μ and σ.

```
x2 = icdf('Normal',y,mu,sigma)
```

```
x2 =

   -1.2816   -0.6745         0    0.6745    1.2816
```

The icdf values are the same as those computed using the probability distribution object.

Compute the Poisson Distribution icdf

Create a Poisson distribution object with the rate parameter, λ, equal to 2.

```
lambda = 2;
pd = makedist('Poisson',lambda);
```

Define the input vector y to contain the probability values at which to calculate the icdf.

```
y = [0.1,0.25,0.5,0.75,0.9];
```

Compute the icdf values for the Poisson distribution at the values in y.

```
x = icdf(pd,y)
```

```
x =

     0     1     2     3     4
```

Each value in x corresponds to a value in the input vector y. For example, at the value y equal to 0.9, the corresponding icdf value x is equal to 4.

Alternatively, you can compute the same icdf values without creating a probability distribution object. Use the `icdf` function and specify a Poisson distribution using the same value for the rate parameter λ.

```
x2 = icdf('Poisson',y,lambda)
```

```
x2 =

     0     1     2     3     4
```

The icdf values are the same as those computed using the probability distribution object.

Input Arguments

`'name'` — Probability distribution name

probability distribution name string

Probability distribution name, specified as one of the following probability distribution name strings.

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
`'Beta'`	"Beta Distribution" on page B-4	a: first shape parameter	b: second shape parameter	—
`'Binomial'`	"Binomial Distribution" on page B-9	n: number of trials	p: probability of success for each trial	—
`'BirnbaumSaund`	"Birnbaum-Saunders Distribution" on page B-13	β: scale parameter	γ: shape parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'Burr'	"Burr Type XII Distribution" on page B-15	α: scale parameter	c: first shape parameter	k: second shape parameter
'Chisquare'	"Chi-Square Distribution" on page B-29	ν: degrees of freedom	—	—
'Exponential'	"Exponential Distribution" on page B-35	μ: mean	—	—
'Extreme Value'	"Extreme Value Distribution" on page B-39	μ: location parameter	σ: scale parameter	—
'F'	"F Distribution" on page B-45	ν_1: numerator degrees of freedom	ν_2: denominator degrees of freedom	—
'Gamma'	"Gamma Distribution" on page B-48	α: shape parameter	b: scale parameter	—
'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-54	k: shape parameter	σ: scale parameter	μ: location parameter
'Generalized Pareto'	"Generalized Pareto Distribution" on page B-60	k: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter
'Geometric'	"Geometric Distribution" on page B-65	p: probability parameter	—	—
'Hypergeometri	"Hypergeometric Distribution" on page B-74	m: size of the population	k: number of items with the desired characteristic in the population	n: number of samples drawn
'InverseGaussi	"Inverse Gaussian Distribution" on page B-77	μ: scale parameter	λ: shape parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'Logistic'	"Logistic Distribution" on page B-91	μ: mean	σ: scale parameter	—
'LogLogistic'	"Loglogistic Distribution" on page B-93	μ: log mean	σ: log scale parameter	—
'Lognormal'	"Lognormal Distribution" on page B-95	μ: log mean	σ: log standard deviation	—
'Nakagami'	"Nakagami Distribution" on page B-113	μ: shape parameter	ω: scale parameter	—
'Negative Binomial'	"Negative Binomial Distribution" on page B-115	r: number of successes	p: probability of success in a single trial	—
'Noncentral F'	"Noncentral F Distribution" on page B-123	ν_1: numerator degrees of freedom	ν_2: denominator degrees of freedom	δ: noncentrality parameter
'Noncentral t'	"Noncentral t Distribution" on page B-126	ν: degrees of freedom	δ: noncentrality parameter	—
'Noncentral Chi-square'	"Noncentral Chi-Square Distribution" on page B-120	ν: degrees of freedom	δ: noncentrality parameter	—
'Normal'	"Normal Distribution" on page B-130	μ: mean	σ: standard deviation	—
'Poisson'	"Poisson Distribution" on page B-138	λ: mean	—	—
'Rayleigh'	"Rayleigh Distribution" on page B-141	b: scale parameter	—	—
'Rician'	"Rician Distribution" on page B-144	s: noncentrality parameter	σ: scale parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'T'	"Student's t Distribution" on page B-146	ν: degrees of freedom	—	—
'tLocationScal	"t Location-Scale Distribution" on page B-154	μ: location parameter	σ: scale parameter	ν: shape parameter
'Uniform'	"Uniform Distribution (Continuous)" on page B-163	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'Discrete Uniform'	"Uniform Distribution (Discrete)" on page B-169	n: maximum observable value	—	—
'Weibull'	"Weibull Distribution" on page B-172	a: scale parameter	b: shape parameter	—

y — Probability values at which to evaluate icdf

scalar value | array of scalar values

Probability values at which to evaluate the icdf, specified as a scalar value, or an array of scalar values.

- If y is a scalar value, and if you specify distribution parameters A, B, or C as arrays, then `cdf` expands it into a constant matrix the same size as `A` and `B`.
- If y is an array, and if you specify distribution parameters A, B, or C as arrays, then y, A, B, and C must all be the same size.

Example: `[0.1,0.25,0.5,0.75,0.9]`

Data Types: `single` | `double`

A — First probability distribution parameter

scalar value | array of scalar values

First probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x and A are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A. If A is a scalar, then `cdf` expands it into a constant matrix the same size as x.

Data Types: `single` | `double`

`B` — Second probability distribution parameter

scalar value | array of scalar values

Second probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x, A, and B are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A and B. If A or B are scalars, then `cdf` expands them into constant matrices the same size as x

Data Types: `single` | `double`

`C` — Third probability distribution parameter

scalar value | array of scalar values

Third probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x, A, B, and C are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A, B, and C. If any of A, B or C are scalars, then `cdf` expands them into constant matrices the same size as x.

Data Types: `single` | `double`

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object created using one of the following.

`makedist`	Create a probability distribution object using specified parameter values.
`fitdist`	Fit a probability distribution object to sample data.
`dfittool`	Fit a probability distribution object to sample data using the interactive Distribution Fitting app.
`paretotails`	Create a Pareto tails object.

`gmdistribution`	Create a Gaussian mixture distribution object.

Output Arguments

x — Inverse cumulative distribution function

array

Inverse cumulative distribution function of the specified probability distribution, returned as an array.

- If you specify distribution parameters A, B, orC, then x is the common size of y, A, B, and C after any necessary scalar expansion.
- If you specify a probability distribution object, pd, then x has the same dimensions as y.

See Also

`cdf` | `mle` | `pdf` | `random`

icdf

Class: piecewisedistribution

Inverse cumulative distribution function for piecewise distribution

Syntax

```
X = icdf(obj,P)
```

Description

`X = icdf(obj,P)` returns an array `X` of values of the inverse cumulative distribution function for the piecewise distribution object `obj`, evaluated at the values in the array `P`.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432

icdf(obj,p)
ans =
   -1.7766
    1.8432
```

See Also

`paretotails` | `cdf`

icdf

Class: ProbDistUnivKernel

Return inverse cumulative distribution function (ICDF) for ProbDistUnivKernel object

Syntax

```
Y = icdf(PD, P)
```

Description

`Y = icdf(PD, P)` returns *Y*, an array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivKernel object *PD*, evaluated at values in *P*.

Input Arguments

PD	An object of the class `ProbDistUnivKernel`.
P	A numeric array of values from `0` to `1` where you want to evaluate the ICDF.

Output Arguments

Y	An array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivKernel object *PD*.

See Also

`icdf`

icdf

Class: ProbDistUnivParam

Return inverse cumulative distribution function (ICDF) for ProbDistUnivParam object

Syntax

```
Y = icdf(PD, P)
```

Description

`Y = icdf(PD, P)` returns *Y*, an array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivParam object *PD*, evaluated at values in *P*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.
P	A numeric array of values from `0` to `1` where you want to evaluate the ICDF.

Output Arguments

Y	An array containing the inverse cumulative distribution function (ICDF) for the ProbDistUnivParam object *PD*.

See Also

`icdf`

icdf

Class: prob.TruncatableDistribution
Package: prob

Inverse cumulative distribution function of probability distribution object

Syntax

```
y = icdf(pd,prob)
```

Description

`y = icdf(pd,prob)` returns the inverse cumulative distribution function (icdf) values of the probability distribution pd at the probabilities in prob.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

`prob` — Probabilities

array of scalar values in the range [0,1]

Probabilities at which to compute the icdf, specified as an array of scalar values in the range [0,1]. For example, specifying `[.25 .5 .75]` returns a vector containing three icdf values corresponding to these probabilities.

Data Types: `single` | `double`

Output Arguments

y — Inverse cumulative distribution function

array

Inverse cumulative distribution function (icdf) values of the specified probability distribution, evaluated at the probabilities in prob, returned as an array. y has the same dimensions as x.

Examples

Compute Standard Normal Critical Values

Create a standard normal distribution object.

```
pd = makedist('Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

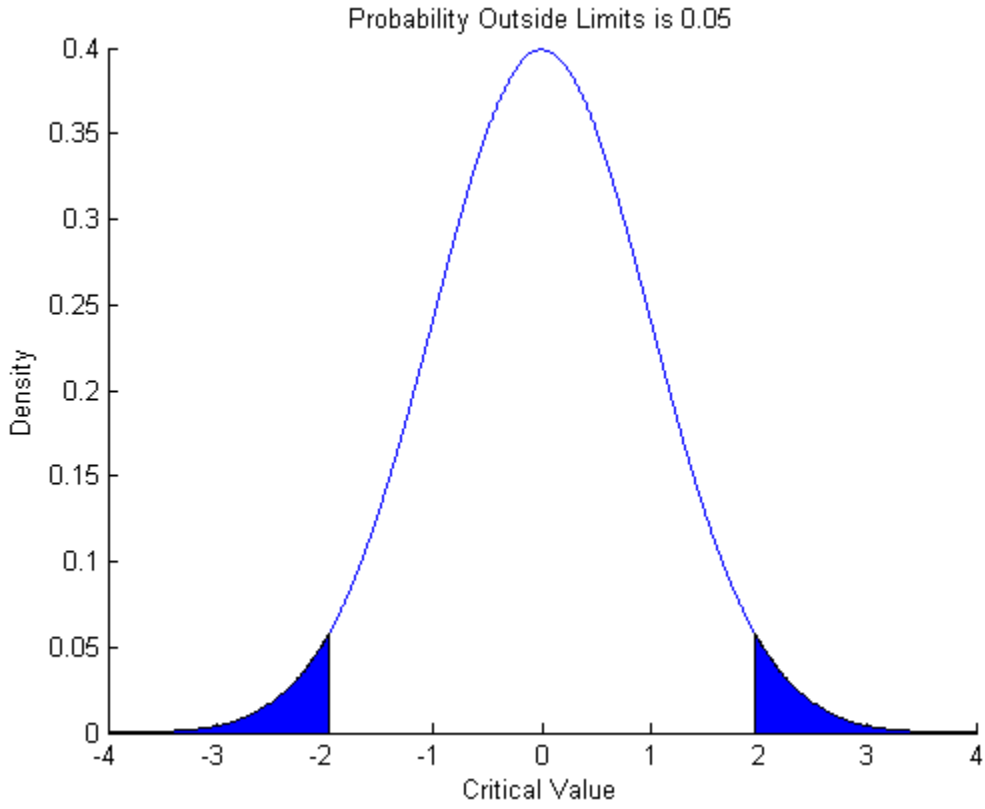
Determine the critical values at the 5% significance level for a test statistic with a standard normal distribution, by computing the upper and lower 2.5% values.

```
y = icdf(pd,[.025,.975])
```

```
y =

   -1.9600    1.9600
```

Plot the cdf and shade the critical regions.

```
p = normspec(y,0,1,'outside')
```



See Also

`cdf` | `dfittool` | `fitdist` | `makedist` | `normspec` | `pdf`

inconsistent

Inconsistency coefficient

Syntax

```
Y = inconsistent(Z)
Y = inconsistent(Z,d)
```

Description

`Y = inconsistent(Z)` computes the inconsistency coefficient for each link of the hierarchical cluster tree `Z`, where `Z` is an (m-1)-by-3 matrix generated by the `linkage` function. The inconsistency coefficient characterizes each link in a cluster tree by comparing its height with the average height of other links at the same level of the hierarchy. The higher the value of this coefficient, the less similar the objects connected by the link.

`Y = inconsistent(Z,d)` computes the inconsistency coefficient for each link in the hierarchical cluster tree `Z` to depth `d`, where `d` is an integer denoting the number of levels of the cluster tree that are included in the calculation. By default, `d=2`.

The output, `Y`, is an (m-1)-by-4 matrix formatted as follows.

Column	Description
1	Mean of the heights of all the links included in the calculation.
2	Standard deviation of the heights of all the links included in the calculation.
3	Number of links included in the calculation.
4	Inconsistency coefficient.

For each link, k, the inconsistency coefficient is calculated as:

$$Y(k,4) = (z(k,3) - Y(k,1)) / Y(k,2)$$

For leaf nodes, nodes that have no further nodes under them, the inconsistency coefficient is set to 0.

Examples

Compute Inconsistency Coefficient

Create the sample data.

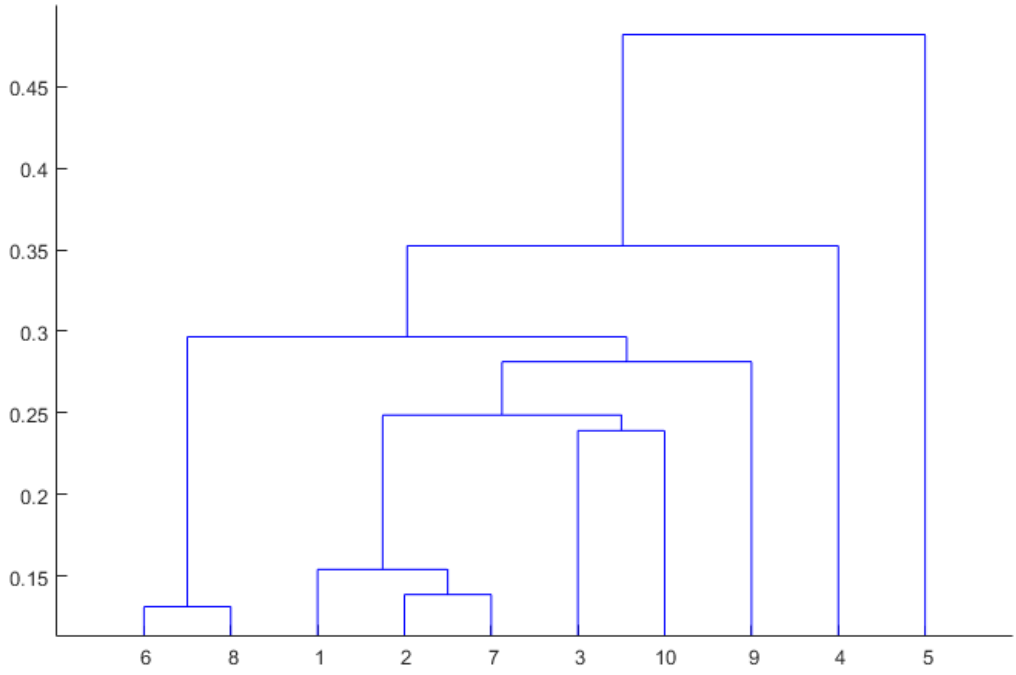
```
X = gallery('uniformdata',[10 2],12);
Y = pdist(X);
```

Generate the hierarchical cluster tree.

```
Z = linkage(Y,'single');
```

Generate a dendrogram plot of the hierarchical cluster tree.

```
dendrogram(Z)
```



Compute the inconsistency coefficient for each link in the cluster tree Z to depth 3.

```
W = inconsistent(Z,3)
```

```
W =

    0.1313         0    1.0000         0
    0.1386         0    1.0000         0
    0.1463    0.0109    2.0000    0.7071
    0.2391         0    1.0000         0
    0.1951    0.0568    4.0000    0.9425
    0.2308    0.0543    4.0000    0.9320
    0.2395    0.0748    4.0000    0.7636
    0.2654    0.0945    4.0000    0.9203
    0.3769    0.0950    3.0000    1.1040
```

References

[1] Jain, A., and R. Dubes. *Algorithms for Clustering Data*. Upper Saddle River, NJ: Prentice-Hall, 1988.

[2] Zahn, C. T. “Graph-theoretical methods for detecting and describing Gestalt clusters.” *IEEE Transactions on Computers*. Vol. C-20, Issue 1, 1971, pp. 68–86.

See Also

`cluster` | `cophenet` | `clusterdata` | `dendrogram` | `linkage` | `pdist` | `squareform`

increaseB

Class: clustering.evaluation.GapEvaluation
Package: clustering.evaluation

Increase reference data sets

Syntax

```
eva_out = increaseB(eva,nref)
```

Description

`eva_out = increaseB(eva,nref)` returns a gap criterion clustering evaluation object eva_out that uses the same evaluation criteria as the input object eva and an additional number of reference data sets as specified by nref.

Input Arguments

`eva` — Clustering evaluation data

clustering evaluation object

Clustering evaluation data, specified as a clustering evaluation object. Create a clustering evaluation object using `evalclusters`.

`nref` — Number of additional reference data sets

positive integer value

Number of additional reference data sets, specified as a positive integer value.

Output Arguments

`eva_out` — Updated clustering evaluation data

clustering evaluation object

Updated clustering evaluation data, returned as a gap criterion clustering evaluation object. eva_out contains evaluation data obtained using the reference data sets from the input object eva plus a number of additional reference data sets as specified in nref.

`increaseB` updates the `B` property of the input object eva to reflect the increase in the number of reference data sets used to compute the gap criterion values. `increaseB` also updates the `CriterionValues` property with gap criterion values computed using the total number of reference data sets. `increaseB` might also update the `OptimalK` and `OptimalY` properties to reflect the optimal number of clusters and optimal clustering solution as determined using the total number of reference data sets. Additionally, `increaseB` might also update the `LogW`, `ExpectedLogW`, `StdLogW`, and `SE` properties.

Examples

Evaluate Clustering Solutions Using Additional Reference Data

Create a gap clustering evaluation object using `evalclusters`, then use `increaseB` to increase the number of reference data sets used to compute the gap criterion values.

Load the sample data.

```
load fisheriris;
```

The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Cluster the flower measurement data using `kmeans`, and use the gap criterion to evaluate proposed solutions of one through five clusters. Use 50 reference data sets.

```
eva = evalclusters(meas,'kmeans','gap','klist',1:5,'B',50)
```

```
eva =

  GapEvaluation with properties:

    NumObservations: 150
         InspectedK: [1 2 3 4 5]
    CriterionValues: [0.0848 0.5920 0.8750 1.0044 1.0462]
           OptimalK: 5
```

The clustering evaluation object `eva` contains data on each proposed clustering solution. The returned results indicate that the optimal number of clusters is five.

The value of the B property of eva shows 50 reference data sets.

```
eva.B
```

```
ans =

    50
```

Increase the number of reference data sets by 50, for a total of 100 sets.

```
eva = increaseB(eva,50)
```

```
eva =

  GapEvaluation with properties:

    NumObservations: 150
         InspectedK: [1 2 3 4 5]
    CriterionValues: [0.0824 0.5899 0.8742 1.0044 1.0463]
           OptimalK: 4
```

The returned results now indicate that the optimal number of clusters is four.

The value of the B property of eva now shows 100 reference data sets.

```
eva.B
```

```
ans =

   100
```

See Also

evalclusters

InputData property

Class: ProbDist

Read-only structure containing information about input data to ProbDist object

Description

`InputData` is a read-only property of the `ProbDist` class. `InputData` is a structure containing information about input data to a ProbDist object. It includes the following fields:

- `data`
- `cens`
- `freq`

Values

Possible values for the three fields in the structure are any data supplied to the `fitdist` function:

- `data` — Data passed to the `fitdist` function when creating the ProbDist object. This field is empty if the ProbDist object was created without fitting to data, that is by using the `ProbDistUnivParam` constructor.
- `cens` — The vector supplied with the `'censoring'` parameter when creating the ProbDist object using the `fitdist` function. This field is empty if the ProbDist object was created without fitting to data, that is by using the `ProbDistUnivParam` constructor.
- `freq` — The vector supplied with the `'frequency'` parameter when creating the ProbDist object using the `fitdist` function. This field is empty if the ProbDist object was created without fitting to data, that is by using the `ProbDistUnivParam` constructor.

Use this information to view and compare the data supplied to create distributions.

interactionplot

Interaction plot for grouped data

Syntax

```
interactionplot(Y,GROUP)
interactionplot(Y,GROUP,'varnames',VARNAMES)
[h,AX,bigax] = interactionplot(...)
```

Description

`interactionplot(Y,GROUP)` displays the two-factor interaction plot for the group means of matrix `Y` with groups defined by entries in the cell array `GROUP`. `Y` is a numeric matrix or vector. If `Y` is a matrix, the rows represent different observations and the columns represent replications of each observation. If `Y` is a vector, the rows give the means of each entry in the cell array `GROUP`. Each cell of `GROUP` must contain a grouping variable that can be a categorical variable, numeric vector, character matrix, or a single-column cell array of strings. `GROUP` can also be a matrix whose columns represent different grouping variables. Each grouping variable must have the same number of rows as `Y`. The number of grouping variables must be greater than 1.

The interaction plot is a matrix plot, with the number of rows and columns both equal to the number of grouping variables. The grouping variable names are printed on the diagonal of the plot matrix. The plot at off-diagonal position (*i*,*j*) is the interaction of the two variables whose names are given at row diagonal (*i*,*i*) and column diagonal (*j*,*j*), respectively.

`interactionplot(Y,GROUP,'varnames',VARNAMES)` displays the interaction plot with user-specified grouping variable names `VARNAMES`. `VARNAMES` is a character matrix or a cell array of strings, one per grouping variable. Default names are `'X1'`, `'X2'`, ...

`[h,AX,bigax] = interactionplot(...)` returns a handle `h` to the figure window, a matrix `AX` of handles to the subplot axes, and a handle `bigax` to the big (invisible) axes framing the subplots.

Examples

Display Interaction Plots

Randomly generate data for a response variable `y` .

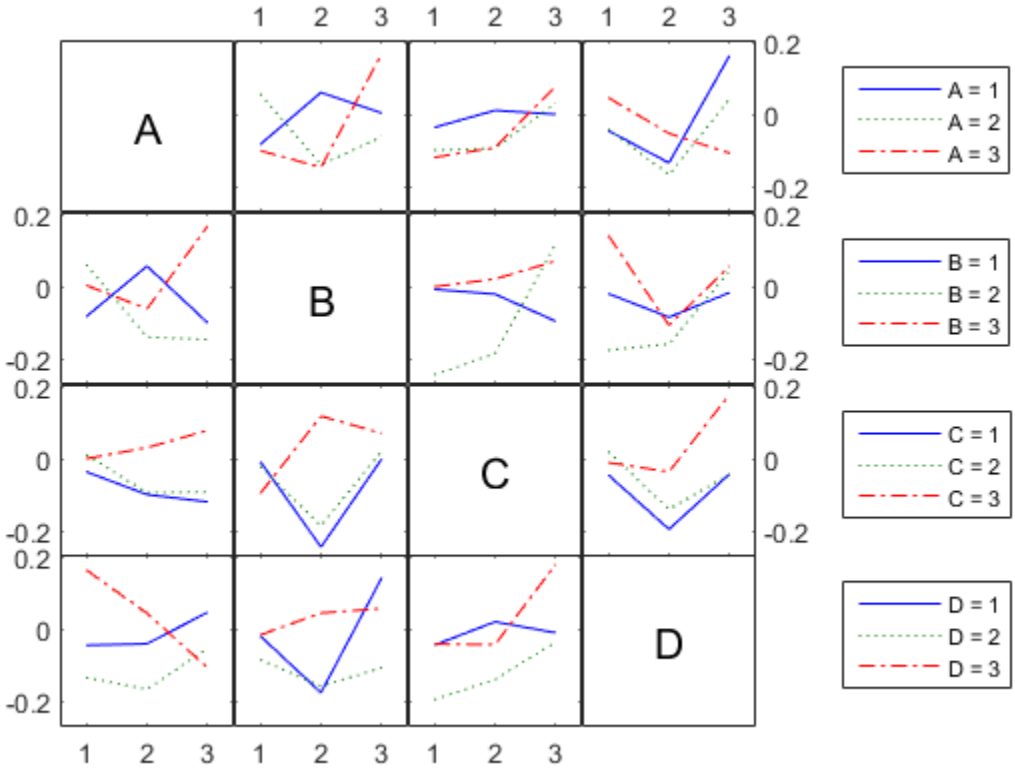
```
rng default;     % For reproducibility
y = randn(1000,1);
```

Randomly generate data for four three-level factors.

```
group = ceil(3*rand(1000,4));
```

Display the interaction plots for the factors and name the factors 'A', 'B', 'C', 'D'.

```
interactionplot(y,group,'varnames',{'A','B','C','D'})
```



See Also

`maineffectsplot` | `multivarichart`

intersect

Class: dataset

Set intersection for dataset array observations

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
C = intersect(A,B)
C = intersect(A,B,vars)
C = intersect(A,B,vars,setOrder)
[C,iA,iB] = intersect( ___ )
```

Description

`C = intersect(A,B)` for `dataset` arrays `A` and `B` returns the common set of observations from the two arrays, with repetitions removed. The observations in the dataset array `C` are in sorted order.

`C = intersect(A,B,vars)` returns the set of common observations from the two arrays, considering only the variables specified in vars, with repetitions removed. The observations in the dataset array C are sorted by those variables.

The values for variables not specified in vars for each observation in C are taken from the corresponding observations in `A`. If there are multiple observations in `A` that correspond to an observation in C, then those values are taken from the first occurrence.

`C = intersect(A,B,vars,setOrder)` returns the observations in C in the order specified by `setOrder`.

`[C,iA,iB] = intersect( ___ )` also returns index vectors iA and iB such that `C = A(iA,:)` and `C = B(iB,:)`. If there are repeated observations in `A` or `B`, then `intersect` returns the index of the first occurrence. You can use any of the previous input arguments.

Input Arguments

`A,B`

Input dataset arrays.

`vars`

Cell array of strings containing variable names or a vector of integers containing variable column numbers, indicating the variables in `A` and `B` that `intersect` considers.

Specify `vars` as `[]` to use its default value of all variables.

`setOrder`

Flag indicating the sorting order for the observations in C. The possible values of `setOrder` are:

`'sorted'`	Observations in C are in sorted order (default).
`'stable'`	Observations in C are in the same order that they appear in `A`.

Output Arguments

`C`

Dataset array with the common set of observations in `A` and `B`, with repetitions removed. C is in sorted order (by default), or the order specified by setOrder.

`iA`

Index vector, indicating the observations in `A` that are common to `B`. The vector `iA` contains the index to the first occurrence of any repeated observations in `A`.

iB

Index vector, indicating the observations in B that are common to A. The vector iB contains the index to the first occurrence of any repeated observations in B.

Examples

Intersection of Two Dataset Arrays

Navigate to the folder containing sample data, and load sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

A = dataset('XLSFile','hospitalSmall.xlsx');
B = dataset('XLSFile','hospitalSmall.xlsx','Sheet',2);
```

Return the intersection and index vectors.

```
[C,iA,iB] = intersect(A,B);
```

```
C =

    id              name          sex        age    wgt    smoke
    'TRW-072'       'WHITE'       'm'        39     202    1
```

There is one observation in common between A and B.

Find the observation in the original dataset arrays.

```
A(iA,:)
```

```
ans =

    id              name          sex        age    wgt    smoke
    'TRW-072'       'WHITE'       'm'        39     202    1
```

```
B(iB,:)
```

```
ans =

    id              name          sex        age    wgt    smoke
    'TRW-072'       'WHITE'       'm'        39     202    1
```

- “Merge Dataset Arrays” on page 2-99

See Also

`dataset` | `ismember` | `setdiff` | `setxor` | `sortrows` | `union` | `unique`

More About

- "Dataset Arrays" on page 2-132

prob.InverseGaussianDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Inverse Gaussian probability distribution object

Description

`prob.InverseGaussianDistribution` is an object consisting of parameters, a model description, and sample data for an inverse Gaussian probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('InverseGaussian')` creates an inverse Gaussian probability distribution object using the default parameter values.

`pd = makedist('InverseGaussian','mu',mu,'lambda',lambda)` creates an inverse Gaussian probability distribution object using the specified parameter values.

Input Arguments

`mu` — Scale parameter

1 (default) | positive scalar value

Scale parameter for the inverse Gaussian distribution, specified as a positive scalar value.

Data Types: `single` | `double`

`lambda` — Shape parameter

1 (default) | positive scalar value

Shape parameter for the inverse Gaussian distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

`mu` — Scale parameter

positive scalar value

Scale parameter for the inverse Gaussian distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`lambda` — Shape parameter

positive scalar value

Shape parameter for the inverse Gaussian distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object

pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Inverse Gaussian Distribution

Also known as the Wald distribution, the inverse Gaussian is used to model nonnegative positively skewed data. Inverse Gaussian distributions have many similarities to standard Gaussian (normal) distributions, which lead to applications in inferential statistics.

The inverse Gaussian distribution uses the following parameters.

Parameter	Description	Support
`mu`	Scale parameter	$\mu > 0$
`lambda`	Shape parameter	$\lambda > 0$

The probability density function (pdf) is

$$f(x \mid \mu,\lambda) = \sqrt{\frac{\lambda}{2\pi x^3}} \exp\left\{-\frac{\lambda}{2\mu^2 x}(x-\mu)^2\right\} \quad ; \quad x > 0 .$$

Examples

Create an Inverse Gaussian Distribution Object Using Default Parameters

Create an inverse Gaussian distribution object using the default parameter values.

```
pd = makedist('InverseGaussian')
```

```
pd =

  InverseGaussianDistribution

  Inverse Gaussian distribution
        mu = 1
    lambda = 1
```

Create an Inverse Gaussian Distribution Object Using Specified Parameters

Create an inverse Gaussian distribution object by specifying parameter values.

```
pd = makedist('InverseGaussian','mu',2,'lambda',4)
```

```
pd =

  InverseGaussianDistribution

  Inverse Gaussian distribution
        mu = 2
    lambda = 4
```

Compute the standard deviation of the distribution.

```
s = std(pd)

s =

    1.4142
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Inverse Gaussian Distribution"
- Class Attributes
- Property Attributes

invpred

Inverse prediction

Syntax

```
X0 = invpred(X,Y,Y0)
[X0,DXLO,DXUP] = invpred(X,Y,Y0)
[X0,DXLO,DXUP] = invpred(X,Y,Y0,name1,val1,name2,val2,...)
```

Description

`X0 = invpred(X,Y,Y0)` accepts vectors `X` and `Y` of the same length, fits a simple regression, and returns the estimated value `X0` for which the height of the line is equal to `Y0`. The output, `X0`, has the same size as `Y0`, and `Y0` can be an array of any size.

`[X0,DXLO,DXUP] = invpred(X,Y,Y0)` also computes 95% inverse prediction intervals. `DXLO` and `DXUP` define intervals with lower bound `X0–DXLO` and upper bound `X0+DXUP`. Both `DXLO` and `DXUP` have the same size as `Y0`.

The intervals are not simultaneous and are not necessarily finite. Some intervals may extend from a finite value to `-Inf` or `+Inf`, and some may extend over the entire real line.

`[X0,DXLO,DXUP] = invpred(X,Y,Y0,name1,val1,name2,val2,...)` specifies optional argument name/value pairs chosen from the following list. Argument names are case insensitive and partial matches are allowed.

Name	Value
`'alpha'`	A value between 0 and 1 specifying a confidence level of `100*(1-alpha)`%. Default is `alpha=0.05` for 95% confidence.
`'predopt'`	Either `'observation'`, the default value to compute the intervals for `X0` at which a new observation could equal `Y0`, or `'curve'` to compute intervals for the `X0` value at which the curve is equal to `Y0`.

Examples

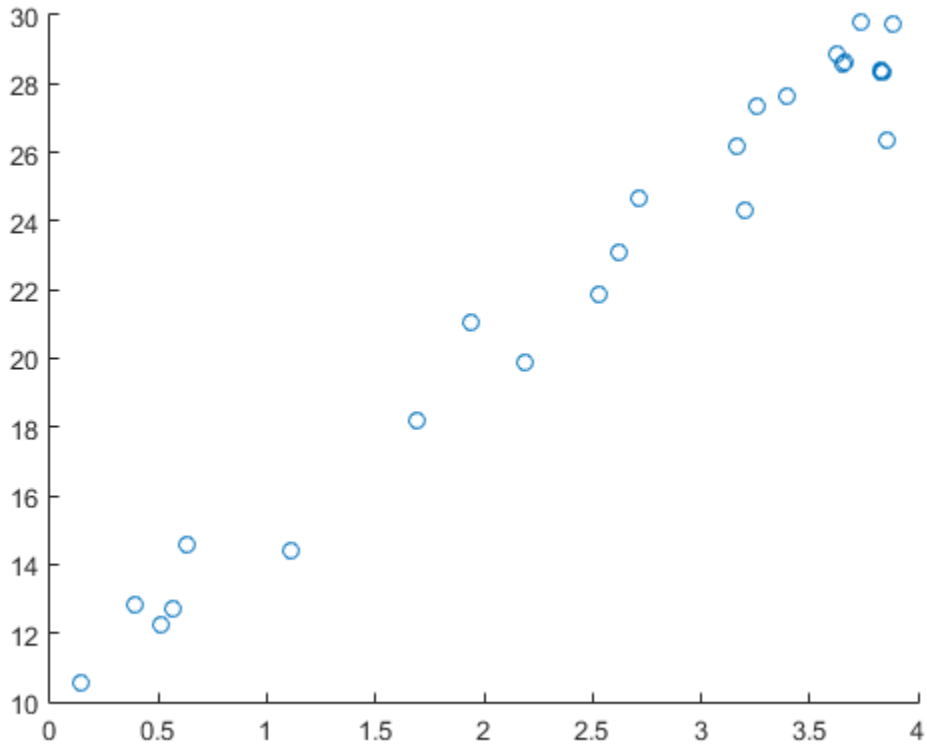
Inverse Prediction

Generate sample data.

```
x = 4*rand(25,1);
y = 10 + 5*x + randn(size(x));
```

Make a scatterplot of the data.

```
scatter(x,y)
```



Predict the *x* value for a given *y* value of 20.

```
x0 = invpred(x,y,20)

x0 =

    1.9967
```

See Also

polyfit | polyconf | polytool | polyval

iqr

Interquartile range

Syntax

```
r = iqr(x)
r = iqr(x,dim)

r = iqr(pd)
```

Description

`r = iqr(x)` returns the interquartile range of the values in x.

`r = iqr(x,dim)` returns the interquartile range along the dimension of x specified by dim.

`r = iqr(pd)` returns the interquartile range of the probability distribution, pd.

Examples

Compute the Interquartile Range

Generate a 4-by-4 matrix of random data from a normal distribution with parameter values μ equal to 10 and σ equal to 1.

```
rng default  % For reproducibility
x = normrnd(10,1,4)
```

```
x =

   10.5377   10.3188   13.5784   10.7254
   11.8339    8.6923   12.7694    9.9369
    7.7412    9.5664    8.6501   10.7147
   10.8622   10.3426   13.0349    9.7950
```

Compute the interquartile range for each column of data.

```
r = iqr(x)
```

```
r =

    2.2086    1.2013    2.5969    0.8541
```

Compute the interquartile range for each row of data.

```
r2 = iqr(x,2)
```

```
r2 =

    1.7237
    2.9870
    1.9449
    1.8797
```

Compute the Normal Distribution Interquartile Range

Create a standard normal distribution object with the mean, μ, equal to 0 and the standard deviation, σ, equal to 1.

```
pd = makedist('Normal',0,1);
```

Compute the interquartile range of the standard normal distribution.

```
r = iqr(pd)
```

```
r =

    1.3490
```

The returned value is the difference between the 75th and the 25th percentile values for the distribution. This is equivalent to computing the difference between the inverse cumulative distribution function (icdf) values at the probabilities y equal to 0.75 and 0.25.

```
r2 = icdf(pd,0.75) - icdf(pd,0.25)
```

```
r2 =

    1.3490
```

Input Arguments

x — Input array

vector | matrix | multidimensional array

Input array, specified as a vector, matrix, or multidimensional array.

Data Types: `single` | `double`

dim — Dimension

1 (default) | positive integer value

Dimension along which the interquartile range is calculated, specified as a positive integer. For example, for a matrix x, when dim is equal to 1, `iqr` returns the interquartile range for the columns of x. When dim is equal to 2, `iqr` returns the interquartile range for the rows of x. For *n*-dimensional arrays, `iqr` operates along the first nonsingleton dimension of `X`.

Data Types: `single` | `double`

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object created using one of the following.

`makedist`	Create a probability distribution object using specified parameter values.
`fitdist`	Fit a probability distribution object to sample data.
`dfittool`	Fit a probability distribution object to sample data using the interactive Distribution Fitting app.
`paretotails`	Create a Pareto tails object.

`gmdistribution`	Create a Gaussian mixture distribution object.

Output Arguments

r — Interquartile range

scalar value

Interquartile range, returned as a scalar value.

- If you input a vector for x, then r is the difference between the 75th and the 25th percentiles of the sample data contained in x.
- If you input a matrix for x, then r is a row vector containing the difference between the 75th and the 25th percentiles of the sample data contained each column of x.
- If you input a probability distribution, pd, then the value of r is the difference between the values of the 75th and 25th percentile of the probability distribution.

See Also

`icdf` | `mad` | `range` | `std`

iqr

Class: ProbDistUnivKernel

Return interquartile range (IQR) for ProbDistUnivKernel object

Syntax

```
Y = iqr(PD)
```

Description

`Y = iqr(PD)` returns *Y*, the interquartile range for the ProbDistUnivKernel object *PD*. The interquartile range is the distance between the 75th and 25th percentiles.

Input Arguments

PD	An object of the class `ProbDistUnivKernel`.

Output Arguments

Y	The value of the interquartile range for the ProbDistUnivKernel object *PD*.

See Also

`iqr` | `ProbDistUnivKernel.icdf`

iqr

Class: ProbDistUnivParam

Return interquartile range (IQR) for ProbDistUnivParam object

Syntax

```
Y = iqr(PD)
```

Description

`Y = iqr(PD)` returns *Y*, the interquartile range for the ProbDistUnivParam object *PD*. The interquartile range is the distance between the 75th and 25th percentiles.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

Y	The value of the interquartile range for the ProbDistUnivParam object *PD*.

See Also

`iqr` | `ProbDistUnivParam.icdf`

iqr

Class: prob.TruncatableDistribution
Package: prob

Interquartile range of probability distribution object

Syntax

```
r = iqr(pd)
```

Description

`r = iqr(pd)` returns the interquartile range r of the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`r` — Interquartile range

scalar value

Interquartile range of the probability distribution, returned as a scalar value. The value of r is the difference between the values of the 75th and 25th percentile of the probability distribution.

Examples

Interquartile Range of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Crete a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the interquartile range of the fitted distribution.

```
r = iqr(pd)
```

```
r =

   11.7634
```

The returned result indicates that the difference between the 75th and 25th percentile of the students' grades is 11.7634.

Use `icdf` to determine the 75th and 25th percentiles of the students' grades.

```
y = icdf(pd,[0.25,0.75])
```

```
y =
   69.1266   80.8900
```

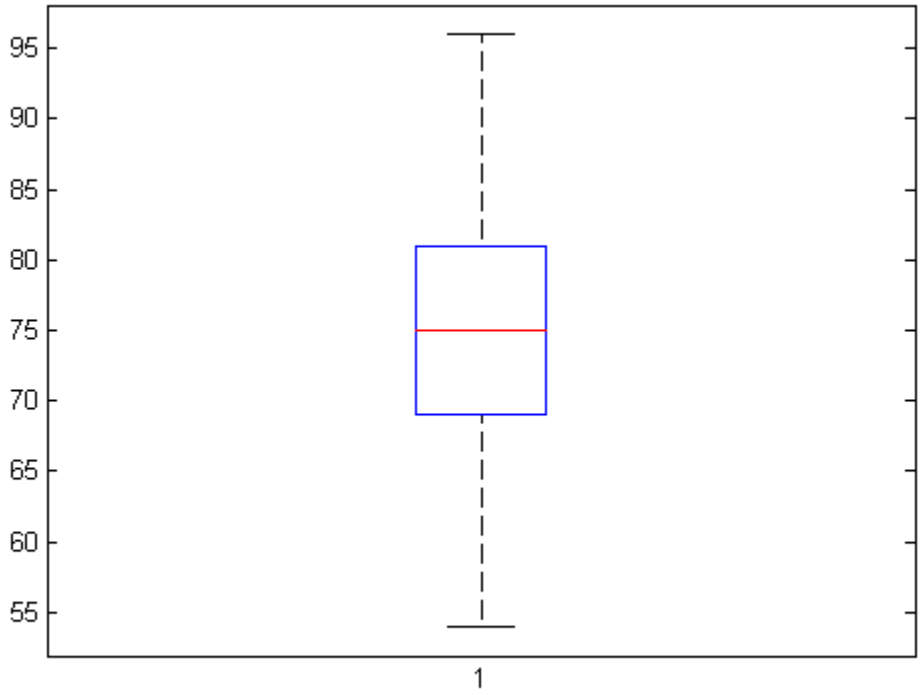
Calculate the difference between the 75th and 25th percentiles. This yields the same result as `iqr`.

```
y(2)-y(1)
```

```
ans =
   11.7634
```

Use `boxplot` to visualize the interquartile range.

```
boxplot(x)
```



The top line of the box shows the 75th percentile, and the bottom line shows the 25th percentile. The center line shows the median, which is the 50th percentile.

See Also

`boxplot` | `dfittool` | `fitdist` | `makedist`

isbranch

Class: classregtree

Test node for branch

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
ib = isbranch(t)
ib = isbranch(t,nodes)
```

Description

`ib = isbranch(t)` returns an *n*-element logical vector `ib` that is `true` for each branch node and `false` for each leaf node.

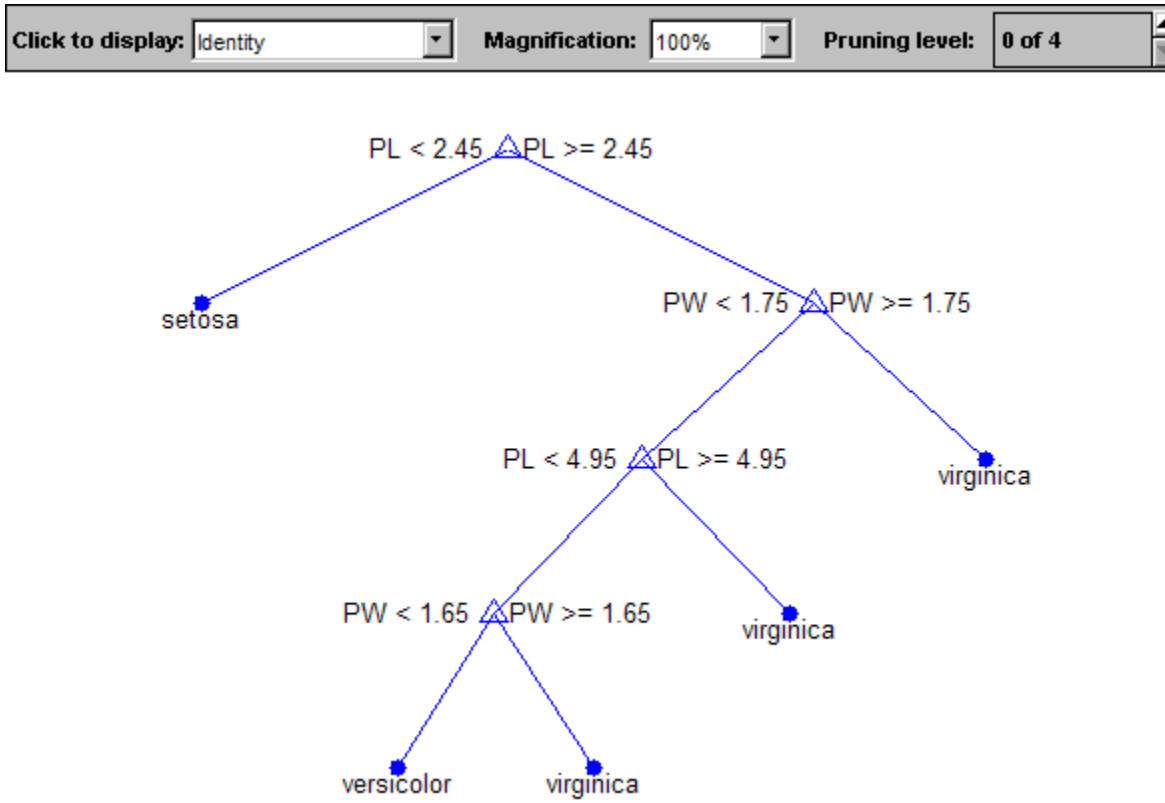
`ib = isbranch(t,nodes)` takes a vector `nodes` of node numbers and returns a vector of logical values for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
```

```
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
ib = isbranch(t)
ib =
     1
     0
     1
     1
     0
```

```
1
0
0
0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes` | `cutvar`

isempty

Class: dataset

True for empty dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
tf = isempty(A)
```

Description

`tf = isempty(A)` returns true (`1`) if `A` is an empty dataset and false (`0`) otherwise. An empty array has no elements, that is `prod(size(A))==0`.

See Also

`size`

islevel

Determine if levels are in nominal or ordinal array

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
tf = islevel(levels,A)
```

Description

`tf = islevel(levels,A)` returns a logical array indicating which of the levels in levels correspond to a level in the nominal or ordinal array A.

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

`levels` — Levels to test

string | cell array of strings | 2-D character matrix

Levels to test, specified as a string, cell array of strings, or 2-D character matrix.

Data Types: `char` | `cell`

Output Arguments

`tf` — Logical array

array the same size as levels

Logical array, returned as an array the same size as levels. tf has value `1` (true) where the corresponding element of levels is the label of a level in the nominal or ordinal array A, even if the level contains no elements. tf has value `0` (false) otherwise.

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`isequal` | `ismember` | `nominal` | `ordinal`

ismember

Class: dataset

Dataset array elements that are members of set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
LiA = ismember(A,B)
LiA = ismember(A,B,vars)
[LiA,LocB] = ismember( ___ )
```

Description

`LiA = ismember(A,B)` for `dataset` arrays A and B returns a vector of logical values the same length as `A`. The output vector, `LiA`, has value `1` (true) in the elements that correspond to observations in `A` that are also present in `B`, and `0` (false) otherwise.

`LiA = ismember(A,B,vars)` returns a vector of logical values the same length as `A`. The output vector, `LiA`, has value `1` (true) in the elements that correspond to observations in `A` that are also present in `B` for the variables specified in vars only, and `0` (false) otherwise.

`[LiA,LocB] = ismember( ___ )` also returns a vector the same length as `A` containing the index to the first observation in B that corresponds to each observation in A, or `0` if there is no such observation. You can use any of the previous input arguments.

Input Arguments

A

Query dataset array, containing the observations to be found in B.

B

Set dataset array. When an observation in A is found in `B`, for all variables or only those variables specified in vars, the corresponding element of LiA is `1`.

vars

Cell array of strings containing variable names or a vector of integers containing variable column numbers, indicating which variables to match observations on in A and B.

Output Arguments

LiA

Vector of logical values the same length as A. LiA has value `1` (true) when the corresponding observation in A is present in B. Otherwise, `LiA` has value `0` (false).

If you specify vars, LiA has value `1` when the corresponding observation in A is present in B for the variables in vars only.

LocB

Vector the same length as A containing the index to the first observation in B that corresponds to each observation in A, for all variables or only those variables specified in vars.

Examples

Find Observations That Are Members of a Dataset Array

Load sample data.

```
load('hospital')
```

```
B = hospital(1:50,1:5);
```

This set dataset array, B, has 50 observations on 5 variables.

Specify a query dataset array.

```
rng('default')
rIx = randsample(100,10);
A = hospital(rIx,1:5)
```

```
A =

              LastName           Sex       Age    Weight    Smoker
    YLN-495    'COLEMAN'         Male      39     188       false
    LQW-768    'TAYLOR'          Female    31     132       false
    DGC-290    'BUTLER'          Male      38     184       true
    DAU-529    'REED'            Male      50     186       true
    REV-997    'ALEXANDER'       Male      25     171       true
    QEQ-082    'COX'             Female    28     111       false
    AGR-528    'SIMMONS'         Male      45     181       false
    PUE-347    'YOUNG'           Female    25     114       false
    HVR-372    'RUSSELL'         Male      44     188       true
    XUE-826    'JACKSON'         Male      25     174       false
```

Check which observations in A are present in B.

```
LiA = ismember(A,B)
```

```
LiA =

     0
     1
     0
     0
     0
     0
     0
     1
     0
     1
```

Display the observations in A that are present in B.

```
A(LiA,:)
```

```
ans =
```

```
            LastName          Sex       Age    Weight    Smoker
    LQW-768    'TAYLOR'          Female    31     132       false
    PUE-347    'YOUNG'           Female    25     114       false
    XUE-826    'JACKSON'         Male      25     174       false
```

Find the location of the observations in B.

```
[~,LocB] = ismember(A,B)
```

```
LocB =

     0
    10
     0
     0
     0
     0
     0
    28
     0
    13
```

Display the observations in B that match observations in A.

```
B(LocB(LocB>0),:)
```

```
ans =

            LastName          Sex       Age    Weight    Smoker
    LQW-768    'TAYLOR'          Female    31     132       false
    PUE-347    'YOUNG'           Female    25     114       false
    XUE-826    'JACKSON'         Male      25     174       false
```

See Also

dataset | intersect | setdiff | setxor | sortrows | union | unique

More About

- “Dataset Arrays” on page 2-132

ismissing

Class: dataset

Find dataset array elements with missing values

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
I = ismissing(ds)
I = ismissing(ds,Name,Value)
```

Description

`I = ismissing(ds)` returns a logical array that indicates which elements in the dataset array, `ds`, contain a missing value. By default, `ismissing` recognizes `NaN` as a missing value in numeric variables, `''` as a missing value in string variables, and `<undefined>` as a missing value in categorical arrays.

- `ds2 = ds(~any(I,2),:)` creates a new dataset array containing only the complete observations in `ds`.
- `ds2 = ds(:,~any(I,1))` creates a new dataset array containing only the variables from `ds` with no missing values.

`I = ismissing(ds,Name,Value)` returns missing value indices with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ds`

`dataset` array

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'NumericTreatAsMissing'`

Vector of numeric values to treat as missing value indicators in floating point ds variables. `ismissing` always treats a `NaN` value as a missing value.

Default:

`'StringTreatAsMissing'`

String or cell array of strings to treat as missing value indicators in string ds variables. `ismissing` always treats the empty string `''` as a missing value.

Output Arguments

`I`

Logical array indicating which elements in ds contain a missing value. `I` is the same size as `ds`, with value `1` for elements that contain a missing value.

See Also

`dataset` | `isempty` | `isnan` | `isundefined` | `replaceWithMissing`

Related Examples

- “Clean Messy and Missing Data” on page 2-113

More About

- “Dataset Arrays” on page 2-132

isvalid

Class: qrandstream

Test handle validity

Syntax

```
tf = isvalid(h)
```

Description

`tf = isvalid(h)` performs an element-wise check for validity on the handle elements of `h`. The result is a logical array of the same dimensions as `h`, where each element is the element-wise validity result.

A handle is invalid if it has been deleted or if it is an element of a handle array and has not yet been initialized.

See Also

`delete` | `qrandstream`

NumIterations property

Class: gmdistribution

Number of iterations

Description

The number of iterations of the algorithm.

Note: This property applies only to `gmdistribution` objects constructed with `fitgmdist`.

---

iwishrnd

Inverse Wishart random numbers

Syntax

```
W = iwishrnd(Tau,df)
W = iwishrnd(Tau,df,DI)
[W,DI] = iwishrnd(Tau,df)
```

Description

`W = iwishrnd(Tau,df)` generates a random matrix `W` from the inverse Wishart distribution with parameters `Tau` and `df`. The inverse of `W` has the Wishart distribution with covariance matrix `Sigma = inv(Tau)` and with `df` degrees of freedom. `Tau` is a symmetric and positive definite matrix.

`W = iwishrnd(Tau,df,DI)` expects `DI` to be the transpose of the inverse of the Cholesky factor of `Tau`, so that `DI'*DI = inv(Tau)`, where `inv` is the MATLAB inverse function. `DI` is lower-triangular and the same size as `Tau`. If you call `iwishrnd` multiple times using the same value of `Tau`, it is more efficient to supply `DI` instead of computing it each time.

`[W,DI] = iwishrnd(Tau,df)` returns `DI` so you can use it as an input in future calls to `iwishrnd`.

Note that different sources use different parametrizations for the inverse Wishart distribution. This function defines the parameter `tau` so that the mean of the output matrix is `Tau/(df-d-1)` where `d` is the dimension of `Tau`.

More About

- “Inverse Wishart Distribution” on page B-78

See Also

`wishrnd`

jackknife

Jackknife sampling

Syntax

```
jackstat = jackknife(jackfun,X)
jackstat = jackknife(jackfun,X,Y,...)
jackstat = jackknife(jackfun,...,'Options',option)
```

Description

`jackstat = jackknife(jackfun,X)` draws jackknife data samples from the `n`-by-`p` data array `X`, computes statistics on each sample using the function `jackfun`, and returns the results in the matrix `jackstat`. `jackknife` regards each row of `X` as one data sample, so there are `n` data samples. Each of the `n` rows of `jackstat` contains the results of applying `jackfun` to one jackknife sample. `jackfun` is a function handle specified with `@`. Row `i` of `jackstat` contains the results for the sample consisting of `X` with the `i`th row omitted:

```
s = x;
s(i,:) = [];
jackstat(i,:) = jackfun(s);
```

If `jackfun` returns a matrix or array, then this output is converted to a row vector for storage in `jackstat`. If `X` is a row vector, it is converted to a column vector.

`jackstat = jackknife(jackfun,X,Y,...)` accepts additional arguments to be supplied as inputs to `jackfun`. They may be scalars, column vectors, or matrices. `jackknife` creates each jackknife sample by sampling with replacement from the rows of the non-scalar data arguments (these must have the same number of rows). Scalar data are passed to `jackfun` unchanged. Non-scalar arguments must have the same number of rows, and each jackknife sample omits the same row from these arguments.

`jackstat = jackknife(jackfun,...,'Options',option)` provides an option to perform jackknife iterations in parallel, if the Parallel Computing Toolbox is available. Set `'Options'` as a structure you create with `statset`. `jackknife` uses the following field in the structure:

`'UseParallel'`	If `true` and if a `parpool` of the Parallel Computing Toolbox is open, use multiple processors to compute jackknife iterations. If the Parallel Computing Toolbox is not installed, or a `parpool` is not open, computation occurs in serial mode. Default is `false`, or serial computation.

Examples

Estimate the bias of the MLE variance estimator of random samples taken from the vector `y` using `jackknife`. The bias has a known formula in this problem, so you can compare the `jackknife` value to this formula.

```
sigma = 5;
y = normrnd(0,sigma,100,1);
m = jackknife(@var, y, 1);
n = length(y);
bias = -sigma^2 / n % known bias formula
jbias = (n - 1)*(mean(m)-var(y,1)) % jackknife bias estimate

bias =
   -0.2500

jbias =
   -0.3378
```

See Also

`bootstrp` | `random` | `randsample` | `histogram` | `ksdensity`

jbtest

Jarque-Bera test

Syntax

```
h = jbtest(x)
h = jbtest(x,alpha)
h = jbtest(x,alpha,mctol)
[h,p] = jbtest(___)
[h,p,jbstat,critval] = jbtest(___)
```

Description

`h = jbtest(x)` returns a test decision for the null hypothesis that the data in vector `x` comes from a normal distribution with an unknown mean and variance, using the Jarque-Bera test. The alternative hypothesis is that it does not come from such a distribution. The result `h` is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = jbtest(x,alpha)` returns a test decision for the null hypothesis at the significance level specified by `alpha`.

`h = jbtest(x,alpha,mctol)` returns a test decision based on a *p*-value computed using a Monte Carlo simulation with a maximum Monte Carlo standard error less than or equal to `mctol`.

`[h,p] = jbtest(___)` also returns the *p*-value `p` of the hypothesis test, using any of the input arguments from the previous syntaxes.

`[h,p,jbstat,critval] = jbtest(___)` also returns the test statistic `jbstat`and the critical value `critval` for the test.

Examples

Test for a Normal Distribution

Load the data set.

```
load carbig;
```

Test the null hypothesis that car mileage, in miles per gallon (MPG), follows a normal distribution across different makes of cars.

```
h = jbtest(MPG)
```

```
h =

     1
```

The returned value of `h = 1` indicates that `jbtest` rejects the null hypothesis at the default 5% significance level.

Test the Hypothesis at a Different Significance Level

Load the data set.

```
load carbig;
```

Test the null hypothesis that car mileage in miles per gallon (MPG) follows a normal distribution across different makes of cars at the 1% significance level.

```
[h,p] = jbtest(MPG,0.01)
```

```
h =

     1


p =

    0.0022
```

The returned value of `h = 1`, and the returned *p*-value less than `α = 0.01` indicate that `jbtest` rejects the null hypothesis.

Test for a Normal Distribution Using Monte Carlo Simulation

Load the data set.

```
load carbig;
```

Test the null hypothesis that car mileage, in miles per gallon (MPG), follows a normal distribution across different makes of cars. Use a Monte Carlo simulation to obtain an exact *p*-value.

```
[h,p,jbstat,critval] = jbtest(MPG,[],0.0001)
h =

     1


p =

    0.0022


jbstat =

   18.2275


critval =

    5.8461
```

The returned value of `h = 1` indicates that `jbtest` rejects the null hypothesis at the default 5% significance level. Additionally, the test statistic, `jbstat`, is larger than the critical value, `critval`, which indicates rejection of the null hypothesis.

Input Arguments

x — Sample data

vector

Sample data for the hypothesis test, specified as a vector. `jbtest` treats `NaN` values in `x` as missing values and ignores them.

Data Types: `single` | `double`

alpha — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as a scalar value in the range (0,1). If `alpha` is in the range [0.001,0.50], and if the sample size is less than or equal to 2000, `jbtest` looks up the critical value for the test in a table of precomputed values. To conduct the test at a significance level outside of these specifications, use `mctol`.

Example: `0.01`

Data Types: `single` | `double`

`mctol` — Maximum Monte Carlo standard error

nonnegative scalar value

Maximum Monte Carlo standard error for the *p*-value, `p`, specified as a nonnegative scalar value. If you specify a value for `mctol`, `jbtest` computes a Monte Carlo approximation for `p` directly, rather than interpolating into a table of precomputed values. `jbtest` chooses the number of Monte Carlo replications large enough to make the Monte Carlo standard error for `p` less than `mctol`.

If you specify a value for `mctol`, you must also specify a value for `alpha`. You can specify `alpha` as `[]` to use the default value of 0.05.

Example: `0.0001`

Data Types: `single` | `double`

Output Arguments

`h` — Hypothesis test result

`1` | `0`

Hypothesis test result, returned as a logical value.

- If `h = 1`, this indicates the rejection of the null hypothesis at the alpha significance level.
- If `h = 0`, this indicates a failure to reject the null hypothesis at the alpha significance level.

`p` — *p*-value

scalar value in the range (0,1)

p-value of the test, returned as a scalar value in the range (0,1). p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

`jbtest` warns when `p` is not found within the tabulated range of [0.001,0.50], and returns either the smallest or largest tabulated value. In this case, you can use `mctol` to compute a more accurate *p*-value.

`jbstat` — Test statistic
nonnegative scalar value

Test statistic for the Jarque-Bera test, returned as a nonnegative scalar value.

`critval` — Critical value
nonnegative scalar value

Critical value for the Jarque-Bera test at the `alpha` significance level, returned as a nonnegative scalar value. If `alpha` is in the range [0.001,0.50], and if the sample size is less than or equal to 2000, `jbtest` looks up the critical value for the test in a table of precomputed values. If you use `mctol`, `jbtest` determines the critical value of the test using a Monte Carlo simulation. The null hypothesis is rejected when `jbstat > critval`.

More About

Jarque-Bera Test

The Jarque-Bera test is a two-sided goodness-of-fit test suitable when a fully specified null distribution is unknown and its parameters must be estimated.

The test is specifically designed for alternatives in the Pearson system of distributions. The test statistic is

$$JB = \frac{n}{6}\left(s^2 + \frac{(k-3)^2}{4}\right),$$

where n is the sample size, s is the sample skewness, and k is the sample kurtosis. For large sample sizes, the test statistic has a chi-square distribution with two degrees of freedom.

Monte Carlo Standard Error

The Monte Carlo standard error is the error due to simulating the p-value.

The Monte Carlo standard error is calculated as

$$SE = \sqrt{\frac{(\hat{p})(1-\hat{p})}{\text{mcreps}}},$$

where $\hat{p}$ is the estimated p-value of the hypothesis test, and `mcreps` is the number of Monte Carlo replications performed. `jbtest` chooses the number of Monte Carlo replications, `mcreps`, large enough to make the Monte Carlo standard error for $\hat{p}$ less than the value specified for `mctol`.

Algorithms

Jarque-Bera tests often use the chi-square distribution to estimate critical values for large samples, deferring to the Lilliefors test (see `lillietest`) for small samples. `jbtest`, by contrast, uses a table of critical values computed using Monte Carlo simulation for sample sizes less than 2000 and significance levels from 0.001 to 0.50. Critical values for a test are computed by interpolating into the table, using the analytic chi-square approximation only when extrapolating for larger sample sizes.

- "Generating Data Using the Pearson System" on page 6-27

References

[1] Jarque, C. M., and A. K. Bera. "A Test for Normality of Observations and Regression Residuals." *International Statistical Review*. Vol. 55, No. 2, 1987, pp. 163–172.

[2] Deb, P., and M. Sefton. "The Distribution of a Lagrange Multiplier Test of Normality." *Economics Letters*. Vol. 51, 1996, pp. 123–130. This paper proposed a Monte Carlo simulation for determining the distribution of the test statistic. The results of this function are based on an independent Monte Carlo simulation, not the results in this paper.

See Also

`adtest` | `kstest` | `lillietest`

johnsrnd

Johnson system random numbers

Syntax

```
r = johnsrnd(quantiles,m,n)
r = johnsrnd(quantiles)
[r,type] = johnsrnd(...)
[r,type,coefs] = johnsrnd(...)
```

Description

`r = johnsrnd(quantiles,m,n)` returns an `m`-by-`n` matrix of random numbers drawn from the distribution in the Johnson system that satisfies the quantile specification given by `quantiles`. `quantiles` is a four-element vector of quantiles for the desired distribution that correspond to the standard normal quantiles [–1.5 –0.5 0.5 1.5]. In other words, you specify a distribution from which to draw random values by designating quantiles that correspond to the cumulative probabilities [0.067 0.309 0.691 0.933]. `quantiles` may also be a `2`-by-`4` matrix whose first row contains four standard normal quantiles, and whose second row contains the corresponding quantiles of the desired distribution. The standard normal quantiles must be spaced evenly.

Note: Because `r` is a random sample, its sample quantiles typically differ somewhat from the specified distribution quantiles.

`r = johnsrnd(quantiles)` returns a scalar value.

`r = johnsrnd(quantiles,m,n,...)` or `r = johnsrnd(quantiles,[m,n,...])` returns an `m`-by-`n`-by-... array.

`[r,type] = johnsrnd(...)` returns the type of the specified distribution within the Johnson system. `type` is `'SN'`, `'SL'`, `'SB'`, or `'SU'`. Set `m` and `n` to zero to identify the distribution type without generating any random values.

The four distribution types in the Johnson system correspond to the following transformations of a normal random variate:

- `'SN'` — Identity transformation (normal distribution)
- `'SL'` — Exponential transformation (lognormal distribution)
- `'SB'` — Logistic transformation (bounded)
- `'SU'` — Hyperbolic sine transformation (unbounded)

`[r,type,coefs] = johnsrnd(...)` returns coefficients `coefs` of the transformation that defines the distribution. `coefs` is `[gamma, eta, epsilon, lambda]`. If `z` is a standard normal random variable and `h` is one of the transformations defined above, `r = lambda*h((z-gamma)/eta)+epsilon` is a random variate from the distribution type corresponding to `h`.

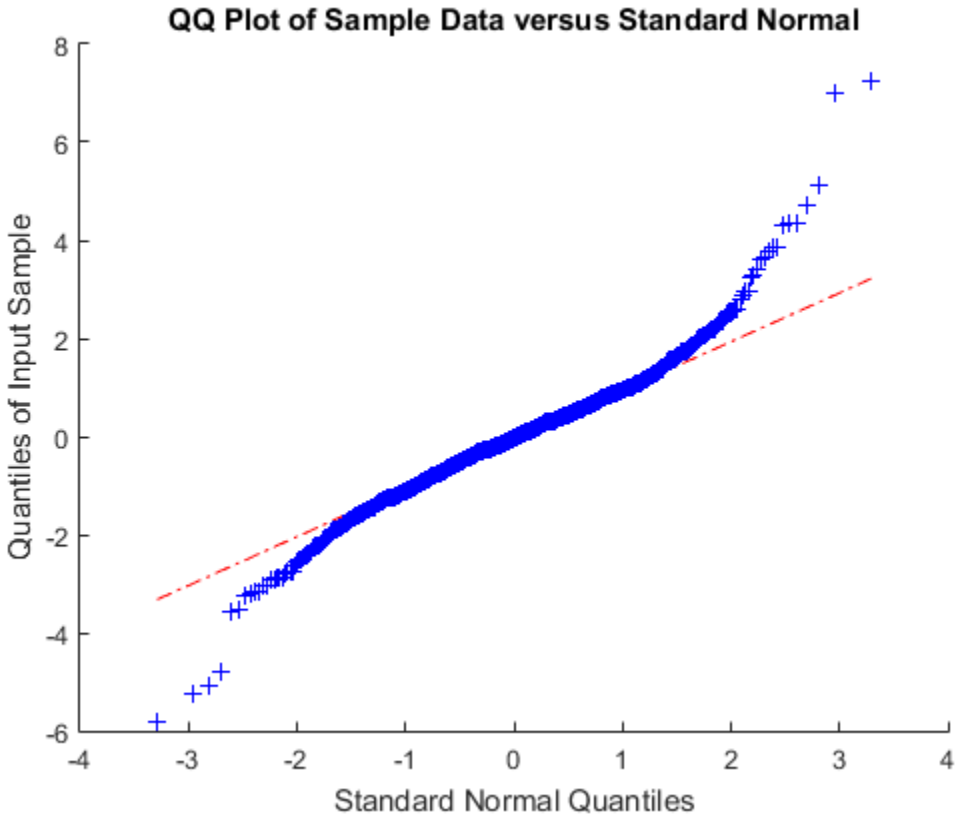
Examples

Generate Random Samples Using the Johnson System

This example shows several different approaches to using the Johnson system of flexible distribution families to generate random numbers and fit a distribution to sample data.

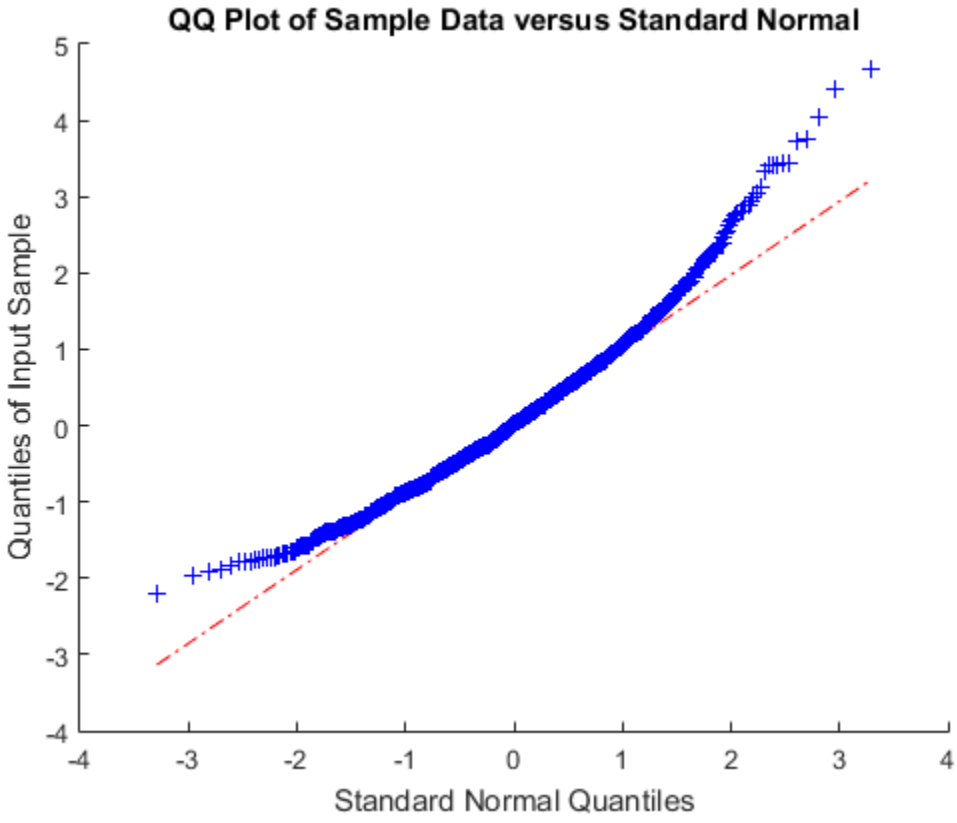
Generate random values with longer tails than a standard normal.

```
rng default;  % For reproducibility
r = johnsrnd([-1.7 -.5 .5 1.7],1000,1);
figure;
qqplot(r);
```



Generate random values skewed to the right.

```
r = johnsrnd([-1.3 -.5 .5 1.7],1000,1);
figure;
qqplot(r);
```



Generate random values that match some sample data well in the right-hand tail.

```
load carbig;
qnorm = [.5 1 1.5 2];
q = quantile(Acceleration, normcdf(qnorm));
r = johnsrnd([qnorm;q],1000,1);
[q;quantile(r,normcdf(qnorm))]
```

```
ans =

   16.7000   18.2086   19.5376   21.7263
   16.6986   18.2220   19.9078   22.0918
```

Determine the distribution type and the coefficients.

```
[r,type,coefs] = johnsrnd([qnorm;q],0)

r =

     []

type =

SU

coefs =

    1.0920    0.5829   18.4382    1.4494
```

More About

- "Johnson System" on page B-80

See Also

`random` | `pearsrnd`

join

Class: dataset

Merge observations

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
C = join(A,B)
C = join(A,B,keys)
C = join(A,B,param1,val1,param2,val2,...)
[C,IB] = join(...)
C = join(A,B,'Type',TYPE,...)
C = join(A,B,'Type',TYPE,'MergeKeys',true,...)
[C,IA,IB] = join(A,B,'Type',TYPE,...)
```

Description

`C = join(A,B)` creates a dataset array `C` by merging observations from the two dataset arrays `A` and `B`. `join` performs the merge by first finding *key variables*, that is, pairs of dataset variables, one in `A` and one in `B`, that share the same name. Each observation in `B` must contain a unique combination of values in the key variables, and must contain all combinations of values that are present in the keys from `A`. `join` then uses these key variables to define a many-to-one correspondence between observations in `A` and those in `B`. `join` uses this correspondence to replicate the observations in `B` and combine them with the observations in `A` to create `C`.

`C = join(A,B,keys)` performs the merge using the variables specified by `keys` as the key variables in both `A` and `B`. `keys` is a positive integer, a vector of positive integers, a variable name, a cell array of variable names, or a logical vector.

C contains one observation for each observation in A. Variables in C include all of the variables from A, as well as one variable corresponding to each variable in B (except for the keys from B). If A and B contain variables with identical names, join adds the suffix '_left' and '_right' to the corresponding variables in C.

C = join(A,B,*param1*,*val1*,*param2*,*val2*,...) specifies optional parameter name/value pairs to control how the dataset variables in A and B are used in the merge. Parameters are:

- 'Keys' — Specifies the variables to use as keys in both A and B.
- 'LeftKeys' — Specifies the variables to use as keys in A.
- 'RightKeys' — Specifies the variables to use as keys in B.

You may provide either the 'Keys' parameter, or both the 'LeftKeys' and 'RightKeys' parameters. The value for these parameters is a positive integer, a vector of positive integers, a variable name, a cell array containing variable names, or a logical vector. 'LeftKeys' or 'RightKeys' must both specify the same number of key variables, and join pairs the left and right keys in the order specified.

- 'LeftVars' — Specifies which variables from A to include in C. By default, join includes all variables from A.
- 'RightVars' — Specifies which variables from B to include in C. By default, join includes all variables from B except the key variables.

You can use 'LeftVars' or 'RightVars' to include or exclude key variables as well as data variables. The value for these parameters is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

[C,IB] = join(...) returns an index vector IB, where join constructs C by horizontally concatenating A(:,LeftVars) and B(IB,RightVars). join can also perform more complicated inner and outer join operations that allow a many-to-many correspondence between A and B, and allow unmatched observations in either A or B.

C = join(A,B,'Type',TYPE,...) performs the join operation specified by TYPE. TYPE is one of 'inner', 'leftouter', 'rightouter', 'fullouter', or 'outer' (which is a synonym for 'fullouter'). For an inner join, C only contains observations corresponding to a combination of key values that occurred in both A and B. For a left (or right) outer join, C also contains observations corresponding to keys in A (or B) that did not match any in B (or A). Variables in C taken from A (or B) contain null values in those observations. A full outer join is equivalent to a left and right outer join. C contains

variables corresponding to the key variables from both A and B, and join sorts the observations in C by the key values.

For inner and outer joins, C contains variables corresponding to the key variables from both A and B by default, as well as all the remaining variables. join sorts the observations in the result C by the key values.

C = join(A,B,'Type',TYPE,'MergeKeys',true,...) includes a single variable in C for each key variable pair from A and B, rather than including two separate variables. For outer joins, join creates the single variable by merging the key values from A and B, taking values from A where a corresponding observation exists in A, and from B otherwise. Setting the 'MergeKeys' parameter to true overrides inclusion or exclusion of any key variables specified via the 'LeftVars' or 'RightVars' parameter. Setting the 'MergeKeys' parameter to false is equivalent to not passing in the 'MergeKeys' parameter.

[C,IA,IB] = join(A,B,'Type',TYPE,...) returns index vectors IA and IB indicating the correspondence between observations in C and those in A and B. For an inner join, join constructs C by horizontally concatenating A(IA,LeftVars) and B(IB,RightVars). For an outer join, IA or IB may also contain zeros, indicating the observations in C that do not correspond to observations in A or B, respectively.

Examples

Create a dataset array from Fisher's iris data:

```
load fisheriris
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);
```

Create a separate dataset array with the diploid chromosome counts for each species of iris:

```
snames = nominal({'setosa';'versicolor';'virginica'});
CC = dataset({snames,'species'},{[38;108;70],'cc'})
CC =
    species       cc
    setosa         38
    versicolor    108
```

```
    virginica      70
```

Broadcast the data in `CC` to the rows of `iris` using the key variable `species` in each dataset:

```
iris2 = join(iris,CC);
iris2([1 2 51 52 101 102],:)
ans =
            species       SL     SW     PL     PW     cc
 Obs1       setosa        5.1    3.5    1.4    0.2     38
 Obs2       setosa        4.9      3    1.4    0.2     38
 Obs51      versicolor      7    3.2    4.7    1.4    108
 Obs52      versicolor    6.4    3.2    4.5    1.5    108
 Obs101     virginica     6.3    3.3      6    2.5     70
 Obs102     virginica     5.8    2.7    5.1    1.9     70
```

Create two datasets and join them using the `'MergeKeys'` flag:

```
% Create two data sets that both contain the key variable
% 'Key1'. The two arrays contain observations with common
% values of Key1, but each array also contains observations
% with values of Key1 not present in the other.
a = dataset({'a' 'b' 'c' 'e' 'h'},[1 2 3 11 17]',...
   'VarNames',{'Key1' 'Var1'})
b = dataset({'a' 'b' 'd' 'e'},[4 5 6 7]',...
   'VarNames',{'Key1' 'Var2'})

% Combine a and b with an outer join, which matches up
% observations with common key values, but also retains
% observations whose key values don't have a match.
% Keep the key values as separate variables in the result.
couter = join(a,b,'key','Key1','Type','outer')

% Join a and b, merging the key values as a single variable
% in the result.
coutermerge = join(a,b,'key','Key1','Type','outer',...
   'MergeKeys',true)

% Join a and b, retaining only observations whose key
% values match.
cinner = join(a,b,'key','Key1','Type','inner',...
   'MergeKeys',true)

a =
```

```
    Key1       Var1
    'a'         1
    'b'         2
    'c'         3
    'e'        11
    'h'        17


b =

    Key1       Var2
    'a'        4
    'b'        5
    'd'        6
    'e'        7


couter =

    Key1_left    Var1    Key1_right    Var2
    'a'            1     'a'             4
    'b'            2     'b'             5
    'c'            3     ''            NaN
    ''           NaN     'd'             6
    'e'           11     'e'             7
    'h'           17     ''            NaN


coutermerge =

    Key1       Var1    Var2
    'a'          1       4
    'b'          2       5
    'c'          3     NaN
    'd'        NaN       6
    'e'         11       7
    'h'         17     NaN


cinner =

    Key1       Var1    Var2
    'a'         1      4
    'b'         2      5
```

```
    'e'         11       7
```

See Also

`sortrows`

KDTreeSearcher

Grow *K*d-tree

Syntax

```
Mdl = KDTreeSearcher(X)
Mdl = KDTreeSearcher(X,Name,Value)
```

Description

`Mdl = KDTreeSearcher(X)` grows a default *K*d-tree (`Mdl`) using the *n*-by-*K* numeric matrix of training data (`X`). `Mdl` is a `KDTreeSearcher` model object that stores the results of the grown *K*d-tree. You can use `Mdl` to search the training data (`X`) for the nearest neighbors to the query data.

`Mdl = KDTreeSearcher(X,Name,Value)` grows a *K*d-tree (`Mdl`) with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify a distance metric or the maximum number of observations in each leaf node (i.e., the bucket size).

Examples

Grow a Default *K* d-Tree

Load Fisher's iris data set.

```
load fisheriris
X = meas;
[n,k] = size(X)
```

```
n =

   150
```

```
k =

     4
```

`X` has 150 observations and 4 predictors.

Grow a 4-dimensional K d-tree using the entire data set as training data.

```
Mdl = KDTreeSearcher(X)
```

```
Mdl =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'euclidean'
    DistParameter: []
                X: [150x4 double]
```

`Mdl` is a `KDTreeSearcher` model object, and its properties appear in the Command Window. It contains information about the grown 4-dimensional K d-tree, such as the distance metric. You can alter property values using dot notation

To find the nearest neighbors in `X` to a batch of query data, pass `Mdl` and the query data to `knnsearch` or `rangesearch`.

Specify the Minkowski Distance for Nearest Neighbor Search

Load Fisher's iris data. Focus on the petal dimensions.

```
load fisheriris
X = meas(:,[3 4]); % Predictors
```

Grow a two-dimensional K d-tree using `createns` and the training data. Specify the Minkowski distance metric.

```
Mdl = createns(X,'NSMethod','kdtree','Distance','Minkowski')
```

```
Mdl =

  KDTreeSearcher with properties:
```

```
       BucketSize: 50
         Distance: 'minkowski'
    DistParameter: 2
                X: [150x2 double]
```

`Mdl` is a `KDTreeSearcher` model object. Access properties of `Mdl` using dot notation. For example, use `Mdl.DistParameter` to access the Minkowski distance exponent.

```
Mdl.DistParameter
```

```
ans =

     2
```

You can pass query data and `Mdl` to:

- searcher.knnsearch to find indices and distances of nearest neighbors.
- searcher.rangesearch to find indices of all nearest neighbors within a distance that you specify.

Search for Nearest Neighbors of Query Data Using the Minkowski Distance

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(1);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
tIdx = ~ismember(1:n,qIdx); % Indices of training data
Q = meas(qIdx,:);
X = meas(tIdx,:);
```

Grow a four-dimensional K d-tree using the training data. Specify to use the Minkowski distance for finding nearest neighbors later.

```
Mdl = createns(X,'NSMethod','kdtree','Distance','minkowski')
```

```
Mdl =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'minkowski'
    DistParameter: 2
                X: [145x4 double]
```

`Mdl` is a `KDTreeSearcher` model object. By default, the Minkowski distance exponent is `2`.

Find the indices of the training data (`X`) that are the two nearest neighbors of each point in the query data (`Q`).

```
IdxNN = knnsearch(Mdl,Q,'K',2)
```

```
IdxNN =

    17     4
     6     2
     1    12
    89    66
   124   100
```

Each row of `NN` corresponds to a query data observation, and the column order corresponds to the order of the nearest neighbors. For example, using the Minkowski distance, the second nearest neighbor of `Q(3,:)` is `X(12,:)`.

Input Arguments

`X` — Training data

numeric matrix

Training data that grows the *K*d-tree, specified as a numeric matrix. `X` has n rows, each corresponding to an observation (i.e., an instance or example), and K columns, each corresponding to a predictor or feature.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Distance','minkowski','P',3,'BucketSize',10` specifies to use the Minkowski distance when searching for nearest neighbors, to use `3` for the Minkowski distance metric exponent, and to use `10` for the bucket size.

`'Distance'` — Distance metric

`'euclidean'` (default) | `'chebychev'` | `'cityblock'` | `'minkowski'`

Distance metric used to find nearest neighbors of query points, specified as the comma-separated pair consisting of `'Distance'` and one of these strings.

Value	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference)
`'cityblock'`	City block distance
`'euclidean'`	Euclidean distance
`'minkowski'`	Minkowski distance

For more details, see “Distance Metrics”.

The software does not use the distance metric for training the *K*d-tree, so you can alter it after training using dot notation.

Example: `'Distance','minkowski'`

Data Types: `char`

`'P'` — Exponent for Minkowski distance metric

`2` (default) | positive scalar

Exponent for the Minkowski distance metric, specified as the comma-separated pair consisting of `'P'` and a positive scalar. If you specify `P` and do not specify `'Distance','minkowski'`, then the software throws an error.

Example: `'P',3`

Data Types: `double` | `single`

`'BucketSize'` — Maximum number of data points in each leaf node
`50` (default) | positive integer

Maximum number of data points in each leaf node of the *K*d-tree, specified as the comma-separated pair consisting of `'BucketSize'` and a positive integer.

Example: `'BucketSize',10`

Data Types: `double` | `single`

Output Arguments

`Mdl` — Grown *K*d-tree
`KDTreeSearcher` model object

Grown *K*d-tree, returned as a `KDTreeSearcher` model object. To search the training data for the nearest neighbors of the query data, pass the query data and `Mdl` to `knnsearch` or `rangesearch`.

More About

- Using KDTreeSearcher Objects
- "*k*-Nearest Neighbor Search and Radius Search" on page 16-11
- "Distance Metrics"

See Also

`createns` | `knnsearch` | `rangesearch`

Introduced in R2010a

Using KDTreeSearcher Objects

Nearest neighbor search using *K*d-tree

`KDTreeSearcher` model objects store results of a nearest neighbors search using the *K*d-tree algorithm. Results that you can store include the training data, the distance metric and its parameters, and the maximal number of data points in each leaf node (i.e., the bucket size). The *K*d-tree algorithm partitions an *n*-by-*K* data set by recursively splitting *n* points in *K*-dimensional space into a binary tree. To find the nearest neighbors of a query observation, `KDTreeSearcher` restricts the training data space to the training observations in the leaf node that the query observation belongs to.

Once you create or train a `KDTreeSearcher` model object, you can search the stored tree to find all neighboring points to the query data by performing a nearest neighbors search using `knnsearch` or radius search using `rangesearch`. The *K*d-tree algorithm is particularly useful when:

- *K* is relatively small (i.e., $K < 10$).
- The training and query sets are not sparse.
- The training and query sets have many observations.

Examples

Grow a Default *K* d-Tree

Load Fisher's iris data set.

```
load fisheriris
X = meas;
[n,k] = size(X)
```

```
n =

   150


k =

     4
```

`X` has 150 observations and 4 predictors.

Grow a 4-dimensional K d-tree using the entire data set as training data.

```
Mdl = KDTreeSearcher(X)
```

```
Mdl =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'euclidean'
    DistParameter: []
                X: [150x4 double]
```

`Mdl` is a `KDTreeSearcher` model object, and its properties appear in the Command Window. It contains information about the grown 4-dimensional K d-tree, such as the distance metric. You can alter property values using dot notation

To find the nearest neighbors in `X` to a batch of query data, pass `Mdl` and the query data to `knnsearch` or `rangesearch`.

Alter Properties of `KDTreeSearcher` Model

Load Fisher's iris data set.

```
load fisheriris
X = meas;
```

Grow a default four-dimensional K d-tree using the entire data set as training data.

```
Mdl = KDTreeSearcher(X)
```

```
Mdl =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'euclidean'
    DistParameter: []
                X: [150x4 double]
```

Specify that the neighbor searcher use the Minkowski metric to compute the distances between the training and query data.

```
Mdl.Distance = 'minkowski'
```

```
Mdl =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'minkowski'
    DistParameter: 2
                X: [150x4 double]
```

Pass `Mdl` and the query data to either `knnsearch` or `rangesearch` to find the nearest neighbors to the points in the query data using the Minkowski distance.

Search for Nearest Neighbors of Query Data Using the Minkowski Distance

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(1);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
tIdx = ~ismember(1:n,qIdx); % Indices of training data
Q = meas(qIdx,:);
X = meas(tIdx,:);
```

Grow a four-dimensional K d-tree using the training data. Specify to use the Minkowski distance for finding nearest neighbors later.

```
Mdl = createns(X,'NSMethod','kdtree','Distance','minkowski')
```

```
Mdl =

  KDTreeSearcher with properties:

      BucketSize: 50
```

```
        Distance: 'minkowski'
    DistParameter: 2
                X: [145x4 double]
```

`Mdl` is a `KDTreeSearcher` model object. By default, the Minkowski distance exponent is `2`.

Find the indices of the training data (`X`) that are the two nearest neighbors of each point in the query data (`Q`).

```
IdxNN = knnsearch(Mdl,Q,'K',2)
```

```
IdxNN =

    17     4
     6     2
     1    12
    89    66
   124   100
```

Each row of `NN` corresponds to a query data observation, and the column order corresponds to the order of the nearest neighbors. For example, using the Minkowski distance, the second nearest neighbor of `Q(3,:)` is `X(12,:)`.

Properties

`Distance` — Distance metric

`'chebychev' | 'cityblock' | 'euclidean' | 'minkowski'`

Distance metric used to find nearest neighbors of query points, specified as one of these strings.

Value	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference)
`'cityblock'`	City block distance
`'euclidean'`	Euclidean distance

Value	Description
`'minkowski'`	Minkowski distance

For more details, see “Distance Metrics”.

The software does not use the distance metric for training the *K*d-tree, so you can alter it after training using dot notation.

Data Types: `char`

`DistParameter` — Distance metric parameter values

`[]` | positive scalar

Distance metric parameter values, specified as empty (`[]`) or as a positive scalar.

If `Distance` is `'minkowski'`, then:

- `DistParameter` is the exponent in the Minkowski distance formula.
- You can alter `DistParameter` of a trained `KDTreeSearcher` model.

Otherwise, `DistParameter` is `[]`, indicating that the specified distance metric formula has no parameters.

Data Types: `single` | `double`

`X` — Training data

numeric matrix

Training data that grows the *K*d-tree, specified as a numeric matrix. `X` has *n* rows, each corresponding to an observation (i.e., an instance or example), and *K* columns, each corresponding to a predictor or feature.

Data Types: `single` | `double`

Object Functions

`knnsearch` `rangesearch`

Create Object

Train a `KDTreeSearcher` model object using `KDTreeSearcher` or `createns`.

See Also

`ExhaustiveSearcher`

More About

- "*k*-Nearest Neighbor Search and Radius Search" on page 16-11
- "Distance Metrics"

Kernel property

Class: ProbDistKernel

Read-only string specifying name of kernel smoothing function for ProbDistKernel object

Description

`Kernel` is a read-only property of the `ProbDistKernel` class. `Kernel` is a string specifying the name of the kernel smoothing function used to create a ProbDistKernel object.

Values

```
'normal'
'box'
'triangle'
'epanechnikov'
```

Use this information to view and compare the kernel smoothing function used to create distributions.

See Also

`ksdensity`

prob.KernelDistribution class

Package: prob
Superclasses: prob.TruncatableDistribution

Kernel probability distribution object

Description

`prob.KernelDistribution` is an object consisting of parameters, a model description, and sample data for a nonparametric kernel-smoothing distribution. Create a `prob.KernelDistribution` object using `fitdist` or `dfittool`.

Construction

`pd = fitdist(x,'Kernel')` creates a probability distribution object by fitting a kernel-smoothing distribution to the data in x.

`pd = fitdist(x,'Kernel',Name,Value)` creates a probability distribution object with additional options specified by one or more name-value pair arguments. For example, you can change the kernel function or specify the kernel bandwidth.

Input Arguments

x — Input data

column vector

Input data to fit with a kernel-smoothing distribution, specified as a column vector of scalar values. `fitdist` ignores `NaN` values in x.

Data Types: `single | double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Kernel'` — Kernel smoother type

`'normal'` (default) | `'box'` | `'triangle'` | `'epanechnikov'`

Kernel smoother type, specified as the comma-separated pair consisting of `'Kernel'` and one of the following kernel smoothing function types:

- `'normal'`
- `'box'`
- `'triangle'`
- `'epanechnikov'`

`'Support'` — Kernel density support

`'unbounded'` (default) | `'positive'` | two-element vector

Kernel density support, specified as the comma-separated pair consisting of `'Support'` and a string or two-element vector. The string must be one of the following.

`'unbounded'`	Density can extend over the whole real line.
`'positive'`	Density is restricted to positive values.

Alternatively, you can specify a two-element vector giving finite lower and upper limits for the support of the density.

Data Types: `single` | `double`

`'Width'` — Bandwidth of kernel smoothing window

scalar value

Bandwidth of the kernel smoothing window, specified as the comma-separated pair consisting of `'Width'` and a scalar value. The default value used by `fitdist` is optimal for estimating normal densities, but you might want to choose a smaller value to reveal features such as multiple modes.

Data Types: `single` | `double`

Properties

`Kernel` — Kernel smoother type

`'normal'` | `'box'` | `'triangle'` | `'epanechnikov'`

Kernel function type, stored as a valid kernel function type name.

`BandWidth` — Bandwidth of kernel smoothing window

positive scalar value

Bandwidth of the kernel smoothing window, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Methods

mean	Mean of probability distribution object
negloglik	Negative loglikelihood
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate

Truncate probability distribution object

Definitions

Kernel Distribution

The kernel distribution is a nonparametric estimation of the probability density function (pdf) of a random variable.

The kernel distribution uses the following options.

Option	Description	Possible Values
`Kernel`	Kernel function type	`normal`, `box`, `triangle`, `epanechnikov`
`BandWidth`	Kernel smoothing parameter	`BandWidth > 0`

The kernel density estimator is

$$\hat{f}_h(x) = \frac{1}{nh}\sum_{i=1}^{n} K\left(\frac{x - x_i}{h}\right) \quad ; \quad -\infty < x < \infty ,$$

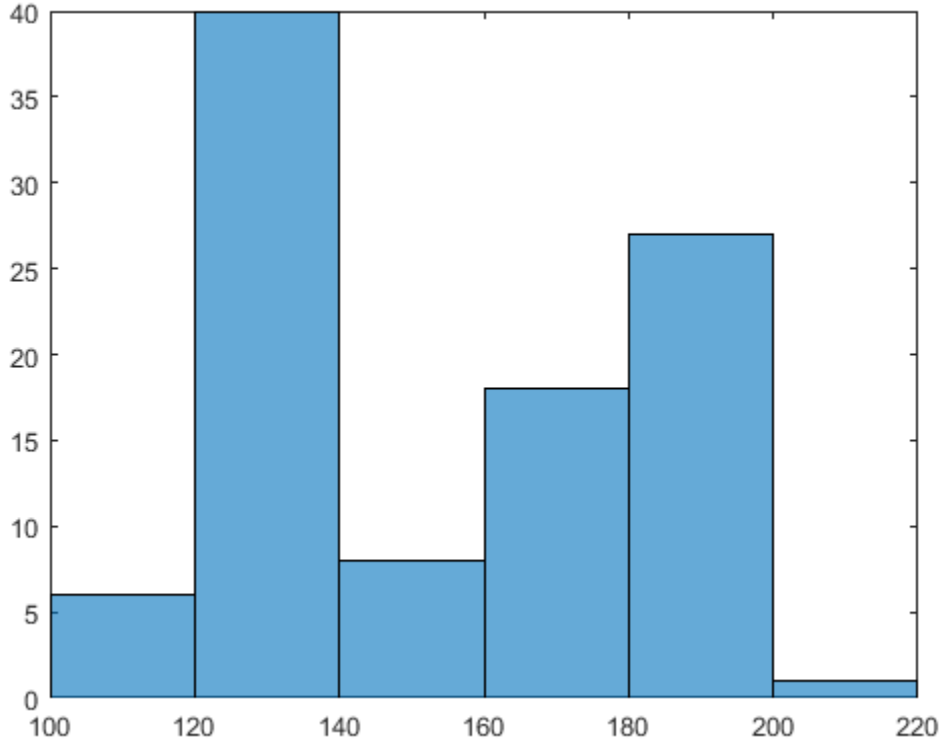
where n is the sample size, $K(\bullet)$ is the kernel function, and h is the bandwidth.

Examples

Fit a Kernel Distribution Object to Data

Load the sample data. Visualize the patient weight data using a histogram.

```
load hospital
histogram(hospital.Weight)
```



The histogram shows that the data has two modes, one for female patients and one for male patients.

Create a probability distribution object by fitting a kernel distribution to the patient weight data.

```
pd_kernel = fitdist(hospital.Weight,'Kernel')
```

```
pd_kernel =

  KernelDistribution

    Kernel = normal
    Bandwidth = 14.3792
```

```
    Support = unbounded
```

For comparison, create another probability distribution object by fitting a normal distribution to the patient weight data.

```
pd_normal = fitdist(hospital.Weight,'Normal')
```

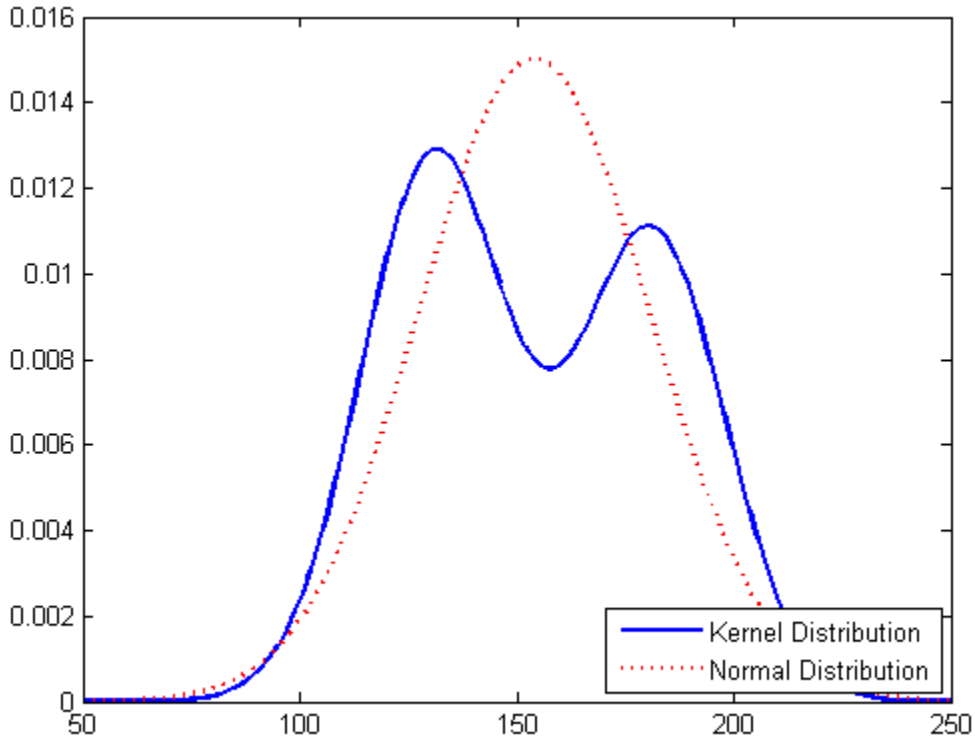
```
pd_normal =

  NormalDistribution

  Normal distribution
       mu =     154   [148.728, 159.272]
    sigma = 26.5714   [23.3299, 30.8674]
```

Define the x values and compute the pdf of each distribution.

```
x = 50:1:250;
pdf_kernel = pdf(pd_kernel,x);
pdf_normal = pdf(pd_normal,x);
```

Plot the pdf of each distribution.

```
plot(x,pdf_kernel,'Color','b','LineWidth',2);
hold on;
plot(x,pdf_normal,'Color','r','LineStyle',':','LineWidth',2);
legend('Kernel Distribution','Normal Distribution','Location','SouthEast');
hold off;
```



Fitting a kernel distribution instead of a unimodal distribution such as the normal reveals the separate modes for the female and male patients.

- "Fit Kernel Distribution Object to Data" on page 5-49

See Also

`dfittool` | `fitdist`

More About

- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40

- “Kernel Distribution”
- Class Attributes
- Property Attributes

kfoldEdge

Classification edge for observations not used for training

Syntax

```
edge = kfoldEdge(CVMdl)
edge = kfoldEdge(CVMdl,Name,Value)
```

Description

`edge = kfoldEdge(CVMdl)` returns the classification edge obtained by the cross-validated ECOC model (`ClassificationPartitionedECOC`) `CVMdl`. For every fold, `kfoldEdge` computes the classification edge for in-fold observations using an ECOC model trained on out-of-fold observations. `CVMdl.X` contains both sets of observations.

`edge = kfoldEdge(CVMdl,Name,Value)` returns the classification edge with additional options specified by one or more Name,Value pair arguments.

For example, specify the number of folds, decoding scheme, or verbosity level.

Input Arguments

`CVMdl` — Cross-validated ECOC model

`ClassificationPartitionedECOC` model

Cross-validated ECOC model, specified as a `ClassificationPartitionedECOC` model. You can create a `ClassificationPartitionedECOC` model by:

- Passing a trained ECOC model (`ClassificationECOC`) to `crossval`
- Training an ECOC model using `fitcecoc` and setting any one of these cross-validation name-value pair arguments: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

`CVMdl.BinaryLoss` (default) | function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in {-1,1,0}) and f_j is the score for observation j.

Value	Description	Score Domain	Formula
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2yf)]/\log(2)$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-yf)$
`'hamming'`	Hamming	$(-\infty,\infty)$ or $[0,1]$	$1 - \text{sign}(yf)$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - yf)$
`'linear'`	Linear	$(-\infty,\infty)$	$1 - yf$
`'quadratic'`	Quadratic	$[0,1]$	$[1 - y(2f - 1)]^2$

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,f)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `CVMdl.CodingMatrix`.
  - `f` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss.

- K is the number of classes.
- L is the number of binary learners.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Folds'` — Fold indices for prediction

`1:Mdl.KFold` (default) | numeric vector of positive integers

Fold indices for prediction, specified as the comma-separated pair consisting of `'Folds'` and a numeric vector of positive integers. The elements of `Folds` must range from `1` through `Mdl.KFold`.

The software only uses the folds specified in `Folds` for prediction.

Example: `'Folds',[1 4 10]`

Data Types: `single` | `double`

`'Mode'` — Edge meaning

`'average'` (default) | `'individual'`

Edge meaning, specified as the comma-separated pair consisting of `'Mode'` and `'average'` or `'individual'`.

This table describes the values.

Value	Description
`'average'`	`edge` is the scalar average over all folds.
`'individual'`	`edge` is a vector of length k containing one edge per fold. k is the number of folds.

Example: `'Mode','individual'`

Data Types: `char`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single` | `double`

Output Arguments

`edge` — Classification edge

numeric scalar | numeric row vector

Classification edge, returned as a numeric scalar or numeric row vector.

If Mode is `'average'`, then `edge` is the average classification edge among all binary learners. Otherwise, `edge` is a 1-by-`L` numeric row vector containing the classification edge for each, respective binary learner, where `L` is the number of binary learners (`size(`CVMdl`.CodingMatrix,2)`).

Data Types: `single` | `double`

Definitions

Classification Edge

The *classification edge* is the weighted mean of the *classification margins*.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margin

The *classification margins* are, for each observation, the difference between the negative loss for the positive class and maximal negative loss among the negative classes. If the margins are on the same scale, then they serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [4].

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} |m_{kj}| \, g(m_{kj}, s_j)}{\sum_{j=1}^{L} |m_{kj}|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Estimate *k*-Fold Cross-Validation Edge of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
```

```
X = meas;
Y = categorical(species);
classOrder = unique(Y);
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'CrossVal','on','Learners',t,'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedModel` model. By default, the software implements 10-fold cross validation. You can alter the number of folds using the `'KFold'` name-value pair argument.

Estimate the average of the out-of-fold edges.

```
edge = kfoldEdge(CVMdl)
```

```
edge =

    0.4825
```

Alternatively, you can obtain the per-fold edges by specifying the name-value pair `'Mode','individual'` in `kfoldEdge`.

Display Individual Edges for Each Cross-Validation Fold

The classification edge is a relative measure of classifier quality. You can determine ill-performing folds by displaying the edges for each fold.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y);
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify to use 8-fold cross validation. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'KFold',8,'Learners',t,'ClassNames',classOrder);
```

Estimate the classification edge for each fold.

```
edges = kfoldEdge(CVMdl,'Mode','individual')
```

```
edges =

    0.4791
    0.4872
    0.4260
    0.5302
    0.5064
    0.4575
    0.4860
    0.4687
```

The edges have similar magnitudes across folds. Ill-performing folds have low edges relative to the other folds.

You can return the classification edge for the entire model by specifying the well-performing folds using the `'Folds'` name-value pair argument.

Select ECOC Model Features by Comparing Cross-Validation Edges

The classifier edge measures the average of the classifier margins. One way to perform feature selection is to compare cross-validation edges from multiple models. Based solely on this criterion, the classifier with the highest edge is the best classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Define these two data sets:

- `fullX` contains all predictors.
- `partX` contains the petal dimensions.

```
fullX = X;
partX = X(:,3:4);
```

Train an ECOC model using SVM binary classifiers for each predictor set, and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(fullX,Y,'CrossVal','on','Learners',t,...
    'ClassNames',classOrder);
PCVMdl = fitcecoc(partX,Y,'CrossVal','on','Learners',t,...
    'ClassNames',classOrder);
```

`CVMdl` and `PCVMdl` are `ClassificationPartitionedECOC` models. By default, the software implements 10-fold cross validation.

Estimate the test-sample edge for each classifier.

```
fullEdge = kfoldEdge(CVMdl)
partEdge = kfoldEdge(PCVMdl)
```

```
fullEdge =

    0.4825


partEdge =

    0.4951
```

`PCVMdl` achieves an edge that is similar to the more complex model `CVMdl`.

- “Quick Start Parallel Computing for Statistics and Machine Learning Toolbox” on page 21-2

References

See Also

`ClassificationECOC` | `ClassificationPartitionedModel` | `edge` | `fitcecoc` | `kfoldMargin` | `kfoldPredict` | `statset`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

kfoldEdge

Class: ClassificationPartitionedEnsemble

Classification edge for observations not used for training

Syntax

```
E = kfoldEdge(obj)
E = kfoldEdge(obj,Name,Value)
```

Description

`E = kfoldEdge(obj)` returns classification edge (average classification margin) obtained by cross-validated classification ensemble `obj`. For every fold, this method computes classification edge for in-fold observations using an ensemble trained on out-of-fold observations.

`E = kfoldEdge(obj,Name,Value)` calculates edge with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

Object of class `ClassificationPartitionedEnsemble`. Create `ens` with `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `ens` from a classification ensemble with `crossval`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'folds'`

Indices of folds ranging from `1` to `ens.KFold`. Use only these folds for predictions.

Default: `1:ens.KFold`

`'mode'`

String representing the meaning of the output edge:

- `'average'` — `edge` is a scalar value, the average over all folds.
- `'individual'` — `edge` is a vector of length `ens.KFold` with one element per fold.
- `'cumulative'` — `edge` is a vector of length `min(ens.NTrainedPerFold)` in which element `J` is obtained by averaging values across all folds for weak learners `1:J` in each fold.

Default: `'average'`

Output Arguments

`E`

The average classification margin. `E` is a scalar or vector, depending on the setting of the `mode` name-value pair.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `obj.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `obj.X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Compute the k-fold edge for an ensemble trained on the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
cvens = crossval(ens);
E = kfoldEdge(cvens)

E =
    3.2078
```

See Also

`kfoldLoss` | `kfoldMargin` | `crossval` | `kfoldPredict` | `kfoldfun`

kfoldEdge

Class: ClassificationPartitionedModel

Classification edge for observations not used for training

Syntax

```
E = kfoldEdge(obj)
E = kfoldEdge(obj,Name,Value)
```

Description

`E = kfoldEdge(obj)` returns classification edge (average classification margin) obtained by cross-validated classification model `obj`. For every fold, this method computes classification edge for in-fold observations using an ensemble trained on out-of-fold observations.

`E = kfoldEdge(obj,Name,Value)` calculates edge with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`obj`

Object of class `ClassificationPartitionedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'folds'`

Indices of folds ranging from `1` to `obj.KFold`. Use only these folds for predictions.

Default: `1:obj.KFold`

`'mode'`

String representing the meaning of the output edge:

- `'average'` — `edge` is a scalar value, the average over all folds.
- `'individual'` — `edge` is a vector of length `obj.KFold` with one element per fold.

Default: `'average'`

Output Arguments

`E`

The average classification margin. `E` is a scalar or vector, depending on the setting of the `mode` name-value pair.

Definitions

Edge

The *edge* is the weighted mean value of the classification *margin*. The weights are class prior probabilities. If you supply additional weights, those weights are normalized to sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

The classification margin is a column vector with the same number of rows as in the matrix X. A high value of margin indicates a more reliable prediction than a low value.

Score

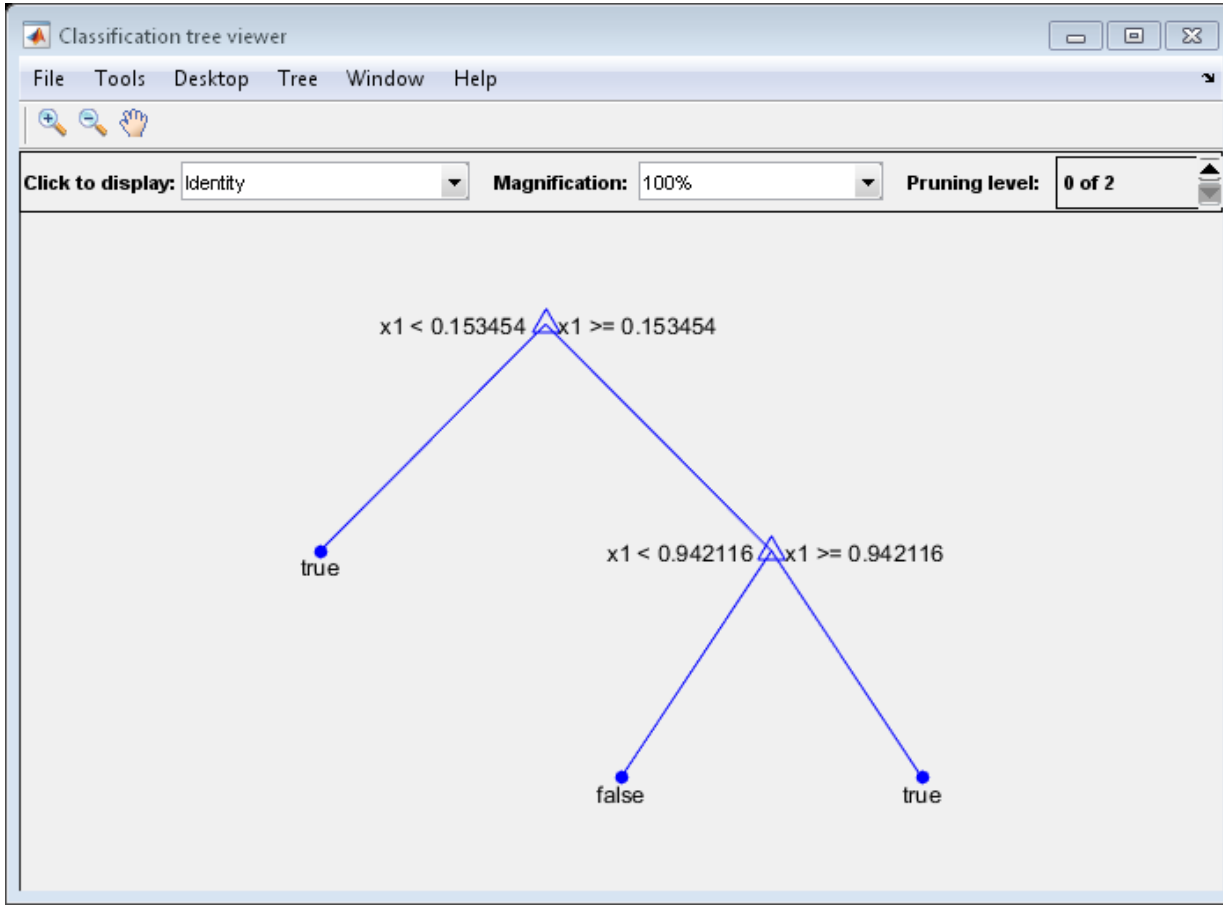
For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see “Posterior Probability” on page 15-7.

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

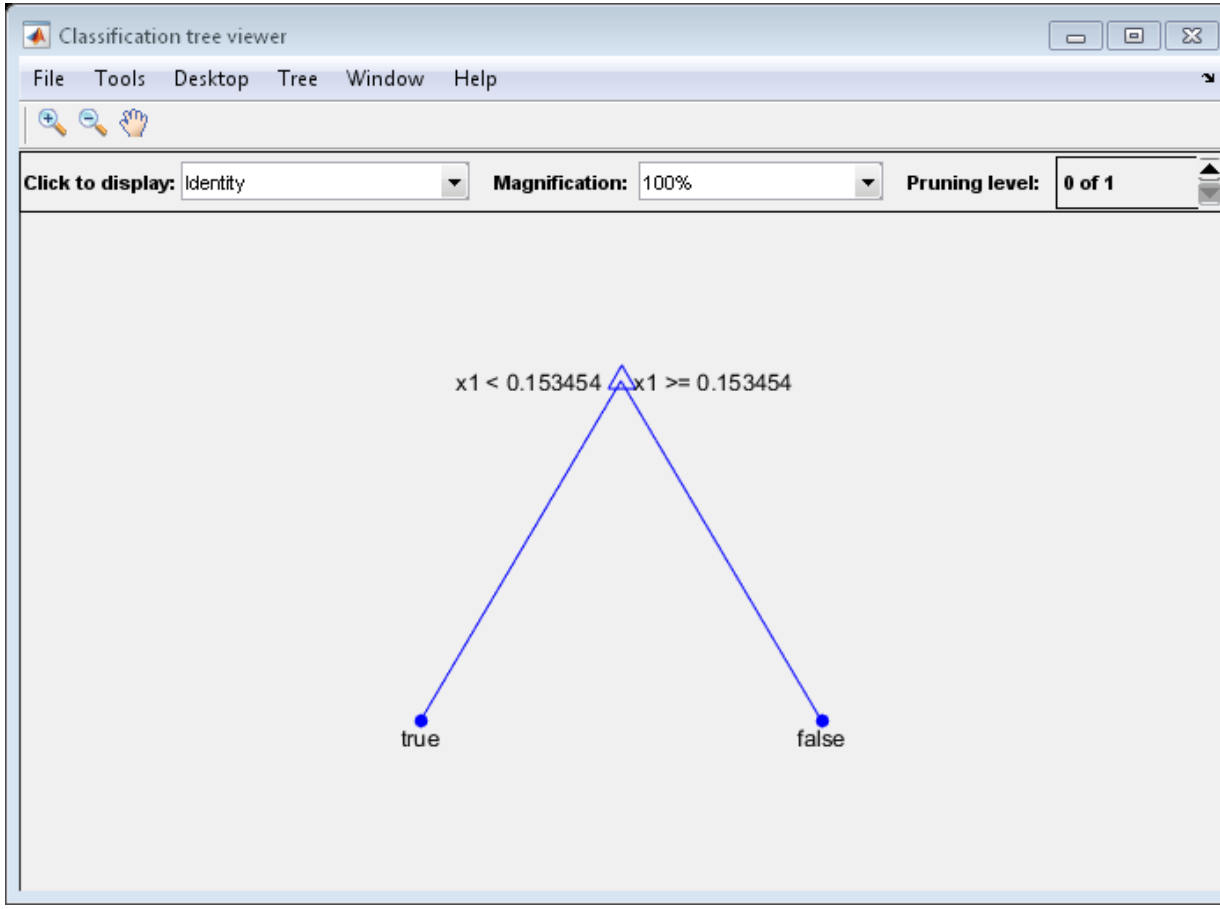
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Esimtate the *k*-fold Edge of a Classifier

Compute the *k*-fold edge for a model trained on Fisher's iris data.

Load Fisher's iris data set.

```
load fisheriris
```

Train a classification tree classifier.

```
tree = fitctree(meas,species);
```

Cross validate the classifier using 10-fold cross validation.

```
cvtree = crossval(tree);
```

Compute the *k*-fold edge.

```
edge = kfoldEdge(cvtree)
```

```
edge =

    0.8578
```

See Also

kfoldMargin | kfoldLoss | kfoldfun | crossval | ClassificationPartitionedModel | kfoldPredict | ClassificationPartitionedEnsemble

kfoldfun

Class: ClassificationPartitionedECOC

Cross validate function

Syntax

```
vals = kfoldfun(CVMdl,fun)
```

Description

`vals = kfoldfun(CVMdl,fun)` cross validates the function `fun` by applying `fun` to the data stored in the cross-validated model `CVMdl`. You must pass `fun` as a function handle.

Input Arguments

`CVMdl` — Cross-validated model

`ClassificationPartitionedECOC` model | `ClassificationPartitionedEnsemble` model | `ClassificationPartitionedModel` model

Cross-validated model, specified as a `ClassificationPartitionedECOC` model, `ClassificationPartitionedEnsemble` model, or a `ClassificationPartitionedModel` model.

`fun` — Cross-validated function

function handle

Cross-validated function, specified as a function handle. `fun` has the syntax

```
testvals = fun(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)
```

- `CMP` is a compact model stored in one element of the CVMdl`.Trained` property.
- `Xtrain` is the training matrix of predictor values.
- `Ytrain` is the training array of response values.
- `Wtrain` are the training weights for observations.

- `Xtest` and `Ytest` are the test data, with associated weights `Wtest`.
- The returned value `testvals` needs the same size across all folds.

Data Types: `function_handle`

Output Arguments

`vals` — Cross-validation results

numeric matrix

Cross-validation results, returned as an numeric matrix. `vals` is the arrays of `testvals` output, concatenated vertically over all folds. For example, if `testvals` from every fold is a numeric vector of length `N`, `kfoldfun` returns a `KFold`-by-`N` numeric matrix with one row per fold.

Data Types: `double`

Examples

Estimate Classification Error Using a Custom Loss Function

Train an ECOC multiclass classifier, and then cross validate it using a custom *k*-fold loss function.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers for each predictor set, and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'CrossVal','on','Learners',t,...
    'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. By default, the software implements 10-fold cross validation.

Compute the classification error (proportion of misclassified observations) for the out-of-fold observations.

```
L = kfoldLoss(CVMdl)
```

```
L =

    0.0400
```

Examine the result when the cost of misclassifying a flower as `'versicolor'` is `10`, and any other error is `1`. Write a function called `noversicolor.m` that attributes a cost of `1` for misclassification, but `10` for misclassifying a flower as `versicolor`, and save it on your MATLAB path.

```
function averageCost = noversicolor(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)
%noversicolor Example custom cross-validation function
%   Attributes a cost of 10 for misclassifying versicolor irises, and 1 for
%   the other irises.  This example function requires the |fisheriris| data
%   set.
Ypredict = predict(CMP,Xtest);
misclassified = not(strcmp(Ypredict,Ytest)); % Different result
classifiedAsVersicolor = strcmp(Ypredict,'versicolor'); % Index of bad decisions
cost = sum(misclassified) + ...
    9*sum(misclassified & classifiedAsVersicolor); % Total differences
averageCost = cost/numel(Ytest); % Average error
end
```

Compute the mean misclassification error with the `noversicolor` cost.

```
foldLoss = kfoldfun(CVMdl,@noversicolor);
mean(foldLoss)
```

```
ans =

    0.0667
```

See Also

`ClassificationECOC` | `ClassificationPartitionedECOC` | `ClassificationPartitionedModel` | `crossval` | `fitcecoc` | `kfoldEdge` | `kfoldLoss` | `kfoldMargin` | `kfoldPredict`

kfoldfun

Class: ClassificationPartitionedModel

Cross validate function

Syntax

```
vals = kfoldfun(CVMdl,fun)
```

Description

`vals = kfoldfun(CVMdl,fun)` cross validates the function `fun` by applying `fun` to the data stored in the cross-validated model `CVMdl`. You must pass `fun` as a function handle.

Input Arguments

`CVMdl` — Cross-validated model

`ClassificationPartitionedECOC` model | `ClassificationPartitionedEnsemble` model | `ClassificationPartitionedModel` model

Cross-validated model, specified as a `ClassificationPartitionedECOC` model, `ClassificationPartitionedEnsemble` model, or a `ClassificationPartitionedModel` model.

`fun` — Cross-validated function

function handle

Cross-validated function, specified as a function handle. `fun` has the syntax

```
testvals = fun(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)
```

- `CMP` is a compact model stored in one element of the CVMdl.`Trained` property.
- `Xtrain` is the training matrix of predictor values.
- `Ytrain` is the training array of response values.

- `Wtrain` are the training weights for observations.
- `Xtest` and `Ytest` are the test data, with associated weights `Wtest`.
- The returned value `testvals` needs the same size across all folds.

Data Types: `function_handle`

Output Arguments

`vals` — Cross-validation results

numeric matrix

Cross-validation results, returned as an numeric matrix. `vals` is the arrays of `testvals` output, concatenated vertically over all folds. For example, if `testvals` from every fold is a numeric vector of length `N`, `kfoldfun` returns a `KFold`-by-`N` numeric matrix with one row per fold.

Data Types: `double`

Examples

Estimate Classification Error Using a Custom Loss Function

Train a classification tree classifier, and then cross validate it using a custom *k*-fold loss function.

Load Fisher's iris data set.

```
load fisheriris
```

Train a classification tree classifier.

```
Mdl = fitctree(meas,species);
```

`Mdl` is a `ClassificationTree` model.

Cross validate `Mdl` using the default 10-fold cross validation. Compute the classification error (proportion of misclassified observations) for the out-of-fold observations.

```
rng(1); % For reproducibility
CVMdl = crossval(Mdl);
```

```
L = kfoldLoss(CVMdl)
```

```
L =

    0.0467
```

Examine the result when the cost of misclassifying a flower as `'versicolor'` is `10`, and any other error is `1`. Write a function called `noversicolor.m` that attributes a cost of `1` for misclassification, but `10` for misclassifying a flower as `versicolor`, and save it on your MATLAB path.

```
function averageCost = noversicolor(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)
%noversicolor Example custom cross-validation function
%   Attributes a cost of 10 for misclassifying versicolor irises, and 1 for
%   the other irises.  This example function requires the |fisheriris| data
%   set.
Ypredict = predict(CMP,Xtest);
misclassified = not(strcmp(Ypredict,Ytest)); % Different result
classifiedAsVersicolor = strcmp(Ypredict,'versicolor'); % Index of bad decisions
cost = sum(misclassified) + ...
    9*sum(misclassified & classifiedAsVersicolor); % Total differences
averageCost = cost/numel(Ytest); % Average error
end
```

Compute the mean misclassification error with the `noversicolor` cost.

```
mean(kfoldfun(CVMdl,@noversicolor))
```

```
ans =

    0.2267
```

See Also

`ClassificationPartitionedModel` | `kfoldEdge` | `kfoldMargin` | `kfoldLoss` | `crossval` | `ClassificationPartitionedECOC` | `kfoldPredict` | `crossval`

kfoldfun

Class: RegressionPartitionedModel

Cross validate function

Syntax

```
vals = kfoldfun(obj,fun)
```

Description

`vals = kfoldfun(obj,fun)` cross validates the function `fun` by applying `fun` to the data stored in the cross-validated model `obj`. You must pass `fun` as a function handle.

Input Arguments

`obj`

Object of class `RegressionPartitionedModel` or `RegressionPartitionedEnsemble`. Create `obj` with `fitrtree` or `fitensemble` along with one of the cross-validation options: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. Alternatively, create `obj` from a regression tree or regression ensemble with `crossval`.

`fun`

A function handle for a cross-validation function. `fun` has the syntax

```
testvals = fun(CMP,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)
```

- `CMP` is a compact model stored in one element of the obj`.Trained` property.
- `Xtrain` is the training matrix of predictor values.
- `Ytrain` is the training array of response values.
- `Wtrain` are the training weights for observations.
- `Xtest` and `Ytest` are the test data, with associated weights `Wtest`.

- The returned value `testvals` must have the same size across all folds.

Output Arguments

`vals`

The arrays of `testvals` output, concatenated vertically over all folds. For example, if `testvals` from every fold is a numeric vector of length `N`, `kfoldfun` returns a `KFold`-by-`N` numeric matrix with one row per fold.

Examples

Cross validate a regression tree, and obtain the mean squared error (see `kfoldLoss`):

```
load imports-85
t = fitrtree(X(:,[4 5]),X(:,16),...
    'predictornames',{'length' 'width'},...
    'responsename','price');
cv = crossval(t);
L = kfoldLoss(cv)

L =
  1.5489e+007
```

Examine the result of simple averaging of responses instead of using predictions:

```
f = @(cmp,Xtrain,Ytrain,Wtrain,Xtest,Ytest,Wtest)...
    mean((Ytest-mean(Ytrain)).^2)
mean(kfoldfun(cv,f))

ans =
  6.3497e+007
```

See Also

`RegressionPartitionedEnsemble` | `kfoldLoss` | `crossval` | `fitrtree` | `kfoldPredict` | `RegressionPartitionedModel`

kfoldLoss

Classification loss for observations not used for training

Syntax

```
loss = kfoldLoss(CVMdl)
loss = kfoldLoss(CVMdl,Name,Value)
```

Description

`loss = kfoldLoss(CVMdl)` returns the classification loss obtained by the cross-validated ECOC model (`ClassificationPartitionedECOC`) `CVMdl`. For every fold, this function computes the classification loss for in-fold observations using a model trained on out-of-fold observations. `CVMdl.X` contains both sets of observations.

`loss = kfoldLoss(CVMdl,Name,Value)` returns the classification loss with additional options specified by one or more Name,Value pair arguments.

For example, specify the number of folds, decoding scheme, or verbosity level.

Input Arguments

`CVMdl` — Cross-validated ECOC model

`ClassificationPartitionedECOC` model

Cross-validated ECOC model, specified as a `ClassificationPartitionedECOC` model. You can create a `ClassificationPartitionedECOC` model by:

- Passing a trained ECOC model (`ClassificationECOC`) to `crossval`
- Training an ECOC model using `fitcecoc` and setting any one of these cross-validation name-value pair arguments: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

`CVMdl.BinaryLoss` (default) | function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in {-1,1,0}) and f_j is the score for observation j.

Value	Description	Score Domain	Formula
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2yf)]/\log(2)$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-yf)$
`'hamming'`	Hamming	$(-\infty,\infty)$ or $[0,1]$	$1 - \text{sign}(yf)$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - yf)$
`'linear'`	Linear	$(-\infty,\infty)$	$1 - yf$
`'quadratic'`	Quadratic	$[0,1]$	$[1 - y(2f - 1)]^2$

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,f)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `CVMdl.CodingMatrix`.
  - `f` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss.

- K is the number of classes.
- L is the number of binary learners.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Folds'` — Fold indices for prediction

`1:Mdl.KFold` (default) | numeric vector of positive integers

Fold indices for prediction, specified as the comma-separated pair consisting of `'Folds'` and a numeric vector of positive integers. The elements of `Folds` must range from `1` through `Mdl.KFold`.

The software only uses the folds specified in `Folds` for prediction.

Example: `'Folds',[1 4 10]`

Data Types: `single` | `double`

`'LossFun'` — Loss function

`'classiferror'` (default) | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or `'classiferror'`.

You can:

- Specify the built-in function `'classiferror'`, then the loss function is the classification error, in other words, the proportion of misclassified observations.
- Specify your own function using function handle notation.

  Suppose that `n = size(X,1)` is the sample size and `k` is the number of classes. Your function needs the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

- The output argument `lossvalue` is a scalar.
- You choose the function name (*`lossfun`*).
- `C` is an `n`-by-`k` logical matrix with rows indicating which class the corresponding observation belongs. The column order corresponds to the class order in `CVMdl.ClassNames`.

  Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q`, for each row. Set every element of row `p` to `0`.
- `S` is an `n`-by-`k` numeric matrix of negated loss values for classes. Each row corresponds to an observation. The column order corresponds to the class order in `CVMdl.ClassNames`. `S` resembles the output argument `negLoss` of `kfoldPredict`.
- `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes its elements to sum to `1`.
- `Cost` is a `k`-by-`k` numeric matrix of misclassification costs. For example, `Cost = ones(K) -eye(K)` specifies a cost of 0 for correct classification, and 1 for misclassification.

Specify your function using `'LossFun',@lossfun`.

Data Types: `function_handle | char`

`'Mode'` — Edge meaning

`'average'` (default) | `'individual'`

Edge meaning, specified as the comma-separated pair consisting of `'Mode'` and `'average'` or `'individual'`.

This table describes the values.

Value	Description
`'average'`	`edge` is the scalar average over all folds.
`'individual'`	`edge` is a vector of length *k* containing one edge per fold. *k* is the number of folds.

Example: `'Mode','individual'`

Data Types: `char`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single` | `double`

Output Arguments

`loss` — Classification loss

numeric scalar | numeric row vector

Classification loss, returned as a numeric scalar or numeric row vector.

If Mode is `'average'`, then `loss` is the average classification loss among all binary learners. Otherwise, `loss` is a 1-by-`L` numeric row vector containing the classification loss for each, respective binary leanrer, where `L` is the number of binary learners (`size(`CVMdl`.CodingMatrix,2)`).

Data Types: `single` | `double`

Definitions

Classification Error

The *classification error* is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j e_j}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is the weight for observation j. The software renormalizes the weights to sum to 1.
- e_j = 1 if the predicted class of observation j differs from its true class, and 0 otherwise.

In other words, it is the proportion of observations that the classifier misclassifies.

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} |m_{kj}| \, g(m_{kj}, s_j)}{\sum_{j=1}^{L} |m_{kj}|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Determine *k*-Fold Cross-Validation Loss of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers, and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'CrossVal','on','Learners',t,'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. By default, the software implements 10-fold cross validation. You can alter the number of folds using the `'KFold'` name-value pair argument.

Estimate the average out-of-fold classification error.

```
L = kfoldLoss(CVMdl)
```

```
L =

    0.0400
```

The average classification error for the folds is 4%.

Alternatively, you can obtain the per-fold losses by specifying the name-value pair `'Mode','individual'` in `kfoldLoss`.

Display Individual Losses for Each Cross-Validation Fold

The classification loss is a measure of classifier quality. You can determine ill-performing folds by displaying the losses for each fold.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y);
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify to use 8-fold cross validation. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'KFold',8,'Learners',t,'ClassNames',classOrder);
```

Estimate the average classification loss across folds, and the losses for each fold.

```
loss = kfoldLoss(CVMdl)
losses = kfoldLoss(CVMdl,'Mode','individual')
```

```
loss =

    0.0333


losses =

    0.0556
    0.0526
    0.1579
         0
         0
         0
         0
         0
```

The third fold misclassifies a much higher portion of observations than any other fold.

Return the classification loss for the entire model by specifying the well-performing folds using the `'Folds'` name-value pair argument.

```
loss = kfoldLoss(CVMdl,'Folds',[1:2 4:8])
```

```
loss =

    0.0153
```

The total classification loss decreased by approximately half its original size.

Consider adjusting parameters of the binary classifiers or the coding design to see if performance for all folds improves.

Determine ECOC Model Quality Using a Custom Cross-Validation Loss

Suppose that it is interesting to know how well a model classifies a particular class. This example shows how to pass such a custom loss function to `kfoldLoss`.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
n = numel(Y);           % Sample size
classOrder = unique(Y)  % Class order
K = numel(classOrder);  % Number of classes
rng(1) % For reproducibility
```

```
classOrder =

     setosa
     versicolor
     virginica
```

Train an ECOC model using SVM binary classifiers, and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'CrossVal','on','Learners',t,'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. By default, the software implements 10-fold cross validation. You can alter the number of folds using the `'KFold'` name-value pair argument.

Compute the negated losses for the out-of-fold observations.

```
[~,negLoss] = kfoldPredict(CVMdl);
```

Create a function that takes the minimal loss for each observation, and then averages the minimal losses across all observations.

```
lossfun = @(C,S,~,~)mean(min(-negLoss,[],2));
```

Compute the cross-validated custom loss.

```
kfoldLoss(CVMdl,'LossFun',lossfun)
```

```
ans =

    0.0101
```

The average, minimal, binary loss for the out-of-fold observations is 0.0101.

- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q, X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `ClassificationPartitionedModel` | `fitcecoc` | `kfoldPredict` | `loss` | `statset`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13

- “Concepts of Parallel Computing in Statistics and Machine Learning Toolbox” on page 21-7

kfoldLoss

Class: ClassificationPartitionedEnsemble

Classification loss for observations not used for training

Syntax

```
L = kfoldLoss(ens)
L = kfoldLoss(ens,Name,Value)
```

Description

`L = kfoldLoss(ens)` returns loss obtained by cross-validated classification model `ens`. For every fold, this method computes classification loss for in-fold observations using a model trained on out-of-fold observations.

`L = kfoldLoss(ens,Name,Value)` calculates loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

Object of class `ClassificationPartitionedEnsemble`. Create `ens` with `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `ens` from a classification ensemble with `crossval`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'folds'`

Indices of folds ranging from `1` to ens`.KFold`. Use only these folds for predictions.

Default: `1:ens.KFold`

`'lossfun '`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-2365
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 22-2365
- `'hinge'` — See "Loss Functions" on page 22-2365.
- `'mincost'` — Smallest misclassification cost as given by the obj`.Cost` matrix. See "Loss Functions" on page 22-2365.

You can write your own loss function in the syntax described in "Loss Functions" on page 22-2365.

Default: `'classiferror'`

`'mode'`

A string for determining the output of `kfoldLoss`:

- `'average'` — L is a scalar, the loss averaged over all folds.
- `'individual'` — L is a vector of length ens`.KFold`, where each entry is the loss for a fold.
- `'cumulative'` — L is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'average'`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'hinge'` — Classification error measure that has the form

$$L=\frac{\sum_{j=1}^{n} w_j \max\left\{0,1-y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of `ens.X`.
- `K` is the number of classes in ens, represented in `ens.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `score` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Find the average cross-validated classification error for an ensemble model of the `ionosphere` data:

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)

L =
    0.0826
```

See Also

`kfoldEdge` | `kfoldMargin` | `crossval` | `kfoldPredict` | `kfoldfun`

kfoldLoss

Class: ClassificationPartitionedModel

Classification loss for observations not used for training

Syntax

```
L = kfoldLoss(obj)
L = kfoldLoss(obj,Name,Value)
```

Description

`L = kfoldLoss(obj)` returns loss obtained by cross-validated classification model `obj`. For every fold, this method computes classification loss for in-fold observations using a model trained on out-of-fold observations.

`L = kfoldLoss(obj,Name,Value)` calculates loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`obj`

Object of class `ClassificationPartitionedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'folds'`

Indices of folds ranging from `1` to obj`.KFold`. Use only these folds for predictions.

Default: `1:obj.KFold`

`'lossfun '`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-2369.
- `'classiferror'` — Fraction of misclassified observations. See "Loss Functions" on page 22-2369.
- `'exponential'` — See "Loss Functions" on page 22-2369.
- `'hinge'` — See "Loss Functions" on page 22-2369.
- `'mincost'` — Smallest misclassification cost as given by the obj`.Cost` matrix. See "Loss Functions" on page 22-2369.

You can write your own loss function in the syntax described in "Loss Functions" on page 22-2369.

Default: `'mincost'`

`'mode'`

A string for determining the output of `kfoldLoss`:

- `'average'` — L is a scalar, the loss averaged over all folds.
- `'individual'` — L is a vector of length obj`.KFold`, where each entry is the loss for a fold.

Default: `'average'`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Classification Error

The default classification error is the fraction of the data X that obj misclassifies, where Y are the true classifications.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when obj misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

  $$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

  $$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'classiferror'` — Predict the label with the largest posterior probability. The loss is then the fraction of misclassified observations.
- `'hinge'` — Classification error measure that has the form

  $$L=\frac{\sum_{j=1}^{n} w_j \max\left\{0,1-y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

  where:

  - w_j is weight j.

  - For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
  - $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.
- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file in this form:

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in the classifier, represented in the `ClassNames` property.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in the `ClassNames` property.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST = ones(K) - eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

Examples

Find the average cross-validated classification error for a model of the `ionosphere` data:

```
load ionosphere
tree = fitctree(X,Y);
```

```
cvtree = crossval(tree);
L = kfoldLoss(cvtree)

L =
    0.1197
```

See Also

`ClassificationPartitionedModel` | `kfoldEdge` | `kfoldMargin` | `kfoldfun` | `crossval` | `kfoldPredict`

How To

- “Examine the Quality of a KNN Classifier” on page 16-29

kfoldLoss

Class: RegressionPartitionedEnsemble

Cross-validation loss of partitioned regression ensemble

Syntax

```
L = kfoldLoss(cvens)
L = kfoldLoss(cvens,Name,Value)
```

Description

`L = kfoldLoss(cvens)` returns the cross-validation loss of `cvens`.

`L = kfoldLoss(cvens,Name,Value)` returns cross-validation loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`cvens`

Object of class `RegressionPartitionedEnsemble`. Create `obj` with `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `obj` from a regression ensemble with `crossval`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'folds'`

Indices of folds ranging from `1` to `cvens.KFold`. Use only these folds for predictions.

Default: `1:cvens.KFold`

`'lossfun'`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `loss` calls it as

```
fun(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length.

- `Y` is the observed response.
- `Yfit` is the predicted response.
- `W` is the observation weights.

The returned value `fun(Y,Yfit,W)` should be a scalar.

Default: `'mse'`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

The loss (mean squared error) between the observations in a fold when compared against predictions made with an ensemble trained on the out-of-fold data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Examples

Find the cross-validation loss for a regression ensemble of the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
rens = fitensemble(X,MPG,'LSboost',100,'Tree');
cvrens = crossval(rens);
L = kfoldLoss(cvrens)

L =
   25.6935
```

See Also

`RegressionPartitionedEnsemble` | `loss` | `kfoldPredict`

kfoldLoss

Class: RegressionPartitionedModel

Cross-validation loss of partitioned regression model

Syntax

```
L = kfoldLoss(cvmodel)
L = kfoldLoss(cvmodel,Name,Value)
```

Description

`L = kfoldLoss(cvmodel)` returns the cross-validation loss of `cvmodel`.

`L = kfoldLoss(cvmodel,Name,Value)` returns cross-validation loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`cvmodel`

Object of class `RegressionPartitionedModel`. Create `obj` with `fitrtree` along with one of the cross-validation options: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. Alternatively, create `obj` from a regression tree with `crossval`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'folds'`

Indices of folds ranging from `1` to `obj.KFold`. Use only these folds for predictions.

Default: `1:obj.KFold`

`'lossfun'`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `kfoldLoss` calls it as

```
fun(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length.

- `Y` is the observed response.
- `Yfit` is the predicted response.
- `W` is the observation weights.

The returned value `fun(Y,Yfit,W)` should be a scalar.

Default: `'mse'`

`'mode'`

One of the following strings:

- `'average'` — L is the average loss over all folds.
- `'individual'` — L is a vector of the individual losses of in-fold observations trained on out-of-fold data.

Default: `'average'`

Output Arguments

`L`

The loss (mean squared error) between the observations in a fold when compared against predictions made with a tree trained on the out-of-fold data. If `mode` is `'individual'`, `L` is a vector of the losses. If `mode` is `'average'`, `L` is the average loss.

Examples

Construct a partitioned regression model, and examine the cross-validation losses for the folds:

```
load carsmall
XX = [Cylinders Displacement Horsepower Weight];
YY = MPG;
cvmodel = fitrtree(XX,YY,'crossval','on');
L = kfoldLoss(cvmodel,'mode','individual')

L =
   44.9635
   11.8525
   18.2046
    9.2965
   29.4329
   54.8659
   24.6446
    8.2085
   19.7593
   16.7394
```

Alternatives

You can avoid constructing a cross-validated tree model by calling `cvLoss` instead of `kfoldLoss`. The cross-validated tree can save time if you are going to examine it more than once.

See Also

`loss` | `kfoldPredict` | `fitrtree`

kfoldMargin

Classification margins for observations not used for training

Syntax

```
margin = kfoldMargin(CVMdl)
margin = kfoldMargin(CVMdl,Name,Value)
```

Description

`margin = kfoldMargin(CVMdl)` returns classification margins obtained by the cross-validated ECOC model (`ClassificationPartitionedECOC`) `CVMdl`. For every fold, this method computes classification margins for in-fold observations using a model trained on out-of-fold observations. `CVMdl.X` contains both sets of observations.

`margin = kfoldMargin(CVMdl,Name,Value)` returns classification margins with additional options specified by one or more Name,Value pair arguments.

For example, specify the binary learner loss function, decoding scheme, or verbosity level.

Input Arguments

`CVMdl` — Cross-validated ECOC model

`ClassificationPartitionedECOC` model

Cross-validated ECOC model, specified as a `ClassificationPartitionedECOC` model. You can create a `ClassificationPartitionedECOC` model by:

- Passing a trained ECOC model (`ClassificationECOC`) to `crossval`
- Training an ECOC model using `fitcecoc` and setting any one of these cross-validation name-value pair arguments: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

`CVMdl.BinaryLoss` (default) | function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in {-1,1,0}) and f_j is the score for observation j.

Value	Description	Score Domain	Formula
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2yf)]/\log(2)$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-yf)$
`'hamming'`	Hamming	$(-\infty,\infty)$ or $[0,1]$	$1 - \text{sign}(yf)$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - yf)$
`'linear'`	Linear	$(-\infty,\infty)$	$1 - yf$
`'quadratic'`	Quadratic	$[0,1]$	$[1 - y(2f - 1)]^2$

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,f)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `CVMdl.CodingMatrix`.
  - `f` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss.

- K is the number of classes.
- L is the number of binary learners.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Options'` — Estimation options

`[ ]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single` | `double`

Output Arguments

`margin` — Classification margins

numeric vector

Classification margins, returned as a numeric vector. `margin` is an `n`-by-1 vector, where each row is the margin of the corresponding observation, and `n` is the number of observations (i.e., `size(`CVMdl`.X,1)`).

Data Types: `single` | `double`

Definitions

Classification Margin

The *classification margins* are, for each observation, the difference between the negative loss for the positive class and maximal negative loss among the negative classes. If the margins are on the same scale, then they serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [4].

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left| m_{kj} \right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Estimate *k*-Fold Cross-Validated Margins of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y);
rng(1); % For reproducibility
```

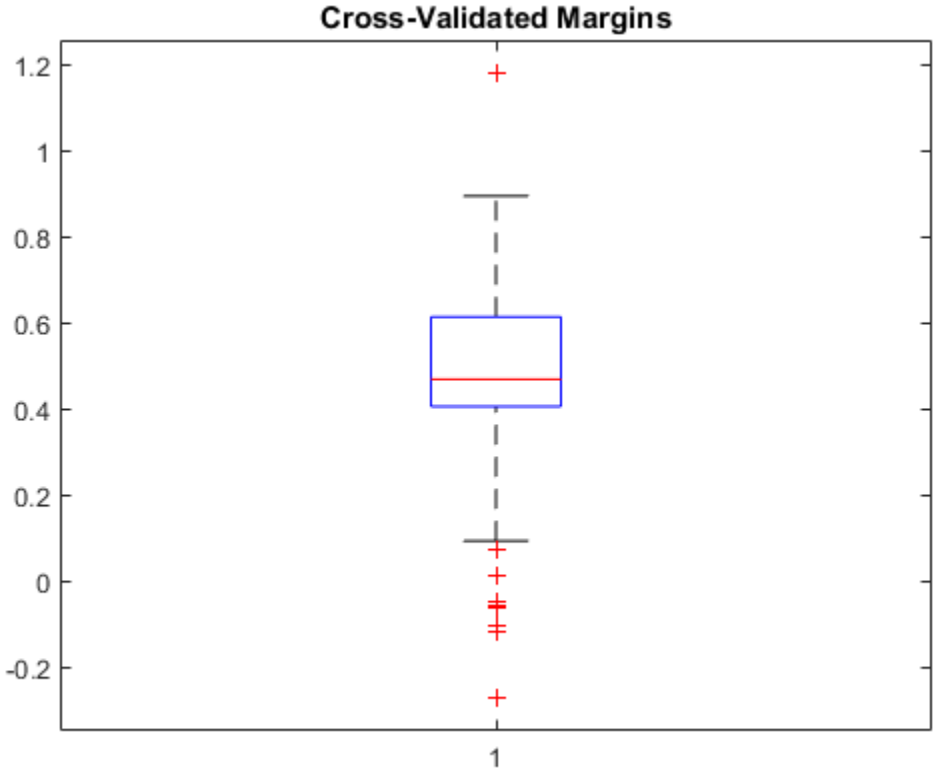
Train an ECOC model using SVM binary classifiers and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'CrossVal','on','Learners',t,'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedModel` model. By default, the software implements 10-fold cross validation. You can alter the number of folds using the `'KFold'` name-value pair argument.

Estimate the out-of-fold margins. Display the distribution of the mnargins using a boxplot.

```
margin = kfoldMargin(CVMdl);

figure;
boxplot(margin);
title('Cross-Validated Margins')
```



An observation margin is the positive-class, negated loss minus the maximum negative-class, negated loss. Classifiers that yield relatively large margins are desirable.

Select ECOC Model Features by Comparing Cross-Validation Margins

The classifier margin measures the average of the classifier margins. One way to perform feature selection is to compare cross-validation margins from multiple models. Based solely on this criterion, the classifier with the greater margins is the best classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
```

```
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Define these two data sets:

- `fullX` contains all predictors.
- `partX` contains the petal dimensions.

```
fullX = X;
partX = X(:,3:4);
```

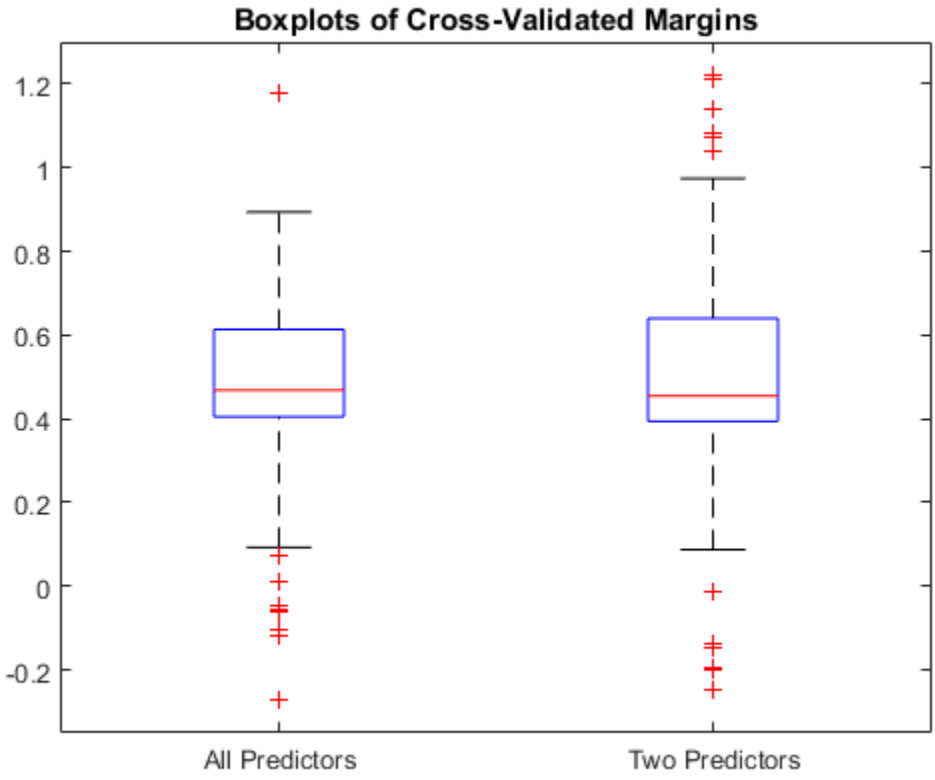
Train an ECOC model using SVM binary classifiers for each predictor set, and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(fullX,Y,'CrossVal','on','Learners',t,...
    'ClassNames',classOrder);
PCVMdl = fitcecoc(partX,Y,'CrossVal','on','Learners',t,...
    'ClassNames',classOrder);
```

`CVMdl` and `PCVMdl` are `ClassificationPartitionedECOC` models. By default, the software implements 10-fold cross validation.

Estimate the test sample margin for each classifier. Specify to use loss-based decoding for aggregating the binary learner results. For each model, display the distribution of the margins using a boxplot.

```
fullMargins = kfoldMargin(CVMdl,'Decoding','lossbased');
partMargins = kfoldMargin(PCVMdl,'Decoding','lossbased');

figure;
boxplot([fullMargins partMargins],'Labels',{'All Predictors','Two Predictors'});
title('Boxplots of Cross-Validated Margins')
```



The margin distributions are approximately the same, but `PCVMdl` is a less complex model, which might make it more desirable.

- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q., X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `ClassificationPartitionedModel` | `fitcecoc` | `kfoldEdge` | `kfoldPredict` | `margin` | `statset`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

kfoldMargin

Class: ClassificationPartitionedModel

Classification margins for observations not used for training

Syntax

```
M = kfoldMargin(obj)
```

Description

`M = kfoldMargin(obj)` returns classification margins obtained by cross-validated classification model `obj`. For every fold, this method computes classification margins for in-fold observations using a model trained on out-of-fold observations.

Input Arguments

`obj`

A partitioned classification model of type `ClassificationPartitionedModel` or `ClassificationPartitionedEnsemble`.

Output Arguments

`M`

The classification margin.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

The classification margin is a column vector with the same number of rows as in the matrix X. A high value of margin indicates a more reliable prediction than a low value.

Score

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 15-7.

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

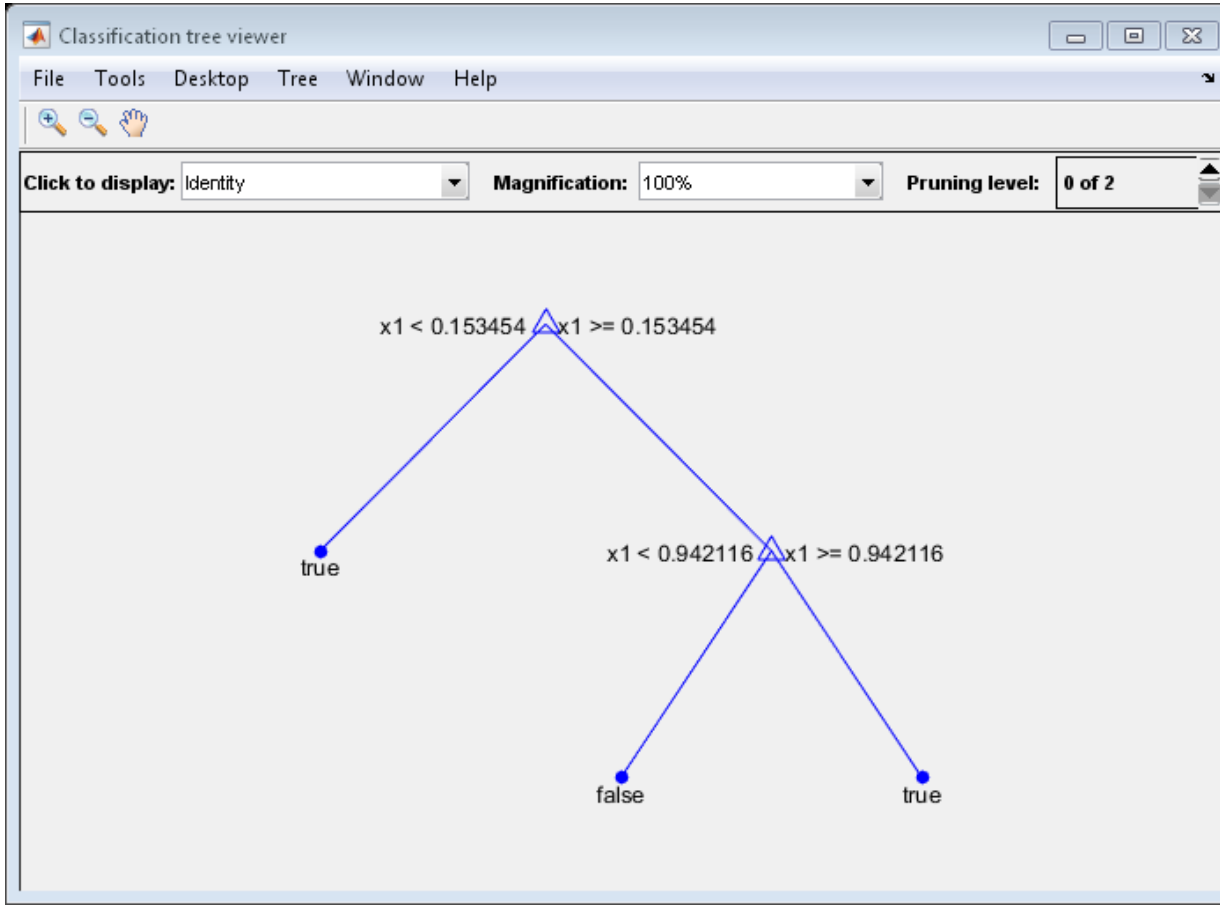
- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

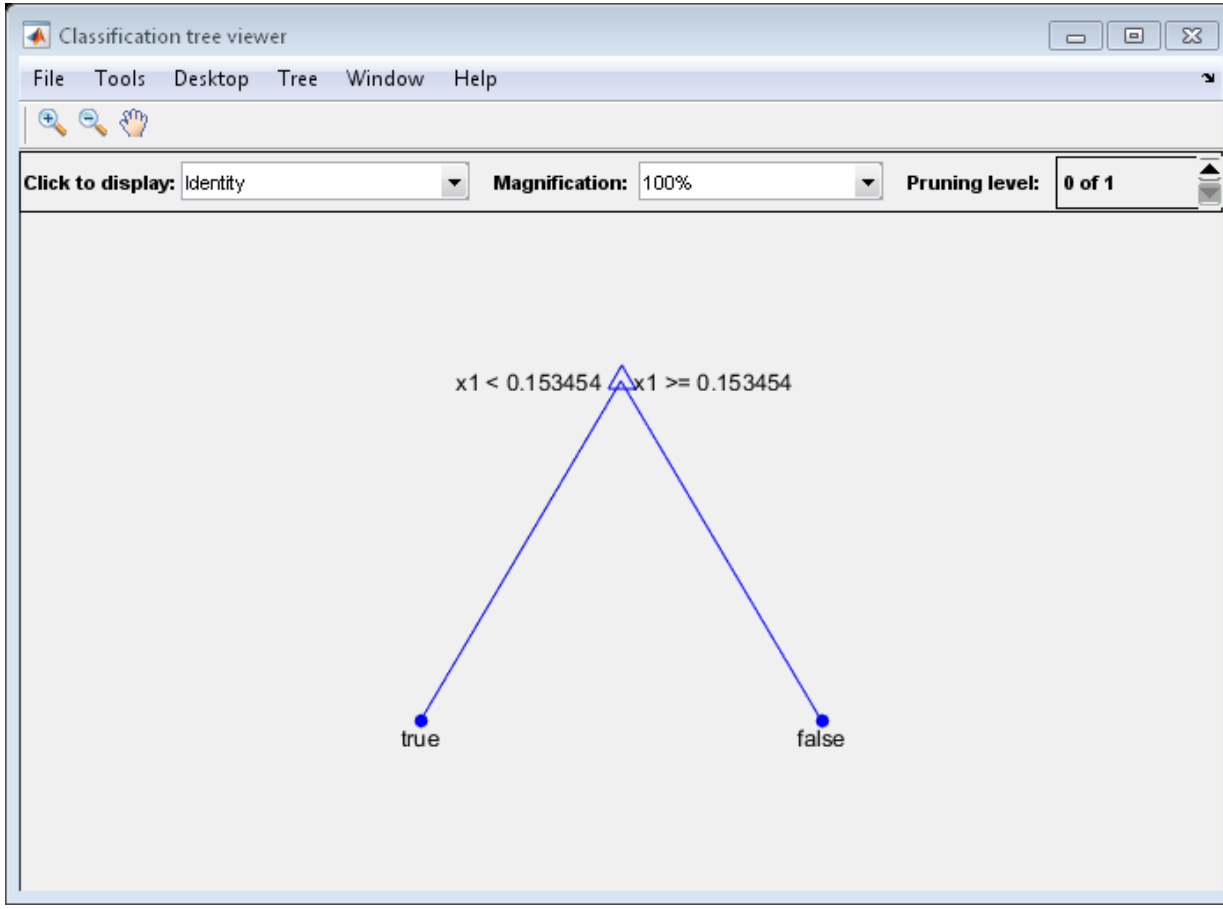
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Esimtate the *k*-fold Margins of a Classifier

Find the *k*-fold margins for an ensemble that classifies the `ionosphere` data.

Load the `ionosphere` data set.

```
load ionosphere
```

Train a classification ensemble of decision trees.

```
Mdl = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
```

Cross validate the classifier using 10-fold cross validation.

```
cvens = crossval(Mdl);
```

Compute the _k_fold margins. Disaply summary statistics for the margins.

```
m = kfoldMargin(cvens);
marginStats = table(min(m),mean(m),max(m),...
    'VariableNames',{'Min','Mean','Max'})
```

```
marginStats =

      Min        Mean       Max
    _______    _______    ______

    -11.312    7.3236     23.517
```

See Also

ClassificationPartitionedModel | kfoldEdge | kfoldLoss | kfoldfun | crossval | kfoldPredict

kfoldPredict

Predict responses for observations not used for training

Syntax

```
label = kfoldPredict(CVMdl)
label = kfoldPredict(CVMdl,Name,Value)
[label,NegLoss,PBScore] = kfoldPredict( ___ )
[label,NegLoss,PBScore,Posterior] = kfoldPredict( ___ )
```

Description

`label = kfoldPredict(CVMdl)` returns class labels predicted by the cross-validated ECOC model (`ClassificationPartitionedECOC`) `CVMdl`. For every fold, `kfoldPredict` predicts class labels for in-fold observations using a model trained on out-of-fold observations. `CVMdl.X` contains both sets of observations.

The software predicts the classification of an observation by assigning the observation to the class yielding the largest negated average binary loss (or, equivalently, the smallest average binary loss).

`label = kfoldPredict(CVMdl,Name,Value)` returns predicted class labels with additional options specified by one or more Name,Value pair arguments.

For example, specify the posterior probability estimation method, decoding scheme, or verbosity level.

`[label,NegLoss,PBScore] = kfoldPredict( ___ )` additionally returns negated values of the average binary loss per class (`NegLoss`) for in-fold observations, and positive-class scores (`PBScore`) for in-fold observations classified by each binary learner.

If the coding matrix varies across folds (that is, if the coding scheme is `sparserandom` or `denserandom`), then `PBScore` is empty (`[]`).

`[label,NegLoss,PBScore,Posterior] = kfoldPredict( ___ )` additionally returns posterior class probability estimates for in-fold observations (`Posterior`).

To obtain posterior class probabilities, you must set `'FitPosterior',1` when training the ECOC model using `fitcecoc`. Otherwise, `kfoldPredict` throws an error.

Input Arguments

`CVMdl` — Cross-validated ECOC model

`ClassificationPartitionedECOC` model

Cross-validated ECOC model, specified as a `ClassificationPartitionedECOC` model. You can create a `ClassificationPartitionedECOC` model by:

- Passing a trained ECOC model (`ClassificationECOC`) to `crossval`
- Training an ECOC model using `fitcecoc` and setting any one of these cross-validation name-value pair arguments: `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

`CVMdl.BinaryLoss` (default) | function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in {-1,1,0}) and f_j is the score for observation j.

Value	Description	Score Domain	Formula
`'binodeviance'`	Binomial deviance	(-∞,∞)	$\log[1 + \exp(-2yf)]/\log(2)$
`'exponential'`	Exponential	(-∞,∞)	$\exp(-yf)$
`'hamming'`	Hamming	(-∞,∞) or [0,1]	$1 - \text{sign}(yf)$
`'hinge'`	Hinge	(-∞,∞)	$\max(0,1 - yf)$
`'linear'`	Linear	(-∞,∞)	$1 - yf$

Value	Description	Score Domain	Formula
`'quadratic'`	Quadratic	[0,1]	$[1 - y(2f - 1)]^2$

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,f)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `CVMdl.CodingMatrix`.
  - `f` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss.
  - K is the number of classes.
  - L is the number of binary learners.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'NumKLInitializations'` — Number of random initial values

`0` (default) | nonnegative integer

Number of random initial values for fitting posterior probabilities by Kullback-Leibler divergence minimization, specified as the comma-separated pair consisting of `'NumKLInitializations'` and a nonnegative integer.

If you do not request the fourth output argument (Posterior) and set `'PosteriorMethod','kl'` (the default), then the software ignores the value of `NumKLInitializations`.

For more details, see "Posterior Estimation Using Kullback-Leibler Divergence" on page 22-3679.

Example: `'NumKLInitializations',5`

Data Types: `single` | `double`

`'Options'` — Estimation options

`[ ]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'PosteriorMethod'` — Posterior probability estimation method

`'kl'` (default) | `'qp'`

Posterior probability estimation method, specified as the comma-separated pair consisting of `'PosteriorMethod'` and `'kl'` or `'qp'`.

- If `PosteriorMethod` is `'kl'`, then the software estimates multiclass posterior probabilities by minimizing the Kullback-Leibler divergence between the predicted and expected posterior probabilities returned by binary learners. For details, see "Posterior Estimation Using Kullback-Leibler Divergence".
- If `PosteriorMethod` is `'qp'`, then the software estimates multiclass posterior probabilities by solving a least-squares problem using quadratic programming. You need an Optimization Toolbox license to use this option. For details, see "Posterior Estimation Using Quadratic Programming".
- If you do not request the fourth output argument (Posterior), then the software ignores the value of `PosteriorMethod`.

Example: `'PosteriorMethod','qp'`

Data Types: `char`

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single | double`

Output Arguments

`label` — Predicted class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Predicted class labels, returned as a categorical or character array, logical or numeric vector, or cell array of strings.

`label`:

- Is the same data type as CVMdl.Y
- Has length equal to the number of rows of CVMdl.X

The software predicts the classification of an observation by assigning the observation to the class yielding the largest negated average binary loss (or, equivalently, the smallest average binary loss).

`NegLoss` — Negated average binary losses

numeric matrix

Negated average binary losses, returned as a numeric matrix. `NegLoss` is an `n`-by-`K` matrix, where `n` is the number of observations (`size(`CVMdl`.X,1)`) and `K` is the number of unique classes (`size(CVMdl.ClassNames,1)`).

`PBScore` — Positive-class scores

numeric matrix

Positive-class scores for each binary learner, returned as a numeric matrix. `PBScore` is an `n`-by-`L` matrix, where `n` is the number of observations (`size(`CVMdl`.X,1)`) and `L` is the number of binary learners (`size(CVMdl.CodingMatrix,2)`).

If the coding matrix varies across folds (that is, if the coding scheme is `sparserandom` or `denserandom`), then `PBScore` is empty (`[]`).

`Posterior` — Posterior class probabilities
numeric matrix

Posterior class probabilities, returned as a numeric matrix. `Posterior` is an `n`-by-`K` matrix, where `n` is the number of observations (`size(`CVMdl`.X,1)`) and `K` is the number of unique classes (`size(CVMdl.ClassNames,1)`).

You must set `'FitPosterior',1` when training the ECOC model using `fitcecoc` to request `Posterior`. Otherwise, the software throws an error.

Definitions

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\arg\min} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} |m_{kj}|\, g(m_{kj}, s_j)}{\sum_{j=1}^{L} |m_{kj}|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Predict *k*-Fold Cross-Validation Labels of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
```

```
classOrder = unique(Y);
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'CrossVal','on','Learners',t,'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedModel` model. By default, the software implements 10-fold cross validation. You can alter the number of folds using the `'KFold'` name-value pair argument.

Predict the out-of-fold labels. Print a random subset of true and predicted labels.

```
labels = kfoldPredict(CVMdl);
idx = randsample(numel(labels),10);
table(Y(idx),labels(idx),...
    'VariableNames',{'TrueLabels','PredictedLabels'})
```

```
ans =

    TrueLabels    PredictedLabels
    __________    _______________

    setosa        setosa
    versicolor    versicolor
    setosa        setosa
    virginica     virginica
    versicolor    versicolor
    setosa        setosa
    virginica     virginica
    virginica     virginica
    setosa        setosa
    setosa        setosa
```

`CVMdl` correctly labeled the out-of-fold observations with indices `idx`.

Predict Cross-Validation Labels of ECOC Models Using Custom Binary Loss Function

Load Fisher's iris data set.

```
load fisheriris
```

```
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
K = numel(classOrder);  % Number of classes
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify to cross validate. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'CrossVal','on','Learners',t,'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedModel` model. By default, the software implements 10-fold cross validation. You can alter the number of folds using the `'KFold'` name-value pair argument.

SVM scores are signed distances from the observation to the decision boundary. Therefore, the domain is $(-\infty,\infty)$. Create a custom binary loss function that:

- Maps the coding design matrix (*M*) and positive-class classification scores (*s*) for each learner to the binary loss for each observation
- Uses linear loss
- Aggregates the binary learner loss using the median.

You can create a separate function for the binary loss function, and then save it on the MATLAB® path. Or, you can specify an anonymous binary loss function.

```
customBL = @(M,s)nanmedian(1 - bsxfun(@times,M,s),2)/2;
```

Predict cross-validation labels and estimate the median binary loss per class. Print the median negative binary losses per class for a random set of 10 out-of-fold observations.

```
[label,NegLoss] = kfoldPredict(CVMdl,'BinaryLoss',customBL);

idx = randsample(numel(label),10);
classOrder
table(Y(idx),label(idx),NegLoss(idx,:),'VariableNames',...
    {'TrueLabel','PredictedLabel','NegLoss'})


classOrder =

     setosa
```

```
     versicolor
     virginica


ans =

    TrueLabel     PredictedLabel                NegLoss
    __________    ______________    ____________________________________

    setosa        versicolor        0.37141       2.1292      -4.0006
    versicolor    versicolor        -1.2167       0.3669     -0.65017
    setosa        versicolor        0.23927         2.08      -3.8193
    virginica     virginica         -1.9154     -0.19947       0.6149
    versicolor    versicolor        -1.3746      0.45535     -0.58076
    setosa        versicolor        0.20061       2.2774      -3.9781
    virginica     versicolor        -1.4928     0.090689    -0.097935
    virginica     virginica         -1.7669     -0.13464       0.4015
    setosa        versicolor        0.19999       1.9113      -3.6113
    setosa        versicolor        0.16108       1.9684      -3.6295
```

The order of the columns corresponds to the elements of `classOrder`. The software predicts the label based on the maximum negated loss. The results seem to indicate that the median of the linear losses might not perform as well as other losses.

Estimate Cross-Validation Posterior Probabilities of ECOC Models

Load Fisher's iris data set. Train the classifier using the petal dimensions as predictors.

```
load fisheriris
X = meas(:,3:4);
Y = categorical(species);
classOrder = unique(Y);
rng(1); % For reproducibility
```

Create an SVM template, and specify the Gaussian kernel. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1,'KernelFunction','gaussian');
```

`t` is an SVM template. Most of its properties are empty. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier using the SVM template, and specify to cross validate. Transform classification scores to class posterior probabilities (returned by

`kfoldPredict`) using the `'FitPosterior'` name-value pair argument. It is good practice to specify the class order.

```
CVMdl = fitcecoc(X,Y,'Learners',t,'CrossVal','on','FitPosterior',true,...
    'ClassNames',classOrder);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. By default, the software uses 10-fold cross validation.

Predict the out-of-fold class posterior probabilities. Specify to use 10 random initial values for the Kullback-Leibler algorithm.

```
[label,~,~,Posterior] = kfoldPredict(CVMdl,'NumKLInitializations',10);
```

The software assigns an observation to the class that yields the smallest average binary loss. Since all binary learners are computing posterior probabilities, the binary loss function is `quadratic`.

Display a random set of results.

```
idx = randsample(size(X,1),10);
CVMdl.ClassNames
table(Y(idx),label(idx),Posterior(idx,:),...
    'VariableNames',{'TrueLabel','PredLabel','Posterior'})
```

```
ans =

     setosa
     versicolor
     virginica


ans =

    TrueLabel     PredLabel                  Posterior
    __________    __________    ___________________________________

    versicolor    versicolor     0.0086394       0.98243     0.0089291
    versicolor    virginica     2.2197e-14       0.12447       0.87553
    setosa        setosa             0.999    0.00022837    0.00076884
    versicolor    versicolor    2.2194e-14       0.98916      0.010839
    virginica     virginica       0.012318      0.012925       0.97476
    virginica     virginica      0.0015571     0.0015638       0.99688
    virginica     virginica      0.0042895     0.0043556       0.99135
```

```
    setosa        setosa             0.999     0.00028329     0.00071382
    virginica     virginica      0.0094719      0.0098229        0.98071
    setosa        setosa             0.999     0.00013562     0.00086192
```

The columns of `Posterior` correspond to the class order of `Mdl.ClassNames`.

Estimate Cross-Validation Posterior Probabilities Using Parallel Computing

Train an error-correcting output codes, multiclass model and estimate posterior probabilities using parallel computing.

Load the `arrhythmia` data set.

```
load arrhythmia
Y = categorical(Y);
tabulate(Y)
n = numel(Y);
K = numel(unique(Y));
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

Several classes are not represented in the data, and many of the other classes have low relative frequencies.

Specify an ensemble learning template that uses the GentleBoost method, and 50 weak, classification tree learners.

```
t = templateEnsemble('GentleBoost',50,'Tree');
```

`t` is a template object. Most of the options are empty (`[ ]`). The software uses default values for all empty options during training.

Since there are many classes, specify a sparse random coding design.

```
rng(1); % For reproducibility
Coding = designecoc(K,'sparserandom');
```

Train an ECOC model using parallel computing, and specify to cross validate and fit posterior probabilities (returned by `kfoldPredict`).

```
pool = parpool;                       % Invokes workers
options = statset('UseParallel',1);
CVMdl = fitcecoc(X,Y,'Learner',t,'Options',options,'Coding',Coding,...
    'FitPosterior',1,'CrossVal','on');
```

```
Starting parallel pool (parpool) using the 'local' profile ... connected to 4 workers.
Warning: One or more folds do not contain points from all the groups.
```

`CVMdl` is a `ClassificationPartitionedECOC` model. By default, the software implements 10-fold cross validation. You can alter the number of folds using the `'KFold'` name-value pair argument.

The pool invokes four workers. The number of workers might vary among systems. Also, there is a good chance that one or more folds do not contain observations from all classes since some classes have low relative frequency.

Estimate posterior probabilities, and display the posterior probability of being classified as not having arrhythmia (class 1) given the data for a random set of out-of-fold observations.

```
[~,~,~,posterior] = kfoldPredict(CVMdl,'Options',options);
idx = randsample(n,10);
table(idx,Y(idx),posterior(idx,1),...
    'VariableNames',{'OOFSampleIndex','TrueLabel','PosteriorNoArrhythmia'})
```

```
ans =

    OOFSampleIndex    TrueLabel    PosteriorNoArrhythmia
    ______________    _________    _____________________

    171               1             0.33654
    221               1             0.85135
     72               16             0.9174
      3               10            0.025649
    202               1              0.8438
    243               1             0.94338
     18               1             0.81789
```

```
 49          6          0.090153
234          1           0.61626
315          1           0.97187
```

- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

Algorithms

The software can estimate class posterior probabilities using quadratic programming or by minimizing the Kullback-Leibler divergence. For the following descriptions of the posterior estimation algorithms, let:

- m_{kj} be the element (k,j) of the coding design matrix M.
- I be the indicator function.
- $\hat{p}_k$ be the class posterior probability estimate for class k of an observation, $k = 1,...,K$.
- r_j be the positive-class posterior probability for binary learner j. That is, r_j is the probability that binary learner j classifies an observation into the positive class, given the training data.

Posterior Estimation Using Kullback-Leibler Divergence

By default, the software minimizes the Kullback-Leibler divergence to estimate class posterior probabilities. The Kullback-Leibler divergence between the expected and observed positive-class posterior probabilities is

$$\Delta(r,r) = \sum_{j=1}^{L} w_j \left[r_j \log \frac{r_j}{r_j} + \left(1 - r_j\right) \log \frac{1 - r_j}{1 - r_j} \right],$$

where $w_j = \sum_{S_j} w_i^*$ is the weight for binary learner j with S_j the set of observation indices that binary learner j is trained on and w_i^* is the weight of observation i. The software minimizes the divergence iteratively. The first step is to choose initial values $\hat{p}_k^{(0)};\ k = 1,...,K$ for the class posterior probabilities.

- If you do not specify NumKLIterations, then the software uses both sets of deterministic initial values described next, and uses the one that minimizes Δ.
  - $\hat{p}_k^{(0)} = 1/K;\ k = 1,...,K.$
  - $\hat{p}_k^{(0)};\ k = 1,...,K$ is the solution of the system

$$M_{01}\hat{p}^{(0)} = r,$$

    where M_{01} is M with all $m_{kj} = -1$ replaced with 0, and r is a vector of positive-class posterior probabilities returned by the L binary learners [2]. The software uses `lsqnonneg` to solve the system.
- If you specify `'NumKLIterations',c`, where `c` is a natural number, then the software does the following to choose $\hat{p}_k^{(0)};\ k = 1,...,K$, and uses the one that minimizes Δ.
  - The software chooses both sets of deterministic initial values as described previously.
  - The software randomly generates `c` vectors of length K using `rand`, and then normalizes each vector to sum to 1.

At iteration t, the software:

1. Computes

$$\hat{r}_j^{(t)} = \frac{\sum_{k=1}^{K} \hat{p}_k^{(t)} I(m_{kj} = +1)}{\sum_{k=1}^{K} \hat{p}_k^{(t)} I(m_{kj} = +1 \cup m_{kj} = -1)}.$$

2. Estimates the next class posterior probability using

$$\hat{p}_k^{(t+1)} = \hat{p}_k^{(t)} \frac{\sum_{j=1}^{L} w_j \left[r_j I\left(m_{kj} = +1\right) + \left(1 - r_j\right) I\left(m_{kj} = -1\right) \right]}{\sum_{j=1}^{L} w_j \left[\hat{r}_j^{(t)} I\left(m_{kj} = +1\right) + \left(1 - \hat{r}_j^{(t)}\right) I\left(m_{kj} = -1\right) \right]}.$$

3 Normalizes $\hat{p}_k^{(t+1)};\ k = 1,...,K$ so that they sum to 1.

4 Checks for convergence.

For more details, see [5] and [7].

Posterior Estimation Using Quadratic Programming

Posterior probability estimation using quadratic programming requires an Optimization Toolbox license. To estimate posterior probabilities for an observation using this method, the software:

1 Estimates the positive-class posterior probabilities, r_j, for binary learners $j = 1,...,L$.

2 Using the relationship between r_j and $\hat{p}_k$ [6], minimizes

$$\sum_{j=1}^{L} \left[-r_j \sum_{k=1}^{K} \hat{p}_k I\left(m_{kj} = -1\right) + \left(1 - r_j\right) \sum_{k=1}^{K} \hat{p}_k I\left(m_{kj} = +1\right) \right]^2$$

with respect to $\hat{p}_k$ and the restrictions

$$0 \le \hat{p}_k \le 1$$
$$\sum_k \hat{p}_k = 1.$$

The software performs minimization using `quadprog`.

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Dietterich, T., and G. Bakiri. "Solving Multiclass Learning Problems Via Error-Correcting Output Codes." *Journal of Artificial Intelligence Research*. Vol. 2, 1995, pp. 263–286.

[3] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[4] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[5] Hastie, T., and R. Tibshirani. "Classification by Pairwise Coupling." *Annals of Statistics*. Vol. 26, Issue 2, 1998, pp. 451–471.

[6] Wu, T. F., C. J. Lin, and R. Weng. "Probability Estimates for Multi-Class Classification by Pairwise Coupling." *Journal of Machine Learning Research*. Vol. 5, 2004, pp. 975–1005.

[7] Zadrozny, B. "Reducing Multiclass to Binary by Coupling Probability Estimates." *NIPS 2001: Proceedings of Advances in Neural Information Processing Systems 14*, 2001, pp. 1041–1048.

See Also

`ClassificationECOC` | `ClassificationPartitionedModel` | `edge` | `fitcecoc` | `predict` | `quadprog` | `statset`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

kfoldPredict

Class: ClassificationPartitionedModel

Predict response for observations not used for training

Syntax

```
label = kfoldPredict(obj)
[label,score] = kfoldPredict(obj)
[label,score,cost] = kfoldPredict(obj)
```

Description

`label = kfoldPredict(obj)` returns class labels predicted by `obj`, a cross-validated classification. For every fold, `kfoldPredict` predicts class labels for in-fold observations using a model trained on out-of-fold observations.

`[label,score] = kfoldPredict(obj)` returns the predicted classification scores for in-fold observations using a model trained on out-of-fold observations.

`[label,score,cost] = kfoldPredict(obj)` returns misclassification costs.

Input Arguments

`obj`

Object of class `ClassificationPartitionedModel` or `ClassificationPartitionedEnsemble`.

Output Arguments

`label`

Vector of class labels of the same type as the response data used in training obj. Each entry of `label` corresponds to a predicted class label for the corresponding row of `X`.

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in `obj.X`, and `K` is the number of classes (in `obj.ClassNames`). `score(i,j)` represents the confidence that row `i` of `obj.X` is of class `j`. For details, see "Definitions" on page 22-2412.

`cost`

Numeric matrix of misclassification costs of size `N`-by-`K`. `cost(i,j)` is the average misclassification cost of predicting that row `i` of `obj.X` is of class `j`.

Definitions

Cost (discriminant analysis)

The *average misclassification cost* is the mean misclassification cost for predictions made by the cross-validated classifiers trained on out-of-fold observations. The matrix of expected costs per observation is defined in "Cost" on page 15-8.

Score

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 15-7.

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

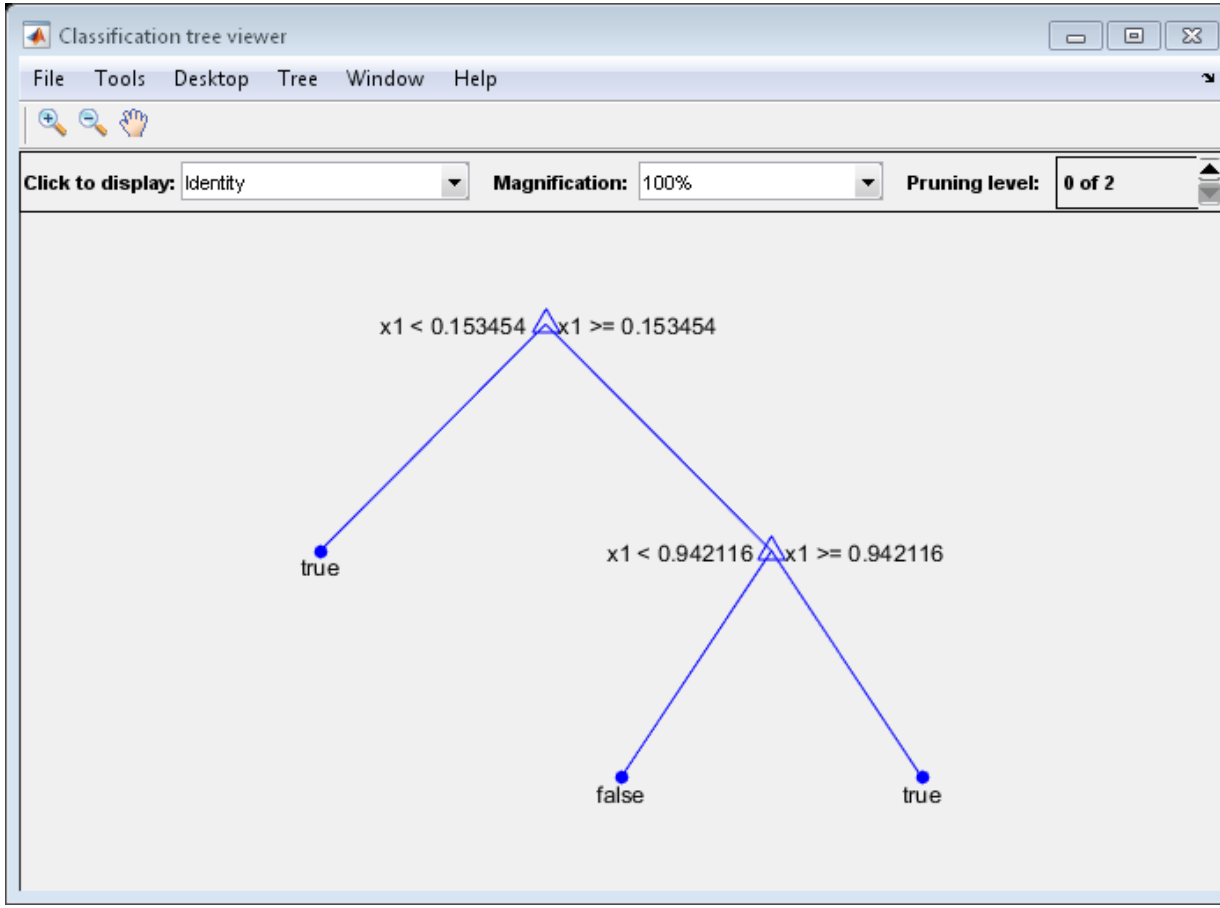
- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

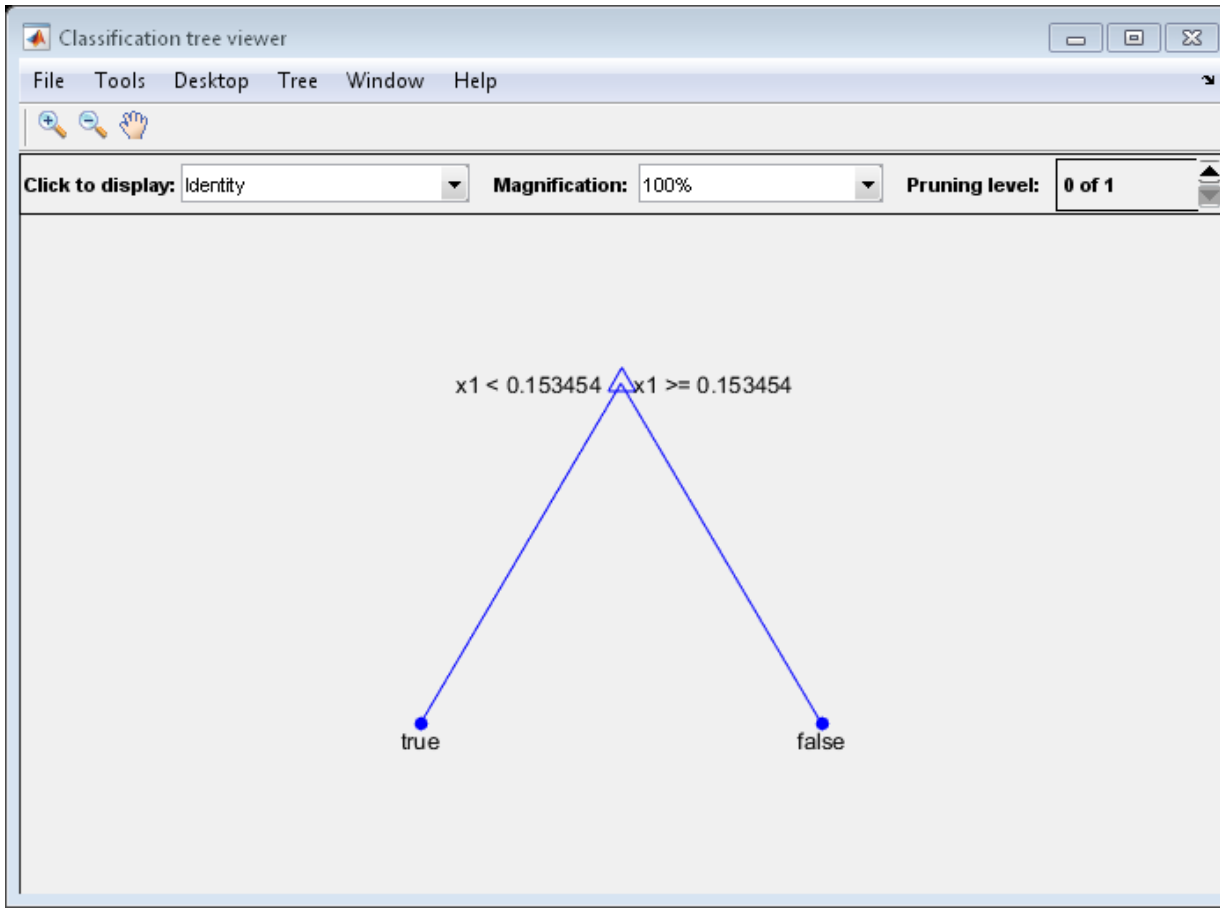
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
```

```
[score X(1:10,:)]

ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Estimate Cross-Validation Predictions from an Ensemble

Find the cross-validation predictions for a model based on Fisher's iris data.

Load Fisher's iris data set.

```
load fisheriris
```

Train an ensemble of classification trees.

```
rng(1); % For reproducibility
Mdl = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
```

Cross valdate the trained ensemble using 10-fold cross validation.

```
CVMdl = crossval(Mdl);
```

Estimate cross-validation predicted labels and scores.

```
[elabel escore] = kfoldPredict(CVMdl);
```

Display the maximum and minimum scores of each class.

```
max(escore)
min(escore)
```

```
ans =

    9.3862    8.9871   10.1866


ans =

    0.0017    3.8359    0.8981
```

See Also

ClassificationPartitionedModel | kfoldEdge | kfoldMargin | kfoldLoss | kfoldfun | crossval

kfoldPredict

Class: RegressionPartitionedModel

Predict response for observations not used for training.

Syntax

```
yfit = kfoldPredict(obj)
```

Description

`yfit = kfoldPredict(obj)` returns the predicted values for the responses of the training data based on `obj`, an object trained on out-of-fold observations.

Input Arguments

`obj`

Object of class `RegressionPartitionedModel`. Create `obj` with `fitrtree` or `fitensemble` along with one of the cross-validation options: `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. Alternatively, create `obj` from a regression tree or regression ensemble with `crossval`.

Output Arguments

`yfit`

A vector of predicted values for the response data based on a model trained on out-of-fold observations.

Examples

Construct a partitioned regression model, and examine the cross-validation loss. The cross-validation loss is the mean squared error between yfit and the true response data:

```
load carsmall
XX = [Cylinders Displacement Horsepower Weight];
YY = MPG;
tree = fitrtree(XX,YY);
cvmodel = crossval(tree);
L = kfoldLoss(cvmodel)

L =
   26.5271

yfit = kfoldPredict(cvmodel);
mean( (yfit - tree.Y).^2 )

ans =
   26.5271
```

See Also

`kfoldLoss` | `fitrtree`

kmeans

k-means clustering

Syntax

```
idx = kmeans(X,k)
idx = kmeans(X,k,Name,Value)
[idx,C] = kmeans(___)
[idx,C,sumd] = kmeans(___)
[idx,C,sumd,D] = kmeans(___)
```

Description

`idx = kmeans(X,k)` performs *k*-means clustering to partition the observations of the *n*-by-*p* data matrix `X` into `k` clusters, and returns an *n*-by-1 vector (`idx`) containing cluster indices of each observation. Rows of `X` correspond to points and columns correspond to variables.

By default, `kmeans` uses the squared Euclidean distance measure and the *k*-means++ algorithm for cluster center initialization.

`idx = kmeans(X,k,Name,Value)` returns the cluster indices with additional options specified by one or more `Name,Value` pair arguments.

For example, specify the cosine distance, the number of times to repeat the clustering using new initial values, or to use parallel computing.

`[idx,C] = kmeans(___)` returns the `k` cluster centroid locations in the `k`-by-*p* matrix `C`.

`[idx,C,sumd] = kmeans(___)` returns the within-cluster sums of point-to-centroid distances in the `k`-by-1 vector `sumd`.

`[idx,C,sumd,D] = kmeans(___)` returns distances from each point to every centroid in the *n*-by-`k` matrix `D`.

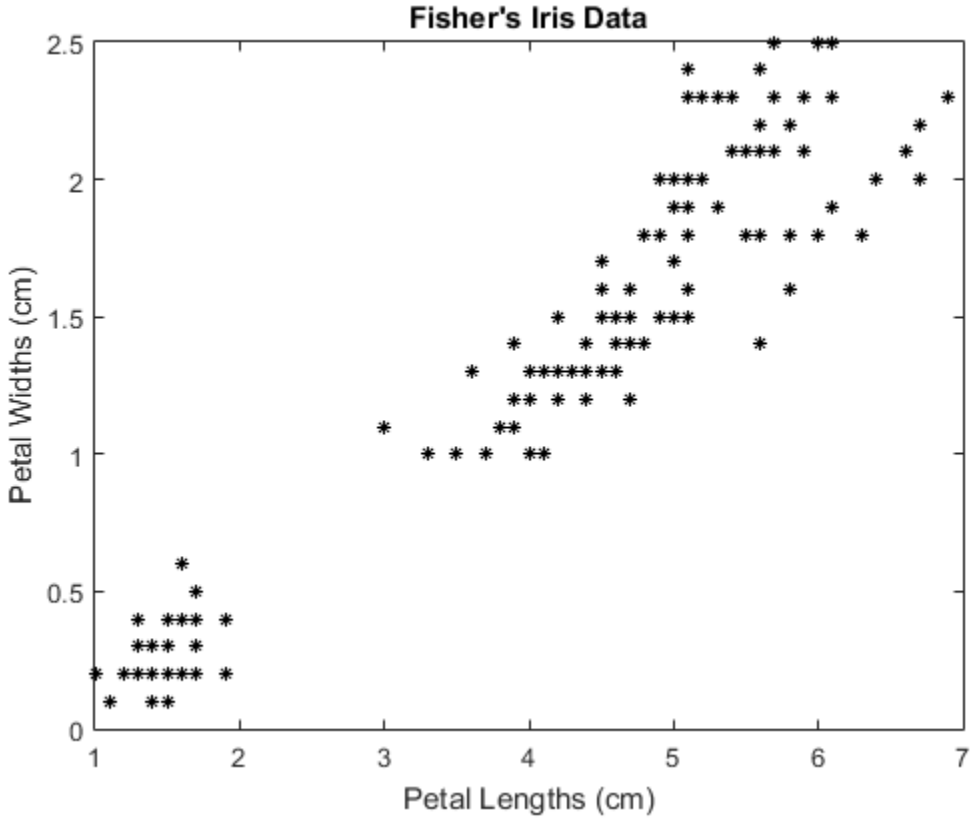
Examples

Train a *k*-Means Clustering Algorithm

Cluster data using *k*-means clustering, then plot the cluster regions.

Load Fisher's iris data set. Use the petal lengths and widths as predictors.

```
load fisheriris
X = meas(:,3:4);

figure;
plot(X(:,1),X(:,2),'k*','MarkerSize',5);
title 'Fisher''s Iris Data';
xlabel 'Petal Lengths (cm)';
ylabel 'Petal Widths (cm)';
```



The larger cluster seems to be split into a lower variance region and a higher variance region. This might indicate that the larger cluster is two, overlapping clusters.

Cluster the data. Specify $k = 3$ clusters.

```
rng(1); % For reproducibility
[idx,C] = kmeans(X,3);
```

`kmeans` uses the *k*-means++ algorithm for centroid initialization and squared Euclidean distance by default. It is good practice to search for lower, local minima by setting the `'Replicates'` name-value pair argument.

`idx` is a vector of predicted cluster indices corrresponding to the observations in `X`. `C` is a 3-by-2 matrix containing the final centroid locations.

Use `kmeans` to compute the distance from each centroid to points on a grid. To do this, pass the centroids (`C`) and points on a grid to `kmeans`, and implement one iteration of the algorithm.

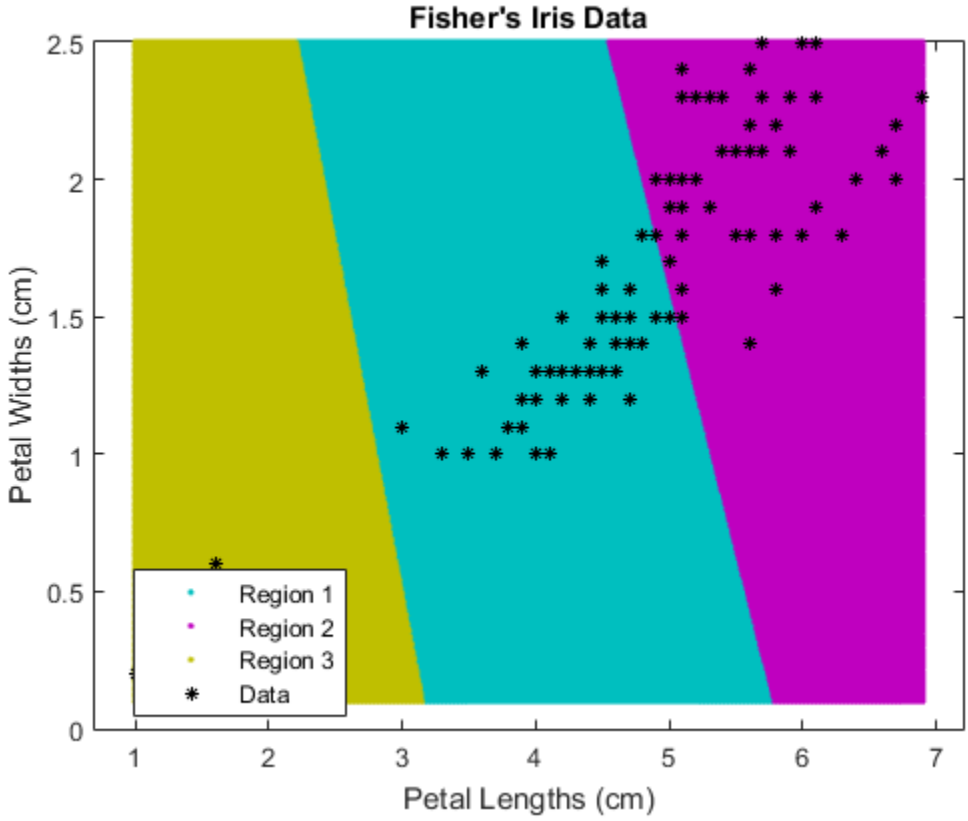
```
x1 = min(X(:,1)):0.01:max(X(:,1));
x2 = min(X(:,2)):0.01:max(X(:,2));
[x1G,x2G] = meshgrid(x1,x2);
XGrid = [x1G(:),x2G(:)]; % Defines a fine grid on the plot

idx2Region = kmeans(XGrid,3,'MaxIter',1,'Start',C);...
    % Assigns each node in the grid to the closest centroid
```

```
Warning: Failed to converge in 1 iterations.
```

`kmeans` displays a warning stating that the algorithm did not converge, which you should expect since the software only implemented one iteration.

Plot the cluster regions.

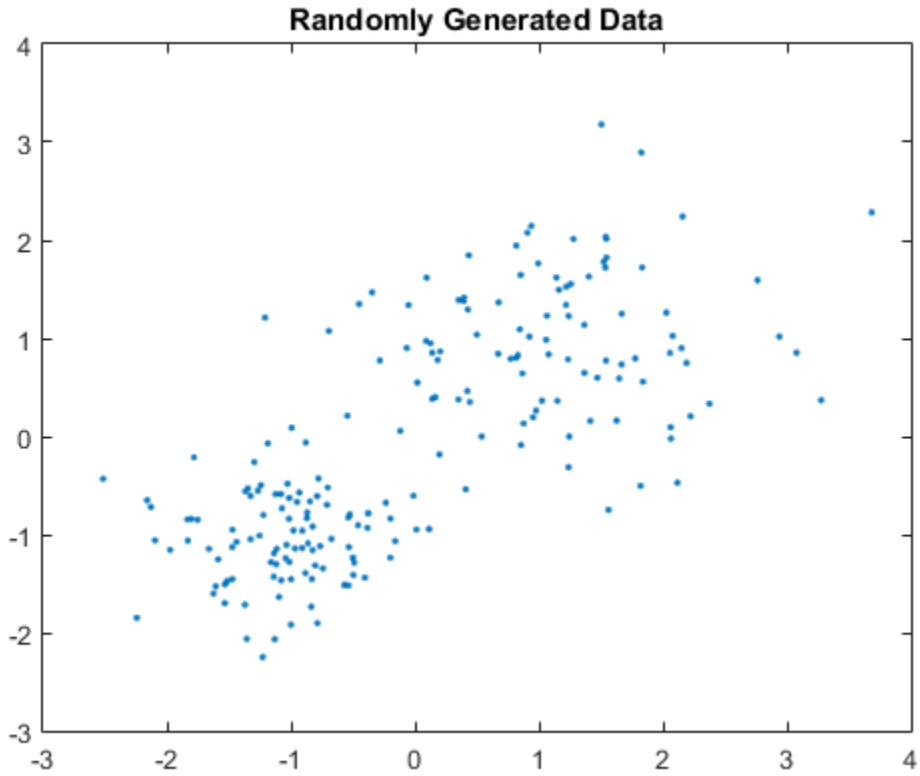
```
figure;
gscatter(XGrid(:,1),XGrid(:,2),idx2Region,...
    [0,0.75,0.75;0.75,0,0.75;0.75,0.75,0],'..');
hold on;
plot(X(:,1),X(:,2),'k*','MarkerSize',5);
title 'Fisher''s Iris Data';
xlabel 'Petal Lengths (cm)';
ylabel 'Petal Widths (cm)';
legend('Region 1','Region 2','Region 3','Data','Location','Best');
hold off;
```



Partition Data into Two Clusters

Randomly generate the sample data.

```
rng default; % For reproducibility
X = [randn(100,2)*0.75+ones(100,2);
    randn(100,2)*0.5-ones(100,2)];

figure;
plot(X(:,1),X(:,2),'.');
title 'Randomly Generated Data';
```



There appears to be two clusters in the data.

Partition the data into two clusters, and choose the best arrangement out of five intializations. Display the final output.

```
opts = statset('Display','final');
[idx,C] = kmeans(X,2,'Distance','cityblock',...
    'Replicates',5,'Options',opts);
```

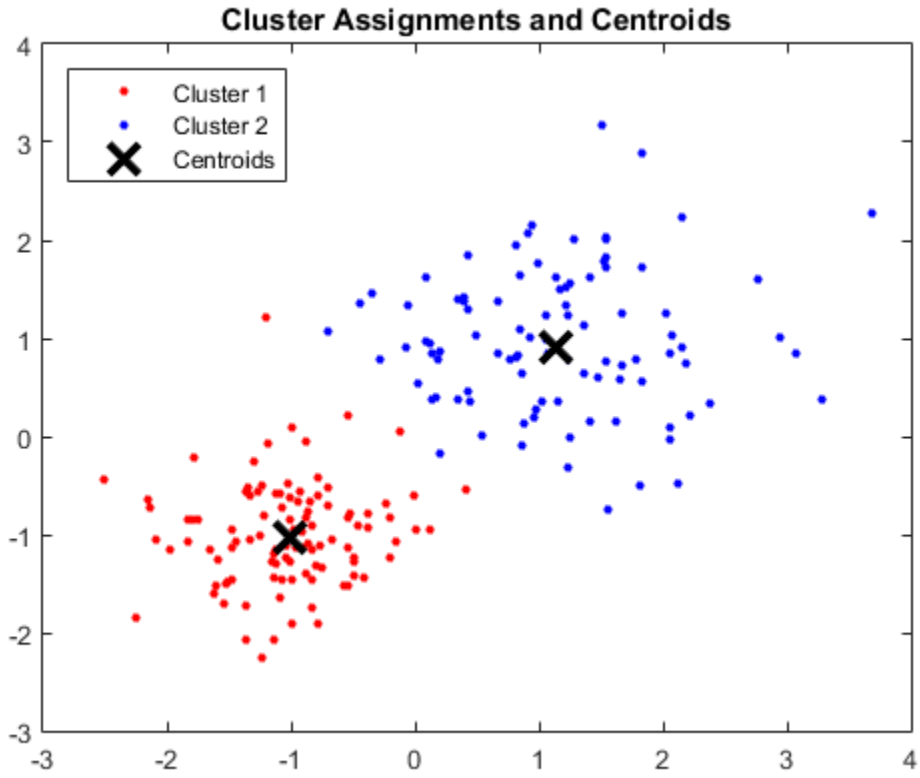
```
Replicate 1, 4 iterations, total sum of distances = 201.533.
Replicate 2, 6 iterations, total sum of distances = 201.533.
Replicate 3, 4 iterations, total sum of distances = 201.533.
Replicate 4, 4 iterations, total sum of distances = 201.533.
Replicate 5, 3 iterations, total sum of distances = 201.533.
```

```
Best total sum of distances = 201.533
```

By default, the software initializes the replicates separatly using *k*-means++.

Plot the clusters and the cluster centroids.

```
figure;
plot(X(idx==1,1),X(idx==1,2),'r.','MarkerSize',12)
hold on
plot(X(idx==2,1),X(idx==2,2),'b.','MarkerSize',12)
plot(C(:,1),C(:,2),'kx',...
     'MarkerSize',15,'LineWidth',3)
legend('Cluster 1','Cluster 2','Centroids',...
       'Location','NW')
title 'Cluster Assignments and Centroids'
hold off
```



You can determine how well separated the clusters are by passing `idx` to silhouette.

Cluster Data Using Parallel Computing

Clustering large data sets might take time, particularly if you use online updates (set by default). If you have a Parallel Computing Toolbox license and you invoke a pool of workers, then `kmeans` runs each clustering task (or replicate) in parallel. Therefore, if `Replicates` > 1, then the parallel computing decreases time to convergence.

Randomly generate a large data set from a Gaussian mixture model.

```
Mu = bsxfun(@times,ones(20,30),(1:20)'); % Gaussian mixture mean
rn30 = randn(30,30);
Sigma = rn30'*rn30; % Symmetric and positive-definite covariance
```

```
Mdl = gmdistribution(Mu,Sigma);

rng(1); % For reproducibility
X = random(Mdl,10000);
```

`Mdl` is a 30-dimensional `gmdistribution` model with 20 components. `X` is a `10000`-by-`30` matrix of data generated from `Mdl`.

Invoke a parallel pool of workers. Specify options for parallel computing.

```
pool = parpool;                       % Invokes workers
stream = RandStream('mlfg6331_64');  % Random number stream
options = statset('UseParallel',1,'UseSubstreams',1,...
    'Streams',stream);
```

```
Starting parallel pool (parpool) using the 'local' profile ... connected to 2 workers.
```

The input argument `'mlfg6331_64'` of `RandStream` specifies to use the multiplicative lagged Fibonacci generator algorithm. `options` is a structure array containing fields that specify options for controlling estimation.

The Command Window indicates that two workers are available. The number of workers might vary on your system.

Cluster the data using k-means clustering. Specify that there are $k = 20$ clusters in the data and increase the number of iterations. Typically, the objective function contains local minima. Specify 10 replicates to help find a lower, local minimum.

```
tic; % Start stopwatch timer
[idx,C,sumd,D] = kmeans(X,20,'Options',options,'MaxIter',10000,...
    'Display','final','Replicates',10);
toc % Terminate stopwatch timer
```

```
Replicate 4, 121 iterations, total sum of distances = 7.58059e+06.
Replicate 7, 234 iterations, total sum of distances = 7.5904e+06.
Replicate 3, 146 iterations, total sum of distances = 7.59086e+06.
Replicate 2, 179 iterations, total sum of distances = 7.57758e+06.
Replicate 6, 118 iterations, total sum of distances = 7.58614e+06.
Replicate 5, 88 iterations, total sum of distances = 7.59462e+06.
Replicate 1, 99 iterations, total sum of distances = 7.57765e+06.
Replicate 9, 147 iterations, total sum of distances = 7.57639e+06.
Replicate 10, 107 iterations, total sum of distances = 7.60079e+06.
Replicate 8, 144 iterations, total sum of distances = 7.58117e+06.
Best total sum of distances = 7.57639e+06
Elapsed time is 123.857736 seconds.
```

The Command Window displays the number of iterations and the terminal objective function value for each replicate. The output arguments contain the results of replicate 9 because it has the lowest total sum of distances.

- "Create Clusters and Determine Separation" on page 14-22
- "Determine the Correct Number of Clusters" on page 14-24
- "Avoid Local Minima" on page 14-27

Input Arguments

X — Data

numeric matrix

Data, specified as a numeric matrix. The rows of X correspond to observations, and the columns correspond to variables.

If X is a numeric vector, then kmeans treats it as an *n*-by-1 data matrix, regardless of its orientation.

Data Types: single | double

k — Number of clusters

positive integer

Number of clusters in the data, specified as a positive integer.

Data Types: single | double

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. Name is the argument name and Value is the corresponding value. Name must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as Name1,Value1,...,NameN,ValueN.

Example: 'Distance','cosine','Replicates',10,'Options',statset('UseParallel',1) specifies the cosine distance, 10 replicate clusters at different starting values, and to use parallel computing.

'Display' — Level of output to display

'off' (default) | 'final' | 'iter'

Level of output to display in the Command Window, specified as the comma-separated pair consisting of `'Display'` and a string. Available options are:

- `'final'` — Displays results of the final iteration
- `'iter'` — Displays results of each iteration
- `'off'` — Displays nothing

Example: `'Display','final'`

Data Types: `char`

`'Distance'` — Distance measure

`'sqeuclidean'` (default) | `'cityblock'` | `'cosine'` | `'correlation'` | `'hamming'`

Distance measure, in `p`-dimensional space, used for minimization, specified as the comma-separated pair consisting of `'Distance'` and a string.

`kmeans` computes centroid clusters differently for the different, supported distance measures. This table summarizes the available distance measures. In the formulae, x is an observation (that is, a row of X) and c is a centroid (a row vector).

Distance Measure	Description	Formula
`'sqeuclidean'`	Squared Euclidean distance (default). Each centroid is the mean of the points in that cluster.	$d(x,c) = (x-c)(x-c)'$
`'cityblock'`	Sum of absolute differences, i.e., the $L1$ distance. Each centroid is the component-wise median of the points in that cluster.	$d(x,c) = \sum_{j=1}^{p} \left\| x_j - c_j \right\|$
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors). Each centroid is the mean of the points in that cluster, after normalizing those points to unit Euclidean length.	$d(x,c) = 1 - \frac{xc'}{\sqrt{(xx')(cc')}}$

Distance Measure	Description	Formula
`'correlation'`	One minus the sample correlation between points (treated as sequences of values). Each centroid is the component-wise mean of the points in that cluster, after centering and normalizing those points to zero mean and unit standard deviation.	$$d(x,c) = 1 - \frac{\left(x-\bar{\vec{x}}\right)\left(c-\bar{\vec{c}}\right)'}{\sqrt{\left(x-\bar{\vec{x}}\right)\left(x-\bar{\vec{x}}\right)'}\sqrt{\left(c-\bar{\vec{c}}\right)\left(c-\right.}}$$ where • $\bar{\vec{x}} = \frac{1}{p}\left(\sum_{j=1}^{p} x_j\right)\vec{1}_p$ • $\bar{\vec{c}} = \frac{1}{p}\left(\sum_{j=1}^{p} c_j\right)\vec{1}_p$ • $\vec{1}_p$ is a row vector of p ones.
`'hamming'`	This measure is only suitable for binary data. It is the proportion of bits that differ. Each centroid is the component-wise median of points in that cluster.	$$d(x,y) = \frac{1}{p}\sum_{j=1}^{p} I\left\{x_j \neq y_j\right\},$$ where I is the indicator function.

Example: `'Distance','cityblock'`

Data Types: `char`

`'EmptyAction'` — Action to take if cluster loses all member observations

`'singleton'` (default) | `'error'` | `'drop'`

Action to take if a cluster loses all its member observations, specified as the comma-separated pair consisting of `'EmptyAction'` and a string. This table summarizes the available options.

Value	Description
`'error'`	Treat an empty cluster as an error.

Value	Description
`'drop'`	Remove any clusters that become empty. `kmeans` sets the corresponding return values in C and D to `NaN`.
`'singleton'`	Create a new cluster consisting of the one point furthest from its centroid (default).

Example: `'EmptyAction','error'`

Data Types: `char`

`'MaxIter'` — Maximum number of iterations

`100` (default) | positive integer

Maximum number of iterations, specified as the comma-separated pair consisting of `'MaxIter'` and a positive integer.

Example: `'MaxIter',1000`

Data Types: `double | single`

`'OnlinePhase'` — Online update flag

`'on'` (default) | `'off'`

Online update flag, specified as the comma-separated pair consisting of `'OnlinePhase'` and `'on'` or `'off'`.

If `OnlinePhase` is `on` (the default), then `kmeans` performs an online update phase in addition to a batch update phase. The online phase can be time consuming for large data sets, but guarantees a solution that is a local minimum of the distance criterion. In other words, the software finds a partition of the data in which moving any single point to a different cluster increases the total sum of distances.

Example: `'OnlinePhase','off'`

Data Types: `char`

`'Options'` — Options for controlling iterative algorithm for minimizing fitting criteria

`[]` (default) | structure array returned by `statset`

Options for controlling the iterative algorithm for minimizing the fitting criteria, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`. These options require Parallel Computing Toolbox.

This table summarizes the available options.

Option	Description
`'Streams'`	A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `kmeans` uses the default stream or streams. If you specify `Streams`, use a single object except when: • You have an open parallel pool • `UseParallel` is `true`. • `UseSubstreams` is `false`. In that case, use a cell array the same size as the parallel pool. If a parallel pool is not open, then `Streams` must supply a single random number stream.
`'UseParallel'`	• If `true`, Replicates > 1, and if a parallel pool of workers from the Parallel Computing Toolbox is open, then the software implements *k*-means on each replicate in parallel. • If the Parallel Computing Toolbox is not installed, or a parallel pool of workers is not open, computation occurs in serial mode. Default is `default`, meaning serial computation.
`'UseSubstreams'`	Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.

To ensure more predictable results, use `parpool` and explicitly create a parallel pool before invoking `kmeans` and setting `'Options',statset('UseParallel',1)`.

Example: `'Options',statset('UseParallel',1)`

Data Types: `struct`

`'Replicates'` — Number of times to repeat clustering using new initial cluster centroid positions

`1` (default) | positive integer

Number of times to repeat clustering using new initial cluster centroid positions, specified as the comma-separated pair consisting of `'Replicates'` and an integer. `kmeans` returns the solution with the lowest sumd.

You can set `'Replicates'` implicitly by supplying a 3-D array as the value for the `'Start'` name-value pair argument.

Example: `'Replicates',5`

Data Types: `double` | `single`

`'Start'` — Method for choosing initial cluster centroid positions

`'plus'` (default) | `'cluster'` | `'sample'` | `'uniform'` | numeric matrix | numeric array

Method for choosing initial cluster centroid positions (or *seeds*), specified as the comma-separated pair consisting of `'Start'` and a string, a numeric matrix, or a numeric array. This table summarizes the available options for choosing seeds.

Value	Description
`'cluster'`	Perform a preliminary clustering phase on a random 10% subsample of `X`. This preliminary phase is itself initialized using `'sample'`.
`'plus'` (default)	Select `k` seeds by implementing the *k*-means++ algorithm for cluster center initialization.
`'sample'`	Select `k` observations from `X` at random.
`'uniform'`	Select `k` points uniformly at random from the range of `X`. Not valid with the Hamming distance.
numeric matrix	`k`-by-*p* matrix of centroid starting locations. The rows of `Start` correspond to seeds. The software infers `k` from the first dimension of `Start`, so you can pass in `[]` for `k`.

Value	Description
numeric array	k-by-*p*-*r* array of centroid starting locations. The rows of each page correspond to seeds. The third dimension invokes replication of the clustering routine. Page *j* contains the set of seeds for replicate *j*. The software infers the number of replicates (specified by the `'Replicates'` name-value pair argument) from the size of the third dimension.

Example: `'Start','sample'`

Data Types: `char` | `double` | `single`

Note: The software treats `NaN`s as missing data, and removes any row of `X` containing at least one `NaN`. Removing rows of `X` reduces the sample size.

Output Arguments

`idx` — Cluster indices

numeric column vector

Cluster indices, returned as a numeric column vector. `idx` has as many rows as `X`, and each row indicates the cluster assignment of the corresponding observation.

`C` — Cluster centroid locations

numeric matrix

Cluster centroid locations, returned as a numeric matrix. `C` is a k-by-*p* matrix, where row *j* is the centroid of cluster *j*.

`sumd` — Within-cluster sums of point-to-centroid distances

numeric column vector

Within-cluster sums of point-to-centroid distances, returned as a numeric column vector. `sumd` is a k-by-1 vector, where element *j* is the sum of point-to-centroid distances within cluster *j*.

D — Distances from each point to every centroid

numeric matrix

Distances from each point to every centroid, returned as a numeric matrix. D is an n-by-k matrix, where element (j,m) is the distance from observation j to centroid m.

More About

k-Means Clustering

k-means clustering, or Lloyd's algorithm [2], is an iterative, data-partitioning algorithm that assigns n observations to exactly one of k clusters defined by centroids, where k is chosen before the algorithm starts.

The algorithm proceeds as follows:

1. Choose k initial cluster centers (*centroid*). For example, choose k observations at random (by using `'Start','sample'`) or use the k-means ++ algorithm for cluster center initialization (the default).
2. Compute point-to-cluster-centroid distances of all observations to each centroid.
3. There are two ways to proceed (specified by OnlinePhase):

   - Batch update — Assign each observation to the cluster with the closest centroid.
   - Online update — Individually assign observations to a different centroid if the reassignment decreases the sum of the within-cluster, sum-of-squares point-to-cluster-centroid distances.

   For more details, see "Algorithms" on page 22-2436.
4. Compute the average of the observations in each cluster to obtain k new centroid locations.
5. Repeat steps 2 through 4 until cluster assignments do not change, or the maximum number of iterations is reached.

k-means++ Algorithm

The *k-means++ algorithm* uses an heuristic to find centroid seeds for k-means clustering. According to Arthur and Vassilvitskii [1], k-means++ improves the running time of Lloyd's algorithm, and the quality of the final solution.

The k-means++ algorithm chooses seeds as follows, assuming the number of clusters is k.

1. Select an observation uniformly at random from the data set, X. The chosen observation is the first centroid, and is denoted c_1.
2. Compute distances from each observation to c_1. Denote the distance observation m is from c_j $d(x_m, c_j)$.
3. Select the next centroid, c_2 at random from X with probability

$$\frac{d^2(x_m, c_1)}{\sum_{j=1}^{n} d^2(x_j, c_1)}.$$

4. To choose center j:
   a. Compute the distances from each observation to each centroid, and assign each observation to its closest centroid.
   b. For $m = 1,...,n$ and $p = 1,...,j-1$, select centroid j at random from X with probability

$$\frac{d^2(x_m, c_p)}{\sum_{\{h; x_h \in C_p\}} d^2(x_h, c_p)},$$

   where C_p is the set of all observations closest to centroid c_p and x_m belongs to C_p.

   That is, select each subsequent center with a probability proportional to the distance from itself to the closest center that you already chose.
5. Repeat step 4 until k centroids are chosen.

Arthur and Vassilvitskii [1] demonstrate, using a simulation study for several cluster orientations, that k-means++ achieves faster convergence to a lower sum of within-cluster, sum-of-squares point-to-cluster-centroid distances than Lloyd's algorithm.

Algorithms

- `kmeans` uses a two-phase iterative algorithm to minimize the sum of point-to-centroid distances, summed over all `k` clusters.

1. This first phase uses *batch updates*, where each iteration consists of reassigning points to their nearest cluster centroid, all at once, followed by recalculation of cluster centroids. This phase occasionally does not converge to solution that is a local minimum. That is, a partition of the data where moving any single point to a different cluster increases the total sum of distances. This is more likely for small data sets. The batch phase is fast, but potentially only approximates a solution as a starting point for the second phase.
2. This second phase uses *online updates*, where points are individually reassigned if doing so reduces the sum of distances, and cluster centroids are recomputed after each reassignment. Each iteration during this phase consists of one pass though all the points. This phase converges to a local minimum, although there might be other local minima with lower total sum of distances. In general, finding the global minimum is solved by an exhaustive choice of starting points, but using several replicates with random starting points typically results in a solution that is a global minimum.

- If Replicates = $r > 1$ and Start is `plus` (the default), then the software selects r possibly different sets of seeds according to the k-means++ algorithm.
- If you enable the `UseParallel` option in Options and `Replicates` > 1, then each worker selects seeds and clusters in parallel.

- "Introduction to *k*-Means Clustering" on page 14-21

References

[1] Arthur, David, and Sergi Vassilvitskii. "K-means++: The Advantages of Careful Seeding." *SODA '07: Proceedings of the Eighteenth Annual ACM-SIAM Symposium on Discrete Algorithms*. 2007, pp. 1027–1035.

[2] Lloyd, Stuart P. "Least Squares Quantization in PCM." *IEEE Transactions on Information Theory*. Vol. 28, 1982, pp. 129–137.

[3] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

[4] Spath, H. *Cluster Dissection and Analysis: Theory, FORTRAN Programs, Examples*. Translated by J. Goldschmidt. New York: Halsted Press, 1985.

See Also

`clusterdata` | `gmdistribution` | `linkage` | `parpool` | `silhouette` | `statset`

kmedoids

k-medoids clustering

Syntax

```
[idx,C] = kmedoids( ___ )
[idx,C,sumd] = kmedoids( ___ )
[idx,C,sumd,D] = kmedoids( ___ )
[idx,C,sumd,D,midx] = kmedoids( ___ )
[idx,C,sumd,D,midx,info] = kmedoids( ___ )
```

Description

`idx = kmedoids(X,k)` performs "k-medoids Clustering" on page 22-2453 to partition the observations of the n-by-p matrix X into k clusters, and returns an n-by-1 vector idx containing cluster indices of each observation. Rows of X correspond to points and columns correspond to variables. By default, `kmedoids` uses squared Euclidean distance measure and the k-means++ algorithm for choosing initial cluster medoid positions.

`idx = kmedoids(X,k,Name,Value)` uses additional options specified by one or more Name,Value pair arguments.

`[idx,C] = kmedoids( ___ )` returns the k cluster medoid locations in the k-by-p matrix C.

`[idx,C,sumd] = kmedoids( ___ )` returns the within-cluster sums of point-to-medoid distances in the k-by-1 vector sumd.

`[idx,C,sumd,D] = kmedoids( ___ )` returns distances from each point to every medoid in the n-by-k matrix D.

`[idx,C,sumd,D,midx] = kmedoids( ___ )` returns the indices midx such that C = X(midx,:). midx is a k-by-1 vector.

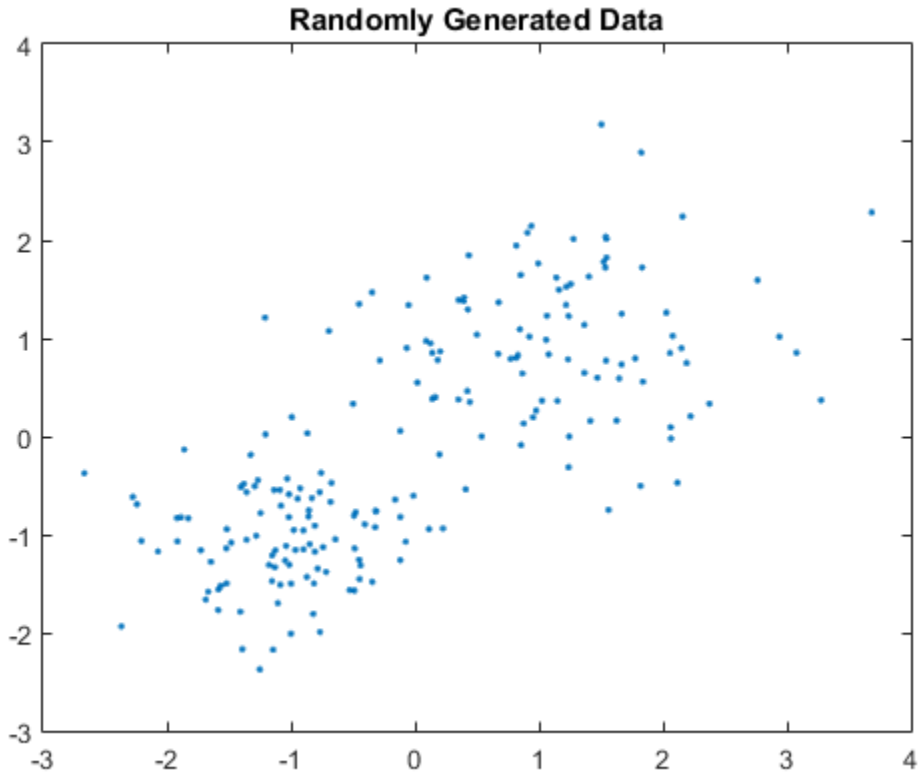
`[idx,C,sumd,D,midx,info] = kmedoids( ___ )` returns a structure info with information about the options used by the algorithm when executed.

Examples

Group Data into Two Clusters

Randomly generate data.

```
rng('default'); % For reproducibility
X = [randn(100,2)*0.75+ones(100,2);
     randn(100,2)*0.55-ones(100,2)];
figure;
plot(X(:,1),X(:,2),'.');
title('Randomly Generated Data');
```



Group data into two clusters using `kmedoids`. Use the `cityblock` distance measure.

```
opts = statset('Display','iter');
[idx,C,sumd,d,midx,info] = kmedoids(X,2,'Distance','cityblock','Options',opts);

   rep     iter          sum
     1        1      209.856
     1        2      209.856
Best total sum of distances = 209.856
```

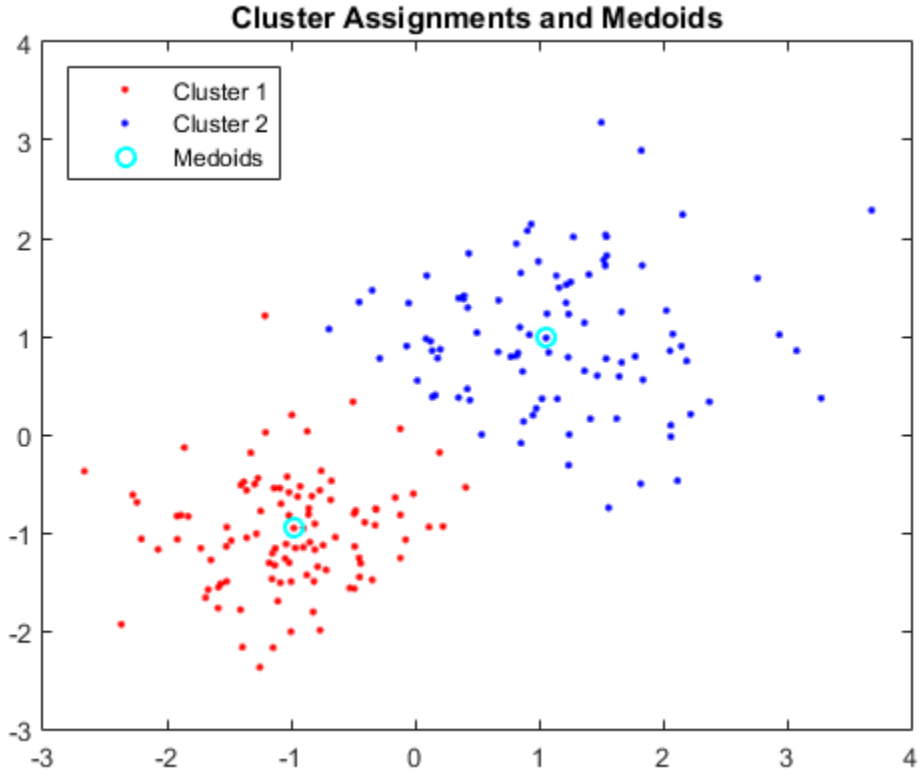
`info` is a struct that contains information about how the algorithm was executed. For example, `bestReplicate` field indicates the replicate that was used to produce the final solution. In this example, the replicate number 1 was used since the default number of replicates is 1 for the default algorithm, which is `pam` in this case.

```
info
```

```
info =

        algorithm: 'pam'
            start: 'plus'
         distance: 'cityblock'
       iterations: 2
    bestReplicate: 1
```

Plot the clusters and the cluster medoids.

```
figure;
plot(X(idx==1,1),X(idx==1,2),'r.','MarkerSize',7)
hold on
plot(X(idx==2,1),X(idx==2,2),'b.','MarkerSize',7)
plot(C(:,1),C(:,2),'co',...
     'MarkerSize',7,'LineWidth',1.5)
legend('Cluster 1','Cluster 2','Medoids',...
       'Location','NW');
title('Cluster Assignments and Medoids');
hold off
```



Cluster Categorical Data Using k-Medoids

This example uses "Mushroom" data set [3][4][5] [6][7] from the UCI machine learning archive [7], described in http://archive.ics.uci.edu/ml/datasets/Mushroom. The data set includes 22 predictors for 8,124 observations of various mushrooms. The predictors are categorical data types. For example, cap shape is categorized with features of `'b'` for bell-shaped cap and `'c'` for conical. Mushroom color is also categorized with features of `'n'` for brown, and `'p'` for pink. The data set also includes a classification for each mushroom of either edible or poisonous.

Since the features of the mushroom data set are categorical, it is not possible to define the mean of several data points, and therefore the widely-used *k*-means clustering algorithm cannot be meaningfully applied to this data set. *k*-medoids is a related

algorithm that partitions data into k distinct clusters, by finding medoids that minimize the sum of dissimilarities between points in the data and their nearest medoid.

The medoid of a set is a member of that set whose average dissimilarity with the other members of the set is the smallest. Similarity can be defined for many types of data that do not allow a mean to be calculated, allowing k-medoids to be used for a broader range of problems than k-means.

Using k-medoids, this example clusters the mushrooms into two groups, based on the predictors provided. It then explores the relationship between those clusters and the classifications of the mushrooms as either edible or poisonous.

This example assumes that you have downloaded the "Mushroom" data set [3][4][5] [6][7] from the UCI database (http://archive.ics.uci.edu/ml/machine-learning-databases/mushroom/) and saved it in your current directory as a text file named agaricus-lepiota.txt. There is no column headers in the data, so `readtable` uses the default variable names.

```
clear all
data = readtable('agaricus-lepiota.txt','ReadVariableNames',false);
```

Display the first 5 mushrooms with their first few features.

```
data(1:5,1:10)
```

```
ans =

    Var1    Var2    Var3    Var4    Var5    Var6    Var7    Var8    Var9    Var10
    ____    ____    ____    ____    ____    ____    ____    ____    ____    _____

    'p'     'x'     's'     'n'     't'     'p'     'f'     'c'     'n'     'k'
    'e'     'x'     's'     'y'     't'     'a'     'f'     'c'     'b'     'k'
    'e'     'b'     's'     'w'     't'     'l'     'f'     'c'     'b'     'n'
    'p'     'x'     'y'     'w'     't'     'p'     'f'     'c'     'n'     'n'
    'e'     'x'     's'     'g'     'f'     'n'     'f'     'w'     'b'     'k'
```

Extract the first column, labeled data for edible and poisonous groups. Then delete the column.

```
labels = data(:,1);
labels = categorical(labels{:,:});
data(:,1) = [];
```

Store the names of predictors (features), which are described in http://archive.ics.uci.edu/ml/machine-learning-databases/mushroom/agaricus-lepiota.names.

```
VarNames = {'cap_shape' 'cap_surface' 'cap_color' 'bruises' 'odor' ...
    'gill_attachment' 'gill_spacing' 'gill_size' 'gill_color' ...
    'stalk_shape' 'stalk_root' 'stalk_surface_above_ring' ...
    'stalk_surface_below_ring' 'stalk_color_above_ring' ...
    'stalk_color_below_ring' 'veil_type' 'veil_color' 'ring_number' ....
    'ring_type' 'spore_print_color' 'population' 'habitat'};
```

Set the variable names.

```
data.Properties.VariableNames = VarNames;
```

There are a total of 2480 missing values denoted as `'?'`.

```
sum(char(data{:,:}) == '?')
```

```
ans =

        2480
```

Based on the inspection of the data set and its description, the missing values belong only to the 11th variable (`stalk_root`). Remove the column from the table.

```
data(:,11) = [];
```

`kmedoids` only accepts numeric data. You need to cast the categories you have into numeric type. The distance function you will use to define the dissimilarity of the data will be based on the double representation of the categorical data.

```
cats = categorical(data{:,:});
data = double(cats);
```

`kmedoids` can use any distance metric supported by pdist2 to cluster. For this example you will cluster the data using the Hamming distance because this is an appropriate distance metric for categorical data as illustrated below. The Hamming distance between two vectors is the percentage of the vector components that differ. For instance, consider these two vectors.

```
v1 = [1 0 2 1];
```

```
v2 = [1 1 2 1];
```

They are equal in the 1st, 3rd and 4th coordinate. Since 1 of the 4 coordinates differ, the Hamming distance between these two vectors is .25.

You can use the function `pdist2` to measure the Hamming distance between the first and second row of data, the numerical representation of the categorical mushroom data. The value .2857 means that 6 of the 21 features of the mushroom differ.

```
pdist2(data(1,:),data(2,:),'hamming')
```

```
ans =

    0.2857
```

In this example, you're clustering the mushroom data into two clusters based on features to see if the clustering corresponds to edibility. The `kmedoids` function is guaranteed to converge to a local minima of the clustering criterion; however, this may not be a global minimum for the problem. It is a good idea to cluster the problem a few times using the `'replicates'` parameter. When `'replicates'` is set to a value, *n*, greater than 1, the k-medoids algorithm is run *n* times, and the best result is returned.

To run `kmedoids` to cluster data into 2 clusters, based on the Hamming distance and to return the best result of 3 replicates, you run the following.

```
rng('default'); %For reproducibility
[IDX, C, SUMD, D, MIDX, INFO] = kmedoids(data,2,'distance','hamming','replicates',3);
```

Let's assume that mushrooms in the predicted group 1 are poisonous and group 2 are all edible. To determine the performance of clustering results, calculate how many mushrooms in group 1 are indeed poisonous and group 2 are edible based on the known labels. In other words, calculate the number of false positives, false negatives, as well as true positives and true negatives.

Construct a confusion matrix (or matching matrix), where the diagonal elements represent the number of true positives and true negatives, respectively. The off-diagonal elements represent false negatives and false positives, respectively. For convenience, use the `confusionmat` function, which calculates a confusion matrix given known labels and predicted labels. Get the predicted label information from the `IDX` variable. `IDX` contains values of 1 and 2 for each data point, representing poisonous and edible groups, respectively.

```
predLabels = labels; %Initialize a vector for predicted labels.
predLabels(IDX==1) = categorical({'p'}); %Assign group 1 to be poisonous.
predLabels(IDX==2) = categorical({'e'}); %Assign group 2 to be edible.
confMatrix = confusionmat(labels,predLabels)
```

```
confMatrix =
```

```
        4176          32
         816        3100
```

Out of 4208 edible mushrooms, 4176 were correctly predicted to be in group 2 (edible group), and 32 were incorrectly predicted to be in group 1 (poisonous group). Similarly, out of 3916 poisonous mushrooms, 3100 were correctly predicted to be in group 1 (poisonous group), and 816 were incorrectly predicted to be in group 2 (edible group).

Given this confusion matrix, calculate the accuracy, which is the proportion of true results (both true positives and true negatives) against the overall data, and precision, which is the proportion of the true positives against all the positive results (true positives and false positives).

```
accuracy = (confMatrix(1,1)+confMatrix(2,2))/(sum(sum(confMatrix)))
```

```
accuracy =

    0.8956
```

```
precision = confMatrix(1,1) / (confMatrix(1,1)+confMatrix(2,1))
```

```
precision =

    0.8365
```

The results indicated that applying the k-medoids algorithm to the categorical features of mushrooms resulted in clusters that were associated with edibility.

Input Arguments

X — Data

numeric matrix

Data, specified as a numeric matrix. The rows of `X` correspond to observations, and the columns correspond to variables.

k — Number of medoids

positive integer

Number of medoids in the data, specified as a positive integer.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example:
`'Distance','euclidean','Replicates',3,'Options',statset('UseParallel',1)`
specifies Euclidean distance, three replicate medoids at different starting values, and to use parallel computing.

`'Algorithm'` — Algorithm to find medoids

`'pam' | 'small' | 'clara' | 'large'`

Algorithm to find medoids, specified as the comma-separated pair consisting of `'Algorithm'` and a string. The default algorithm depends on the number of rows of X.

- If the number of rows of X is less than 3000, `'pam'` is the default algorithm.
- If the number of rows is between 3000 and 10000, `'small'` is the default algorithm.
- For all other cases, `'large'` is the default algorithm.

You can override the default choice by explicitly stating the algorithm. This table summarizes the available algorithms.

Algorithm	Description
`'pam'`	Partitioning Around Medoids (PAM) is the classical algorithm for solving the *k*-medoids problem described in [1]. After applying the initialization function to select initial medoid positions, the program performs the swap-step of the PAM algorithm, that is, it searches over all possible swaps between medoids and non-medoids to see if the sum of medoid to cluster member distances goes down. You can specify which initialization function to use via the `'Start'` name-value pair argument. The algorithm proceeds as follows. **1** Build-step: Each of *k* clusters is associated with a potential medoid. This assignment is performed using a technique specified by the `'Start'` name-value pair argument.

Algorithm	Description
	2 Swap-step: Within each cluster, each point is tested as a potential medoid by checking if the sum of within-cluster distances gets smaller using that point as the medoid. If so, the point is defined as a new medoid. Every point is then assigned to the cluster with the closest medoid. The algorithm iterates the build- and swap-steps until the medoids do not change, or other termination criteria are met. The algorithm can produce better solutions than the other algorithms in some situations, but it can be prohibitively long running.
`'small'`	Use an algorithm similar to the k-means algorithm to find k medoids. This option employs a variant of the Lloyd's iterations based on [2]. The algorithm proceeds as follows. 1 For each point in each cluster, calculate the sum of distances from the point to every other point in the cluster. Choose the point that minimizes the sum as the new medoid. 2 Update the cluster membership for each data point to reflect the new medoid. The algorithm repeats these steps until no further updates occur or other termination criteria are met. The algorithm has an optional PAM-like online update phase (specified by the `'OnlinePhase'` name-value pair argument) that improves cluster quality. It tends to return higher quality solutions than the `clara` or `large` algorithms, but it may not be the best choice for very large data.

Algorithm	Description
`'clara'`	Clustering LARge Applications (CLARA) [1] repeatedly performs the PAM algorithm on random subsets of the data. It aims to overcome scaling challenges posed by the PAM algorithm through sampling. The algorithm proceeds as follows. **1** Select a subset of the data and apply the PAM algorithm to the subset. **2** Assign points of the full data set to clusters by picking the closest medoid. The algorithm repeats these steps until the medoids do not change, or other termination criteria are met. For the best performance, it is recommended that you perform multiple replicates. By default, the program performs five replicates. Each replicate samples `s` rows from X (specified by `'NumSamples'` name-value pair argument) to perform clustering on. By default, `40+2*k` samples are selected.
`'large'`	This is similar to the `small` scale algorithm and repeatedly performs searches using a k-means like update. However, the algorithm examines only a random sample of cluster members during each iteration. The user-adjustable parameter, `'PercentNeighbors'`, controls the number of neighbors to examine. If there is no improvement after the neighbors are examined, the algorithm terminates the local search. The algorithm performs a total of *r* replicates (specified by `'Replicates'` name-value pair argument) and returns the best clustering result. The algorithm has an optional PAM-like online phase (specified by the `'OnlinePhase'` name-value pair argument) that improves cluster quality.

Example: `'Algorithm','pam'`

`'OnlinePhase'` — Flag to perform PAM-like online update phase
`'on'` (default) | `'off'`

A flag to perform PAM-like online update phase, specified as a comma-separated pair consisting of `'OnlinePhase'` and `'on'` or `'off'`.

If it is `on`, then `kmedoids` performs a PAM-like update to the medoids after the Lloyd iterations in the `small` and `large` algorithms. During this online update phase, the algorithm chooses a small subset of data points in each cluster that are the furthest from and nearest to medoid. For each chosen point, it reassigns the clustering of the entire data set and check if this creates a smaller sum of distances than the best known.

In other words, the swap considerations are limited to the points near the medoids and far from the medoids. The near points are considered in order to refine the clustering. The far points are considered in order to escape local minima. Turning on this feature tends to improve the quality of solutions generated by both algorithms. Total run time tends to increase as well, but the increase typically is less than one iteration of PAM.

Example: `OnlinePhase,'off'`

`'Distance'` — Distance measure

`'sqeuclidean'` (default) | `'euclidean'` | `'seuclidean'` | `'cityblock'` | `'minkowski'` | `'chebychev'` | `'mahalanobis'` | `'cosine'` | `'correlation'` | `'spearman'` | `'hamming'` | `'jaccard'` | custom distance function

Distance measure, in p-dimensional space, specified as the comma-separate pair consisting of `'Distance'` and a string. `kmedoids` minimizes the sum of medoid to cluster member distances. See `pdist` for the definition of each distance measure. `kmedoids` supports all distance measures supported by `pdist`.

Example: `'Distance','hamming'`

`'Options'` — Options to control iterative algorithm to minimize fitting criteria

`[ ]` (default) | structure array returned by `statset`

Options to control the iterative algorithm to minimize fitting criteria, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`. This table summarizes these options.

Option	Description
`Display`	Level of display output. Choices are `'off'` (default) and `'iter'`.
`MaxIter`	Maximum number of iterations allowed. The default is `100`.
`UseParallel`	If `true` and a `parpool` is open, compute in parallel. If Parallel Computing Toolbox is not available, or a `parpool` is not open,

Option	Description
	computation occurs in serial mode. The default is `false`, meaning serial computation.
`UseSubstreams`	Set to `true` to compute in parallel in a reproducible fashion. The default is `false`. To compute reproducibly, you must also set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
`Streams`	A `RandStream` object or cell array of such objects. For details about these options and parallel computing in Statistics and Machine Learning Toolbox, see "Speed Up Statistical Computations" or enter `help parallelstats` at the command line.

Example: `'Options',statset('Display','off')`

`'Replicates'` — Number of times to repeat clustering using new initial cluster medoid positions

positive integer

Number of times to repeat clustering using new initial cluster medoid positions, specified as a positive integer. The default value depends on the choice of algorithm. For `pam` and `small`, the default is 1. For `clara`, the default is 5. For `large`, the default is 3.

Example: `'Replicates',4`

`'NumSamples'` — Number of samples to take from data when executing clara algorithm

`40+2*k` (default) | positive integer

Number of samples to take from the data when executing the `clara` algorithm, specified as a positive integer. The default number of samples is calculated as `40+2*k`.

Example: `'NumSamples',160`

`'PercentNeighbors'` — Percent of data set to examine using large algorithm

0.001 (default) | scalar value between 0 and 1

Percent of the data set to examine using the `large` algorithm, specified as a positive number.

The program examines `percentneighbors*size(X,1)` number of neighbors for the medoids. If there is no improvement in the within-cluster sum of distances, then the algorithm terminates.

The value of this parameter between 0 and 1, where a value closer to 1 tends to give higher quality solutions, but the algorithm takes longer to run, and a value closer to 0 tends to give lower quality solutions, but finishes faster.

Example: `'PercentNeighbors',0.01`

`'Start'` — Method for choosing initial cluster medoid positions

`'plus'` (default) | `'sample'` | `'cluster'` | matrix

Method for choosing initial cluster medoid positions, specified as the comma-separated pair consisting of `'Start'` and a string or a matrix. This table summarizes the available methods.

Method	Description
`'plus'` (default)	Select k observations from X according to the *k*-means++ algorithm for cluster center initialization.
`'sample'`	Select k observations from X at random.
`'cluster'`	Perform preliminary clustering phase on a random subsample (10%) of X. This preliminary phase is itself initialized using `sample`, that is, the observations are selected at random.
matrix	A custom k-by-*p* matrix of starting locations. In this case, you can pass in `[]` for the k input argument, and `kmedoids` infers k from the first dimension of the matrix. You can also supply a 3-D array, implying a value for `'Replicates'` from the array's third dimension.

Example: `'Start','sample'`

Output Arguments

`idx` — Medoid indices

numeric column vector

Medoid indices, returned as a numeric column vector. idx has as many rows as X, and each row indicates the medoid assignment of the corresponding observation.

`C` — Cluster medoid locations

numeric matrix

Cluster medoid locations, returned as a numeric matrix. C is a *k*-by-*p* matrix, where row *j* is the medoid of cluster *j*

`sumd` — Within-cluster sums of point-to-medoid distances

numeric column vector

Within-cluster sums of point-to-medoid distances, returned as a numeric column vector. sumd is a k-by1 vector, where element *j* is the sum of point-to-medoid distances within cluster *j*.

`D` — Distances from each point to every medoid

numeric matrix

Distances from each point to every medoid, returned as a numeric matrix. `D` is an *n*-by-k matrix, where element (*j*,*m*) is the distance from observation *j* to medoid *m*.

`midx` — Index to `X`

column vector

Index to X, returned as a column vector of indices. midx is a k-by-1 vector and the indices satisfy `C = X(midx,:)`.

`info` — Algorithm information

struct

Algorithm information, returned as a struct. info contains options used by the function when executed such as *k*-medoid clustering algorithm (`algorithm`), method used to choose initial cluster medoid positions (`start`), distance measure (`distance`), number of iterations taken in the best replicate (`iterations`) and the replicate number of the returned results (`bestReplicate`).

More About

k-medoids Clustering

k-medoids clustering is a partitioning method commonly used in domains that require robustness to outlier data, arbitrary distance metrics, or ones for which the mean or median does not have a clear definition.

It is similar to *k*-means, and the goal of both methods is to divide a set of measurements or observations into *k* subsets or clusters so that the subsets minimize the sum of distances between a measurement and a center of the measurement's cluster. In the *k*-means algorithm, the center of the subset is the mean of measurements in the subset, often called a centroid. In the *k*-medoids algorithm, the center of the subset is a member of the subset, called a medoid.

The *k*-medoids algorithm returns medoids which are the actual data points in the data set. This allows you to use the algorithm in situations where the mean of the data does not exist within the data set. This is the main difference between *k*-medoids and *k*-means where the centroids returned by *k*-means may not be within the data set. Hence *k*-medoids is useful for clustering categorical data where a mean is impossible to define or interpret.

The function `kmedoids` provides several iterative algorithms that minimize the sum of distances from each object to its cluster medoid, over all clusters. One of the algorithms is called partitioning around medoids (PAM) [1] which proceeds in two steps.

1. Build-step: Each of *k* clusters is associated with a potential medoid. This assignment is performed using a technique specified by the `'Start'` name-value pair argument.
2. Swap-step: Within each cluster, each point is tested as a potential medoid by checking if the sum of within-cluster distances gets smaller using that point as the medoid. If so, the point is defined as a new medoid. Every point is then assigned to the cluster with the closest medoid.

The algorithm iterates the build- and swap-steps until the medoids do not change, or other termination criteria are met.

You can control the details of the minimization using several optional input parameters to `kmedoids`, including ones for the initial values of the cluster medoids, and for the maximum number of iterations. By default, `kmedoids` uses the *k*-means++ algorithm for cluster medoid initialization and the squared Euclidean metric to determine distances.

References

[1] Kaufman, L., and Rousseeuw, P. J. (2009). Finding Groups in Data: An Introduction to Cluster Analysis. Hoboken, New Jersey: John Wiley & Sons, Inc.

[2] Park, H-S, and Jun, C-H. (2009). A simple and fast algorithm for K-medoids clustering. Expert Systems with Applications. 36, 3336-3341.

[3] Schlimmer,J.S. (1987). Concept Acquisition Through Representational Adjustment (Technical Report 87-19). Doctoral disseration, Department of Information and Computer Science, University of California, Irvine.

[4] Iba,W., Wogulis,J., and Langley,P. (1988). Trading off Simplicity and Coverage in Incremental Concept Learning. In Proceedings of the 5th International Conference on Machine Learning, 73-79. Ann Arbor, Michigan: Morgan Kaufmann.

[5] Duch W, A.R., and Grabczewski, K. (1996) Extraction of logical rules from training data using backpropagation networks. Proc. of the The 1st Online Workshop on Soft Computing, 19-30, pp. 25-30.

[6] Duch, W., Adamczak, R., Grabczewski, K., Ishikawa, M., and Ueda, H. (1997). Extraction of crisp logical rules using constrained backpropagation networks - comparison of two new approaches. Proc. of the European Symposium on Artificial Neural Networks (ESANN'97), Bruge, Belgium 16-18.

[7] Bache, K. and Lichman, M. (2013). UCI Machine Learning Repository [http://archive.ics.uci.edu/ml]. Irvine, CA: University of California, School of Information and Computer Science.

See Also

`clusterdata` | `evalclusters` | `kmeans` | `linkage` | `linkage` | `pdist` | `silhouette`

knnsearch

k-nearest neighbors search using *K*d-tree or exhaustive search

Syntax

```
Idx = knnsearch(Mdl,Y)
Idx = knnsearch(Mdl,Y,Name,Value)
[Idx,D] = knnsearch(___)
```

Description

`Idx = knnsearch(Mdl,Y)` searches for the nearest neighbor (i.e., the closest point, row, or observation) in `Mdl.X` to each point (i.e., row or observation) in the query data `Y` using an exhaustive search or a *K*d-tree. `knnsearch` returns `Idx`, which is a column vector of the indices in `Mdl.X` representing the nearest neighbors.

`Idx = knnsearch(Mdl,Y,Name,Value)` returns the indices of the closest points in `Mdl.X` to `Y` with additional options specified by one or more `Name,Value` pair arguments. For example, specify the number of nearest neighbors to search for, distance metric different from the one stored in `Mdl.Distance`. You can also specify which action to take if the closest distances are tied.

`[Idx,D] = knnsearch(___)` additionally returns the matrix `D` using any of the input arguments in the previous syntaxes. `D` contains the distances between each observation in `Y` that correspond to the closest observations in `Mdl.X`. The function arranges the columns of `D` in ascending order by closeness, with respect to the distance metric.

Examples

Search for Nearest Neighbors Using a *K* d-tree and Exhaustive Search

`knnsearch` accepts `ExhaustiveSearcher` or `KDTreeSearcher` model objects to search the training data for the nearest neighbors to the query data. An `ExhaustiveSearcher` model invokes the exhaustive searcher algorithm, and a `KDTreeSearcher` model defines a *K* d-tree, which `knnsearch` uses to search for nearest neighbors.

Load Fisher's iris data set. Randomly reserve five observations from the data for query data.

```
load fisheriris
rng(1); % For reproducibility
n = size(meas,1);
idx = randsample(n,5);
X = meas(~ismember(1:n,idx),:); % Training data
Y = meas(idx,:);                % Query data
```

The variable `meas` contains 4 predictors.

Grow a default four-dimensional K d-tree.

```
MdlKDT = KDTreeSearcher(X)
```

```
MdlKDT =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'euclidean'
    DistParameter: []
                X: [145x4 double]
```

`MdlKDT` is a `KDTreeSearcher` model object. You can alter its writable properties using dot notation.

Prepare an exhaustive nearest neighbors searcher.

```
MdlES = ExhaustiveSearcher(X)
```

```
MdlES =

  ExhaustiveSearcher with properties:

        Distance: 'euclidean'
    DistParameter: []
                X: [145x4 double]
```

`MdlKDT` is an `ExhaustiveSearcher` model object. It contains the options, such as the distance metric, to use to find nearest neighbors.

Alternatively, you can grow a *K* d-tree or prepare an exhaustive nearest neighbors searcher using `createns`.

Search the training data for the nearest neighbors indices that correspond to each query observation. Conduct both types of searches using the default settings. By default, the number of neighbors to search for per query observation is 1.

```
IdxKDT = knnsearch(MdlKDT,Y);
IdxES = knnsearch(MdlES,Y);
[IdxKDT IdxES]
```

```
ans =

    17    17
     6     6
     1     1
    89    89
   124   124
```

In this case, the results of the search are the same.

Search for Nearest Neighbors of Query Data Using the Minkowski Distance

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(1);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
X = meas(~ismember(1:n,qIdx),:);
Y = meas(qIdx,:);
```

Grow a four-dimensional *K* d-tree using the training data. Specify to use the Minkowski distance for finding nearest neighbors later.

```
Mdl = KDTreeSearcher(X,'Distance','minkowski')
```

```
Mdl =
```

```
  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'minkowski'
    DistParameter: 2
                X: [145x4 double]
```

`Mdl` is a `KDTreeSearcher` model object. By default, the Minkowski distance exponent is `2`.

Find the indices of the training data (`X`) that are the two nearest neighbors of each point in the query data (`Y`).

```
Idx = knnsearch(Mdl,Y,'K',2)
```

```
Idx =

    17     4
     6     2
     1    12
    89    66
   124   100
```

Each row of `Idx` corresponds to a query data observation, and the column order corresponds to the order of the nearest neighbors, with respect to ascending distance. For example, using the Minkowski distance, the second nearest neighbor of `Y(3,:)` is `X(12,:)`.

Include Ties in Nearest Neighbors Search

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(4);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
X = meas(~ismember(1:n,qIdx),:);
Y = meas(qIdx,:);
```

Grow a four-dimensional K d-tree using the training data. Specify to use the Minkowski distance for finding nearest neighbors later.

```
Mdl = KDTreeSearcher(X);
```

`Mdl` is a `KDTreeSearcher` model object. By default, the distance metric for finding nearest neighbors is the Euclidean metric.

Find the indices of the training data (`X`) that are the seven nearest neighbors of each point in the query data (`Y`).

```
[Idx,D] = knnsearch(Mdl,Y,'K',7,'IncludeTies',true);
```

`Idx` and `D` are five-element cell arrays of vectors, with each vector having at least seven elements.

Display the lengths of the vectors in `Idx`.

```
cellfun('length',Idx)
```

```
ans =

     8
     7
     7
     7
     7
```

Because cell `1` contains a vector with length greater than $k = 7$, query observation 1 (`Y(1,:)`) is equally close to at least two observations in `X`.

Display the indices of the nearest neighbors to `Y(1,:)` and their distances.

```
nn5 = Idx{1}
nn5d = D{1}
```

```
nn5 =

    91    98    67    69    71    93    88    95


nn5d =
```

```
Columns 1 through 7

  0.1414    0.2646    0.2828    0.3000    0.3464    0.3742    0.3873

Column 8

  0.3873
```

Training observations `88` and `95` are 0.3873 cm away from query observation `1`.

Input Arguments

`Mdl` — Nearest neighbors searcher

`ExhaustiveSearcher` model object | `KDTreeSearcher` model object

Nearest neighbors searcher, specified as an `ExhaustiveSearcher` or `KDTreeSearcher` model object, respectively. To create `Mdl`, with the appropriate mode creator. You can also use `createns`.

If `Mdl` is an `ExhaustiveSearcher` model, then `knnsearch` searches for nearest neighbors using an exhaustive search. Otherwise, `knnsearch` uses the grown *K*d-tree to search for nearest neighbors.

`Y` — Query data

numeric matrix

Query data, specified as a numeric matrix.

`Y` is an *m*-by-*K* matrix. Rows of `Y` correspond to observations (i.e., examples), and columns correspond to predictors (i.e., variables or features). `Y` must have the same number of columns as the training data stored in `Mdl.X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'K',2,'Distance','minkowski'` specifies to find the two nearest neighbors of `Mdl.X` to each point in `Y` and to use the Minkowski distance metric.

For Both Nearest Neighbor Searchers

`'Distance'` — Distance metric
`Mdl.Distance` (default) | `'cityblock'` | `'euclidean'` | `'mahalanobis'` | `'minkowski'` | `'seuclidean'` | function handle | ...

Distance metric used to find neighbors of the training data to the query observations, specified as the comma-separated pair consisting of `'Distance'` and a string or function handle.

For both types of nearest neighbor searchers, `Mdl` supports these distance metrics.

Value	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference)
`'cityblock'`	City block distance
`'euclidean'`	Euclidean distance
`'minkowski'`	Minkowski distance

If Mdl is an `ExhaustiveSearcher` model object, then `knnsearch` supports these distance metrics.

Value	Description
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values)
`'cosine'`	One minus the cosine of the included angle between observations (row vectors)
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ

Value	Description
'mahalanobis'	Mahalanobis distance
'seuclidean'	Standardized Euclidean distance
'spearman'	One minus the sample Spearman's rank correlation between observations (treated as sequences of values)

If Mdl is an ExhaustiveSearcher model object, then you can also specify a function handle for a custom distance metric using @ (for example, @distfun). The custom distance function must:

- Have the form function D2 = distfun(ZI, ZJ)
- Take as arguments:
  - A 1-by-*K* vector ZI containing a single row from X or from the query points Y
  - An *m*-by-*K* matrix ZJ containing multiple rows of X or Y
- Return an *m*-by-1 vector of distances D2, whose *j*th element is the distance between the observations ZI and ZJ(*j*,:)

For more details, see "Distance Metrics".

Example: 'Distance','minkowski'

Data Types: char | function_handle

'IncludeTies' — Flag to include nearest neighbors that have the same distance from query observations

false (0) (default) | true (1)

Flag to include nearest neighbors that have the same distance from query observations, specified as the comma-separated pair consisting of 'IncludeTies' and false (0) or true (1).

If IncludeTies is true, then:

- knnsearch includes all nearest neighbors whose distances are equal to the Kth smallest distance in the output arguments.
- Idx and D are *m*-by-1 cell arrays such that each cell contains a vector of at least K indices and distances, respectively. Each vector in D contains arranged distances

in ascending order. Each row in `Idx` contains the indices of the nearest neighbors corresponding to these smallest distances in `D`.

If `IncludeTies` is `false`, then `knnsearch` chooses the observation with the smallest index among the observations that have the same distance from a query point.

Example: `'IncludeTies',true`

`'K'` — Number of nearest neighbors to search for in the training data per query observation

1 (default) | positive integer

Number of nearest neighbors to search for in the training data per query observation, specified as the comma-separated pair consisting of `'IncludeTies'` and a positive integer.

Example: `'K',2`

Data Types: `single` | `double`

`'P'` — Exponent for Minkowski distance metric

2 (default) | positive scalar

Exponent for the Minkowski distance metric, specified as the comma-separated pair consisting of `'P'` and a positive scalar. If you specify `P` and do not specify `'Distance','minkowski'`, then the software throws an error.

Example: `'P',3`

Data Types: `double` | `single`

For Exhaustive Nearest Neighbor Searchers

`'Cov'` — Covariance matrix for Mahalanobis distance metric

`nancov(X)` (default) | positive definite matrix

Covariance matrix for the Mahalanobis distance metric, specified as the comma-separated pair consisting of `'Cov'` and a positive definite matrix. `Cov` is a K-by-K matrix, where K is the number of columns of X. If you specify `Cov` and do not specify `'Distance','mahalanobis'`, then `knnsearch` throws an error.

Example: `'Cov',eye(3)`

Data Types: `double` | `single`

'Scale' — Scale parameter value for standard Euclidean distance metric

nanstd(X) (default) | nonnegative numeric vector

Scale parameter value for the standard Euclidean distance metric, specified as the comma-separated pair consisting of 'Scale' and a nonnegative numeric vector. Scale has length K, where K is the number of columns of X.

The software scales each difference between the training and query data using the corresponding element of Scale. If you specify Scale and do not specify 'Distance','seuclidean', then knnsearch throws an error.

Example: 'Scale',quantile(X,0.75) - quantile(X,0.25)

Data Types: double | single

Note: If you specify 'Distance', 'Cov', 'P', or 'Scale', then Mdl.Distance and Mdl.DistParameter do not change value.

Output Arguments

Idx — Training data indices of nearest neighbors

numeric matrix | cell array of numeric vectors

Training data indices of nearest neighbors, returned as a numeric matrix or cell array of numeric vectors.

- If you do not specify IncludeTies (false by default), then Idx is an m-by-K numeric matrix, where m is the number of rows in Y and K is the number of searched nearest neighbors. Idx(j,k) indicates that Mdl.X(Idx(j,k),:) is the observation with the kth smallest distance to the query observation Y(j,:).
- If you specify 'IncludeTies',true, then Idx is an m-by-1 cell array such that cell j (Idx{j}) contains a vector of at least K indices of the closest observations in Mdl.X to the query observation Y(j,:). The function arranges the elements of the vectors in ascending order by distance.

D — Distances of nearest neighbors to the query data

numeric matrix | cell array of numeric vectors

Distances of the nearest neighbors to the query data, returned as a numeric matrix or cell array of numeric vectors.

- If you do not specify IncludeTies (`false` by default), then `D` is an *m*-by-K numeric matrix, where *m* is the number of rows in Y and `K` is the number of searched nearest neighbors. `D(j,k)` is the distance `Mdl.X(Idx(j,k),:)` is from the query observation `Y(j,:)` with respect to the distance metric, and it represents the `k`th smallest distance.
- If you specify `'IncludeTies',true`, then D is an *m*-by-`1` cell array such that cell `j` (`D{j}`) contains a vector of at least K distances of the closest observations in `Mdl.X` to the query observation `Y(j,:)`. The function arranges the elements of the vectors in ascending order by distance.

Alternatives

- `knnsearch` is an object function that requires an `ExhaustiveSearcher` or a `KDTreeSearcher` model object and query data. Under equivalent conditions, `knnsearch` returns the same results as `knnsearch` when you specify the name-value pair argument `'NSMethod','exhaustive'` or `'NSMethod','kdtree'`, respectively.
- For *k*-nearest neighbors classification, see `fitcknn` and `ClassificationKNN`.

More About

Algorithms

For positive integer `K`, `knnsearch` finds the `K` points in `Mdl.X` that are nearest each `Y` point. In contrast, for positive scalar `r`, `rangesearch` finds all the points in `Mdl.X` that are within a distance `r` of each `Y` point.

- Using ExhaustiveSearcher Objects
- Using KDTreeSearcher Objects
- "*k*-Nearest Neighbor Search and Radius Search" on page 16-11
- "Distance Metrics"

References

[1] Friedman, J. H., Bentely, J., and Finkel, R. A. (1977). "An Algorithm for Finding Best Matches in Logarithmic Expected Time." *ACM Transactions on Mathematical Software* Vol. 3, Issue 3, Sept. 1977, pp. 209–226.

See Also

`ClassificationKNN` | `createns` | `ExhaustiveSearcher` | `fitcknn` | `KDTreeSearcher` | `knnsearch` | `rangesearch`

Introduced in R2010a

knnsearch

Find *k*-nearest neighbors using data

Syntax

```
IDX = knnsearch(X,Y)
[IDX,D] = knnsearch(X,Y)
[IDX,D] = knnsearch(X,Y,'Name',Value)
```

Description

`IDX = knnsearch(X,Y)` finds the nearest neighbor in `X` for each point in `Y`. `IDX` is a column vector with *my* rows. Each row in `IDX` contains the index of nearest neighbor in `X` for the corresponding row in `Y`.

`[IDX,D] = knnsearch(X,Y)` returns an *my*-by-1 vector `D` containing the distances between each observation in `Y` and the corresponding closest observation in `X`. That is, `D(i)` is the distance between `X(IDX(i),:)` and `Y(i,:)`.

`[IDX,D] = knnsearch(X,Y,'Name',Value)` accepts one or more optional comma-separated name-value pair arguments. Specify `Name` inside single quotes.

`knnsearch` does not save a search object. To create a search object, use `createns`.

Input Arguments

X

An *mx*-by-*n* numeric matrix. Rows of `X` correspond to observations and columns correspond to variables.

Y

An *my*-by-*n* numeric matrix of query points. Rows of `Y` correspond to observations and columns correspond to variables.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'K'`

Positive integer specifying the number of nearest neighbors in `X` for each point in `Y`. Default is 1. `IDX` and `D` are *my*-by-`K` matrices. `D` sorts the distances in each row in ascending order. Each row in `IDX` contains the indices of the `K` closest neighbors in `X` corresponding to the `K` smallest distances in `D`.

`'IncludeTies'`

A logical value indicating whether `knnsearch` includes all the neighbors whose distance values are equal to the `K`th smallest distance. If `IncludeTies` is `true`, `knnsearch` includes all these neighbors. In this case, `IDX` and `D` are *my*-by-`1` cell arrays. Each row in `IDX` and `D` contains a vector with at least `K` numeric numbers. `D` sorts the distances in each vector in ascending order. Each row in `IDX` contains the indices of the closest neighbors corresponding to these smallest distances in `D`.

Default: `false`

`'NSMethod'`

Nearest neighbors search method. Value is either:

- `'kdtree'` — Creates and uses a `K`d-tree to find nearest neighbors. This is the default value when the number of columns of `X` is less than 10, `X` is not sparse, and the distance measure is one of the following measures. `'kdtree'` is only valid when the distance measure is one of the following:
  - `'euclidean'`
  - `'cityblock'`
  - `'minkowski'`
  - `'chebychev'`
- `'exhaustive'` — Uses the exhaustive search algorithm by computing the distance values from all the points in `X` to each point in `Y` to find nearest neighbors.

`'Distance'`

A string or a function handle specifying the distance metric. The value can be one of the following:

- `'euclidean'` — Euclidean distance (default).
- `'seuclidean'` — Standardized Euclidean distance. Each coordinate difference between rows in `X` and the query matrix is scaled by dividing by the corresponding element of the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use the `Scale` argument.
- `'cityblock'` — City block distance.
- `'chebychev'` — Chebychev distance (maximum coordinate difference).
- `'minkowski'` — Minkowski distance. The default exponent is 2. To specify a different exponent, use the `'P'` argument.
- `'mahalanobis'` — Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is `nancov(X)`. To change the value of `C`, use the `Cov` parameter.
- `'cosine'` — 1 minus the cosine of the included angle between observations (treated as vectors).
- `'correlation'` — One minus the sample linear correlation between observations (treated as sequences of values).
- `'spearman'` — One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
- `'hamming'` — Hamming distance, which is the percentage of coordinates that differ.
- `'jaccard'` — One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.
- custom distance function — A distance function specified using `@` (for example, `@distfun`). A custom distance function must
  - Have the form `function D2 = distfun(ZI,ZJ)`
  - Take as arguments:
    - A 1-by-n vector `ZI` containing a single row from `X` or from the query points `Y`
    - An m2-by-n matrix `ZJ` containing multiple rows of `X` or `Y`
  - Return an m2-by-1 vector of distances `D2`, whose jth element is the distance between the observations `ZI` and `ZJ(j,:)`

For more information on these distance metrics, see “Distance Metrics”.

`'P'`

A positive scalar, p, indicating the exponent of the Minkowski distance. This parameter is only valid if the `Distance` is `'minkowski'`. Default is 2.

`'Cov'`

A positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This parameter is only valid when `Distance` is `'mahalanobis'`. Default is `nancov(X)`.

`'Scale'`

A vector `S` containing nonnegative values, with length equal to the number of columns in `X`. Each coordinate of `X` and each query point is scaled by the corresponding element of `S` when computing the standardized Euclidean distance. This argument is only valid when `Distance` is `'seuclidean'`. Default is `nanstd(X)`.

`'BucketSize'`

The maximum number of data points in the leaf node of the *k*d-tree. This argument is only meaningful when using the *k*d-tree search method. Default is 50.

Examples

Classify Using k-Nearest Neighbors

Find the 10 nearest neighbors in `x` to each point in `y` using first the `'minkowski'` distance metric with a p value of `5`, and then using the `'chebychev'` distance metric.

Load Fisher's iris data set

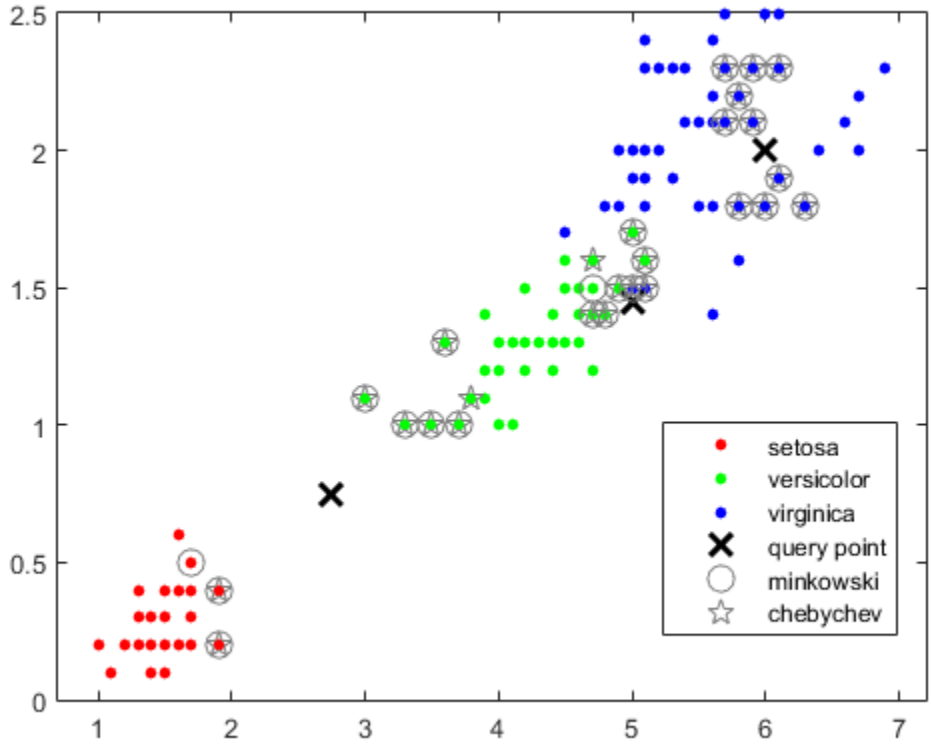
```
load fisheriris
x = meas(:,3:4);
y = [5 1.45;6 2;2.75 .75];
```

Perform a `knnsearch` between `x` and the query points in `y`, using first Minkowski then Chebychev distance metrics.

```
[n,d]=knnsearch(x,y,'k',10,'distance','minkowski','p',5);
[ncb,dcb] = knnsearch(x,y,'k',10,...
   'distance','chebychev');
```

Visualize the results of the two different nearest neighbors searches. Plot the training data. Plot an X for the query points. Use circles to denote the Minkowski nearest neighbors. Use pentagrams to denote the Chebychev nearest neighbors.

```
gscatter(x(:,1),x(:,2),species)
line(y(:,1),y(:,2),'marker','x','color','k',...
   'markersize',10,'linewidth',2,'linestyle','none')
line(x(n,1),x(n,2),'color',[.5 .5 .5],'marker','o',...
   'linestyle','none','markersize',10)
line(x(ncb,1),x(ncb,2),'color',[.5 .5 .5],'marker','p',...
   'linestyle','none','markersize',10)
legend('setosa','versicolor','virginica','query point',...
'minkowski','chebychev','Location','best')
```



Alternatives

`knnsearch` is the object function of `ExhaustiveSearcher` and `KDTreeSearcher` models for a *k*-nearest neighbors search. If you set the `NSMethod` name-value pair argument to the appropriate value (`'exhaustive'` for an exhaustive search or `'kdtree'` for a *K*d-tree), then the search results are equivalent to conducting a distance search using `knnsearch` and without using model objects.

More About

Tips

- For a fixed positive integer `K`, `knnsearch` finds the `K` points in `X` that are nearest each point in `Y`. In contrast, for a fixed positive real value `r`, `rangesearch` finds all the points in `X` that are within a distance `r` of each point in `Y`.

Algorithms

For information on a specific search algorithm, see "Distance Metrics".

- Using ExhaustiveSearcher Objects
- Using KDTreeSearcher Objects
- "*k*-Nearest Neighbor Search and Radius Search" on page 16-11
- "Distance Metrics"

References

[1] Friedman, J. H., Bentely, J., and Finkel, R. A. (1977) An Algorithm for Finding Best Matches in Logarithmic Expected Time, ACM Transactions on Mathematical Software 3, 209.

See Also

`createns` | `ExhaustiveSearcher` | `KDTreeSearcher` | `knnsearch`

kruskalwallis

Kruskal-Wallis test

Syntax

```
p = kruskalwallis(x)
p = kruskalwallis(x,group)
p = kruskalwallis(x,group,displayopt)
[p,tbl,stats] = kruskalwallis( ___ )
```

Description

`p = kruskalwallis(x)` returns the *p*-value for the null hypothesis that the data in each column of the matrix x comes from the same distribution, using a Kruskal-Wallis test. The alternative hypothesis is that not all samples come from the same distribution. `kruskalwallis` also returns an ANOVA table and a box plot.

`p = kruskalwallis(x,group)` returns the *p*-value for a test of the null hypothesis that the data in each categorical group, as specified by the grouping variable group comes from the same distribution. The alternative hypothesis is that not all groups come from the same distribution.

`p = kruskalwallis(x,group,displayopt)` returns the *p*-value of the test and lets you display or suppress the ANOVA table and box plot.

`[p,tbl,stats] = kruskalwallis( ___ )` also returns the ANOVA table as the cell array `tbl` and the structure `stats` containing information about the test statistics.

Examples

Test Data Samples for the Same Distribution

Create two different normal probability distribution objects. The first distribution has `mu = 0` and `sigma = 1`, and the second distribution has `mu = 2` and `sigma = 1`.

```
pd1 = makedist('Normal');
pd2 = makedist('Normal','mu',2,'sigma',1);
```

Create a matrix of sample data by generating random numbers from these two distributions.

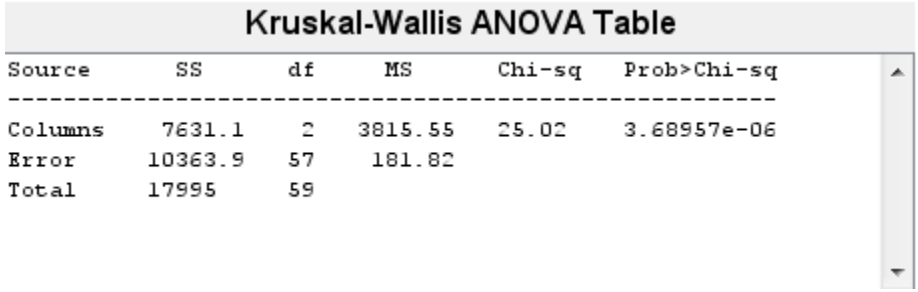
```
rng('default'); % for reproducibility
x = [random(pd1,20,2),random(pd2,20,1)];
```

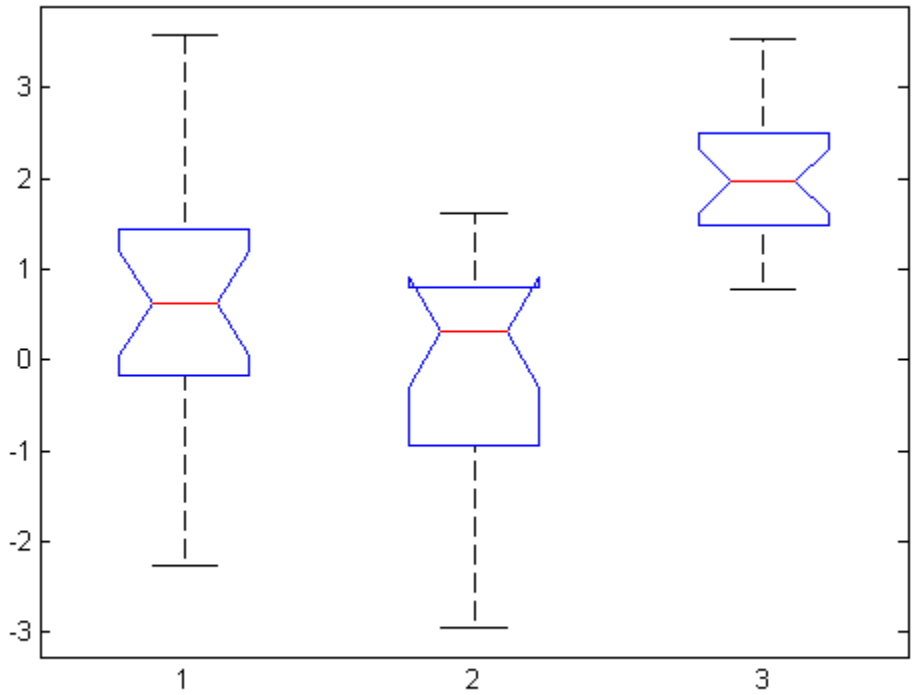
The first two columns of `x` contain data generated from the first distribution, while the third column contains data generated from the second distribution.

Test the null hypothesis that the sample data from each column in `x` comes from the same distribution.

```
p = kruskalwallis(x)
```

```
p =

   3.6896e-06
```





The returned value of `p` indicates that `kruskalwallis` rejects the null hypothesis that all three data samples come from the same distribution at a 1% significance level. The ANOVA table provides additional test results, and the box plot visually presents the summary statistics for each column in `x`.

Conduct Followup Tests for Unequal Medians

Create two different normal probability distribution objects. The first distribution has `mu = 0` and `sigma = 1`. The second distribution has `mu = 2` and `sigma = 1`.

```
pd1 = makedist('Normal');
pd2 = makedist('Normal','mu',2,'sigma',1);
```

Create a matrix of sample data by generating random numbers from these two distributions.

```
rng('default'); % for reproducibility
x = [random(pd1,20,2),random(pd2,20,1)];
```

The first two columns of `x` contain data generated from the first distribution, while the third column contains data generated from the second distribution.

Test the null hypothesis that the sample data from each column in `x` comes from the same distribution. Suppress the output displays, and generate the structure `stats` to use in further testing.

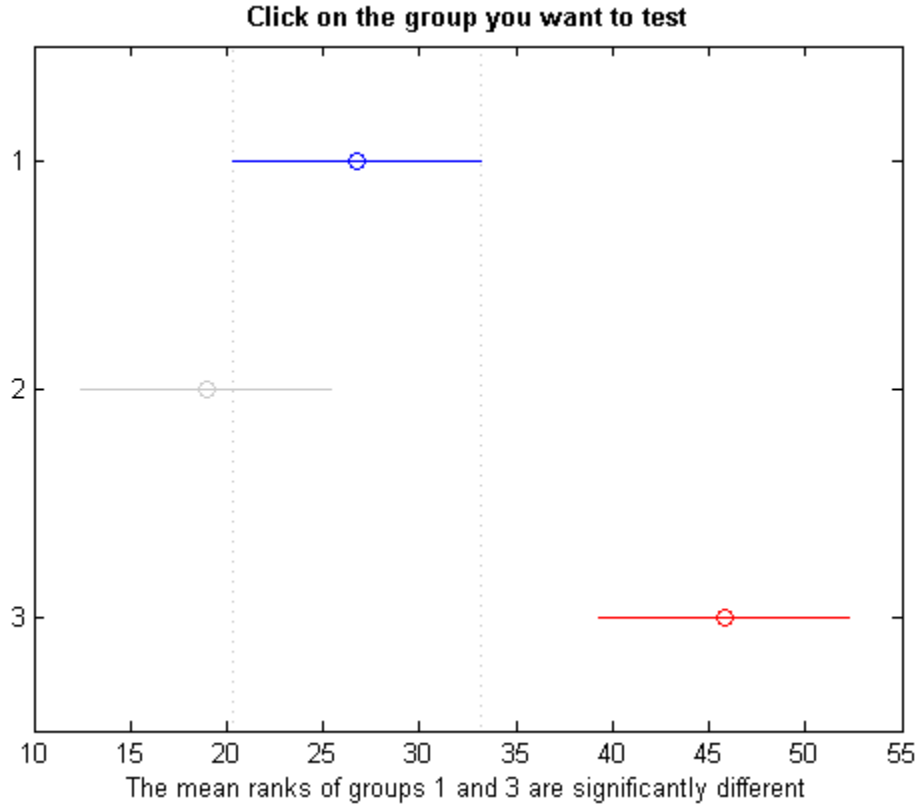
```
[p,tbl,stats] = kruskalwallis(x,[],'off')
```

```
p =

   3.6896e-06


tbl =

  Columns 1 through 4

    'Source'     'SS'            'df'    'MS'
    'Columns'    [7.6311e+03]    [ 2]    [3.8155e+03]
    'Error'      [1.0364e+04]    [57]    [  181.8228]
    'Total'      [     17995]    [59]              []

  Columns 5 through 6

    'Chi-sq'     'Prob>Chi-sq'
    [25.0200]    [ 3.6896e-06]
           []                []
           []                []


stats =

       gnames: [3x1 char]
            n: [20 20 20]
       source: 'kruskalwallis'
    meanranks: [26.7500 18.9500 45.8000]
         sumt: 0
```

The returned value of `p` indicates that the test rejects the null hypothesis at the 1% significance level. You can use the structure `stats` to perform additional followup testing. The cell array `tbl` contains the same data as the graphical ANOVA table, including column and row labels.

Conduct a followup test to identify which data sample comes from a different distribution.

```
c = multcompare(stats)

Note: Intervals can be used for testing but are not simultaneous confidence intervals.

c =

    1.0000    2.0000   -5.1435    7.8000   20.7435
    1.0000    3.0000  -31.9935  -19.0500   -6.1065
    2.0000    3.0000  -39.7935  -26.8500  -13.9065
```



The results indicate that there is a significant difference between groups 1 and 3, so the test rejects the null hypothesis that the data in these two groups comes from the same distribution. The same is true for groups 2 and 3. However, there is not a significant difference between groups 1 and 2, so the test does not reject the null hypothesis that these two groups come from the same distribution. Therefore, these results suggest that the data in groups 1 and 2 come from the same distribution, and the data in group 3 comes from a different distribution.

Test for the Same Distribution Across Groups

Create a vector, `strength`, containing measurements of the strength of metal beams. Create a second vector, `alloy`, containing strings indicating the type of metal alloy from which the corresponding beam is made.

```
strength = [82 86 79 83 84 85 86 87 74 82 ...
            78 75 76 77 79 79 77 78 82 79];

alloy = {'st','st','st','st','st','st','st','st',...
         'al1','al1','al1','al1','al1','al1',...
         'al2','al2','al2','al2','al2','al2'};
```

Test the null hypothesis that the beam strength measurements have the same distribution across all three alloys.

```
p = kruskalwallis(strength,alloy,'off')
```

```
p =

    0.0018
```

The returned value of `p` indicates that the test rejects the null hypothesis at the 1% significance level.

Input Arguments

x — Sample data

vector | matrix

Sample data for the hypothesis test, specified as a vector or an *m*-by-*n* matrix. If `x` is an *m*-by-*n* matrix, each of the *n* columns represents an independent sample containing *m* mutually independent observations.

Data Types: `single` | `double`

group — Grouping variable

categorical variable | vector | character array | cell array

Grouping variable, specified as a categorical variable, vector, character array, or cell array.

- If `x` is a vector, then each element in `group` identifies the group to which the corresponding element in `x` belongs, and `group` must be a vector of the same length as `x`. If a row of `group` contains an empty cell or empty string, that row and the corresponding observation in `x` are disregarded. `NaN` values in either `x` or `group` are similarly ignored.

- If `x` is a matrix, then each column in `x` represents a different group, and you can use `group` to specify labels for these columns. The number of elements in `group` and the number of columns in `x` must be equal.

The labels contained in `group` also annotate the box plot.

Example:
`{'red','blue','green','blue','red','blue','green','green','red'}`

Data Types: `single` | `double` | `char`

`displayopt` — Display option
`'on'` (default) | `'off'`

Display option, specified as `'on'` or `'off'`. If `displayopt` is `'on'`, `kruskalwallis` displays the following figures:

- An ANOVA table containing the sums of squares, degrees of freedom, and other quantities calculated based on the ranks of the data in x.
- A box plot of the data in each column of the data matrix x. The box plots are based on the actual data values, rather than on the ranks.

If `displayopt` is `'off'`, `kruskalwallis` does not display these figures.

If you specify a value for `displayopt`, you must also specify a value for `group`. If you do not have a grouping variable, specify `group` as `[]`.

Example: `'off'`

Output Arguments

`p` — *p*-value
scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

`tbl` — ANOVA table
cell array

ANOVA table of test results, returned as a cell array. `tbl` includes the sums of squares, degrees of freedom, and other quantities calculated based on the ranks of the data in x, as well as column and row labels.

`stats` — Test data
structure

Test data, returned as a structure. You can perform followup multiple comparison tests on pairs of sample medians by using `multcompare`, with `stats` as the input value.

More About

Kruskal-Wallis Test

The Kruskal-Wallis test is a nonparametric version of classical one-way ANOVA, and an extension of the Wilcoxon rank sum test to more than two groups. It compares the medians of the groups of data in `x` to determine if the samples come from the same population (or, equivalently, from different populations with the same distribution).

The Kruskal-Wallis test uses ranks of the data, rather than numeric values, to compute the test statistics. It finds ranks by ordering the data from smallest to largest across all groups, and taking the numeric index of this ordering. The rank for a tied observation is equal to the average rank of all observations tied with it. The *F*-statistic used in classical one-way ANOVA is replaced by a chi-square statistic, and the *p*-value measures the significance of the chi-square statistic.

The Kruskal-Wallis test assumes that all samples come from populations having the same continuous distribution, apart from possibly different locations due to group effects, and that all observations are mutually independent. By contrast, classical one-way ANOVA replaces the first assumption with the stronger assumption that the populations have normal distributions.

- “Grouping Variables” on page 2-52

See Also

`anova1` | `boxplot` | `friedman` | `multcompare` | `ranksum`

ksdensity

Kernel smoothing function estimate

Syntax

```
[f,xi] = ksdensity(x)
[f,xi] = ksdensity(x,pts)
[f,xi] = ksdensity(x,pts,Name,Value)
[f,xi,bw] = ksdensity( ___ )

ksdensity( ___ )
ksdensity(ax, ___ )
```

Description

`[f,xi] = ksdensity(x)` returns a probability density estimate, `f`, for the sample in the vector `x`. The estimate is based on a normal kernel function, and is evaluated at 100 equally spaced points, `xi`, that cover the range of the data in `x`.

`ksdensity` works best with continuously distributed samples.

`[f,xi] = ksdensity(x,pts)` returns a probability density estimate, `f`, for the sample in the vector `x`, evaluated at the specified values in vector `pts`. Here, the `xi` and `pts` vectors contain identical values.

`[f,xi] = ksdensity(x,pts,Name,Value)` returns a probability density estimate, `f`, for the sample in the vector `x`, with additional options specified by one or more `Name,Value` pair arguments.

For example, you can define the function type `ksdensity` evaluates, such as probability density, cumulative probability, survivor function, and so on. Or you can specify the bandwidth of the smoothing window.

`[f,xi,bw] = ksdensity( ___ )` also returns the bandwidth of the kernel smoothing window, `bw`. The default bandwidth is the optimal for normal densities.

`ksdensity( ___ )` plots the kernel smoothing function estimate.

`ksdensity(ax, ___ )` plots the results using axes with the handle, `ax`, instead of the current axes returned by `gca`.

Examples

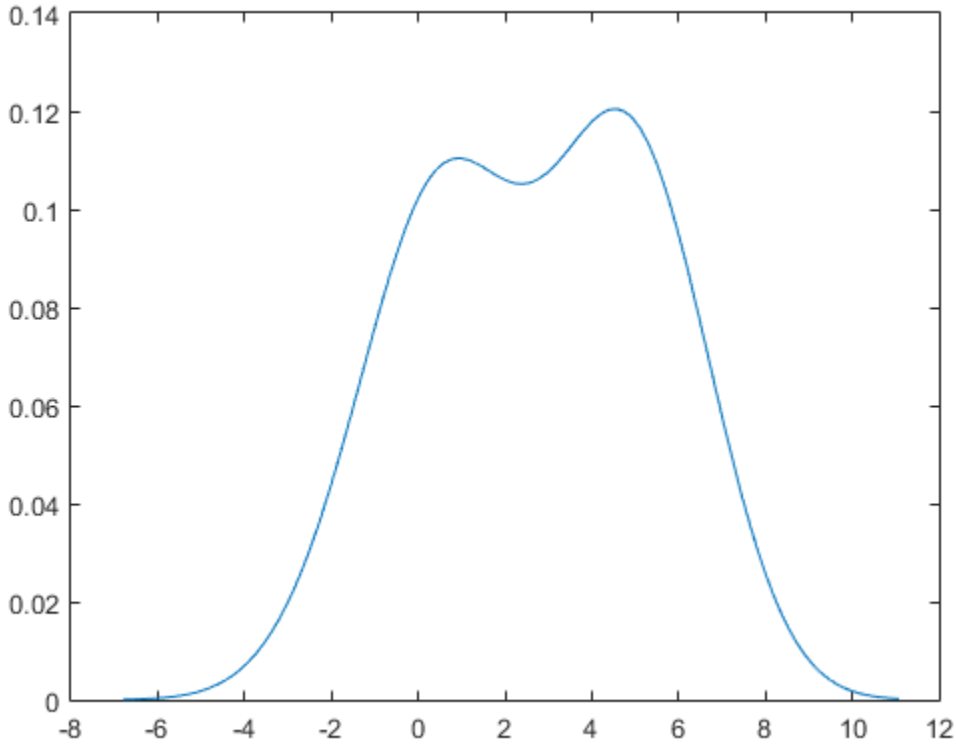
Estimate Density

Generate a sample data set from a mixture of two normal distributions.

```
rng default  % for reproducibility
x = [randn(30,1); 5+randn(30,1)];
```

Plot the estimated density.

```
[f,xi] = ksdensity(x);
figure
plot(xi,f);
```



The density estimate shows the bimodality of the sample.

Estimate Cumulative Distribution Function at Specified Values

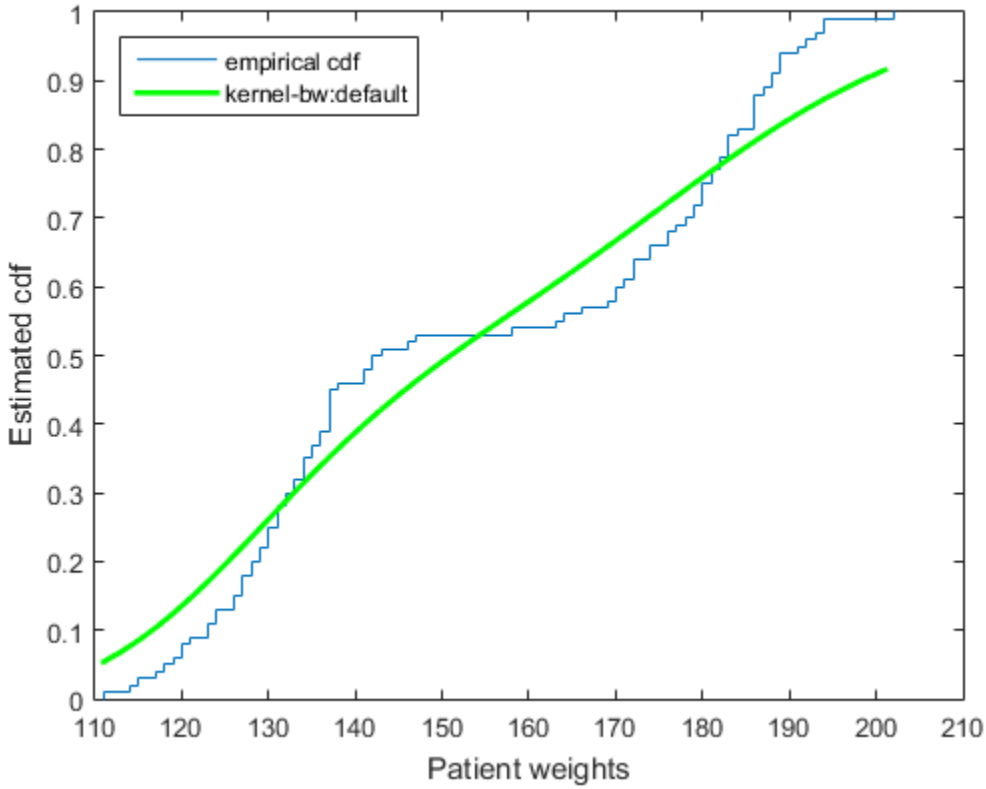
Load the sample data.

```
load hospital
```

Compute and plot the estimated cdf evaluated at a specified set of values.

```
pts = (min(hospital.Weight):2:max(hospital.Weight));
figure()
ecdf(hospital.Weight)
hold on
```

```
[f,xi,bw] = ksdensity(hospital.Weight,pts,'support','positive',...
 'function','cdf');
plot(xi,f,'-g','LineWidth',2)
legend('empirical cdf','kernel-bw:default','Location','NorthWest')
xlabel('Patient weights')
ylabel('Estimated cdf')
```



`ksdensity` seems to smooth the cumulative distribution function estimate too much. An estimate with a smaller bandwidth might produce a closer estimate to the empirical cumulative distribution function.

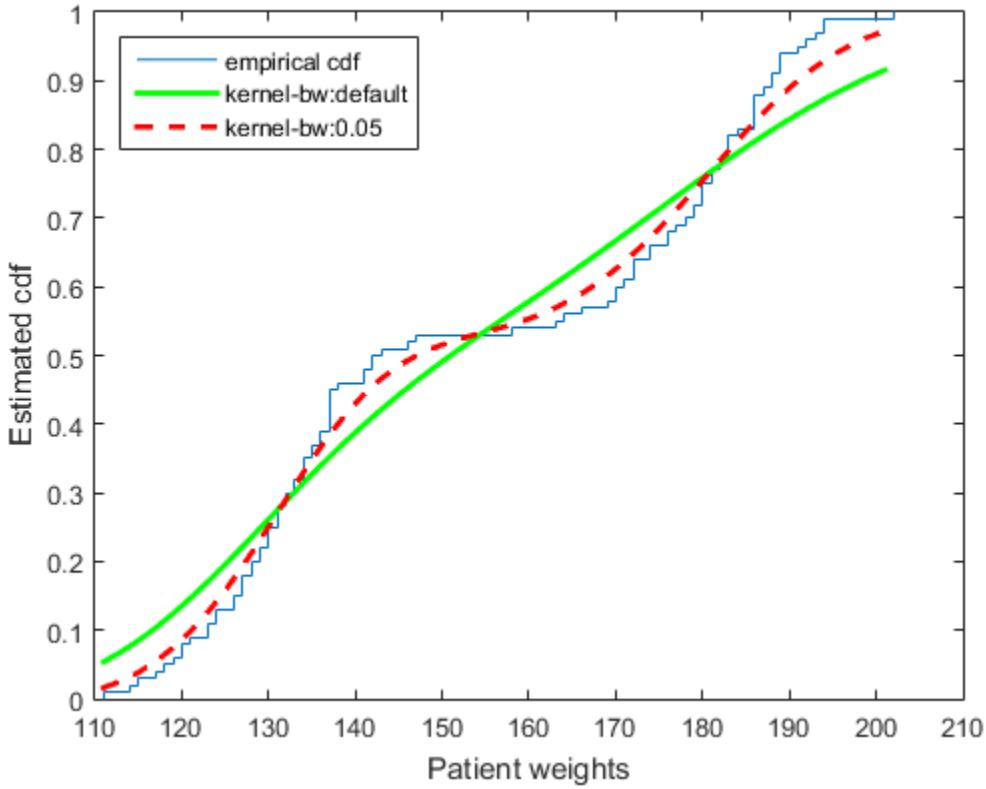
Return the bandwidth of the smoothing window.

`bw`

```
bw =

    0.1070
```

Plot the cumulative distribution function estimate using a smaller bandwidth.

```
[f,xi] = ksdensity(hospital.Weight,pts,'support','positive',...
 'function','cdf','bandwidth',0.05);
plot(xi,f,'--r','LineWidth',2)
legend('empirical cdf','kernel-bw:default','kernel-bw:0.05',...
 'Location','NorthWest')
hold off
```



The `ksdensity` estimate with a smaller bandwidth matches the empirical cumulative distribution function better.

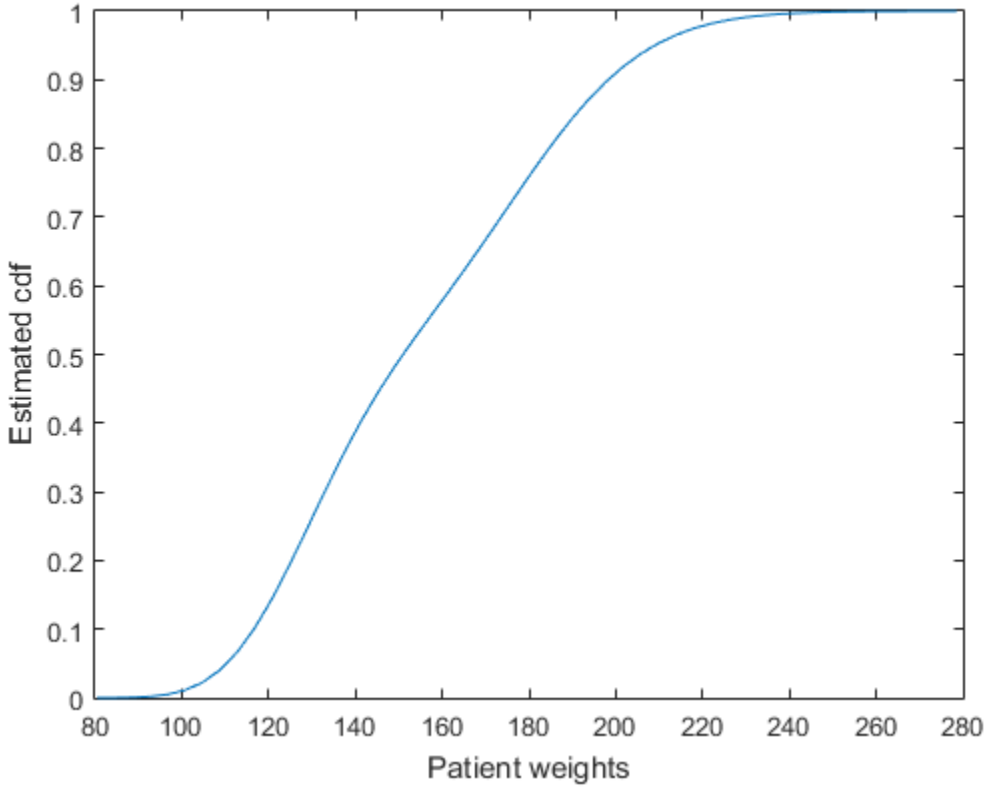
Plot Estimated Cumulative Density Function for Given Number of Points

Load the sample data.

```
load hospital
```

Plot the estimated cdf evaluated at 50 equally spaced points.

```
figure()
ksdensity(hospital.Weight,'support','positive','function','cdf',...
'npoints',50)
xlabel('Patient weights')
ylabel('Estimated cdf')
```



Estimate Survivor and Cumulative Hazard for Censored Failure Data

Generate sample data from an exponential distribution with mean 3.

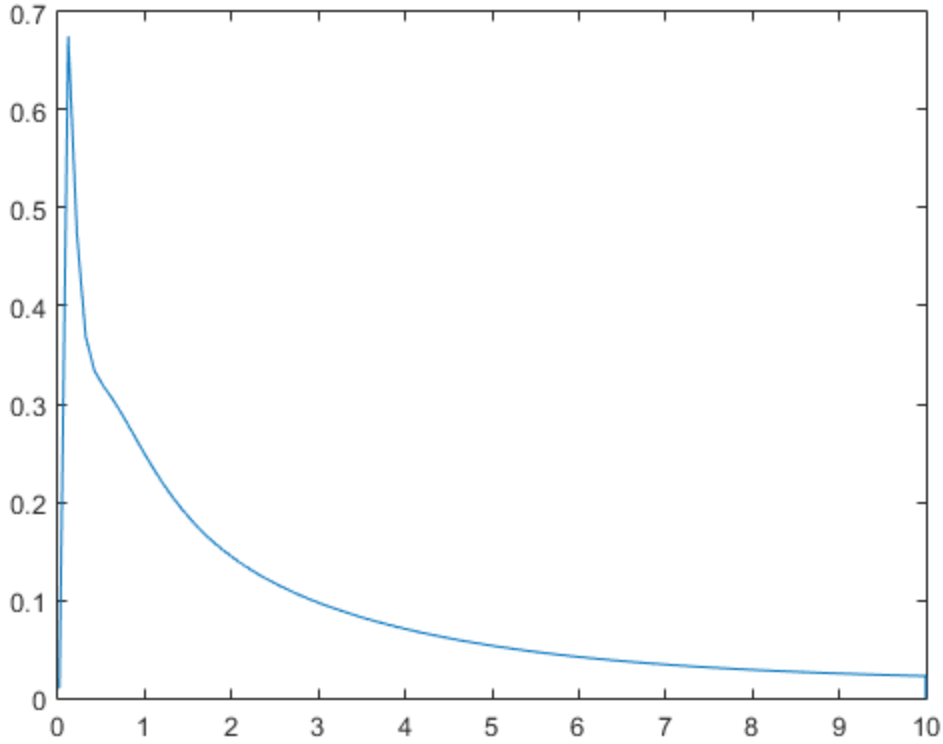
```
rng default  % for reproducibility
x = random('exp',3,100,1);
```

Create a logical vector that indicates censoring. Here, observations with lifetimes longer than 10 are censored.

```
T = 10;
cens = (x>10);
```

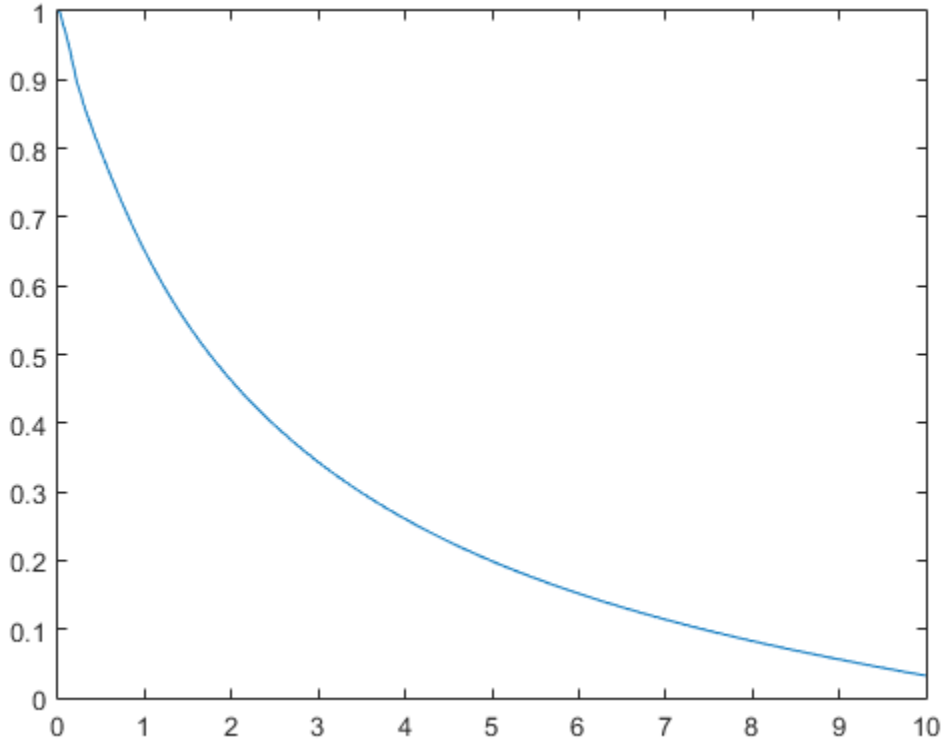
Compute and plot the estimated density function.

```
figure
ksdensity(x,'support','positive','censoring',cens);
```



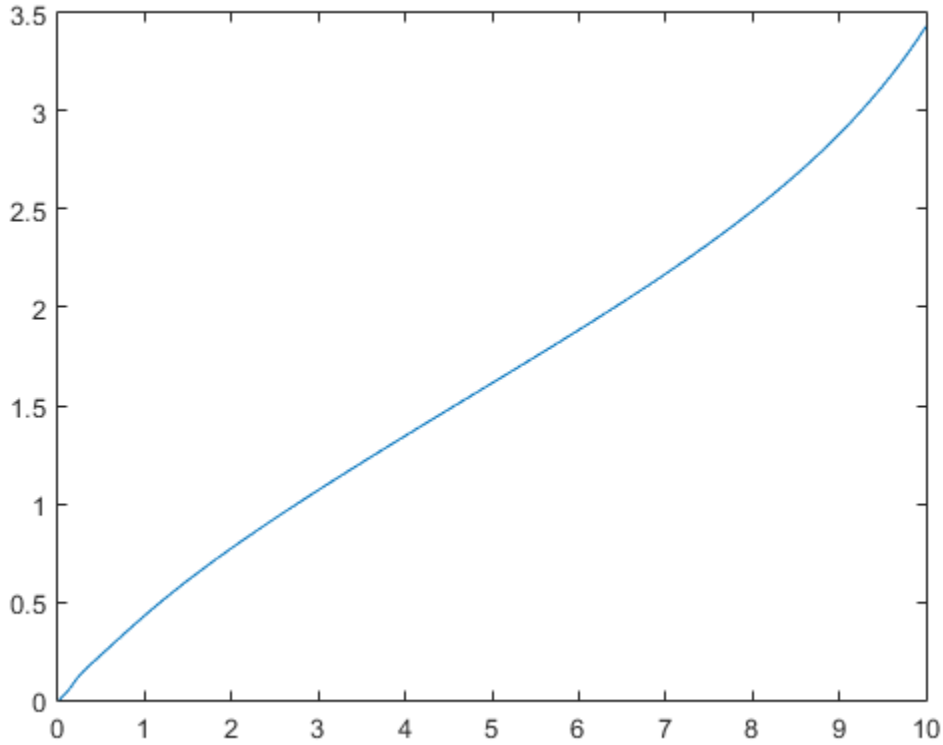
Compute and plot the survivor function.

```
figure
ksdensity(x,'support','positive','censoring',cens,...
'function','survivor');
```



Compute and plot the cumulative hazard function.

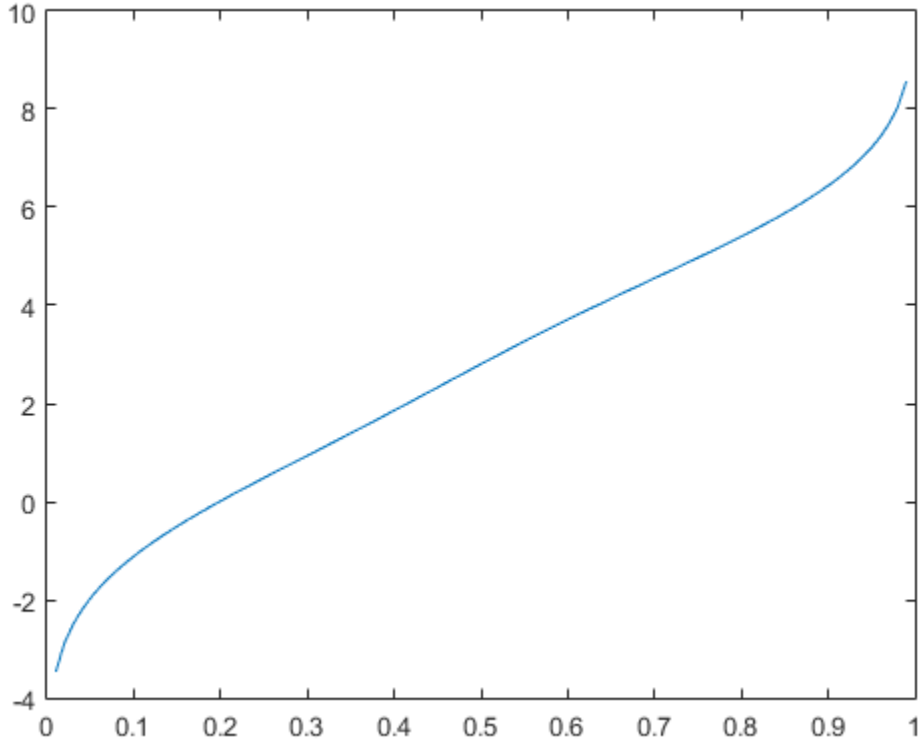
```
figure
ksdensity(x,'support','positive','censoring',cens,...
'function','cumhazard');
```



Estimate Inverse Cumulative Distribution Function for Specified Probability Values

Generate a mixture of two normal distributions, and plot the estimated inverse cumulative distribution function at a specified set of probability values.

```
rng default  % for reproducibility
x = [randn(30,1); 5+randn(30,1)];
pi = linspace(.01,.99,99);
figure
ksdensity(x,pi,'function','icdf');
```



Return Bandwidth of Smoothing Window

Generate a mixture of two normal distributions.

```
rng default  % For reproducibility
x = [randn(30,1); 5+randn(30,1)];
```

Return the bandwidth of the smoothing window for the probability density estimate.

```
[f,xi,bw] = ksdensity(x);
bw
```

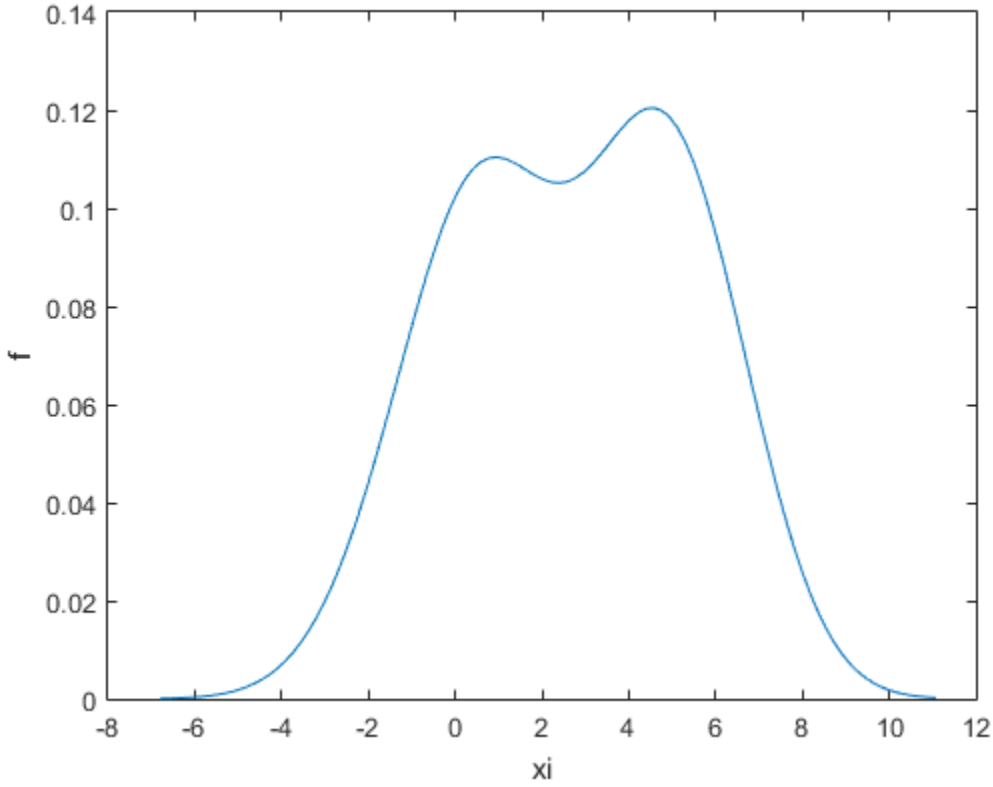
```
bw =
```

```
    1.5141
```

The default bandwidth is optimal for normal densities.

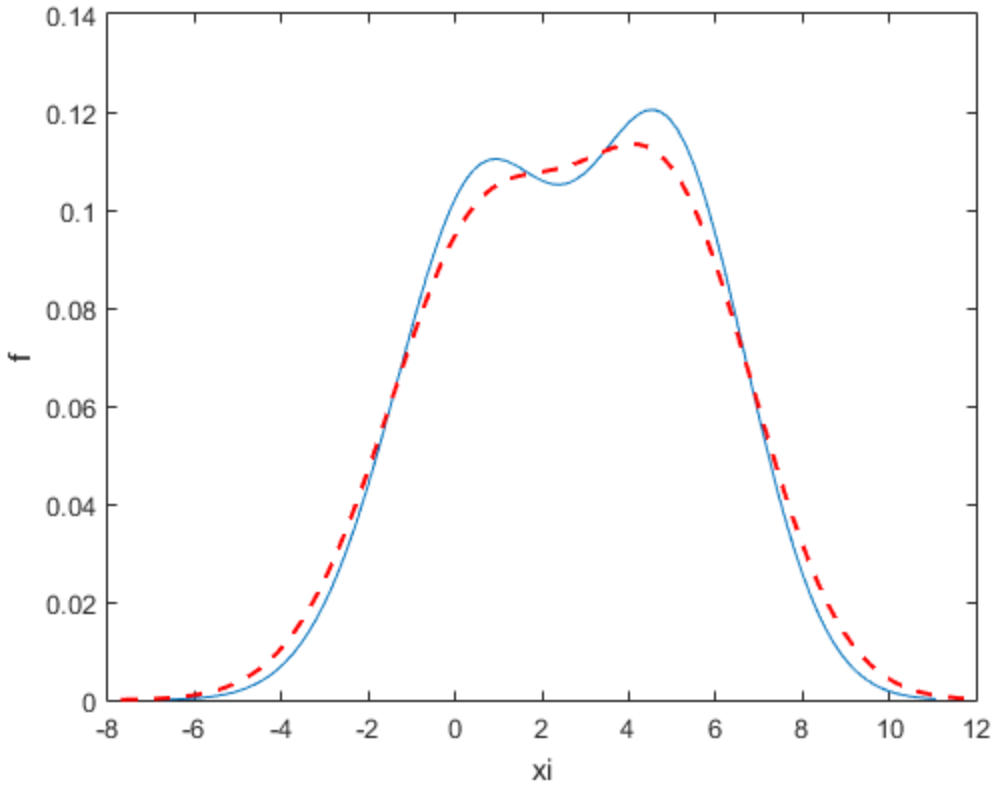
Plot the estimated density.

```
figure
plot(xi,f);
xlabel('xi')
ylabel('f')
hold on
```



Plot the density using an increased bandwidth value.

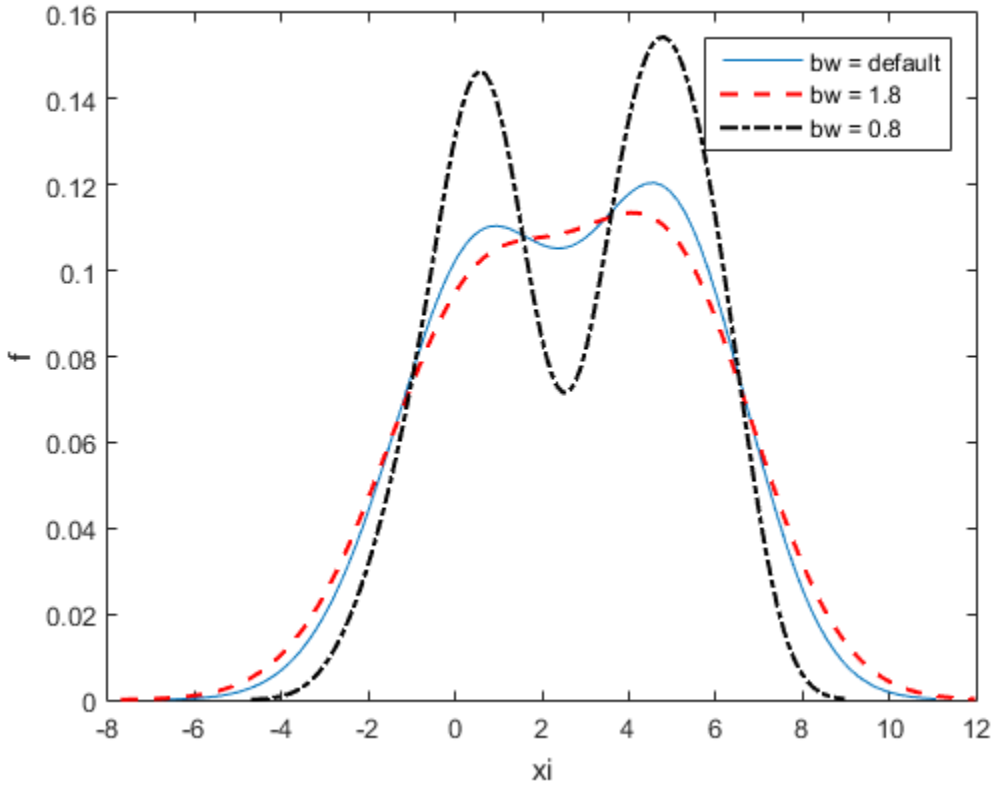
```
[f,xi] = ksdensity(x,'width',1.8);
plot(xi,f,'--r','LineWidth',1.5)
```



A higher bandwidth further smooths the density estimate, which might mask some characteristics of the distribution.

Now, plot the density using a decreased bandwidth value.

```
[f,xi] = ksdensity(x,'width',0.8);
plot(xi,f,'-.k','LineWidth',1.5)
legend('bw = default','bw = 1.8','bw = 0.8')
hold off
```



A smaller bandwidth smooths the density estimate less, which exaggerates some characteristics of the sample.

- "Fit Kernel Distribution Using ksdensity" on page 5-54
- "Fit Distributions to Grouped Data Using ksdensity" on page 5-57

Input Arguments

x — Sample data

column vector

Sample data, for which `ksdensity` returns f values, specified as a column vector.

Example: `[f,xi] = ksdensity(x)`

Data Types: `single` | `double`

`pts` — Points to evaluate `f`

vector

Points to evaluate f at, specified as a vector. `pts` can be a row or column vector. `f` has the same dimensions as `pts`.

Example: `pts = (0:1:25); ksdensity(x,pts);`

Data Types: `single` | `double`

`ax` — Axes handle

handle

Axes handle for the figure `ksdensity` plots to, specified as a handle.

For example, if `h` is a handle for a figure, then `ksdensity` can plot to that figure as follows.

Example: `ksdensity(h,x)`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'censoring',cens,'kernel','triangle','npoints',20,'function','cdf'` specifies that `ksdensity` estimates the cdf by evaluating at 20 equally spaced points that covers the range of data, using the triangle kernel smoothing function and accounting for the censored data information in vector `cens`.

`'censoring'` — Logical vector

vector of 0s (default) | vector of 0s and 1s

Logical vector indicating which entries are censored, specified as a vector of binary values. A value of 0 indicates there is no censoring, 1 indicates that observation is censored. Default is there is no censoring.

Example: `'censoring',censdata`

Data Types: `logical`

`'kernel'` — Type of kernel smoother

`'normal'` (default) | `'box'` | `'triangle'` | `'epanechnikov'` | `function handle` | `string`

Type of kernel smoother, specified as the comma-separated pair consisting of `'kernel'` and one of the following.

- `'normal'` (default)
- `'box'`
- `'triangle'`
- `'epanechnikov'`
- You can also specify a custom kernel function, as a function handle or as a string, e.g., `@normpdf` or `'normpdf'`. This calls the function with one argument that is an array of distances between data values and locations where the density is evaluated. The function must return an array of the same size containing corresponding values of the kernel function.

  When `'function'` is `'pdf'`, this kernel function returns density values. Otherwise, it returns cumulative probability values.

  Specifying a custom kernel when `'function'` is `'icdf'` returns an error.

If `'support'` is `'positive'`, then `ksdensity` transforms x using a log function, estimates the density of the transformed values, and transforms back to the original scale. If `'support'` is a vector `[L U]`, then `ksdensity` uses the transformation `log((X-L)/(U-X))`. The `width` parameter and bw outputs are on the scale of the transformed values.

Example: `'kernel','box'`

Data Types: `char` | `function_handle`

`'npoints'` — Number of equally spaced points

100 (default) | scalar value

Number of equally spaced points in `xi`, specified as the comma-separated pair consisting of `'npoints'` and a scalar value.

For instance, for a kernel smooth estimate of a specified function at 80 equally spaced points within the range of sample data, input:

Example: `'npoints',80`

Data Types: `single` | `double`

`'support'` — Support for the density

`'unbounded'` (default) | `'positive'` | two-element vector, `[L U]`

Support for the density, specified as the comma-separated pair consisting of `'support'` and one of the following.

`'unbounded'`	Default. Allow the density to extend over the whole real line.
`'positive'`	Restrict the density to positive values.
Two-element vector, `[L U]`	Give the finite lower and upper bounds for the support of the density.

Example: `'support','positive'`

Example: `'support',[0 10]`

Data Types: `single` | `double` | `char`

`'weights'` — Weights for each x value

vector

Weights for each x value, specified as the comma-separated pair consisting of `'weights'` and a vector of the same length as x.

For instance, if the weights for the data values are in vector `xw`, then you can specify the weights as follows.

Example: `'weights',xw`

Data Types: `single` | `double`

`'bandwidth'` — Bandwidth of the kernel smoothing window

optimal value for normal densities (default) | scalar value

The bandwidth of the kernel-smoothing window, which is a function of the number of points in `x`, specified as the comma-separated pair consisting of `'width'` and a scalar. The default is optimal for estimating normal densities, but you might want to choose a larger or smaller value to smooth more or less.

Example: `'bandwidth',0.8`

Data Types: `single` | `double`

`'function'` — Function to estimate

`'pdf'` (default) | `'cdf'` | `'icdf'` | `'survivor'` | `'cumhazard'`

Function to estimate, specified as the comma-separated pair consisting of `'function'` and one of the following.

`'pdf'`	Default. Probability density function.
`'cdf'`	Cumulative distribution function.
`'icdf'`	Inverse cumulative distribution function. For `'icdf'`, `f = ksdensity(x,pi,'function','icdf')` computes the estimated inverse cdf of the values in `x`, and evaluates it at the probability values specified in `pi`.
`'survivor'`	Survivor function.
`'cumhazard'`	Cumulative hazard function.

Example: `'function','icdf'`

Data Types: `char`

Output Arguments

`f` — Estimated function values

vector

Estimated function values, returned as a vector of the same dimension as xi or pts.

`xi` — Evaluation points

100 equally spaced points (default) | vector

Evaluation points at which `ksdensity` calculates f, returned as a vector. Default is 100 equally spaced points that cover the range of data in x.

`bw` — Bandwidth of smoothing window

scalar value

Bandwidth of smoothing window, returned as a scalar value.

More About

- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Supported Distributions" on page 5-17

References

[1] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis*. New York: Oxford University Press Inc., 1997.

See Also

`histogram`

kstest

One-sample Kolmogorov-Smirnov test

Syntax

```
h = kstest(x)
h = kstest(x,Name,Value)
[h,p] = kstest( ___ )
[h,p,ksstat,cv] = kstest( ___ )
```

Description

`h = kstest(x)` returns a test decision for the null hypothesis that the data in vector x comes from a standard normal distribution, against the alternative that it does not come from such a distribution, using the one-sample Kolmogorov-Smirnov test. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, or `0` otherwise.

`h = kstest(x,Name,Value)` returns a test decision for the one-sample Kolmogorov-Smirnov test with additional options specified by one or more name-value pair arguments. For example, you can test for a distribution other than standard normal, change the significance level, or conduct a one-sided test.

`[h,p] = kstest( ___ )` also returns the *p*-value p of the hypothesis test, using any of the input arguments from the previous syntaxes.

`[h,p,ksstat,cv] = kstest( ___ )` also returns the value of the test statistic ksstat and the approximate critical value cv of the test.

Examples

Test for a Standard Normal Distribution

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
test1 = grades(:,1);
```

Test the null hypothesis that the data comes from a normal distribution with a mean of 75 and a standard deviation of 10. Use these parameters to center and scale each element of the data vector since, by default, `kstest` tests for a standard normal distribution.

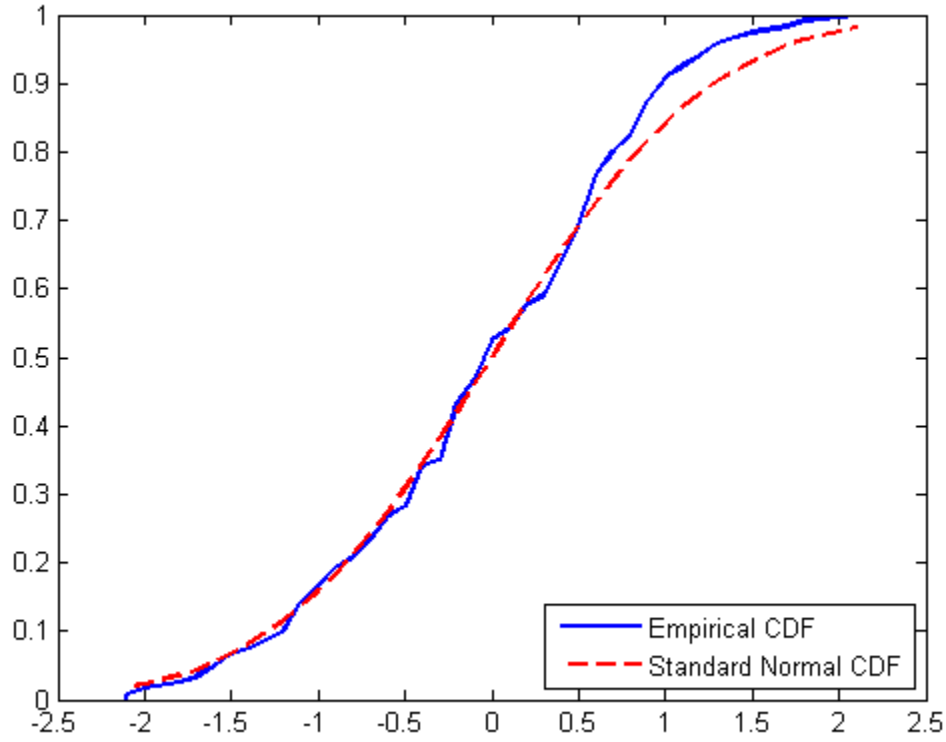
```
x = (test1-75)/10;
h = kstest(x)
```

```
h =
 0
```

The returned value of `h = 0` indicates that `kstest` fails to reject the null hypothesis at the default 5% significance level.

Plot the empirical cumulative distribution function (cdf) and the standard normal cdf for a visual comparison.

```
[f,x_values] = ecdf(x);
F = plot(x_values,f);
set(F,'LineWidth',2);
hold on;
G = plot(x_values,normcdf(x_values,0,1),'r-');
set(G,'LineWidth',2);
legend([F G],...
       'Empirical CDF','Standard Normal CDF',...
       'Location','SE');
```



The plot shows the similarity between the empirical cdf of the centered and scaled data vector and the cdf of the standard normal distribution.

Specify the Hypothesized Distribution Using a Two-Column Matrix

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Specify the hypothesized distribution as a two-column matrix. Column 1 contains the data vector `x`. Column 2 contains cdf values evaluated at each value in `x` for a

hypothesized Student's t distribution with a location parameter of 75, a scale parameter of 10, and one degree of freedom.

```
test_cdf = [x,cdf('tlocationscale',x,75,10,1)];
```

Test if the data are from the hypothesized distribution.

```
h = kstest(x,'CDF',test_cdf)
```

```
h =
 1
```

The returned value of `h = 1` indicates that `kstest` rejects the null hypothesis at the default 5% significance level.

Specify the Hypothesized Distribution Using a Probability Distribution Object

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Create a probability distribution object to test if the data comes from a Student's t distribution with a location parameter of 75, a scale parameter of 10, and one degree of freedom.

```
test_cdf = makedist('tlocationscale','mu',75,'sigma',10,'nu',1);
```

Test the null hypothesis that the data comes from the hypothesized distribution.

```
h = kstest(x,'CDF',test_cdf)
```

```
h =
 1
```

The returned value of `h = 1` indicates that `kstest` rejects the null hypothesis at the default 5% significance level.

Test the Hypothesis at Different Significance Levels

Load the sample data. Create a vector containing the first column of the students' exam grades.

```
load examgrades;
test1 = grades(:,1);
```

Create a probability distribution object to test if the data comes from a Student's t distribution with a location parameter of 75, a scale parameter of 10, and one degree of freedom.

```
test_cdf = makedist('tlocationscale','mu',75,'sigma',10,'nu',1);
```

Test the null hypothesis that data comes from the hypothesized distribution at the 1% significance level.

```
[h,p] = kstest(x,'CDF',test_cdf,'Alpha',0.01)
```

```
h =
     1

p =
    0.0021
```

The returned value of `h = 1` indicates that `kstest` rejects the null hypothesis at the 1% significance level.

Conduct a One-Sided Hypothesis Test

Load the sample data. Create a vector containing the third column of the stock return data matrix.

```
load stockreturns;
x = stocks(:,3);
```

Test the null hypothesis that the data comes from a standard normal distribution, against the alternative hypothesis that the population cdf of the data is larger than the standard normal cdf.

```
[h,p,k,c] = kstest(x,'Tail','larger')
```

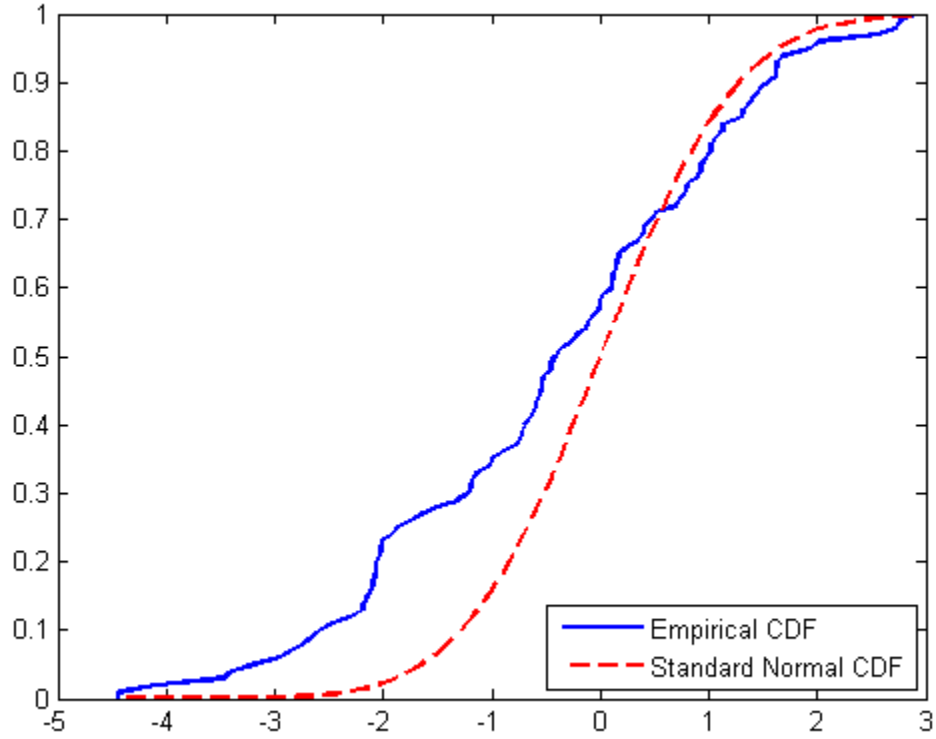
```
h =
 1
p =
 5.0854e-05
k =
 0.2197
c =
```

```
0.1207
```

The returned value of `h = 1` indicates that `kstest` rejects the null hypothesis in favor of the alternative hypothesis at the default 5% significance level.

Plot the empirical cdf and the standard normal cdf for a visual comparison.

```
[f,x_values] = ecdf(x);
J = plot(x_values,f);
hold on;
K = plot(x_values,normcdf(x_values),'r--');
set(J,'LineWidth',2);
set(K,'LineWidth',2);
legend([J K],'Empirical CDF','Standard Normal CDF','Location','SE');
```



The plot shows the difference between the empirical cdf of the data vector `x` and the cdf of the standard normal distribution.

Input Arguments

`x` — Sample data

vector

Sample data, specified as a vector.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Alpha',0.01` specifies a right-tailed hypothesis test at the 1% significance level.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'CDF'` — cdf of hypothesized continuous distribution

matrix | probability distribution object

cdf of hypothesized continuous distribution, specified the comma-separated pair consisting of `'CDF'` and either a two-column matrix or a continuous probability distribution object. When CDF is a matrix, column 1 contains a set of possible x values, and column 2 contains the corresponding hypothesized cumulative distribution function values $G(x)$. The calculation is most efficient if CDF is specified such that column 1 contains the values in the data vector x. If there are values in x not found in column 1 of CDF, `kstest` approximates $G(x)$ by interpolation. All values in x must lie in the interval

between the smallest and largest values in the first column of CDF. By default, `kstest` tests for a standard normal distribution.

The one-sample Kolmogorov-Smirnov test is only valid for continuous cumulative distribution functions, and requires CDF to be predetermined. The result is not accurate if CDF is estimated from the data. To test x against the normal, lognormal, extreme value, Weibull, or exponential distribution without specifying distribution parameters, use `lillietest` instead.

Data Types: `single` | `double`

`'Tail'` — Type of alternative hypothesis

`'unequal'` (default) | `'larger'` | `'smaller'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'unequal'`	Test the alternative hypothesis that the cdf of the population from which x is drawn is not equal to the cdf of the hypothesized distribution.
`'larger'`	Test the alternative hypothesis that the cdf of the population from which x is drawn is greater than the cdf of the hypothesized distribution.
`'smaller'`	Test the alternative hypothesis that the cdf of the population from which x is drawn is less than the cdf of the hypothesized distribution.

If the values in the data vector x tend to be larger than expected from the hypothesized distribution, the empirical distribution function of x tends to be smaller, and vice versa.

Example: `'Tail','larger'`

Output Arguments

h — Hypothesis test result

`1` | `0`

Hypothesis test result, returned as a logical value.

- If h = `1`, this indicates the rejection of the null hypothesis at the Alpha significance level.

- If h = 0, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value
scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

`ksstat` — Test statistic
nonnegative scalar value

Test statistic of the hypothesis test, returned as a nonnegative scalar value.

`cv` — Critical value
nonnegative scalar value

Critical value, returned as a nonnegative scalar value.

More About

One-Sample Kolmogorov-Smirnov Test

The one-sample Kolmogorov-Smirnov test is a nonparametric test of the null hypothesis that the population cdf of the data is equal to the hypothesized cdf.

The two-sided test for "unequal" cdf functions tests the null hypothesis against the alternative that the population cdf of the data is not equal to the hypothesized cdf. The test statistic is the maximum absolute difference between the empirical cdf calculated from x and the hypothesized cdf:

$$D^* = \max_x \left(\left| \hat{F}(x) - G(x) \right| \right),$$

where $\hat{F}(x)$ is the empirical cdf and $G(x)$ is the cdf of the hypothesized distribution.

The one-sided test for a "larger" cdf function tests the null hypothesis against the alternative that the population cdf of the data is greater than the hypothesized cdf.

The test statistic is the maximum amount by which the empirical cdf calculated from x exceeds the hypothesized cdf:

$$D^* = \max_x \left(\hat{F}(x) - G(x) \right).$$

The one-sided test for a "smaller" cdf function tests the null hypothesis against the alternative that the population cdf of the data is less than the hypothesized cdf. The test statistic is the maximum amount by which the hypothesized cdf exceeds the empirical cdf calculated from x:

$$D^* = \max_x \left(G(x) - \hat{F}(x) \right).$$

`kstest` computes the critical value cv using an approximate formula or by interpolation in a table. The formula and table cover the range $0.01 \le \texttt{alpha} \le 0.2$ for two-sided tests and $0.005 \le \texttt{alpha} \le 0.1$ for one-sided tests. cv is returned as `NaN` if `alpha` is outside this range.

Algorithms

`kstest` decides to reject the null hypothesis by comparing the p-value p with the significance level Alpha, not by comparing the test statistic ksstat with the critical value cv. Since cv is approximate, comparing ksstat with cv occasionally leads to a different conclusion than comparing p with Alpha.

References

[1] Massey, F. J. "The Kolmogorov-Smirnov Test for Goodness of Fit." *Journal of the American Statistical Association*. Vol. 46, No. 253, 1951, pp. 68–78.

[2] Miller, L. H. "Table of Percentage Points of Kolmogorov Statistics." *Journal of the American Statistical Association*. Vol. 51, No. 273, 1956, pp. 111–121.

[3] Marsaglia, G., W. Tsang, and J. Wang. "Evaluating Kolmogorov's Distribution." *Journal of Statistical Software*. Vol. 8, Issue 18, 2003.

See Also

`adtest` | `kstest2` | `lillietest`

kstest2

Two-sample Kolmogorov-Smirnov test

Syntax

```
h = kstest2(x1,x2)
h = kstest2(x1,x2,Name,Value)
[h,p] = kstest2(___)
[h,p,ks2stat] = kstest2(___)
```

Description

`h = kstest2(x1,x2)` returns a test decision for the null hypothesis that the data in vectors x1 and x2 are from the same continuous distribution, using the two-sample Kolmogorov-Smirnov test. The alternative hypothesis is that x1 and x2 are from different continuous distributions. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = kstest2(x1,x2,Name,Value)` returns a test decision for a two-sample Kolmogorov-Smirnov test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level or conduct a one-sided test.

`[h,p] = kstest2(___)` also returns the asymptotic *p*-value p, using any of the input arguments from the previous syntaxes.

`[h,p,ks2stat] = kstest2(___)` also returns the test statistic ks2stat.

Examples

Test Two Samples for the Same Distribution

Generate sample data from two different Weibull distributions.

```
rng(1);     % For reproducibility
x1 = wblrnd(1,1,1,50);
x2 = wblrnd(1.2,2,1,50);
```

Test the null hypothesis that data in vectors `x1` and `x2` comes from populations with the same distribution.

```
h = kstest2(x1,x2)
```

```
h =
 1
```

The returned value of `h = 1` indicates that `kstest` rejects the null hypothesis at the default 5% significance level.

Test the Hypothesis at Different Significance Levels

Generate sample data from two different Weibull distributions.

```
rng(1);      % For reproducibility
x1 = wblrnd(1,1,1,50);
x2 = wblrnd(1.2,2,1,50);
```

Test the null hypothesis that data vectors `x1` and `x2` are from populations with the same distribution at the 1% significance level.

```
[h,p] = kstest2(x1,x2,'Alpha',0.01)
```

```
h =
 0
p =
 0.0317
```

The returned value of `h = 0` indicates that `kstest` does not reject the null hypothesis at the 1% significance level.

One-Sided Hypothesis Test

Generate sample data from two different Weibull distributions.

```
rng(1);      % For reproducibility
x1 = wblrnd(1,1,1,50);
x2 = wblrnd(1.2,2,1,50);
```

Test the null hypothesis that data in vectors `x1` and `x2` comes from populations with the same distribution, against the alternative hypothesis that the cdf of the distribution of `x1` is larger than the cdf of the distribution of `x2`.

```
[h,p,k] = kstest2(x1,x2,'Tail','larger')
```

```
h =
 1
p =
 0.0158
k =
 0.2800
```

The returned value of `h = 1` indicates that `kstest` rejects the null hypothesis, in favor of the alternative hypothesis that the cdf of the distribution of `x1` is larger than the cdf of the distribution of `x2`, at the default 5% significance level. The returned value of `k` is the test statistic for the two-sample Kolmogorov-Smirnov test.

Input Arguments

`x1` — Sample data

vector

Sample data from the first sample, specified as a vector. Data vectors x1 and x2 do not need to be the same size.

Data Types: `single` | `double`

`x2` — Sample data

vector

Sample data from the second sample, specified as a vector. Data vectors x1 and x2 do not need to be the same size.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example:

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single | double`

`'Tail'` — Type of alternative hypothesis

`'unequal'` (default) | `'larger'` | `'smaller'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'unequal'`	Test the alternative hypothesis that the empirical cdf of x1 is unequal to the empirical cdf of x2.
`'larger'`	Test the alternative hypothesis that the empirical cdf of x1 is larger than the empirical cdf of x2.
`'smaller'`	Test the alternative hypothesis that the empirical cdf of x1 is smaller than the empirical cdf of x2.

If the data values in x1 tend to be larger than those in x2, the empirical distribution function of x1 tends to be smaller than that of x2, and vice versa.

Example: `'Tail','larger'`

Output Arguments

h — Hypothesis test result

`1` | `0`

Hypothesis test result, returned as a logical value.

- If h = `1`, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = `0`, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — Asymptotic *p*-value

scalar value in the range (0,1)

Asymptotic *p*-value of the test, returned as a scalar value in the range (0,1). p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. The asymptotic *p*-value becomes very accurate for large sample sizes, and is believed to be reasonably accurate for sample sizes `n1` and `n2`, such that `(n1*n2)/(n1 + n2)` ≥ 4.

`ks2stat` — Test statistic
nonnegative scalar value

Test statistic, returned as a nonnegative scalar value.

More About

Two-Sample Kolmogorov-Smirnov Test

The two-sample Kolmogorov-Smirnov test is a nonparametric hypothesis test that evaluates the difference between the cdfs of the distributions of the two sample data vectors over the range of *x* in each data set.

The two-sided test uses the maximum absolute difference between the cdfs of the distributions of the two data vectors. The test statistic is

$$D^* = \max_x\left(\left|F_1(x) - F_2(x)\right|\right),$$

where $\hat{F}_1(x)$ is the proportion of x1 values less than or equal to *x* and $\hat{F}_2(x)$ is the proportion of x2 values less than or equal to *x*.

The one-sided test uses the actual value of the difference between the cdfs of the distributions of the two data vectors rather than the absolute value. The test statistic is

$$D^* = \max_x\left(F_1(x) - F_2(x)\right).$$

Algorithms

In `kstest2`, the decision to reject the null hypothesis is based on comparing the *p*-value p with the significance level Alpha, not by comparing the test statistic ks2stat with a critical value.

References

[1] Massey, F. J. "The Kolmogorov-Smirnov Test for Goodness of Fit." *Journal of the American Statistical Association*. Vol. 46, No. 253, 1951, pp. 68–78.

[2] Miller, L. H. "Table of Percentage Points of Kolmogorov Statistics." *Journal of the American Statistical Association*. Vol. 51, No. 273, 1956, pp. 111–121.

[3] Marsaglia, G., W. Tsang, and J. Wang. "Evaluating Kolmogorov's Distribution." *Journal of Statistical Software*. Vol. 8, Issue 18, 2003.

See Also

`adtest` | `kstest` | `lillietest`

kurtosis

Kurtosis

Syntax

```
k = kurtosis(X)
k = kurtosis(X,flag)
k = kurtosis(X,flag,dim)
```

Description

`k = kurtosis(X)` returns the sample kurtosis of `X`. For vectors, `kurtosis(x)` is the kurtosis of the elements in the vector `x`. For matrices `kurtosis(X)` returns the sample kurtosis for each column of `X`. For N-dimensional arrays, `kurtosis` operates along the first nonsingleton dimension of `X`.

`k = kurtosis(X,flag)` specifies whether to correct for bias (`flag` is `0`) or not (`flag` is `1`, the default). When `X` represents a sample from a population, the kurtosis of `X` is biased, that is, it will tend to differ from the population kurtosis by a systematic amount that depends on the size of the sample. You can set `flag` to `0` to correct for this systematic bias.

`k = kurtosis(X,flag,dim)` takes the kurtosis along dimension `dim` of `X`.

`kurtosis` treats `NaN`s as missing values and removes them.

Examples

```
X = randn([5 4])
X =
  1.1650  1.6961  -1.4462  -0.3600
  0.6268  0.0591  -0.7012  -0.1356
  0.0751  1.7971   1.2460  -1.3493
  0.3516  0.2641  -0.6390  -1.2704
  -0.6965  0.8717  0.5774  0.9846
```

```
k = kurtosis(X)
k =
  2.1658  1.2967  1.6378  1.9589
```

More About

Algorithms

Kurtosis is a measure of how outlier-prone a distribution is. The kurtosis of the normal distribution is 3. Distributions that are more outlier-prone than the normal distribution have kurtosis greater than 3; distributions that are less outlier-prone have kurtosis less than 3.

The kurtosis of a distribution is defined as

$$k = \frac{E(x-\mu)^4}{\sigma^4}$$

where μ is the mean of x, σ is the standard deviation of x, and $E(t)$ represents the expected value of the quantity t. `kurtosis` computes a sample version of this population value.

Note Some definitions of kurtosis subtract 3 from the computed value, so that the normal distribution has kurtosis of 0. The `kurtosis` function does not use this convention.

When you set `flag` to 1, the following equation applies:

$$k_1 = \frac{\frac{1}{n}\sum_{i=1}^{n}(x_i-\bar{x})^4}{\left(\frac{1}{n}\sum_{i=1}^{n}(x_i-\bar{x})^2\right)^2}$$

When you set `flag` to 0, the following equation applies:

$$k_0 = \frac{n-1}{(n-2)(n-3)}\left((n+1)k_1 - 3(n-1)\right) + 3$$

This bias-corrected formula requires that `X` contain at least four elements.

See Also

`mean` | `moment` | `skewness` | `std` | `var`

lasso

Regularized least-squares regression using lasso or elastic net algorithms

Syntax

```
B = lasso(X,Y)
[B,FitInfo] = lasso(X,Y)
[B,FitInfo] = lasso(X,Y,Name,Value)
```

Description

`B = lasso(X,Y)` returns fitted least-squares regression coefficients for a set of regularization coefficients Lambda.

`[B,FitInfo] = lasso(X,Y)` returns a structure containing information about the fits.

`[B,FitInfo] = lasso(X,Y,Name,Value)` fits regularized regressions with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`X`

Numeric matrix with `n` rows and `p` columns. Each row represents one observation, and each column represents one predictor (variable).

`Y`

Numeric vector of length `n`, where `n` is the number of rows of X. `Y(i)` is the response to row `i` of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'`

Scalar value from `0` to `1` (excluding `0`) representing the weight of lasso (L^1) versus ridge (L^2) optimization. `Alpha = 1` represents lasso regression, `Alpha` close to `0` approaches ridge regression, and other values represent elastic net optimization. See "Definitions" on page 22- .

Default: `1`

`'CV'`

Method `lasso` uses to estimate mean squared error:

- `K`, a positive integer — `lasso` uses `K`-fold cross validation.
- `cvp`, a `cvpartition` object — `lasso` uses the cross-validation method expressed in `cvp`. You cannot use a `'leaveout'` partition with `lasso`.
- `'resubstitution'` — `lasso` uses X and Y to fit the model and to estimate the mean squared error, without cross validation.

Default: `'resubstitution'`

`'DFmax'`

Maximum number of nonzero coefficients in the model. `lasso` returns results only for Lambda values that satisfy this criterion.

Default: `Inf`

`'Lambda'`

Vector of nonnegative `Lambda` values. See "Definitions" on page 22- .

- If you do not supply `Lambda`, `lasso` calculates the largest value of `Lambda` that gives a nonnull model. In this case, `LambdaRatio` gives the ratio of the smallest to the largest value of the sequence, and NumLambda gives the length of the vector.
- If you supply `Lambda`, `lasso` ignores `LambdaRatio` and NumLambda.

Default: Geometric sequence of `NumLambda` values, the largest just sufficient to produce `B = 0`

`'LambdaRatio'`

Positive scalar, the ratio of the smallest to the largest Lambda value when you do not set `Lambda`.

If you set `LambdaRatio = 0`, `lasso` generates a default sequence of `Lambda` values, and replaces the smallest one with `0`.

Default: `1e-4`

`'MCReps'`

Positive integer, the number of Monte Carlo repetitions for cross validation.

- If `CV` is `'resubstitution'` or a `cvpartition` of type `'resubstitution'`, `MCReps` must be `1`.
- If `CV` is a `cvpartition` of type `'holdout'`, `MCReps` must be greater than `1`.

Default: `1`

`'NumLambda'`

Positive integer, the number of Lambda values `lasso` uses when you do not set `Lambda`. `lasso` can return fewer than `NumLambda` fits if the if the residual error of the fits drops below a threshold fraction of the variance of `Y`.

Default: `100`

`'Options'`

Structure that specifies whether to cross validate in parallel, and specifies the random stream or streams. Create the `Options` structure with `statset`. Option fields:

- `UseParallel` — Set to `true` to compute in parallel. Default is `false`.
- `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. Default is `false`.

- `Streams` — A `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `lasso` uses the default stream.

`'PredictorNames'`

Cell array of strings representing names of the predictor variables, in the order in which they appear in X.

Default: `{}`

`'RelTol'`

Convergence threshold for the coordinate descent algorithm (see Friedman, Tibshirani, and Hastie [3]). The algorithm terminates when successive estimates of the coefficient vector differ in the L^2 norm by a relative amount less than `RelTol`.

Default: `1e-4`

`'Standardize'`

Boolean value specifying whether `lasso` scales X before fitting the models. This affects whether the regularization is applied to the coefficients on the standardized scale or original scale. The results are always presented on the original data scale.

X and Y are always centered.

Default: `true`

`'Weights'`

Observation weights, a nonnegative vector of length `n`, where `n` is the number of rows of X. `lasso` scales `Weights` to sum to `1`.

Default: `1/n * ones(n,1)`

Output Arguments

`B`

Fitted coefficients, a `p`-by-`L` matrix, where `p` is the number of predictors (columns) in X, and `L` is the number of Lambda values.

`FitInfo`

Structure containing information about the model fits.

Field in FitInfo	Description
`Intercept`	Intercept term β_0 for each linear model, a 1-by-`L` vector
`Lambda`	Lambda parameters in ascending order, a 1-by-`L` vector
`Alpha`	Value of Alpha parameter, a scalar
`DF`	Number of nonzero coefficients in B for each value of `Lambda`, a 1-by-`L` vector
`MSE`	Mean squared error (MSE), a 1-by-`L` vector

If you set the CV name-value pair to cross validate, the `FitInfo` structure contains additional fields.

Field in FitInfo	Description
`SE`	The standard error of MSE for each `Lambda`, as calculated during cross validation, a 1-by-`L` vector
`LambdaMinMSE`	The `Lambda` value with minimum MSE, a scalar
`Lambda1SE`	The largest `Lambda` such that MSE is within one standard error of the minimum, a scalar
`IndexMinMSE`	The index of `Lambda` with value `LambdaMinMSE`, a scalar
`Index1SE`	The index of `Lambda` with value `Lambda1SE`, a scalar

Examples

Remove Redundant Predictors

Construct a data set with redundant predictors, and identify those predictors using cross-validated `lasso`.

Create a matrix `X` of 100 five-dimensional normal variables and a response vector `Y` from just two components of `X`, with small added noise.

```
X = randn(100,5);
r = [0;2;0;-3;0]; % only two nonzero coefficients
Y = X*r + randn(100,1)*.1; % small added noise
```

Construct the default lasso fit.

```
B = lasso(X,Y);
```

Find the coefficient vector for the 25th value in `B`.

```
B(:,25)
```

```
ans =

         0
    1.6093
         0
   -2.5865
         0
```

`lasso` identifies and removes the redundant predictors.

Plot a Regularized Fit with Cross Validation

Visually examine the cross-validated error of various levels of regularization.

Load the `acetylene` data and prepare the data with interactions for fitting.

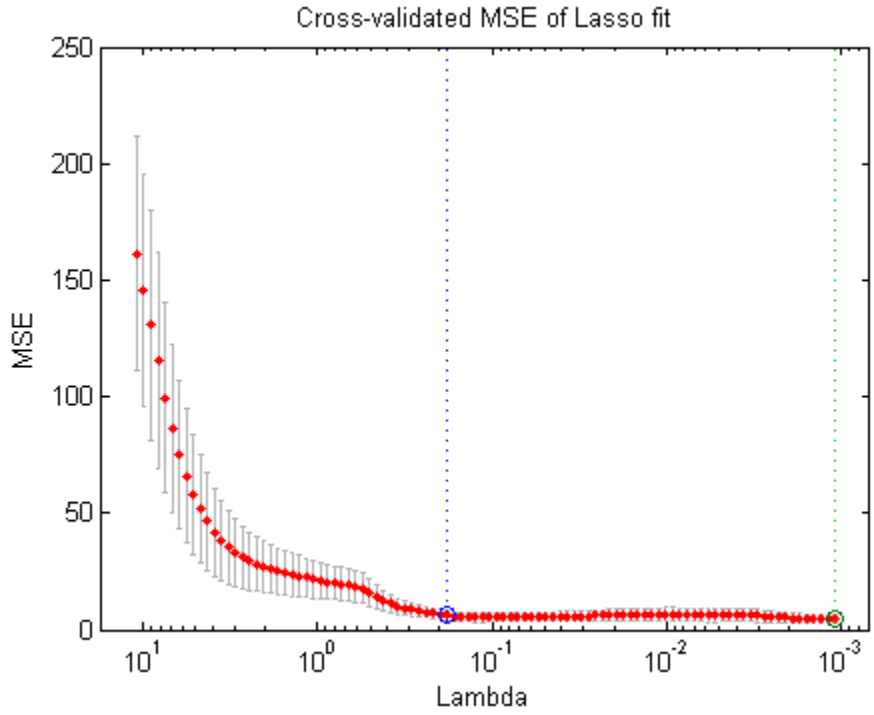
```
load acetylene
Xs = [x1 x2 x3];
X = x2fx(Xs,'interaction');
X(:,1) = []; % No constant term
```

Construct the lasso fit using ten-fold cross validation. Include the `FitInfo` output so you can plot the result.

```
[B FitInfo] = lasso(X,y,'CV',10);
```

Plot the cross-validated fits.

```
lassoPlot(B,FitInfo,'PlotType','CV');
```



More About

Lasso

For a given value of λ, a nonnegative parameter, `lasso` solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)^2+\lambda\sum_{j=1}^{p}\left|\beta_j\right|\right),$$

where

- N is the number of observations.
- y_i is the response at observation i.

- x_i is data, a vector of p values at observation i.
- λ is a nonnegative regularization parameter corresponding to one value of Lambda.
- The parameters β_0 and β are scalar and p-vector respectively.

As λ increases, the number of nonzero components of β decreases.

The lasso problem involves the L^1 norm of β, as contrasted with the elastic net algorithm.

Elastic Net

For an α strictly between 0 and 1, and a nonnegative λ, elastic net solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{2N}\sum_{i=1}^{N}\left(y_i-\beta_0-x_i^T\beta\right)^2+\lambda P_\alpha(\beta)\right),$$

where

$$P_\alpha(\beta)=\frac{(1-\alpha)}{2}\|\beta\|_2^2+\alpha\|\beta\|_1=\sum_{j=1}^{p}\left(\frac{(1-\alpha)}{2}\beta_j^2+\alpha\left|\beta_j\right|\right).$$

Elastic net is the same as lasso when $\alpha = 1$. As α shrinks toward 0, elastic net approaches `ridge` regression. For other values of α, the penalty term $P_\alpha(\beta)$ interpolates between the L^1 norm of β and the squared L^2 norm of β.

- "Lasso and Elastic Net"

References

[1] Tibshirani, R. *Regression shrinkage and selection via the lasso.* Journal of the Royal Statistical Society, Series B, Vol 58, No. 1, pp. 267–288, 1996.

[2] Zou, H. and T. Hastie. *Regularization and variable selection via the elastic net.* Journal of the Royal Statistical Society, Series B, Vol. 67, No. 2, pp. 301–320, 2005.

[3] Friedman, J., R. Tibshirani, and T. Hastie. *Regularization paths for generalized linear models via coordinate descent.* Journal of Statistical Software, Vol 33, No. 1, 2010. http://www.jstatsoft.org/v33/i01

[4] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning,* 2nd edition. Springer, New York, 2008.

See Also

`lassoPlot` | `ridge`

lassoglm

Lasso or elastic net regularization for generalized linear model regression

Syntax

```
B = lassoglm(X,Y)
[B,FitInfo] = lassoglm(X,Y)
[B,FitInfo] = lassoglm(X,Y,distr)
[B,FitInfo] = lassoglm(X,Y,distr,Name,Value)
```

Description

`B = lassoglm(X,Y)` returns penalized maximum-likelihood fitted coefficients for a generalized linear model of the response `Y` to the data matrix `X`. `Y` are assumed to have a Gaussian probability distribution.

`[B,FitInfo] = lassoglm(X,Y)` returns a structure containing information about the fits.

`[B,FitInfo] = lassoglm(X,Y,distr)` fits the model using the probability distribution type for `Y` as specified in `distr`.

`[B,FitInfo] = lassoglm(X,Y,distr,Name,Value)` fits regularized generalized linear regressions with additional options specified by one or more Name,Value pair arguments.

Input Arguments

X

Numeric matrix with `n` rows and `p` columns. Each row represents one observation, and each column represents one predictor (variable).

Y

When `distr` is not `'binomial'`, `Y` is a numeric vector or categorical array of length `n`, where `n` is the number of rows of X. `Y(i)` is the response to row `i` of `X`.

When `distr` is `'binomial'`, `Y` is either a:

- Numeric vector of length `n`, where each entry represents success (`1`) or failure (`0`)
- Logical vector of length `n`, where each entry represents success or failure
- Categorical array of length `n`, where each entry represents success or failure
- Two column numeric matrix, where the first column contains the number of successes for each observation, and the second column contains the total number of trials

`distr`

Distributional family for the nonsystematic variation in the responses, a string. Choices:

- `'normal'`
- `'binomial'`
- `'poisson'`
- `'gamma'`
- `'inverse gaussian'`

By default, `lassoglm` uses the canonical link function corresponding to `distr`. Specify another link function using the `'link'` name-value pair.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'`

Scalar value from `0` to `1` (excluding `0`) representing the weight of lasso (L^1) versus ridge (L^2) optimization. `Alpha = 1` represents lasso regression, and other values represent elastic net optimization. `Alpha` close to `0` approaches ridge regression. See “Definitions” on page 22- .

Default: 1

`'CV'`

Method `lassoglm` uses to estimate deviance:

- K, a positive integer — lassoglm uses K-fold cross validation.
- cvp, a cvpartition object — lassoglm uses the cross-validation method expressed in cvp. You cannot use a 'leaveout' partition with lassoglm.
- 'resubstitution' — lassoglm uses X and Y to fit the model and to estimate the deviance, without cross validation.

Default: 'resubstitution'

'DFmax'

Maximum number of nonzero coefficients in the model. lassoglm returns results for Lambda values that satisfy this criterion.

Default: Inf

'Lambda'

Vector of nonnegative Lambda values. See “Lasso” on page 22-2539.

- If you do not supply Lambda, lassoglm estimates the largest value of Lambda that gives a nonnull model. In this case, LambdaRatio gives the ratio of the smallest to the largest value of the sequence, and NumLambda gives the length of the vector.
- If you supply Lambda, lassoglm ignores LambdaRatio and NumLambda.

Default: Geometric sequence of NumLambda values, the largest just sufficient to produce B = 0

'LambdaRatio'

Positive scalar, the ratio of the smallest to the largest Lambda value when you do not explicitly set Lambda.

If you set LambdaRatio = 0, lassoglm generates a default sequence of Lambda values, and replaces the smallest one with 0.

Default: 1e-4

'Link'

Specify the mapping between the mean μ of the response and the linear predictor Xb.

Value	Description
`'comploglog'`	$\log(-\log((1-\mu))) = Xb$
`'identity'`, default for the distribution `'normal'`	$\mu = Xb$
`'log'`, default for the distribution `'poisson'`	$\log(\mu) = Xb$
`'logit'`, default for the distribution `'binomial'`	$\log(\mu/(1-\mu)) = Xb$
`'loglog'`	$\log(-\log(\mu)) = Xb$
`'probit'`	$\Phi^{-1}(\mu) = Xb$, where Φ is the normal (Gaussian) CDF function
`'reciprocal'`, default for the distribution `'gamma'`	$\mu^{-1} = Xb$
`p` (a number), default for the distribution `'inverse gaussian'` (with $p = -2$)	$\mu^p = Xb$
Cell array of the form `{FL FD FI}`, containing three function handles, created using `@`, that define the link (`FL`), the derivative of the link (`FD`), and the inverse link (`FI`). Equivalently, can be a structure of function handles with field `Link` containing `FL`, field `Derivative` containing `FD`, and field `Inverse` containing `FI`.	User-specified link function (see "Custom Link Function" on page 10-16)

`'MCReps'`

Positive integer, the number of Monte Carlo repetitions for cross validation.

- If `CV` is `'resubstitution'` or a `cvpartition` of type `'resubstitution'`, `MCReps` must be `1`.
- If `CV` is a `cvpartition` of type `'holdout'`, `MCReps` must be greater than `1`.

Default: `1`

'NumLambda'

Positive integer, the number of Lambda values `lassoglm` uses when you do not set `Lambda`. `lassoglm` can return fewer than `NumLambda` fits if the deviance of the fits drops below a threshold fraction of the null deviance (deviance of the fit without any predictors `X`).

Default: `100`

'Offset'

Numeric vector with the same number of rows as `X`. `lassoglm` uses `Offset` as an additional predictor variable, but keeps its coefficient value fixed at `1.0`.

'Options'

Structure that specifies whether to cross validate in parallel, and specifies the random stream or streams. Create the `Options` structure with `statset`. Option fields:

- `UseParallel` — Set to `true` to compute in parallel. Default is `false`.
- `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. Default is `false`.
- `Streams` — `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `lassoglm` uses the default stream.

'PredictorNames'

Cell array of strings representing names of the predictor variables, in the order in which they appear in X.

Default: `{}`

'RelTol'

Convergence threshold for the coordinate descent algorithm (see Friedman, Tibshirani, and Hastie [3]). The algorithm terminates when successive estimates of the coefficient vector differ in the L^2 norm by a relative amount less than `RelTol`.

Default: `1e-4`

`'Standardize'`

Boolean value specifying whether `lassoglm` scales X before fitting the models. This affects whether the regularization is applied to the coefficients on the standardized scale or original scale. The results are always presented on the original scale.

Default: `true`

`'Weights'`

Observation weights, a nonnegative vector of length `n`, where `n` is the number of rows of X. At least two values must be positive.

Default: `1/n * ones(n,1)`

Output Arguments

`B`

Fitted coefficients, a `p`-by-`L` matrix, where `p` is the number of predictors (columns) in X, and `L` is the number of Lambda values.

`FitInfo`

Structure containing information about the model fits.

Field in FitInfo	Description
`Alpha`	Value of Alpha parameter, a scalar.
`Deviance`	Deviance of the fitted model for each value of `Lambda`, a `1`-by-`L` vector. If cross validation was performed, the values for `Deviance` represent the estimated expected deviance of the model applied to new data, as calculated by cross validation. Otherwise, `Deviance` is the deviance of the fitted model applied to the data used to perform the fit.
`DF`	Number of nonzero coefficients in B for each `Lambda` value, a `1`-by-`L` vector.
`Intercept`	Intercept term β_0 for each linear model, a `1`-by-`L` vector.

Field in FitInfo	Description
`Lambda`	`Lambda` parameters in ascending order, a 1-by-`L` vector.

If you set the CV name-value pair to cross validate, the `FitInfo` structure contains additional fields.

Field in FitInfo	Description
`IndexMinDeviance`	Index of `Lambda` with value `LambdaMinDeviance`, a scalar.
`Index1SE`	Index of `Lambda` with value `Lambda1SE`, a scalar.
`LambdaMinDeviance`	`Lambda` value with minimum expected deviance, as calculated by cross validation, a scalar.
`Lambda1SE`	Largest `Lambda` such that `Deviance` is within one standard error of the minimum, a scalar.
`SE`	Standard error of `Deviance` for each `Lambda`, as calculated during cross validation, a 1-by-`L` vector.

Examples

Lasso Regularization of a Generalized Linear Model

Construct data from a Poisson model, and identify the important predictors using `lassoglm`.

Create data with 20 predictors, and Poisson responses using just three of the predictors, plus a constant.

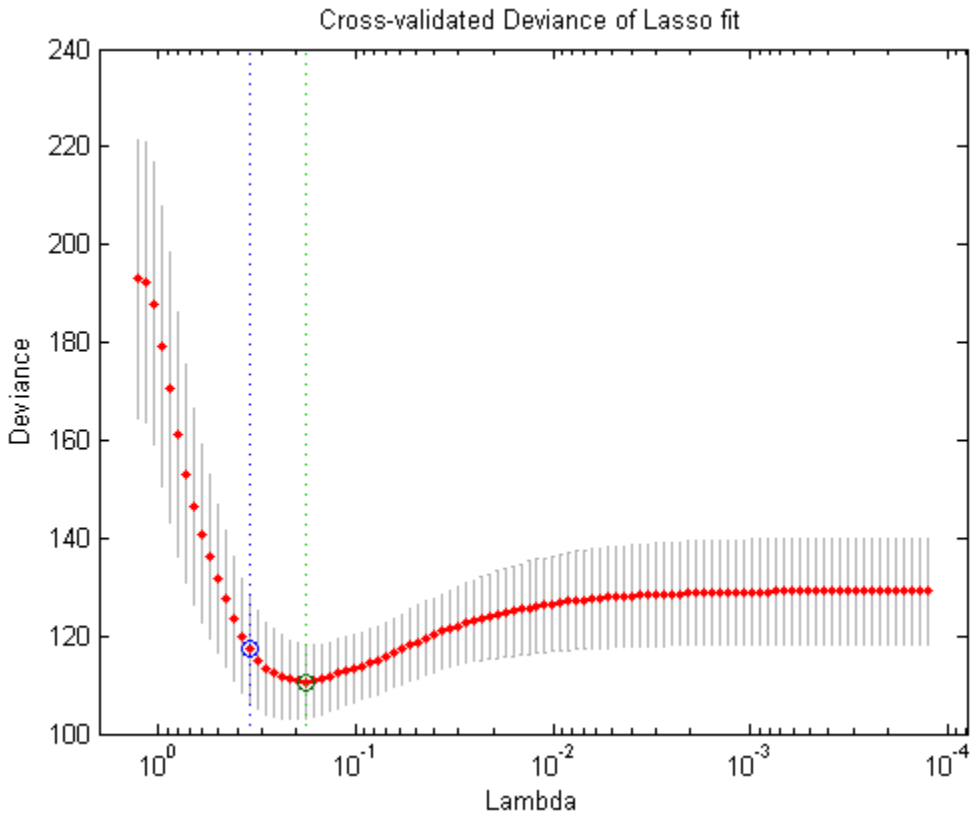
```
rng('default') % for reproducibility
X = randn(100,20);
mu = exp(X(:,[5 10 15])*[.4;.2;.3] + 1);
y = poissrnd(mu);
```

Construct a cross-validated lasso regularization of a Poisson regression model of the data.

```
[B FitInfo] = lassoglm(X,y,'poisson','CV',10);
```

Examine the cross-validation plot to see the effect of the `Lambda` regularization parameter.

```
lassoPlot(B,FitInfo,'plottype','CV');
```



The green circle and dashed line locate the `Lambda` with minimal cross-validation error. The blue circle and dashed line locate the point with minimal cross-validation error plus one standard deviation.

Find the nonzero model coefficients corresponding to the two identified points.

```
minpts = find(B(:,FitInfo.IndexMinDeviance))
```

```
minpts =

     3
     5
```

```
     6
    10
    11
    15
    16

min1pts = find(B(:,FitInfo.Index1SE))

min1pts =

     5
    10
    15
```

The coefficients from the minimal plus one standard error point are exactly those coefficients used to create the data.

- "Regularize Poisson Regression" on page 10-45
- "Regularize Logistic Regression" on page 10-48
- "Regularize Wide Data in Parallel" on page 10-55

More About

Link Function

A link function $f(\mu)$ maps a distribution with mean μ to a linear model with data X and coefficient vector b using the formula
$f(\mu) = Xb$.

Find the formulas for the link functions in the `Link` name-value pair description. Here, "typical" means a link function that is typically used for the listed distribution.

Distributional Family	Link Function (typical, {default})
`'normal'`	`{'identity'}`
`'binomial'`	`'comploglog'`, `'loglog'`, `'probit'`, `{'logit'}`
`'poisson'`	`{'log'}`
`'gamma'`	`{'reciprocal'}`
`'inverse gaussian'`	`{-2}`

Lasso

For a nonnegative value of λ, `lasso` solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{N}\text{Deviance}\left(\beta_0,\beta\right)+\lambda\sum_{j=1}^{p}\left|\beta_j\right|\right),$$

where

- Deviance is the deviance of the model fit to the responses using intercept β_0 and predictor coefficients β. The formula for Deviance depends on the `distr` parameter you supply to `lassoglm`. Minimizing the λ-penalized deviance is equivalent to maximizing the λ-penalized log likelihood.
- N is the number of observations.
- λ is a nonnegative regularization parameter corresponding to one value of Lambda.
- Parameters β_0 and β are scalar and p-vector respectively.

As λ increases, the number of nonzero components of β decreases.

The lasso problem involves the L^1 norm of β, as contrasted with the elastic net algorithm.

Elastic Net

For an α strictly between 0 and 1, and a nonnegative λ, elastic net solves the problem

$$\min_{\beta_0,\beta}\left(\frac{1}{N}\text{Deviance}\left(\beta_0,\beta\right)+\lambda P_\alpha\left(\beta\right)\right),$$

where

$$P_\alpha\left(\beta\right)=\frac{(1-\alpha)}{2}\|\beta\|_2^2+\alpha\|\beta\|_1=\sum_{j=1}^{p}\left(\frac{(1-\alpha)}{2}\beta_j^2+\alpha\left|\beta_j\right|\right).$$

Elastic net is the same as lasso when $\alpha = 1$. For other values of α, the penalty term $P_\alpha(\beta)$ interpolates between the L^1 norm of β and the squared L^2 norm of β. As α shrinks toward 0, elastic net approaches `ridge` regression.

- “Lasso Regularization of Generalized Linear Models” on page 10-45

References

[1] Tibshirani, R. *Regression Shrinkage and Selection via the Lasso.* Journal of the Royal Statistical Society, Series B, Vol. 58, No. 1, pp. 267–288, 1996.

[2] Zou, H. and T. Hastie. *Regularization and Variable Selection via the Elastic Net.* Journal of the Royal Statistical Society, Series B, Vol. 67, No. 2, pp. 301–320, 2005.

[3] Friedman, J., R. Tibshirani, and T. Hastie. *Regularization Paths for Generalized Linear Models via Coordinate Descent.* Journal of Statistical Software, Vol. 33, No. 1, 2010. http://www.jstatsoft.org/v33/i01

[4] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning,* 2nd edition. Springer, New York, 2008.

[5] Dobson, A. J. *An Introduction to Generalized Linear Models,* 2nd edition. Chapman & Hall/CRC Press, New York, 2002.

[6] McCullagh, P., and J. A. Nelder. *Generalized Linear Models,* 2nd edition. Chapman & Hall/CRC Press, New York, 1989.

[7] Collett, D. *Modelling Binary Data,* 2nd edition. Chapman & Hall/CRC Press, New York, 2003.

See Also

`glmfit` | `lasso` | `lassoPlot` | `ridge`

lassoPlot

Trace plot of lasso fit

Syntax

```
ax = lassoPlot(B)
ax = lassoPlot(B,FitInfo)
ax = lassoPlot(B,FitInfo,Name,Value)
[ax,figh] = lassoPlot(B,...)
```

Description

`ax = lassoPlot(B)` creates a trace plot of the values in `B` against the L^1 norm of `B`. `ax` is a handle to the plot axis.

`ax = lassoPlot(B,FitInfo)` creates a plot with type depending on the data type of `FitInfo` and the value, if any, of the plotType name-value pair.

`ax = lassoPlot(B,FitInfo,Name,Value)` creates a plot with additional options specified by one or more Name,Value pair arguments.

`[ax,figh] = lassoPlot(B,...)` returns a handle to the figure window.

Input Arguments

`B`

Coefficients of a sequence of regression fits, as returned from the `lasso` or `lassoglm` functions. `B` is a `p`-by-`NLambda` matrix, where `p` is the number of predictors, and each column of `B` is a set of coefficients `lasso` calculates using one `Lambda` penalty value.

`FitInfo`

Information controlling the plot:

- `FitInfo` is a structure, especially as returned from `lasso` or `lassoglm` — `lassoPlot` creates a plot based on the PlotType name-value pair.

- `FitInfo` is a vector — `lassoPlot` forms the *x*-axis of the plot from the values in `FitInfo`. The length of `FitInfo` must equal the number of columns of `B`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Parent'`

Axis in which to draw the plot.

Default: New plot

`'PlotType'`

Choose the plot type when you give a FitInfo vector or structure:

FitInfo Type	PlotType	Plot
Vector or Structure	`'L1'`	`plotLasso` creates the *x*-axis from the L^1 norm of the coefficients in B. The *x*-axis at the top of the plot contains the degrees of freedom (`df`), meaning the number of nonzero coefficients of `B`.
Structure	`'Lambda'`	`plotLasso` creates the x-axis from the `Lambda` field of `FitInfo`. The x-axis at the top of the plot contains the degrees of freedom (`df`), meaning the number of nonzero coefficients of `B`.
Cross-Validated Structure	`'CV'`	• For each `Lambda`, plots an estimate of the mean squared prediction error on new data for the model fitted by `lasso` with that value of `Lambda`. • Plots error bars for the estimates. • Plots the value of `Lambda` with minimum cross-validated MSE. • Plots the greatest `Lambda` that is within one standard error of minimum MSE (so makes the sparsest model within that region).

Default: `'L1'`

`'PredictorNames'`

Cell array of strings to label each coefficient of B. If the length of `PredictorNames` is less than the number of rows of `B`, the remaining labels are padded with default values.

`lassoPlot` uses the predictor names in `FitInfo` only if:

- You created `FitInfo` with a call to `lasso` that included a `PredictorNames` name-value pair.
- You call `lassoPlot` *without* a `PredictorNames` name-value pair.
- You include `FitInfo` in your `lassoPlot` call.

Default: `{'B1','B2',...}`

`'XScale'`

- `'linear'` for linear x-axis
- `'log'` for logarithmic scaled x-axis

Default: `'linear'`, except `'log'` for the `'CV'` plot type

Output Arguments

`ax`

Handle to the axis of the plot (see "Coordinate System").

`figh`

Handle to the figure window (see "Special Object Identifiers").

Examples

Lasso Plot with Default Plot Type

Load the sample data

```
load acetylene
```

Prepare the design matrix for lasso fit with interactions.

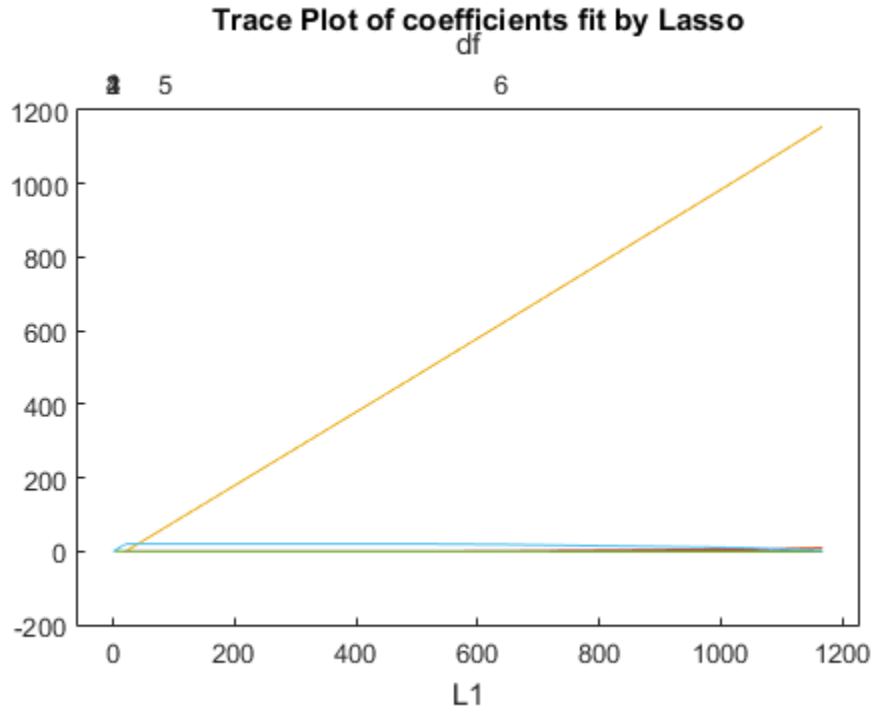
```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
```

Fit a regularized model of the data using `lasso` .

```
B = lasso(D,y);
```

Plot the fits with the default plot type.

```
lassoPlot(B);
```



Lasso Plot with Lambda Plot Type

Load the sample data.

```
load acetylene
```

Prepare the data for lasso fit with interactions.

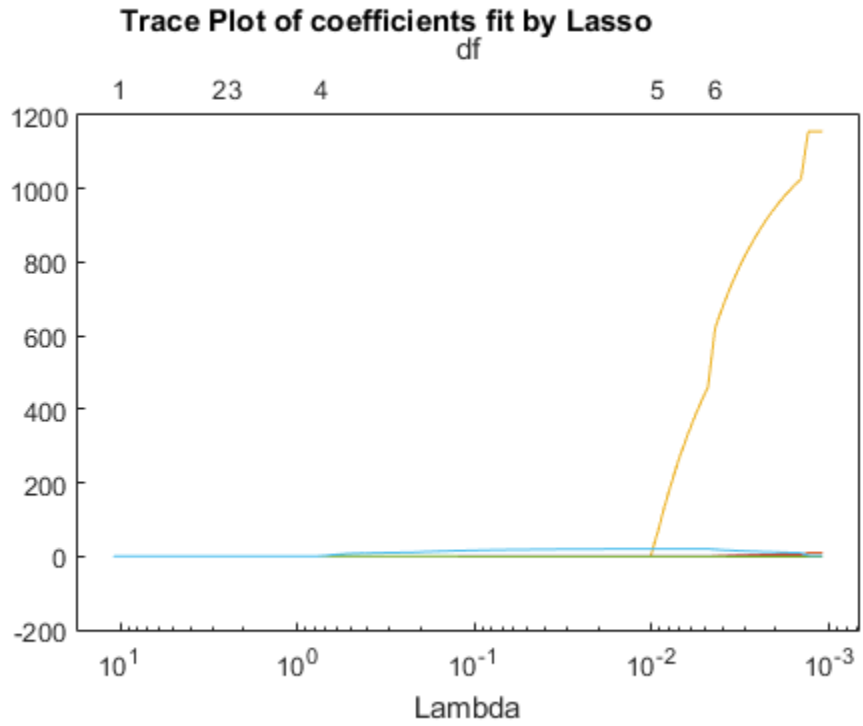
```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
```

Fit a regularized model of the data with `lasso` .

```
[B FitInfo] = lasso(D,y);
```

Plot the fits with the `Lambda` plot type and logarithmic scaling.

```
lassoPlot(B,FitInfo,'PlotType','Lambda','XScale','log');
```



Lasso Plot with Cross-Validated Fits

Load the sample data.

```
load acetylene
```

Prepare the design matrix for a lasso fit with interactions.

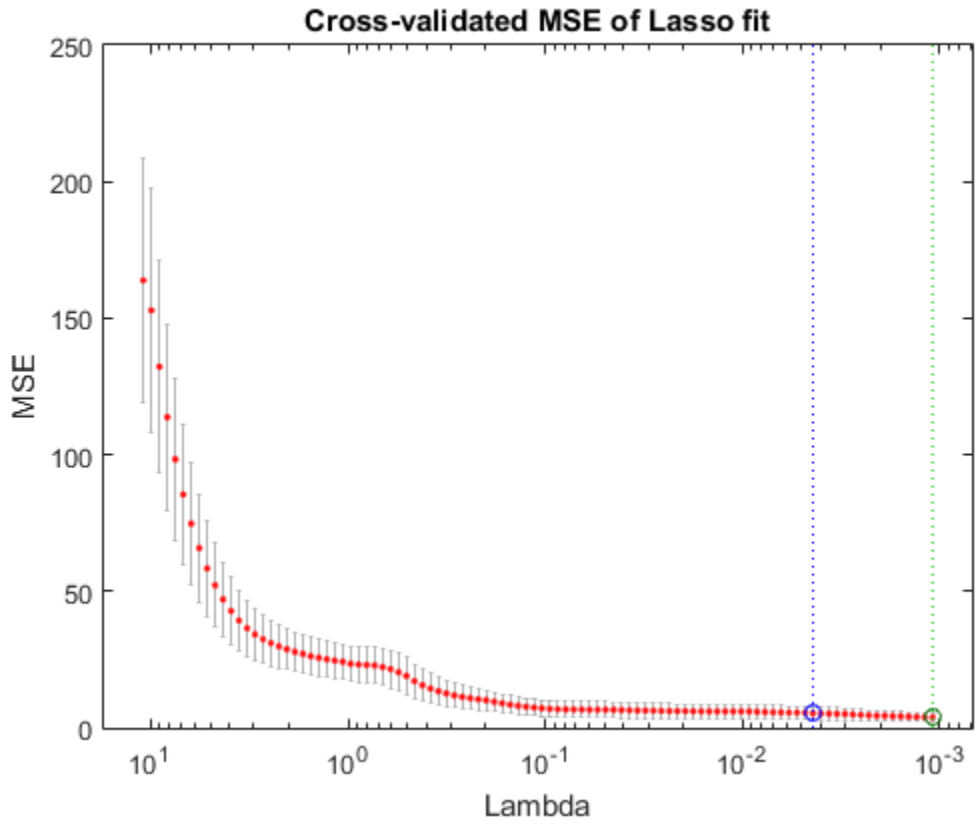
```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
D(:,1) = []; % No constant term
```

Fit a regularized model of the data with `lasso` and cross validation.

```
[B FitInfo] = lasso(D,y,'CV',10);
```

Plot the cross-validated fits.

```
lassoPlot(B,FitInfo,'PlotType','CV');
```



More About

- "Lasso and Elastic Net"

See Also

`lasso` | `lassoglm`

le

Class: qrandstream

Less than or equal relation for handles

Syntax

```
h1 <= h2
```

Description

Handles are equal if they are handles for the same object. All comparisons use a number associated with each handle object. Nothing can be assumed about the result of a handle comparison except that the repeated comparison of two handles in the same MATLAB session will yield the same result. The order of handle values is purely arbitrary and has no connection to the state of the handle objects being compared.

`h1 <= h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise `<=` result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = le(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `ge` | `gt` | `ne` | `eq` | `lt`

Leap property

Class: qrandset

Interval between points

Description

Number of points to leap over and omit for each point taken from the sequence. The `Leap` property of a point set contains a positive integer which specifies the number of points in the sequence to leap over and omit for every point taken. The default `Leap` value is 0, which corresponds to taking every point from the sequence.

Leaping is a technique used to improve the quality of a point set. However, you must choose the `Leap` values with care; many `Leap` values create sequences that fail to touch on large sub-hyper-rectangles of the unit hypercube, and so fail to be a uniform quasi-random point set.

Choosing Leap Values for Halton Sets

A known rule for choosing `Leap` values for Halton sets is to set it to (`P`-1) where `P` is a prime number that has not been used to generate one of the dimensions, i.e. for a `k`-dimensional point set `P` would be the (`k`+1)th or greater prime.

Examples

Experiment with different leap values:

```
% No leaping produces the standard Halton sequence.
P = haltonset(5);
P(1:5,:)

% Set a leap of 1.  The point set now includes every other
% point from the sequence.
P.Leap = 1;
P(1:5,:)
```

See Also

`net` | `qrandset` | `subsref` | `haltonset` | `Skip`

length

Class: dataset

Length of dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
n = length(A)
```

Description

`n = length(A)` returns the number of observations in the dataset `A`. `length` is equivalent to `size(A,1)`.

See Also

`size`

length

Class: qrandset

Length of point set

Syntax

```
length(p)
```

Description

`length(p)` returns the number of points in the point set `p`. It is equivalent to `size(p, 1)`.

See Also

`qrandset` | `size`

levelcounts

Element counts by level of a nominal or ordinal array

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
C = levelcounts(A)
C = levelcounts(A,dim)
```

Description

`C = levelcounts(A)` returns counts of the number of elements in the nominal or ordinal array A equal to each of the possible levels in A into the vector C, which has as many elements as A has levels.

- If A is a matrix, then C is a matrix of column counts.
- If A is an *N*-dimensional array, `levelcounts` operates along the first nonsingleton dimension.

`C = levelcounts(A,dim)` operates along the dimension dim.

Examples

Count Observations in Each Level

Create a nominal array from string data in a cell array.

```
colors = nominal({'r','b','g';'g','r','b';'b','r','g'},...
                 {'blue','green','red'})
```

```
colors =

     red        blue      green
     green      red       blue
     blue       red       green
```

Count the number of observations of each level in each column.

```
levelcounts(colors)
```

```
ans =

     1     1     1
     1     0     2
     1     2     0
```

Count the number of observations of each level in each row.

```
levelcounts(colors,2)
```

```
ans =

     1     1     1
     1     1     1
     1     1     1
```

Alternatively, you can use `summary` to display the counts with their labels. The default is to count elements in each column.

```
summary(colors)
```

```
     blue       1      1      1
     green      1      0      2
     red        1      2      0
```

You can also count elements in each row.

```
summary(colors,2)
```

```
    blue      green      red
       1          1        1
       1          1        1
       1          1        1
```

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

dim — Dimension along which to count

positive integer value

Dimension along which to count the number of elements in each level, specified as a positive integer value. For example, if the dimension is `1`, then `levelcounts` counts along each column, while if the dimension is `2`, then `levelcounts` counts along each row.

Data Types: `double` | `single`

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`nominal` | `ordinal` | `summary`

leverage

Leverage

Syntax

```
h = leverage(data)
h = leverage(data,model)
```

Description

`h = leverage(data)` finds the leverage of each row (point) in the matrix `data` for a linear additive regression model.

`h = leverage(data,model)` finds the leverage on a regression, using a specified model type, where *`model`* can be one of these strings:

- `'linear'` - includes constant and linear terms
- `'interaction'` - includes constant, linear, and cross product terms
- `'quadratic'` - includes interactions and squared terms
- `'purequadratic'` - includes constant, linear, and squared terms

Leverage is a measure of the influence of a given observation on a regression due to its location in the space of the inputs.

Examples

One rule of thumb is to compare the leverage to $2p/n$ where n is the number of observations and p is the number of parameters in the model. For the Hald data set this value is 0.7692.

```
load hald
h = max(leverage(ingredients,'linear'))
h =
  0.7004
```

Since 0.7004 < 0.7692, there are no high leverage points using this rule.

More About

Algorithms

```
[Q,R] = qr(x2fx(data,'model'));

leverage = (sum(Q'.*Q'))'
```

- `regstats`

References

[1] Goodall, C. R. “Computation Using the QR Decomposition.” *Handbook in Statistics*. Vol. 9, Amsterdam: Elsevier/North-Holland, 1993.

lhsdesign

Latin hypercube sample

Syntax

```
X = lhsdesign(n,p)
X = lhsdesign(...,'smooth','off')
X = lhsdesign(...,'criterion',criterion)
X = lhsdesign(...,'iterations',k)
```

Description

`X = lhsdesign(n,p)` returns an *n*-by-*p* matrix, `X`, containing a latin hypercube sample of `n` values on each of `p` variables. For each column of `X`, the `n` values are randomly distributed with one from each interval `(0,1/n)`, `(1/n,2/n)`, ..., `(1-1/n,1)`, and they are randomly permuted.

`X = lhsdesign(...,'smooth','off')` produces points at the midpoints of the above intervals: `0.5/n`, `1.5/n`, ..., `1-0.5/n`. The default is `'on'`.

`X = lhsdesign(...,'criterion',criterion)` iteratively generates latin hypercube samples to find the best one according to the criterion *`criterion`*, which can be one of the following strings.

Criterion	Description
`'none'`	No iteration.
`'maximin'`	Maximize minimum distance between points. This is the default.
`'correlation'`	Reduce correlation.

`X = lhsdesign(...,'iterations',k)` iterates up to `k` times in an attempt to improve the design according to the specified criterion. The default is `k = 5`.

See Also

`haltonset` | `sobolset` | `lhsnorm` | `unifrnd`

lhsnorm

Latin hypercube sample from normal distribution

Syntax

```
X = lhsnorm(mu,sigma,n)
X = lhsnorm(mu,sigma,n,flag)
[X,Z] = lhsnorm(...)
```

Description

`X = lhsnorm(mu,sigma,n)` returns an *n*-by-*p* matrix, `X`, containing a latin hypercube sample of size `n` from a *p*-dimensional multivariate normal distribution with mean vector, `mu`, and covariance matrix, `sigma`.

`X` is similar to a random sample from the multivariate normal distribution, but the marginal distribution of each column is adjusted so that its sample marginal distribution is close to its theoretical normal distribution.

`X = lhsnorm(mu,sigma,n,flag)` controls the amount of smoothing in the sample. If `flag` is `'off'`, each column has points equally spaced on the probability scale. In other words, each column is a permutation of the values `G(0.5/n), G(1.5/n), ..., G(1-0.5/n)`, where`G` is the inverse normal cumulative distribution for that column's marginal distribution. If `flag` is `'on'` (the default), each column has points uniformly distributed on the probability scale. For example, in place of `0.5/n` you use a value having a uniform distribution on the interval `(0/n,1/n)`.

`[X,Z] = lhsnorm(...)` also returns `Z`, the original multivariate normal sample before the marginals are adjusted to obtain `X`.

References

[1] Stein, M. “Large sample properties of simulations using latin hypercube sampling.” *Technometrics*. Vol. 29, No. 2, 1987, pp. 143–151. Correction, Vol. 32, p. 367.

See Also

`lhsdesign` | `mvnrnd`

lillietest

Lilliefors test

Syntax

```
h = lillietest(x)
h = lillietest(x,Name,Value)
[h,p] = lillietest( ___ )
[h,p,kstat,critval] = lillietest( ___ )
```

Description

`h = lillietest(x)` returns a test decision for the null hypothesis that the data in vector x comes from a distribution in the normal family, against the alternative that it does not come from such a distribution, using a Lilliefors test. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = lillietest(x,Name,Value)` returns a test decision with additional options specified by one or more name-value pair arguments. For example, you can test the data against a different distribution family, change the significance level, or calculate the *p*-value using a Monte Carlo approximation.

`[h,p] = lillietest( ___ )` also returns the *p*-value p, using any of the input arguments from the previous syntaxes.

`[h,p,kstat,critval] = lillietest( ___ )` also returns the test statistic kstat and the critical value critval for the test.

Examples

Test for a Normal Distribution

Load the sample data. Test the null hypothesis that car mileage, in miles per gallon (`MPG`), follows a normal distribution across different makes of cars.

```
load carbig.mat;
```

```
[h,p,k,c] = lillietest(MPG)
```

```
Warning: P is less than the smallest tabulated value, returning 0.001.
h =
 1
p =
 1.0000e-003
k =
 0.0789
c =
 0.0451
```

The test statistic `k` is greater than the critical value `c`, so `lillietest` returns a result of `h = 1` to indicate rejection of the null hypothesis at the default 5% significance level. The warning indicates that the returned *p*-value is the smallest value in the table of precomputed values. To find a more accurate *p*-value, use MCTol to run a Monte Carlo approximation.

Test the Hypothesis at Different Significance Levels

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that the sample data comes from a normal distribution at the 1% significance level.

```
[h,p] = lillietest(x,'Alpha',0.01)
```

```
h =
 0
p =
 0.0348
```

The returned value of `h = 0` indicates that `lillietest` does not reject the null hypothesis at the 1% significance level.

Test for an Exponential Distribution

Load the sample data. Test the null hypothesis that car mileage, in miles per gallon (`MPG`), follows an exponential distribution across different makes of cars.

```
load carbig.mat;
```

```
h = lillietest(MPG,'Distr','exp')

h =
 1
```

The returned value of `h = 1` indicates that `lillietest` rejects the null hypothesis at the default 5% significance level.

Determine the *p*-value Using Monte Carlo Approximation

Load the sample data. Test the null hypothesis that car mileage, in miles per gallon (`MPG`), follows a normal distribution across different makes of cars. Determine the *p*-value using a Monte Carlo approximation with a maximum Monte Carlo standard error of `1e-4`.

```
load carbig.mat;
[h,p] = lillietest(MPG,'MCTol',1e-4)

h =
 1
p =
 0
```

The returned value of `h = 1` indicates that `lillietest` rejects the null hypothesis that the data comes from a normal distribution at the 5% significance level.

Input Arguments

x — Sample data

vector

Sample data, specified as a vector.

Data Types: `single | double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Distr','exp','Alpha',0.01` tests the null hypothesis that the population distribution belongs to the exponential distribution family at the 1% significance level.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

- If MCTol is not used, Alpha must be in the range [0.001,0.50].
- If MCTol is used, Alpha must be in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Distr'` — Distribution family

`'norm'` (default) | `'exp'` | `'ev'`

Distribution family for the hypothesis test, specified as the comma-separated pair consisting of `'Distr'` and one of the following.

`'norm'`	Normal distribution
`'exp'`	Exponential distribution
`'ev'`	Extreme value distribution

Example: `'Distr','exp'`

`'MCTol'` — Maximum Monte Carlo standard error

scalar value in the range (0,1)

Maximum Monte Carlo standard error for p, the *p*-value of the test, specified as the comma-separated pair consisting of `'MCTol'` and a scalar value in the range (0,1).

Example: `'MCTol',0.001`

Data Types: `single` | `double`

Output Arguments

`h` — Hypothesis test result

`1` | `0`

Hypothesis test result, returned as a logical value.

- If h = `1`, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = `0`, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value
scalar value in the range (0,1)

p-value of the test, returned as a scalar value in the range (0,1). p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

- If MCTol is not used, p is computed using inverse interpolation into the table of critical values, and is returned as a scalar value in the range [0.001,0.50]. `lillietest` warns when p is not found within the tabulated range and returns either the smallest or largest tabulated value.
- If MCTol is used, `lillietest` conducts a Monte Carlo simulation to compute a more accurate *p*-value, and p is returned as a scalar value in the range (0,1).

`kstat` — Test statistic
nonnegative scalar value

Test statistic, returned as a nonnegative scalar value.

`critval` — Critical value
nonnegative scalar value

Critical value for the hypothesis test, returned as a nonnegative scalar value.

More About

Lilliefors Test

The Lilliefors test is a two-sided goodness-of-fit test suitable when the parameters of the null distribution are unknown and must be estimated. This is in contrast to the one-sample Kolmogorov-Smirnov test, which requires the null distribution to be completely specified.

The Lilliefors test statistic is:

$$D^* = \max_x \left| F(x) - G(x) \right|,$$

where $\hat{F}(x)$ is the empirical cdf of the sample data and $G(x)$ is the cdf of the hypothesized distribution with estimated parameters equal to the sample parameters.

`lillietest` can be used to test whether the data vector x has a lognormal or Weibull distribution by applying a transformation to the data vector and running the appropriate Lilliefors test:

- To test x for a lognormal distribution, test if `log(x)` has a normal distribution.
- To test x for a Weibull distribution, test if `log(x)` has an extreme value distribution.

The Lilliefors test cannot be used when the null hypothesis is not a location-scale family of distributions.

Monte Carlo Standard Error

The Monte Carlo standard error is the error due to simulating the *p*-value.

The Monte Carlo standard error is calculated as:

$$SE = \sqrt{\frac{(\hat{p})(1-\hat{p})}{\text{mcreps}}},$$

where $\hat{p}$ is the estimated *p*-value of the hypothesis test, and `mcreps` is the number of Monte Carlo replications performed.

The number of Monte Carlo replications, `mcreps`, is determined such that the Monte Carlo standard error for $\hat{p}$ less than the value specified for MCTol.

Algorithms

To compute the critical value for the hypothesis test, `lillietest` interpolates into a table of critical values pre-computed using Monte Carlo simulation for sample sizes less than 1000 and significance levels between 0.001 and 0.50. The table used by `lillietest` is larger and more accurate than the table originally introduced by

Lilliefors. If a more accurate *p*-value is desired, or if the desired significance level is less than 0.001 or greater than 0.50, the MCTol input argument can be used to run a Monte Carlo simulation to calculate the *p*-value more exactly.

When the computed value of the test statistic is greater than the critical value, `lillietest` rejects the null hypothesis at significance level Alpha.

`lillietest` treats `NaN` values in x as missing values and ignores them.

References

[1] Conover, W. J. *Practical Nonparametric Statistics*. Hoboken, NJ: John Wiley & Sons, Inc., 1980.

[2] Lilliefors, H. W. "On the Kolmogorov-Smirnov test for the exponential distribution with mean unknown." *Journal of the American Statistical Association*. Vol. 64, 1969, pp. 387–389.

[3] Lilliefors, H. W. "On the Kolmogorov-Smirnov test for normality with mean and variance unknown." *Journal of the American Statistical Association*. Vol. 62, 1967, pp. 399–402.

See Also

`adtest` | `cdfplot` | `jbtest` | `kstest` | `kstest2`

LinearModel class

Linear regression model class

Description

An object comprising training data, model description, diagnostic information, and fitted coefficients for a linear regression. Predict model responses with the `predict` or `feval` methods.

Construction

`mdl = fitlm(tbl)` or `mdl = fitlm(X,y)` create a linear model of a table or dataset array `tbl`, or of the responses `y` to a data matrix `X`. For details, see `fitlm`.

`mdl = stepwiselm(tbl)` or `mdl = stepwiselm(X,y)` create a linear model of a table or dataset array `tbl`, or of the responses `y` to a data matrix `X`, with unimportant predictors excluded. For details, see `stepwiselm`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see “Grouping Variables” on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

X — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single | double | logical`

y — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single | double`

Properties

CoefficientCovariance

Covariance matrix of coefficient estimates.

CoefficientNames

Cell array of strings containing a label for each coefficient.

Coefficients

Coefficient values stored as a table. `Coefficients` has one row for each coefficient and these columns:

- `Estimate` — Estimated coefficient value
- `SE` — Standard error of the estimate
- `tStat` — t statistic for a test that the coefficient is zero
- `pValue` — p-value for the t statistic

To obtain any of these columns as a vector, index into the property using dot notation. For example, in `mdl` the estimated coefficient vector is

```
beta = mdl.Coefficients.Estimate
```

Use `coefTest` to perform other tests on the coefficients.

`DFE`

Degrees of freedom for error (residuals), equal to the number of observations minus the number of estimated coefficients.

`Diagnostics`

Table with the same number of rows as the input data (`tbl` or `X`). `Diagnostics` contains diagnostics helpful in finding outliers and influential observations. Many diagnostics describe the effect on the fit of deleting single observations. `Diagnostics` contains the following fields.

Field	Meaning	Utility
`Leverage`	Diagonal elements of `HatMatrix`	`Leverage` indicates to what extent the predicted value for an observation is determined by the observed value for that observation. A value close to `1` indicates that the prediction is largely determined by that observation, with little contribution from the other observations. A value close to `0` indicates the fit is largely determined by the other observations. For a model with `P` coefficients and `N` observations, the average value of `Leverage` is `P/N`. An observation with `Leverage` larger than `2*P/N` can be regarded as having high leverage.
`CooksDistance`	Cook's measure of scaled change in fitted values	`CooksDistance` is a measure of scaled change in fitted values. An observation with `CooksDistance` larger than three times the mean Cook's distance can be an outlier.
`Dffits`	Delete-1 scaled differences in fitted values vs. observation number	`Dffits` is the scaled change in the fitted values for each observation that would result from excluding that observation from the fit. Values with an absolute value larger than `2*sqrt(P/N)` may be considered influential.
`S2_i`	Delete-1 variance vs. observation number	`S2_i` is a set of residual variance estimates obtained by deleting each observation in turn. These can be compared with the value of the `MSE` property.

Field	Meaning	Utility
`CovRatio`	Delete-1 ratio of determinant of covariance vs. observation number	`CovRatio` is the ratio of the determinant of the coefficient covariance matrix with each observation deleted in turn to the determinant of the covariance matrix for the full model. Values larger than `1+3*P/N` or smaller than `1-3*P/N` indicate influential points.
`Dfbetas`	Delete-1 scaled differences in covariance estimates vs. observation number	`Dfbetas` is an `N`-by-`P` matrix of the scaled change in the coefficient estimates that would result from excluding each observation in turn. Values larger than `3/sqrt(N)` in absolute value indicate that the observation has a large influence on the corresponding coefficient.
`HatMatrix`	Projection matrix to compute fitted from observed responses	`HatMatrix` is an `N`-by-`N` matrix such that `Fitted = HatMatrix*Y`, where `Y` is the response vector and `Fitted` is the vector of fitted response values.

Rows not used in the fit because of missing values (in `ObservationInfo.Missing`) contain `NaN` values.

Rows not used in the fit because of excluded values (in `ObservationInfo.Excluded`) contain `NaN` values, with the following exception: Delete-1 diagnostics refer to the statistic with and without that observation (row) included in the fit. These diagnostics help identify important observations.

`Fitted`

Predicted response to the input data by using the model. Use `predict` to compute predictions for other predictor values, or to compute confidence bounds on `Fitted`.

`Formula`

Object containing information about the model.

`LogLikelihood`

Log likelihood of the model distribution at the response values, with mean fitted from the model, and other parameters estimated as part of the model fit.

ModelCriterion

AIC and other information criteria for comparing models. A structure with fields:

- AIC — Akaike information criterion
- AICc — Akaike information criterion corrected for sample size
- BIC — Bayesian information criterion
- CAIC — Consistent Akaike information criterion

To obtain any of these values as a scalar, index into the property using dot notation. For example, in a model mdl, the AIC value aic is:

```
aic = mdl.ModelCriterion.AIC
```

MSE

Mean squared error (residuals), SSE/DFE.

NumCoefficients

Number of coefficients in the model, a positive integer. NumCoefficients includes coefficients that are set to zero when the model terms are rank deficient.

NumEstimatedCoefficients

Number of estimated coefficients in the model, a positive integer. NumEstimatedCoefficients does not include coefficients that are set to zero when the model terms are rank deficient. NumEstimatedCoefficients is the degrees of freedom for regression.

NumObservations

Number of observations the fitting function used in fitting. This is the number of observations supplied in the original table, dataset, or matrix, minus any excluded rows (set with the Excluded name-value pair) or rows with missing values.

NumPredictors

Number of variables fitlm used as predictors for fitting.

NumVariables

Number of variables in the data. NumVariables is the number of variables in the original table or dataset, or the total number of columns in the predictor matrix and

response vector when the fit is based on those arrays. It includes variables, if any, that are not used as predictors or as the response.

`ObservationInfo`

Table with the same number of rows as the input data (`tbl` or `X`).

Field	Description
`Weights`	Observation weights. Default is all `1`.
`Excluded`	Logical value, `1` indicates an observation that you excluded from the fit with the `Exclude` name-value pair.
`Missing`	Logical value, `1` indicates a missing value in the input. Missing values are not used in the fit.
`Subset`	Logical value, `1` indicates the observation is not excluded or missing, so is used in the fit.

`ObservationNames`

Cell array of strings containing the names of the observations used in the fit.

- If the fit is based on a table or dataset containing observation names, `ObservationNames` uses those names.
- Otherwise, `ObservationNames` is an empty cell array

`PredictorNames`

Cell array of strings, the names of the predictors used in fitting the model.

`Residuals`

Table of residuals, with one row for each observation and these variables.

Field	Description
`Raw`	Observed minus fitted values.
`Pearson`	Raw residuals divided by RMSE.
`Standardized`	Raw residuals divided by their estimated standard deviation.

Field	Description
`Studentized`	Residual divided by an independent estimate of the residual standard deviation. The residual for observation i is divided by an estimate of the error standard deviation based on all observations except for observation i.

To obtain any of these columns as a vector, index into the property using dot notation. For example, in a model `mdl`, the ordinary raw residual vector `r` is:

```
r = mdl.Residuals.Raw
```

Rows not used in the fit because of missing values (in `ObservationInfo.Missing`) contain `NaN` values.

Rows not used in the fit because of excluded values (in `ObservationInfo.Excluded`) contain `NaN` values, with the following exceptions:

- `raw` contains the difference between the observed and predicted values.
- `standardized` is the residual, standardized in the usual way.
- `studentized` matches the standardized values because this residual is not used in the estimate of the residual standard deviation.

`ResponseName`

String giving naming the response variable.

`RMSE`

Root mean squared error (residuals), `sqrt(MSE)`.

`Robust`

Structure that is empty unless `fitlm` constructed the model using robust regression.

Field	Description
`WgtFun`	Robust weighting function, such as `'bisquare'` (see `robustfit`)
`Tune`	Value specified for tuning parameter (can be `[]`)

Field	Description
`Weights`	Vector of weights used in final iteration of robust fit

`Rsquared`

Proportion of total sum of squares explained by the model. The ordinary R-squared value relates to the `SSR` and `SST` properties:
`Rsquared = SSR/SST = 1 - SSE/SST`.

For a linear or nonlinear model, `Rsquared` is a structure with two fields:

- `Ordinary` — Ordinary (unadjusted) R-squared
- `Adjusted` — R-squared adjusted for the number of coefficients

For a generalized linear model, `Rsquared` is a structure with five fields:

- `Ordinary` — Ordinary (unadjusted) R-squared
- `Adjusted` — R-squared adjusted for the number of coefficients
- `LLR` — Log-likelihood ratio
- `Deviance` — Deviance
- `AdjGeneralized` — Adjusted generalized R-squared

To obtain any of these values as a scalar, index into the property using dot notation. For example, the adjusted R-squared value in `mdl` is

```
r2 = mdl.Rsquared.Adjusted
```

`SSE`

Sum of squared errors (residuals).

The Pythagorean theorem implies
`SST = SSE + SSR`.

`SSR`

Regression sum of squares, the sum of squared deviations of the fitted values from their mean.

The Pythagorean theorem implies
`SST = SSE + SSR`.

SST

Total sum of squares, the sum of squared deviations of `y` from `mean(y)`.

The Pythagorean theorem implies
`SST = SSE + SSR`.

Steps

Structure that is empty unless `stepwiselm` constructed the model.

Field	Description
`Start`	Formula representing the starting model
`Lower`	Formula representing the lower bound model, these terms that must remain in the model
`Upper`	Formula representing the upper bound model, model cannot contain more terms than `Upper`
`Criterion`	Criterion used for the stepwise algorithm, such as `'sse'`
`PEnter`	Value of the parameter, such as `0.05`
`PRemove`	Value of the parameter, such as `0.10`
`History`	Table representing the steps taken in the fit

The `History` table has one row for each step including the initial fit, and the following variables (columns).

Field	Description
`Action`	Action taken during this step, one of: • `'Start'` — First step • `'Add'` — A term is added • `'Remove'` — A term is removed
`TermName`	• `'Start'` step: The starting model specification • `'Add'` or `'Remove'` steps: The term moved in that step
`Terms`	Terms matrix (see `modelspec` of `fitlm`)
`DF`	Regression degrees of freedom after this step

Field	Description
`delDF`	Change in regression degrees of freedom from previous step (negative for steps that remove a term)
`Deviance`	Deviance (residual sum of squares) at that step
`FStat`	F statistic that led to this step
`PValue`	p-value of the F statistic

`VariableInfo`

Table containing metadata about `Variables`. There is one row for each term in the model, and the following columns.

Field	Description
`Class`	String giving variable class, such as `'double'`
`Range`	Cell array giving variable range: • Continuous variable — Two-element vector `[min,max]`, the minimum and maximum values • Categorical variable — Cell array of distinct variable values
`InModel`	Logical vector, where `true` indicates the variable is in the model
`IsCategorical`	Logical vector, where `true` indicates a categorical variable

`VariableNames`

Cell array of strings containing names of the variables in the fit.

- If the fit is based on a table or dataset, this property provides the names of the variables in that table or dataset.
- If the fit is based on a predictor matrix and response vector, `VariableNames` is the values in the `VarNames` name-value pair of the fitting method.
- Otherwise the variables have the default fitting names.

`Variables`

Table containing the data, both observations and responses, that the fitting function used to construct the fit. If the fit is based on a table or dataset array, `Variables` contains

all of the data from that table or dataset array. Otherwise, `Variables` is a table created from the input data matrix `X` and response vector `y`.

Methods

addTerms	Add terms to linear regression model
anova	Analysis of variance for linear model
coefCI	Confidence intervals of coefficient estimates of linear model
coefTest	Linear hypothesis test on linear regression model coefficients
disp	Display linear regression model
dwtest	Durbin-Watson test of linear model
feval	Evaluate linear regression model prediction
fit	Create linear regression model
plot	Scatter plot or added variable plot of linear model
plotAdded	Added variable plot or leverage plot for linear model
plotAdjustedResponse	Adjusted response plot for linear regression model
plotDiagnostics	Plot diagnostics of linear regression model

plotEffects	Plot main effects of each predictor in linear regression model
plotInteraction	Plot interaction effects of two predictors in linear regression model
plotResiduals	Plot residuals of linear regression model
plotSlice	Plot of slices through fitted linear regression surface
predict	Predict response of linear regression model
random	Simulate responses for linear regression model
removeTerms	Remove terms from linear model
step	Improve linear regression model by adding or removing terms
stepwise	Create linear regression model by stepwise regression

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Definitions

Hat Matrix

The *hat matrix H* is defined in terms of the data matrix *X*:

$H = X(X^TX)^{-1}X^T$.

The diagonal elements H_{ii} satisfy

$$0 \le h_{ii} \le 1$$
$$\sum_{i=1}^{n} h_{ii} = p,$$

where n is the number of observations (rows of X), and p is the number of coefficients in the regression model.

Leverage

The *leverage* of observation i is the value of the ith diagonal term, h_{ii}, of the hat matrix H. Because the sum of the leverage values is p (the number of coefficients in the regression model), an observation i can be considered to be an outlier if its leverage substantially exceeds p/n, where n is the number of observations.

Cook's Distance

Cook's distance is the scaled change in fitted values. Each element in `CooksDistance` is the normalized change in the vector of coefficients due to the deletion of an observation. The Cook's distance, D_i, of observation i is

$$D_i = \frac{\sum_{j=1}^{n} \left(\hat{y}_j - \hat{y}_{j(i)}\right)^2}{p\,MSE},$$

where

- $\hat{y}_j$ is the jth fitted response value.
- $\hat{y}_{j(i)}$ is the jth fitted response value, where the fit does not include observation i.
- MSE is the mean squared error.

- p is the number of coefficients in the regression model.

Cook's distance is algebraically equivalent to the following expression:

$$D_i = \frac{r_i^2}{p\,MSE}\left(\frac{h_{ii}}{(1-h_{ii})^2}\right),$$

where r_i is the ith residual, and h_{ii} is the ith leverage value.

`CooksDistance` is an n-by-1 column vector in the `Diagnostics` table of the `LinearModel` object.

Examples

Linear Regression Model of Matrix Data

Fit a linear model of the Hald data.

Load the data.

```
load hald
X = ingredients; % predictor variables
y = heat; % response
```

Fit a default linear model to the data.

```
mdl = fitlm(X,y)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4

Estimated Coefficients:
                   Estimate    SE         tStat       pValue
    (Intercept)      62.405     70.071      0.8906     0.39913
    x1               1.5511    0.74477      2.0827    0.070822
    x2              0.51017    0.72379     0.70486      0.5009
    x3              0.10191    0.75471     0.13503     0.89592
    x4             -0.14406    0.70905    -0.20317     0.84407
```

```
Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 2.45
R-squared: 0.982,  Adjusted R-Squared 0.974
F-statistic vs. constant model: 111, p-value = 4.76e-07
```

Linear Regression with Categorical Predictor and Nonlinear Model

Fit a model of a table that contains a categorical predictor. Use a nonlinear response formula.

Load the `carsmall` data.

```
load carsmall
```

Construct a table containing continuous predictor variable `Weight`, nominal predictor variable `Year`, and response variable `MPG`.

```
tbl = table(MPG,Weight);
tbl.Year = nominal(Model_Year);
```

Create a fitted model of `MPG` as a function of `Year`, `Weight`, and Weight^2. (You don't have to include `Weight` explicitly in your formula because it is a lower-order term of Weight^2.

```
mdl = fitlm(tbl,'MPG ~ Year + Weight^2')
```

```
mdl =

Linear regression model:
    MPG ~ 1 + Weight + Year + Weight^2

Estimated Coefficients:
                   Estimate      SE            tStat      pValue
    (Intercept)       54.206       4.7117      11.505    2.6648e-19
    Weight         -0.016404    0.0031249     -5.2493    1.0283e-06
    Year_76           2.0887      0.71491      2.9215     0.0044137
    Year_82           8.1864      0.81531      10.041    2.6364e-16
    Weight^2       1.5573e-06   4.9454e-07      3.149     0.0022303

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 2.78
R-squared: 0.885,  Adjusted R-Squared 0.88
F-statistic vs. constant model: 172, p-value = 5.52e-41
```

`fitlm` creates two dummy (indicator) variables for the nominal variate, `Year`. The dummy variable `Year_76` takes the value 1 if model year is 1976 and takes the value 0 if it is not. The dummy variable `Year_82` takes the value 1 if model year is 1982 and takes the value 0 if it is not. And the year 1970 is the reference year. The corresponding model is

$$\hat{MPG} = 54.206 - 0.0164(Weight) + 2.0887(Year\_76) + 8.1864(Year\_82) + (1.557e-06)(Weight)^2$$

Robust Linear Regression Model

Fit a linear regression model of the Hald data using robust fitting.

Load the data.

```
load hald
X = ingredients; % predictor variables
y = heat; % response
```

Fit a robust linear model to the data.

```
mdl = fitlm(X,y,'linear','RobustOpts','on')
```

```
mdl =

Linear regression model (robust fit):
    y ~ 1 + x1 + x2 + x3 + x4

Estimated Coefficients:
                   Estimate    SE         tStat       pValue
    (Intercept)       60.09     75.818     0.79256      0.4509
    x1               1.5753    0.80585      1.9548    0.086346
    x2               0.5322    0.78315     0.67957     0.51596
    x3              0.13346     0.8166     0.16343     0.87424
    x4             -0.12052     0.7672    -0.15709     0.87906

Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 2.65
R-squared: 0.979,  Adjusted R-Squared 0.969
F-statistic vs. constant model: 94.6, p-value = 9.03e-07
```

- “Linear Regression Workflow” on page 9-41
- “Robust Regression versus Standard Least-Squares Fit” on page 9-128

Algorithms

The main fitting algorithm is QR decomposition. For robust fitting, the algorithm is `robustfit`.

Alternatives

To remove redundant predictors in linear regression using lasso or elastic net, use the `lasso` function.

To regularize a regression with correlated terms using ridge regression, use the `ridge` or `lasso` functions.

To regularize a regression with correlated terms using partial least squares, use the `plsregress` function.

See Also

`fitlm` | `stepwiselm`

How To

- “Linear Regression” on page 9-11

LinearMixedModel class

Linear mixed-effects model class

Description

A `LinearMixedModel` object represents a model of a response variable with fixed and random effects. It comprises data, a model description, fitted coefficients, covariance parameters, design matrices, residuals, residual plots, and other diagnostic information for a linear mixed-effects model. You can predict model responses with the `predict` function and generate random data at new design points using the `random` function.

Construction

You can fit a linear mixed-effects model using `fitlme(tbl,formula)` if your data is in a table or dataset array. Alternatively, if your model is not easily described using a formula, you can create matrices to define the fixed and random effects, and fit the model using `fitlmematrix(X,y,Z,G)`.

Input Arguments

`tbl` — Input data

table | `dataset` array

Input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or `dataset` array. The predictor variables can be continuous or grouping variables (see "Grouping Variables" on page 2-52). You must specify the model for the variables using formula.

Data Types: `single` | `double` | `char` | `cell`

`formula` — Formula for model specification

string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`

Formula for model specification, specified as a string of the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`. For a full description, see "Formula" on page 22-2595.

Example: `'y ~ treatment +(1|block)'`

X — Fixed-effects design matrix

n-by-*p* matrix

Fixed-effects design matrix, specified as an *n*-by-*p* matrix, where *n* is the number of observations, and *p* is the number of fixed-effects predictor variables. Each row of `X` corresponds to one observation, and each column of `X` corresponds to one variable.

Data Types: `single | double`

y — Response values

n-by-1 vector

Response values, specified as an *n*-by-1 vector, where *n* is the number of observations.

Data Types: `single | double`

Z — Random-effects design

n-by-*q* matrix | cell array of *R* *n*-by-*q*(*r*) matrices, *r* = 1, 2, ..., *R*

Random-effects design, specified as either of the following.

- If there is one random-effects term in the model, then `Z` must be an *n*-by-*q* matrix, where *n* is the number of observations and *q* is the number of variables in the random-effects term.
- If there are *R* random-effects terms, then `Z` must be a cell array of length *R*. Each cell of `Z` contains an *n*-by-*q*(*r*) design matrix `Z{r}`, *r* = 1, 2, ..., *R*, corresponding to each random-effects term. Here, *q*(*r*) is the number of random effects term in the *r*th random effects design matrix, `Z{r}`.

Data Types: `single | double | cell`

G — Grouping variable or variables

n-by-1 vector | cell array of *R* *n*-by-1 vectors

Grouping variable or variables, specified as either of the following.

- If there is one random-effects term, then `G` must be an *n*-by-1 vector corresponding to a single grouping variable with *M* levels or groups.

  `G` can be a categorical vector, numeric vector, character array, or cell array of strings.

- If there are multiple random-effects terms, then `G` must be a cell array of length R. Each cell of `G` contains a grouping variable `G{r}`, $r = 1, 2, ..., R$, with $M(r)$ levels.

  `G{r}` can be a categorical vector, numeric vector, character array, or cell array of strings.

Data Types: `single | double | char | cell`

Properties

`Coefficients` — Fixed-effects coefficient estimates

dataset array

Fixed-effects coefficient estimates and related statistics, stored as a dataset array containing the following fields.

`Name`	Name of the term.
`Estimate`	Estimated value of the coefficient.
`SE`	Standard error of the coefficient.
`tStat`	t-statistics for testing the null hypothesis that the coefficient is equal to zero.
`DF`	Degrees of freedom for the t-test. Method to compute `DF` is specified by the `'DFMethod'` name-value pair argument. `Coefficients` always uses the `'Residual'` method for `'DFMethod'`.
`pValue`	p-value for the t-test.
`Lower`	Lower limit of the confidence interval for coefficient. `Coefficients` always uses the 95% confidence level, i.e.`'alpha'` is 0.05.
`Upper`	Upper limit of confidence interval for coefficient. `Coefficients` always uses the 95% confidence level, i.e.`'alpha'` is 0.05.

You can change `'DFMethod'` and `'alpha'` while computing confidence intervals for or testing hypotheses involving fixed- and random-effects, using the `coefCI` and `coefTest` methods.

`CoefficientCovariance` — Covariance of the estimated fixed-effects coefficients

p-by-p matrix

Covariance of the estimated fixed-effects coefficients of the linear mixed-effects model, stored as a p-by-p matrix, where p is the number of fixed-effects coefficients.

You can display the covariance parameters associated with the random effects using the `covarianceParameters` method.

Data Types: `double`

`CoefficientNames` — Names of the fixed-effects coefficients

1-by-p cell array of strings

Names of the fixed-effects coefficients of a linear mixed-effects model, stored as a 1-by-p cell array of strings.

Data Types: `cell`

`DFE` — Residual degrees of freedom

positive integer value

Residual degrees of freedom, stored as a positive integer value. $DFE = n - p$, where n is the number of observations, and p is the number of fixed-effects coefficients.

This corresponds to the `'Residual'` method of calculating degrees of freedom in the `fixedEffects` and `randomEffects` methods.

Data Types: `double`

`FitMethod` — Method used to fit the linear mixed-effects model

`ML | REML`

Method used to fit the linear mixed-effects model, stored as either of the following strings.

- `ML`, if the fitting method is maximum likelihood
- `REML`, if the fitting method is restricted maximum likelihood

Data Types: `char`

`Formula` — Specification of the fixed- and random-effects terms, and grouping variables

object

Specification of the fixed-effects terms, random-effects terms, and grouping variables that define the linear mixed-effects model, stored as an object.

For more information on how to specify the model to fit using a formula, see "Formula" on page 22-2595.

`LogLikelihood` — Maximized log or restricted log likelihood

scalar value

Maximized log likelihood or maximized restricted log likelihood of the fitted linear mixed-effects model depending on the fitting method you choose, stored as a scalar value.

Data Types: `double`

`ModelCriterion` — Model criterion

dataset array

Model criterion to compare fitted linear mixed-effects models, stored as a dataset array with the following columns.

`AIC`	Akaike Information Criterion
`BIC`	Bayesian Information Criterion
`Loglikelihood`	Log likelihood value of the model
`Deviance`	–2 times the log likelihood of the model

If n is the number of observations used in fitting the model, and p is the number of fixed-effects coefficients, then for calculating AIC and BIC,

- The total number of parameters is $nc + p + 1$, where nc is the total number of parameters in the random-effects covariance excluding the residual variance
- The effective number of observations is
  - n, when the fitting method is maximum likelihood (ML)
  - $n - p$, when the fitting method is restricted maximum likelihood (REML)

`MSE` — ML or REML estimate

positive scalar value

ML or REML estimate, based on the fitting method used for estimating σ^2, stored as a positive scalar value. σ^2 is the residual variance or variance of the observation error term of the linear mixed-effects model.

Data Types: `double`

`NumCoefficients` — Number of fixed-effects coefficients

positive integer value

Number of fixed-effects coefficients in the fitted linear mixed-effects model, stored as a positive integer value.

Data Types: `double`

`NumEstimatedCoefficients` — Number of estimated fixed-effects coefficients

positive integer value

Number of estimated fixed-effects coefficients in the fitted linear mixed-effects model, stored as a positive integer value.

Data Types: `double`

`NumObservations` — Number of observations

positive integer value

Number of observations used in the fit, stored as a positive integer value. This is the number of rows in the table or dataset array, or the design matrices minus the excluded rows or rows with `NaN` values.

Data Types: `double`

`NumPredictors` — Number of predictors

positive integer value

Number of variables used as predictors in the linear mixed-effects model, stored as a positive integer value.

Data Types: `double`

`NumVariables` — Total number of variables

positive integer value

Total number of variables including the response and predictors, stored as a positive integer value.

- If the sample data is in a table or dataset array `tbl`, `NumVariables` is the total number of variables in `tbl` including the response variable.

- If the fit is based on matrix input, `NumVariables` is the total number of columns in the predictor matrix or matrices, and response vector.

`NumVariables` includes variables, if there are any, that are not used as predictors or as the response.

Data Types: `double`

`ObservationInfo` — Information about the observations

table

Information about the observations used in the fit, stored as a table.

`ObservationInfo` has one row for each observation and the following four columns.

`Weights`	The value of the weighted variable for that observation. Default value is 1.
`Excluded`	`true`, if the observation was excluded from the fit using the `'Exclude'` name-value pair argument, `false`, otherwise. 1 stands for `true` and 0 stands for `false`.
`Missing`	`true`, if the observation was excluded from the fit because any response or predictor value is missing, `false`, otherwise. Missing values include `NaN` for numeric variables, empty cells for cell arrays, blank rows for character arrays, and the `<undefined>` value for categorical arrays.
`Subset`	`true`, if the observation was used in the fit, `false`, if it was not used because it is missing or excluded.

Data Types: `table`

`ObservationNames` — Names of observations

cell array of strings

Names of observations used in the fit, stored as a cell array of strings.

- If the data is in a table or dataset array, `tbl`, containing observation names, `ObservationNames` has those names.
- If the data is provided in matrices, or a table or dataset array without observation names, then `ObservationNames` is an empty cell array.

Data Types: `cell`

`PredictorNames` — Names of predictors

cell array of strings

Names of the variables that you use as predictors in the fit, stored as a cell array of strings that has the same length as `NumPredictors`.

Data Types: `cell`

`ResponseName` — Names of response variable

character string

Name of the variable used as the response variable in the fit, stored as a character string.

Data Types: `char`

`Rsquared` — Proportion of variability in the response explained by the fitted model

structure

Proportion of variability in the response explained by the fitted model, stored as a structure. It is the multiple correlation coefficient or R-squared. `Rsquared` has two fields.

`Ordinary`	R-squared value, stored as a scalar value in a structure. `Rsquared.Ordinary = 1 – SSE./SST`
`Adjusted`	R-squared value adjusted for the number of fixed-effects coefficients, stored as a scalar value in a structure. `Rsquared.Adjusted = 1 – (SSE./SST)*(DFT./DFE)`, where `DFE = n – p`, `DFT = n – 1`, and `n` is the total number of observations, `p` is the number of fixed-effects coefficients.

Data Types: `struct`

`SSE` — Error sum of squares
positive scalar value

Error sum of squares, that is, sum of the squared conditional residuals, stored as a positive scalar value.

`SSE = sum((y – F).^2)`, where `y` is the response vector, and `F` is the fitted conditional response of the linear mixed-effects model. The conditional model has contributions from both fixed and random effects.

Data Types: `double`

`SSR` — Regression sum of squares
positive scalar value

Regression sum of squares, that is, the sum of squares explained by the linear mixed-effects regression, stored as a positive scalar value. It is the sum of squared deviations of the conditional fitted values from their mean.

`SSR = sum((F – mean(F)).^2)`, where `F` is the fitted conditional response of the linear mixed-effects model. The conditional model has contributions from both fixed and random effects.

Data Types: `double`

`SST` — Total sum of squares
positive scalar value

Total sum of squares, that is, the sum of the squared deviations of the observed response values from their mean, stored as a positive scalar value.

`SST = sum((y – mean(y)).^2) = SSR + SSE`, where `y` is the response vector.

Data Types: `double`

`Variables` — Variables
table

Variables, stored as a table.

- If the fit is based on a table or dataset array `tbl`, then `Variables` is identical to `tbl`.

- If the fit is based on matrix input, then `Variables` is a table containing all the variables in the predictor matrix or matrices, and response variable.

Data Types: `table`

`VariableInfo` — Information about the variables

table

Information about the variables used in the fit, stored as a table.

`VariableInfo` has one row for each variable and contains the following four columns.

`Class`	Class of the variable (`'double'`, `'cell'`, `'nominal'`, and so on).
`Range`	Value range of the variable. • For a numerical variable, it is a two-element vector of the form `[min,max]`. • For a cell or categorical variable, it is a cell or categorical array containing all unique values of the variable.
`InModel`	`true`, if the variable is a predictor in the fitted model. `false`, if the variable is not in the fitted model.
`IsCategorical`	`true`, if the variable has a type that is treated as a categorical predictor, such as cell, logical, or categorical, or if it is specified as categorical by the `'Categorical'` name-value pair argument of the `fit` method. `false`, if it is a continuous predictor.

Data Types: `table`

`VariableNames` — Names of the variables

cell array of strings

Names of the variables used in the fit, stored as a cell array of strings.

- If sample data is in a table or dataset array `tbl`, `VariableNames` contains the names of the variables in `tbl`.
- If sample data is in matrix format, then `VariableInfo` includes variable names you supply while fitting the model. If you do not supply the variable names, then `VariableInfo` contains the default names.

Data Types: `cell`

Methods

anova	Analysis of variance for linear mixed-effects model
coefCI	Confidence intervals for coefficients of linear mixed-effects model
coefTest	Hypothesis test on fixed and random effects of linear mixed-effects model
compare	Compare linear mixed-effects models
covarianceParameters	Extract covariance parameters of linear mixed-effects model
designMatrix	Fixed- and random-effects design matrices
disp	Display linear mixed-effects model
fit	Fit linear mixed-effects model using tables
fitmatrix	Fit linear mixed-effects model using design matrices
fitted	Fitted responses from a linear mixed-effects model

fixedEffects	Estimates of fixed effects and related statistics
plotResiduals	Plot residuals of linear mixed-effects model
predict	Predict response of linear mixed-effects model
random	Generate random responses from fitted linear mixed-effects model
randomEffects	Estimates of random effects and related statistics
residuals	Residuals of fitted linear mixed-effects model
response	Response vector of the linear mixed-effects model

Definitions

Formula

In general, a formula for model specification is a string of the form `'y ~ terms'`. For the linear mixed-effects models, this formula is in the form `'y ~ fixed + (random1|grouping1) + ... + (randomR|groupingR)'`, where `fixed` and `random` contain the fixed-effects and the random-effects terms.

Suppose a table `tbl` contains the following:

- A response variable, `y`
- Predictor variables, X_j, which can be continuous or grouping variables
- Grouping variables, g_1, g_2, ..., g_R,

where the grouping variables in X_j and g_r can be categorical, logical, character arrays, or cell arrays of strings.

Then, in a formula of the form, `'y ~ fixed + (random1|g1) + ... + (randomR|gR)'`, the term `fixed` corresponds to a specification of the fixed-effects design matrix `X`, $random_1$ is a specification of the random-effects design matrix Z_1 corresponding to grouping variable g_1, and similarly $random_R$ is a specification of the random-effects design matrix Z_R corresponding to grouping variable g_R. You can express the `fixed` and `random` terms using Wilkinson notation.

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1.*X2 (elementwise multiplication of X1 and X2)`
`X1:X2`	`X1.*X2` only
`- X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`. Here are some examples for linear mixed-effects model specification.

Examples:

Formula	Description
`'y ~ X1 + X2'`	Fixed effects for the intercept, `X1` and `X2`. This is equivalent to `'y ~ 1 + X1 + X2'`.

Formula	Description
`'y ~ -1 + X1 + X2'`	No intercept and fixed effects for `X1` and `X2`. The implicit intercept term is suppressed by including `-1`.
`'y ~ 1 + (1 | g1)'`	Fixed effects for the intercept plus random effect for the intercept for each level of the grouping variable `g1`.
`'y ~ X1 + (1 | g1)'`	Random intercept model with a fixed slope.
`'y ~ X1 + (X1 | g1)'`	Random intercept and slope, with possible correlation between them. This is equivalent to `'y ~ 1 + X1 + (1 + X1| g1)'`.
`'y ~ X1 + (1 | g1) + (-1 + X1 | g1)'`	Independent random effects terms for intercept and slope.
`'y ~ 1 + (1 | g1) + (1 | g2) + (1 | g1:g2)'`	Random intercept model with independent main effects for `g1` and `g2`, plus an independent interaction effect.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Random Intercept Model with Categorical Predictor

Load the sample data.

```
load flu
```

The `flu` dataset array has a `Date` variable, and 10 variables containing estimated influenza rates (in 9 different regions, estimated from Google searches, plus a nationwide estimate from the Center for Disease Control and Prevention, CDC).

To fit a linear-mixed effects model, your data must be in a properly formatted dataset array. To fit a linear mixed-effects model with the influenza rates as the responses

and region as the predictor variable, combine the nine columns corresponding to the regions into a tall array. The new dataset array, `flu2`, must have the response variable, `FluRate`, the nominal variable, `Region`, that shows which region each estimate is from, and the grouping variable `Date`.

```
flu2 = stack(flu,2:10,'NewDataVarName','FluRate',...
    'IndVarName','Region');
flu2.Date = nominal(flu2.Date);
```

Fit a linear mixed-effects model with fixed effects for region and a random intercept that varies by `Date`.

Because region is a nominal variable, `fitlme` takes the first region, `NE`, as the reference and creates eight dummy variables representing the other eight regions. For example, $I[MidAtl]$ is the dummy variable representing the region `MidAtl`. For details, see "Dummy Indicator Variables" on page 2-55.

The corresponding model is

$$\begin{aligned} y_{im} &= \beta_0 + \beta_1 I[MidAtl]_i + \beta_2 I[ENCentral]_i + \beta_3 I[WNCentral]_i + \beta_4 I[SAtl]_i \\ &\quad + \beta_5 I[ESCentral]_i + \beta_6 I[WSCentral]_i + \beta_7 I[Mtn]_i + \beta_8 I[Pac]_i + b_{0m} + \varepsilon_{im}, \quad m = 1,2,\ldots,52, \end{aligned}$$

where y_{im} is the observation i for level m of grouping variable `Date`, β_j, j = 0, 1, ..., 8, are the fixed-effects coefficients, b_{0m} is the random effect for level m of the grouping variable `Date`, and ε_{im} is the observation error for observation i. The random effect has the prior distribution, $b \sim N(0,\sigma^2_b)$ and the error term has the distribution, $\varepsilon \sim N(0,\sigma^2)$.

```
lme = fitlme(flu2,'FluRate ~ 1 + Region + (1|Date)')
```

```
Linear mixed-effects model fit by ML

Model information:
    Number of observations             468
    Fixed effects coefficients           9
    Random effects coefficients         52
    Covariance parameters                2

Formula:
    FluRate ~ 1 + Region + (1|Date)
```

```
Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    318.71    364.35    -148.36          296.71

Fixed effects coefficients (95% CIs):
    Name                      Estimate    SE          tStat      DF     pValue        L
    '(Intercept)'               1.2233    0.096678     12.654    459     1.085e-31
    'Region_MidAtl'           0.010192    0.052221    0.19518    459       0.84534
    'Region_ENCentral'        0.051923    0.052221     0.9943    459        0.3206
    'Region_WNCentral'         0.23687    0.052221     4.5359    459    7.3324e-06
    'Region_SAtl'             0.075481    0.052221     1.4454    459       0.14902
    'Region_ESCentral'         0.33917    0.052221      6.495    459    2.1623e-10
    'Region_WSCentral'           0.069    0.052221     1.3213    459       0.18705
    'Region_Mtn'              0.046673    0.052221    0.89377    459       0.37191
    'Region_Pac'              -0.16013    0.052221    -3.0665    459     0.0022936

Random effects covariance parameters (95% CIs):
Group: Date (52 Levels)
    Name1               Name2               Type         Estimate    Lower     Upper
    '(Intercept)'       '(Intercept)'       'std'        0.6443      0.5297    0.7836

Group: Error
    Name            Estimate    Lower      Upper
    'Res Std'       0.26627     0.24878    0.285
```

The *p*-values 7.3324e-06 and 2.1623e-10 respectively show that the fixed effects of the flu rates in regions `WNCentral` and `ESCentral` are significantly different relative to the flu rates in region `NE`.

The confidence limits for the standard deviation of the random-effects term, σ^2_b, do not include 0 (0.5297, 0.78368), which indicates that the random-effects term is significant. You can also test the significance of the random-effects terms using the `compare` method.

The estimated value of an observation is the sum of the fixed effects and the random-effect value at the grouping variable level corresponding to that observation. For example, the estimated best linear unbiased predictor (BLUP) of the flu rate for region `WNCentral` in week 10/9/2005 is

$$\begin{aligned}\hat{y}_{WNCentral,10/9/2005} &= \hat{\beta}_0 + \hat{\beta}_3 I[WNCentral] + \hat{b}_{10/9/2005} \\ &= 1.2233 + 0.23687 - 0.1718 \\ &= 1.28837.\end{aligned}$$

This is the fitted conditional response, since it includes contribution to the estimate from both the fixed and random effects. You can compute this value as follows.

```
beta = fixedEffects(lme);
[~,~,STATS] = randomEffects(lme); % Compute the random-effects statistics (STATS)
STATS.Level = nominal(STATS.Level);
y_hat = beta(1) + beta(4) + STATS.Estimate(STATS.Level=='10/9/2005')
```

```
y_hat =

    1.2884
```

You can simply display the fitted value using the `fitted` method.

```
F = fitted(lme);
F(flu2.Date == '10/9/2005' & flu2.Region == 'WNCentral')
```

```
ans =

    1.2884
```

Compute the fitted marginal response for region `WNCentral` in week 10/9/2005.

```
F = fitted(lme,'Conditional',false);
F(flu2.Date == '10/9/2005' & flu2.Region == 'WNCentral')
```

```
ans =

    1.4602
```

Linear Mixed-Effects Model with a Random Slope

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower and cylinders, and potentially correlated random effect for intercept and acceleration grouped by model year. This model corresponds to

$$MPG_{im} = \beta_0 + \beta_1 Acc_i + \beta_2 HP + b_{0m} + b_{1m} Acc_{im} + \varepsilon_{im}, \quad m = 1,2,3,$$

with the random-effects terms having the following prior distribution

$$b_m = \begin{pmatrix} b_{0m} \\ b_{1m} \end{pmatrix} \sim N\left(0, \begin{pmatrix} \sigma_0^2 & \sigma_{0,1} \\ \sigma_{0,1} & \sigma_1^2 \end{pmatrix}\right),$$

where $D(\theta)$ is the covariance matrix.

First, prepare the design matrices for fitting the linear mixed-effects model.

```
X = [ones(406,1) Acceleration Horsepower];
Z = [ones(406,1) Acceleration];
Model_Year = nominal(Model_Year);
G = Model_Year;
```

Now, fit the model using `fitlmematrix` with the defined design matrices and grouping variables. Use the `'fminunc'` optimization algorithm.

```
lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept','Acceleration'}},'RandomEffectGroups',{'Model_Year'},...
'FitMethod','REML')
```

```
lme =


Linear mixed-effects model fit by REML

Model information:
    Number of observations             392
    Fixed effects coefficients           3
    Random effects coefficients         26
    Covariance parameters                4

Formula:
    y ~ Intercept + Acceleration + Horsepower + (Intercept + Acceleration | Model_Year)

Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    2202.9    2230.7    -1094.5          2188.9

Fixed effects coefficients (95% CIs):
    Name                 Estimate    SE           tStat      DF     pValue        Lowe
    'Intercept'            50.064      2.3176      21.602    389    1.4185e-68      45
    'Acceleration'        -0.57897     0.13843    -4.1825    389    3.5654e-05    -0.8
    'Horsepower'          -0.16958    0.0073242    -23.153    389    3.5289e-75    -0.1
```

```
Random effects covariance parameters (95% CIs):
Group: Model_Year (13 Levels)
    Name1                Name2                Type          Estimate    Lower      U
    'Intercept'          'Intercept'          'std'            3.72       1.5215
    'Acceleration'       'Intercept'          'corr'        -0.8769     -0.98275    -
    'Acceleration'       'Acceleration'       'std'          0.3593      0.19418

Group: Error
    Name             Estimate    Lower     Upper
    'Res Std'        3.6913      3.4331    3.9688
```

The fixed effects coefficients display includes the estimate, standard errors (`SE`), and the 95% confidence interval limits (`Lower` and `Upper`). The *p*-values for (`pValue`) indicate that all three fixed-effects coefficients are significant.

The confidence intervals for the standard deviations and the correlation between the random effects for intercept and acceleration do not include zeros, hence they seem significant. Use the `compare` method to test for the random effects.

Display the covariance matrix of the estimated fixed-effects coefficients.

```
lme.CoefficientCovariance
```

```
ans =

    5.3711   -0.2809   -0.0126
   -0.2809    0.0192    0.0005
   -0.0126    0.0005    0.0001
```

The diagonal elements show the variances of the fixed-effects coefficient estimates. For example, the variance of the estimate of the intercept is 5.3711. Note that the standard errors of the estimates are the square roots of the variances. For example, the standard error of the intercept is 2.3176, which is `sqrt(5.3711)`.

The off-diagonal elements show the correlation between the fixed-effects coefficient estimates. For example, the correlation between the intercept and acceleration is –0.2809 and the correlation between acceleration and horsepower is 0.0005.

Display the coefficient of determination for the model.

```
lme.Rsquared
```

```
ans =
```

```
    Ordinary: 0.7826
    Adjusted: 0.7815
```

The adjusted value is the R-squared value adjusted for the number of predictors in the model.

See Also

`fitlme` | `fitlmematrix`

linhyptest

Linear hypothesis test

Syntax

```
p = linhyptest(beta,COVB,c,H,dfe)
[p,t,r] = linhyptest(...)
```

Description

`p = linhyptest(beta,COVB,c,H,dfe)` returns the *p* value `p` of a hypothesis test on a vector of parameters. `beta` is a vector of *k* parameter estimates. `COVB` is the *k*-by-*k* estimated covariance matrix of the parameter estimates. `c` and `H` specify the null hypothesis in the form `H*b = c`, where `b` is the vector of unknown parameters estimated by `beta`. `dfe` is the degrees of freedom for the `COVB` estimate, or `Inf` if `COVB` is known rather than estimated.

`beta` is required. The remaining arguments have default values:

- `COVB = eye(k)`
- `c = zeros(k,1)`
- `H = eye(K)`
- `dfe = Inf`

If `H` is omitted, `c` must have *k* elements and it specifies the null hypothesis values for the entire parameter vector.

Note: The following functions return outputs suitable for use as the `COVB` input argument to `linhyptest`: `nlinfit`, `coxphfit`, `glmfit`, `mnrfit`, `regstats`, `robustfit`. `nlinfit` returns `COVB` directly; the other functions return `COVB` in `stats.covb`.

`[p,t,r] = linhyptest(...)` also returns the test statistic `t` and the rank `r` of the hypothesis matrix `H`. If `dfe` is `Inf` or is not given, `t*r` is a chi-square statistic with `r`

degrees of freedom . If `dfe` is specified as a finite value, `t` is an *F* statistic with `r` and `dfe` degrees of freedom.

`linhyptest` performs a test based on an asymptotic normal distribution for the parameter estimates. It can be used after any estimation procedure for which the parameter covariances are available, such as `regstats` or `glmfit`. For linear regression, the *p*-values are exact. For other procedures, the *p*-values are approximate, and may be less accurate than other procedures such as those based on a likelihood ratio.

Examples

Fit a multiple linear model to the data in `hald.mat`:

```
load hald
stats = regstats(heat,ingredients,'linear');
beta = stats.beta
beta =
   62.4054
    1.5511
    0.5102
    0.1019
   -0.1441
```

Perform an *F*-test that the last two coefficients are both 0:

```
SIGMA = stats.covb;
dfe = stats.fstat.dfe;
H = [0 0 0 1 0;0 0 0 0 1];
c = [0;0];
[p,F] = linhyptest(beta,SIGMA,c,H,dfe)
p =
    0.4668
F =
    0.8391
```

See Also

`regstats` | `glmfit` | `robustfit` | `mnrfit` | `nlinfit` | `coxphfit`

linkage

Agglomerative hierarchical cluster tree

Syntax

```
Z = linkage(X)
Z = linkage(X,method)
Z = linkage(X,method,metric)
Z = linkage(X,method,pdist_inputs)
Z = linkage(X,method,metric,'savememory',value)
Z = linkage(Y)
Z = linkage(Y,method)
```

Description

`Z = linkage(X)` returns a matrix `Z` that encodes a tree of hierarchical clusters of the rows of the real matrix `X`.

`Z = linkage(X,method)` creates the tree using the specified *`method`*, where *`method`* describes how to measure the distance between clusters.

`Z = linkage(X,method,metric)` performs clustering using the distance measure `metric` to compute distances between the rows of `X`.

`Z = linkage(X,method,pdist_inputs)` passes parameters to the `pdist` function, which is the function that computes the distance between rows of `X`.

`Z = linkage(X,method,metric,'savememory',value)` uses a memory-saving algorithm when *`value`* is `'true'`, and uses the standard algorithm when *`value`* is `'false'`.

`Z = linkage(Y)` uses a vector representation `Y` of a distance matrix. `Y` can be a distance matrix as computed by `pdist`, or a more general dissimilarity matrix conforming to the output format of `pdist`.

`Z = linkage(Y,method)` creates the tree using the specified *`method`*, where *`method`* describes how to measure the distance between clusters.

Input Arguments

X

Matrix with two or more rows. The rows represent observations, the columns represent categories or dimensions.

method

Algorithm for computing distance between clusters.

Method	Description
`'average'`	Unweighted average distance (UPGMA)
`'centroid'`	Centroid distance (UPGMC), appropriate for Euclidean distances only
`'complete'`	Furthest distance
`'median'`	Weighted center of mass distance (WPGMC), appropriate for Euclidean distances only
`'single'`	Shortest distance
`'ward'`	Inner squared distance (minimum variance algorithm), appropriate for Euclidean distances only
`'weighted'`	Weighted average distance (WPGMA)

Default: `'single'`

metric

Any distance metric that the `pdist` function accepts.

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in X is scaled by dividing by the corresponding element of the standard deviation `S=nanstd(X)`. To specify another value for `S`, use `D=pdist(X,'seuclidean',S)`.
`'cityblock'`	City block metric.

Metric	Description
`'minkowski'`	Minkowski distance. The default exponent is 2. To specify a different exponent, use `D = pdist(X,'minkowski',P)`, where `P` is a scalar positive value of the exponent.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist(X,'mahalanobis',C)`, where the matrix `C` is symmetric and positive definite.
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.

custom distance function	A distance function specified using @:
	`D = pdist(X,@distfun)`
	
	A distance function must be of form
	
	`d2 = distfun(XI,XJ)`
	taking as arguments a 1-by-n vector `XI`, corresponding to a single row of `X`, and an m2-by-n matrix `XJ`, corresponding to multiple rows of `X`. `distfun` must accept a matrix `XJ` with an arbitrary number of rows. `distfun` must return an m2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

Default: `'euclidean'`

`pdist_inputs`

A cell array of parameters accepted by the `pdist` function. For example, to set the *`metric`* to `minkowski` and use an exponent of `5`, set `pdist_inputs` to `{'minkowski',5}`.

`savememory`

A string, either `'on'` or `'off'`. When applicable, the `'on'` setting causes `linkage` to construct clusters without computing the distance matrix. `savememory` is applicable when:

- `linkage` is `'centroid'`, `'median'`, or `'ward'`
- `distance` is `'euclidean'` (default)

When `savememory` is `'on'`, `linkage` run time is proportional to the number of dimensions (number of columns of `X`). When `savememory` is `'off'`, `linkage` memory requirement is proportional to N^2, where `N` is the number of observations. So choosing the best (least-time) setting for `savememory` depends on the problem dimensions, number of observations, and available memory. The default `savememory` setting is a rough approximation of an optimal setting.

Default: `'on'` when `X` has 20 columns or fewer, or the computer does not have enough memory to store the distance matrix; otherwise `'off'`

`Y`

A vector of distances with the same format as the output of the `pdist` function:

- A row vector of length $m(m–1)/2$, corresponding to pairs of observations in a matrix `X` with m rows
- Distances arranged in the order (2,1), (3,1), ..., (m,1), (3,2), ..., (m,2), ..., (m,m–1))

`Y` can be a more general dissimilarity matrix conforming to the output format of `pdist`.

Output Arguments

`Z`

`Z` is a (`m` – 1)-by-3 matrix, where `m` is the number of observations in the original data. Columns 1 and 2 of `Z` contain cluster indices linked in pairs to form a binary tree. The

leaf nodes are numbered from 1 to `m`. Leaf nodes are the singleton clusters from which all higher clusters are built. Each newly-formed cluster, corresponding to row `Z(I,:)`, is assigned the index `m+I`. `Z(I,1:2)` contains the indices of the two component clusters that form cluster `m+I`. There are `m`-1 higher clusters which correspond to the interior nodes of the clustering tree. `Z(I,3)` contains the linkage distances between the two clusters merged in row `Z(I,:)`.

For example, suppose there are 30 initial nodes and at step 12 cluster 5 and cluster 7 are combined. Suppose their distance at that time is 1.5. Then `Z(12,:)` will be `[5, 7, 1.5]`. The newly formed cluster will have index 12 + 30 = 42. If cluster 42 appears in a later row, it means the cluster created at step 12 is being combined into some larger cluster.

Examples

Compare Cluster Assignments to Clusters

Load the sample data.

```
load fisheriris
```

Compute four clusters of the Fisher iris data using Ward linkage and ignoring species information.

```
Z = linkage(meas,'ward','euclidean');
c = cluster(Z,'maxclust',4);
```

See how the cluster assignments correspond to the three species.

```
crosstab(c,species)
```

```
ans =

     0    25     1
     0    24    14
     0     1    35
    50     0     0
```

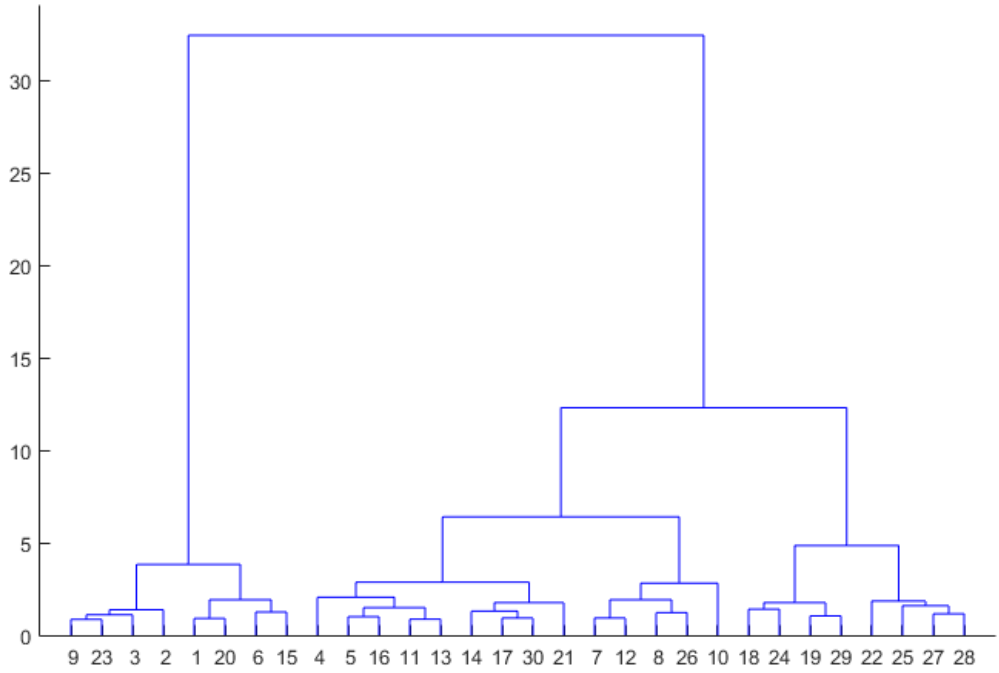
Display the first five rows of Z.

```
firstfive = Z(1:5,:)
```

```
firstfive =

  102.0000  143.0000         0
    8.0000   40.0000    0.1000
    1.0000   18.0000    0.1000
   10.0000   35.0000    0.1000
  129.0000  133.0000    0.1000
```

Create a dendrogram plot of `Z` .

```
dendrogram(Z)
```



Cluster Data and Plot the Result

Randomly generate the sample data with 20000 observations.

```
rng default; % For reproducibility
X = rand(20000,3);
```

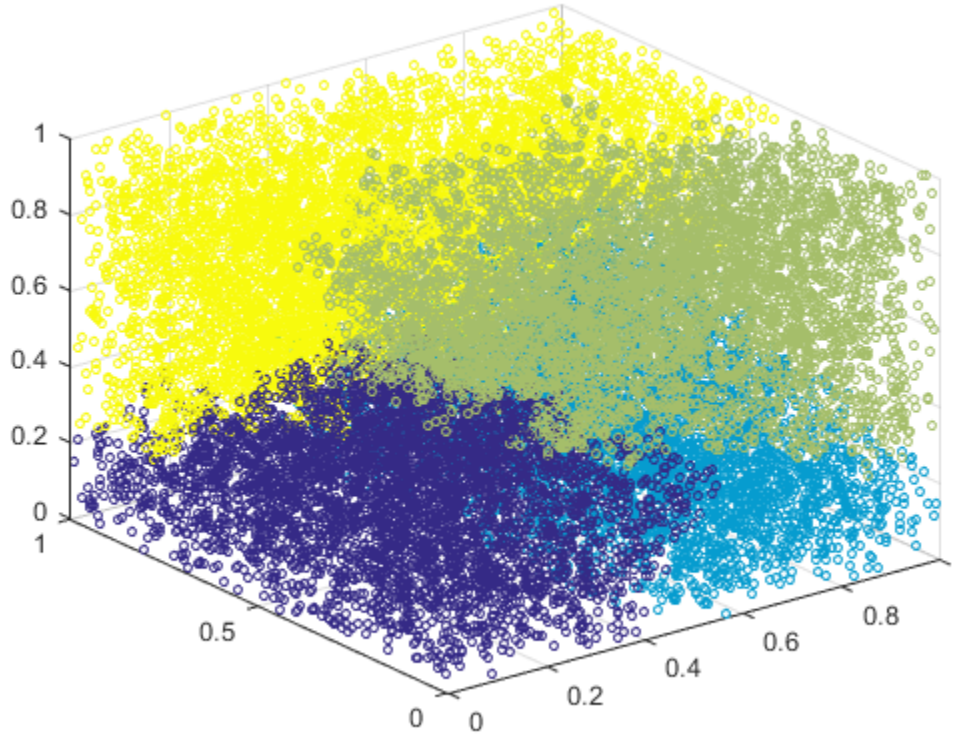
Create a hierarchical cluster tree using Ward's linkage.

```
Z = linkage(X,'ward','euclidean','savememory','on');
```

If you set `savememory` to `'off'` , you can get an out-of-memory error if your machine doesn't have enough memory to hold the distance matrix.

Cluster data into four groups and plot the result.

```
c = cluster(Z,'maxclust',4);
scatter3(X(:,1),X(:,2),X(:,3),10,c)
```



More About

Linkages

The following notation is used to describe the linkages used by the various methods:

- Cluster `r` is formed from clusters `p` and `q`.
- n_r is the number of objects in cluster r.
- x_{ri} is the `i`th object in cluster `r`.
- *Single linkage*, also called *nearest neighbor*, uses the smallest distance between objects in the two clusters:

$$d(r,s) = \min(dist(x_{ri}, x_{sj})), i \in (i,\ldots,n_r), j \in (1,\ldots,n_s)$$

- *Complete linkage*, also called *furthest neighbor*, uses the largest distance between objects in the two clusters:

$$d(r,s) = \max(dist(x_{ri}, x_{sj})), i \in (1,\ldots,n_r), j \in (1,\ldots,n_s)$$

- *Average linkage* uses the average distance between all pairs of objects in any two clusters:

$$d(r,s) = \frac{1}{n_r n_s} \sum_{i=1}^{n_r} \sum_{j=1}^{n_s} dist(x_{ri}, x_{sj})$$

- *Centroid linkage* uses the Euclidean distance between the centroids of the two clusters:

$$d(r,s) = \left\| \bar{x}_r - \bar{x}_s \right\|_2$$

where

$$\bar{x}_r = \frac{1}{n_r} \sum_{i=1}^{n_r} x_{ri}$$

- *Median linkage* uses the Euclidean distance between weighted centroids of the two clusters,

$$d(r,s) = \left\| \tilde{x}_r - \tilde{x}_s \right\|_2$$

where $\tilde{x}_r$ and $\tilde{x}_s$ are weighted centroids for the clusters *r* and *s*. If cluster *r* was created by combining clusters *p* and *q*, $\tilde{x}_r$ is defined recursively as

$$\tilde{x}_r = \frac{1}{2}(\tilde{x}_p + \tilde{x}_q)$$

- *Ward's linkage* uses the incremental sum of squares; that is, the increase in the total within-cluster sum of squares as a result of joining two clusters. The within-cluster

sum of squares is defined as the sum of the squares of the distances between all objects in the cluster and the centroid of the cluster. The sum of squares measure is equivalent to the following distance measure $d(r,s)$, which is the formula `linkage` uses:

$$d(r,s) = \sqrt{\frac{2n_r n_s}{(n_r + n_s)}} \left\| \bar{x}_r - \bar{x}_s \right\|_2,$$

where

- $\| \ \|_2$ is Euclidean distance
- $\bar{x}_r$ and $\bar{x}_s$ are the centroids of clusters r and s
- n_r and n_s are the number of elements in clusters r and s

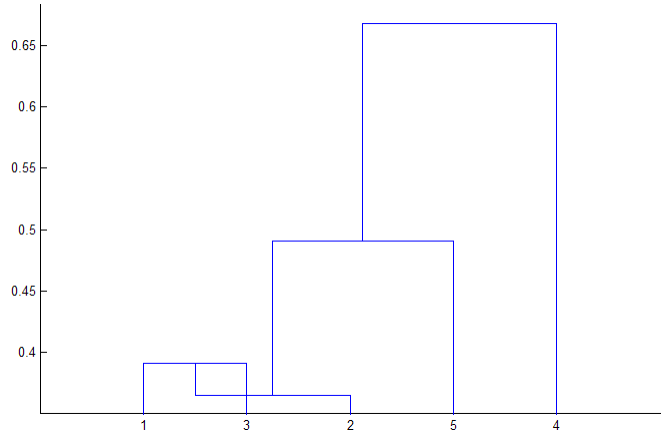
In some references the Ward linkage does not use the factor of 2 multiplying $n_r n_s$. The `linkage` function uses this factor so the distance between two singleton clusters is the same as the Euclidean distance.

- *Weighted average linkage* uses a recursive definition for the distance between two clusters. If cluster r was created by combining clusters p and q, the distance between r and another cluster s is defined as the average of the distance between p and s and the distance between q and s:

$$d(r,s) = \frac{\left(d(p,s) + d(q,s)\right)}{2}$$

Tips

- Computing `linkage(Y)` can be slow when `Y` is a vector representation of the distance matrix. For the `'centroid'`, `'median'`, and `'ward'` methods, `linkage` checks whether `Y` is a Euclidean distance. Avoid this time-consuming check by passing in `X` instead of `Y`.
- The `centroid` and `median` methods can produce a cluster tree that is not monotonic. This occurs when the distance from the union of two clusters, r and s, to a third cluster is less than the distance between r and s. In this case, in a dendrogram drawn with the default orientation, the path from a leaf to the root node takes some downward steps. To avoid this, use another method. The following image shows a nonmonotonic cluster tree.



In this case, cluster 1 and cluster 3 are joined into a new cluster, while the distance between this new cluster and cluster 2 is less than the distance between cluster 1 and cluster 3. This leads to a nonmonotonic tree.

- You can provide the output `Z` to other functions including `dendrogram` to display the tree, `cluster` to assign points to clusters, `inconsistent` to compute inconsistent measures, and `cophenet` to compute the cophenetic correlation coefficient.

See Also

`cluster` | `clusterdata` | `cophenet` | `dendrogram` | `inconsistent` | `kmeans` | `pdist` | `silhouette` | `squareform`

prob.LogisticDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Logistic probability distribution object

Description

`prob.LogisticDistribution` is an object consisting of parameters, a model description, and sample data for a logistic probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Logistic')` creates a logistic probability distribution object using the default parameter values.

`pd = makedist('Logistic','mu',mu,'sigma',sigma)` creates a logistic probability distribution object using the specified parameter values.

Input Arguments

`mu` — Mean

0 (default) | scalar value

Mean of the logistic distribution, specified as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

1 (default) | nonnegative scalar value

Scale parameter of the logistic distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

Properties

`mu` — Mean

scalar value

Mean of the logistic distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

nonnegative scalar value

Scale parameter of the logistic distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Logistic Distribution

The logistic distribution is used for growth models and in logistic regression. It has longer tails and a higher kurtosis than the normal distribution.

The logistic distribution uses the following parameters.

Parameter	Description	Support
`mu`	Mean	$-\infty < \mu < \infty$
`sigma`	Scale parameter	$\sigma \geq 0$

The probability density function (pdf) is

$$f(x \mid \mu,\sigma) = \frac{\exp\left\{\frac{x-\mu}{\sigma}\right\}}{\sigma\left(1+\exp\left\{\frac{x-\mu}{\sigma}\right\}\right)^2} \quad ; \quad -\infty < x < \infty.$$

Examples

Create a Logistic Distribution Object Using Default Parameters

Create a logistic distribution object using the default parameter values.

```
pd = makedist('Logistic')
```

```
pd =

  LogisticDistribution

  Logistic distribution
       mu = 0
    sigma = 1
```

Create a Logistic Distribution Object Using Specified Parameters

Create a logistic distribution object by specifying parameter values.

```
pd = makedist('Logistic', 'mu',2,'sigma',4)
```

```
pd =

  LogisticDistribution

  Logistic distribution
       mu = 2
    sigma = 4
```

Compute the standard deviation of the distribution.

```
s = std(pd)
```

```
s =
```

```
    7.2552
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Logistic Distribution"
- Class Attributes
- Property Attributes

prob.LoglogisticDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Loglogistic probability distribution object

Description

`prob.LoglogisticDistribution` is an object consisting of parameters, a model description, and sample data for a loglogistic probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Loglogistic')` creates a loglogistic probability distribution object using the default parameter values.

`pd = makedist('Loglogistic','mu',mu,'sigma',sigma)` creates a loglogistic probability distribution object using the specified parameter values .

Input Arguments

`mu` — Log mean

0 (default) | positive scalar value

Log mean for the loglogistic distribution, specified as a positive scalar value.

Data Types: `single` | `double`

`sigma` — Log scale parameter

1 (default) | positive scalar value

Log scale parameter for the loglogistic distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

`mu` — Log mean

positive scalar value

Log mean for the loglogistic distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`sigma` — Log scale parameter

positive scalar value

Log scale parameter for the loglogistic distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Loglogistic Distribution

The loglogistic distribution is closely related to the logistic distribution. If x is distributed loglogistically with parameters μ and σ, then $\log(x)$ is distributed logistically with mean and standard deviation. This distribution is often used in survival analysis to model events that experience an initial rate increase, followed by a rate decrease.

The loglogistic distribution uses the following parameters.

Parameter	Description	Support
`mu`	Log mean	$\mu > 0$
`sigma`	Log scale parameter	$\sigma > 0$

The probability density function (pdf) is

$$f(x \mid \mu,\sigma) = \frac{1}{\sigma}\frac{1}{x}\frac{e^z}{\left(1+e^z\right)^2} \quad ; \quad x \geq 0,$$

where $z = \dfrac{\log(x)-\mu}{\sigma}$.

Examples

Create a Loglogistic Distribution Object Using Default Parameters

Create a loglogistic distribution object using the default parameter values.

```
pd = makedist('Loglogistic')
```

```
pd =

  LoglogisticDistribution

  Log-Logistic distribution
       mu = 0
    sigma = 1
```

Create a Loglogistic Distribution Object Using Specified Parameters

Create a loglogistic distribution object by specifying the parameter values.

```
pd = makedist('Loglogistic','mu',5,'sigma',2)
```

```
pd =

  LoglogisticDistribution

  Log-Logistic distribution
       mu = 5
    sigma = 2
```

Generate random numbers from the loglogistic distribution and compute their log values.

```
rng(19) % for reproducibility
x = random(pd,10000,1);
logx = log(x);
```

Compute the mean of the log values.

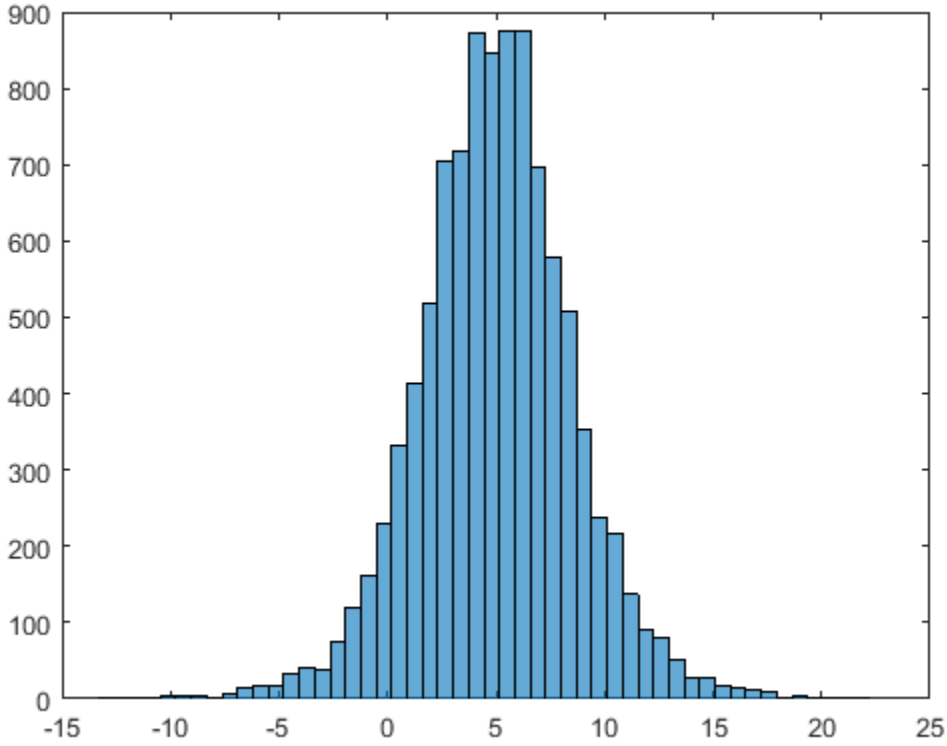
```
m = mean(logx)
```

```
m =

    4.9828
```

The mean of the log of `x` is equal to the `mu` parameter of `x`, since `x` has a loglogistic distribution.

Plot `logx`.

```
histogram(logx,50)
```



The plot shows that the log values of `x` have a logistic distribution.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Working with Probability Distributions" on page 5-3
- "Loglogistic Distribution"
- Class Attributes
- Property Attributes

logncdf

Lognormal cumulative distribution function

Syntax

```
p = logncdf(x,mu,sigma)
[p,plo,pup] = logncdf(x,mu,sigma,pcov,alpha)
[p,plo,pup] = logncdf( ___ ,'upper')
```

Description

`p = logncdf(x,mu,sigma)` returns values at `x` of the lognormal cdf with distribution parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `x`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `x`, `mu`, or `sigma` is expanded to a constant array with the same dimensions as the other inputs.

`[p,plo,pup] = logncdf(x,mu,sigma,pcov,alpha)` returns confidence bounds for `p` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated `parameters`. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `plo` and `pup` are arrays of the same size as `p` containing the lower and upper confidence bounds.

`[p,plo,pup] = logncdf( ___ ,'upper')` returns the complement of the lognormal cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities. You can use `'upper'` with any of the previous syntaxes.

`logncdf` computes confidence bounds for `p` using a normal approximation to the distribution of the estimate

$$\frac{x-\hat{\mu}}{\hat{\sigma}}$$

and then transforming those bounds to the scale of the output `p`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov`

from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The lognormal cdf is

$$p = F(x \mid \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_0^x \frac{e^{\frac{-(\ln(t)-\mu)^2}{2\sigma^2}}}{t} dt$$

Examples

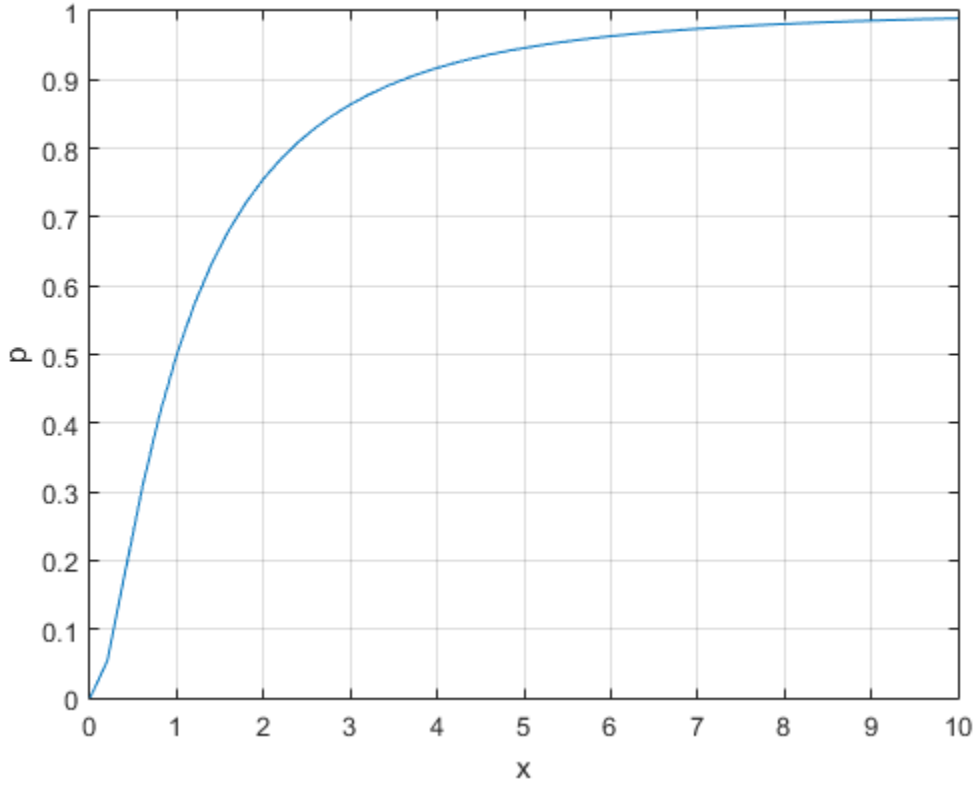
Compute the Lognormal Distribution cdf

Compute the cdf of a lognormal distribution with `mu = 0` and `sigma = 1`.

```
x = (0:0.2:10);
y = logncdf(x,0,1);
```

Plot the cdf.

```
plot(x,y);
grid;
xlabel('x');
ylabel('p');
```



More About

- "Lognormal Distribution" on page B-95

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 102–105.

See Also

cdf | lognpdf | logninv | lognstat | lognfit | lognlike | lognrnd

lognfit

Lognormal parameter estimates

Syntax

```
parmhat = lognfit(data)
[parmhat,parmci] = lognfit(data)
[parmhat,parmci] = lognfit(data,alpha)
[...] = lognfit(data,alpha,censoring)
[...] = lognfit(data,alpha,censoring,freq)
[...] = lognfit(data,alpha,censoring,freq,options)
```

Description

`parmhat = lognfit(data)` returns a vector of maximum likelihood estimates `parmhat(1) = mu` and `parmhat(2) = sigma` of parameters for a lognormal distribution fitting `data`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution.

`[parmhat,parmci] = lognfit(data)` returns 95% confidence intervals for the parameter estimates `mu` and `sigma` in the 2-by-2 matrix `parmci`. The first column of the matrix contains the lower and upper confidence bounds for parameter `mu`, and the second column contains the confidence bounds for parameter `sigma`.

`[parmhat,parmci] = lognfit(data,alpha)` returns 100(1 - `alpha`) % confidence intervals for the parameter estimates, where `alpha` is a value in the range `(0 1)` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = lognfit(data,alpha,censoring)` accepts a Boolean vector `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = lognfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. Typically, `freq` contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = lognfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates when there is censoring. The lognormal fit function accepts an `options` structure which can be created using the function `statset`. Enter `statset('lognfit')` to see the names and default values of the parameters that `lognfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Note: With no censoring, `lognfit` computes `sigma` using the square root of the unbiased estimator of the variance. With censoring, `sigma` is the maximum likelihood estimate.

Examples

This example generates 100 independent samples of lognormally distributed data with $\mu = 0$ and $\sigma = 3$. `parmhat` estimates μ and σ and `parmci` gives 99% confidence intervals around `parmhat`. Notice that `parmci` contains the true values of μ and σ.

```
data = lognrnd(0,3,100,1);
[parmhat,parmci] = lognfit(data,0.01)
parmhat =
  -0.2480  2.8902
parmci =
  -1.0071  2.4393
   0.5111  3.5262
```

More About

- “Lognormal Distribution” on page B-95

See Also

`mle` | `lognlike` | `lognpdf` | `logncdf` | `logninv` | `lognstat` | `lognrnd`

logninv

Lognormal inverse cumulative distribution function

Syntax

```
X = logninv(P,mu,sigma)
[X,XLO,XUP] = logninv(P,mu,sigma,pcov,alpha)
```

Description

`X = logninv(P,mu,sigma)` returns values at `P` of the inverse lognormal cdf with distribution parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `mu`, or `sigma` is expanded to a constant array with the same dimensions as the other inputs.

`[X,XLO,XUP] = logninv(P,mu,sigma,pcov,alpha)` returns confidence bounds for `X` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

`logninv` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\hat{\mu} + \hat{\sigma} q$$

where q is the `P`th quantile from a normal distribution with mean 0 and standard deviation 1. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The lognormal inverse function is defined in terms of the lognormal cdf as

$$x = F^{-1}(p \mid \mu,\sigma) = \{x : F(x \mid \mu,\sigma) = p\}$$

where

$$p = F(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_0^x \frac{e^{\frac{-(\ln(t)-\mu)^2}{2\sigma^2}}}{t} dt$$

Examples

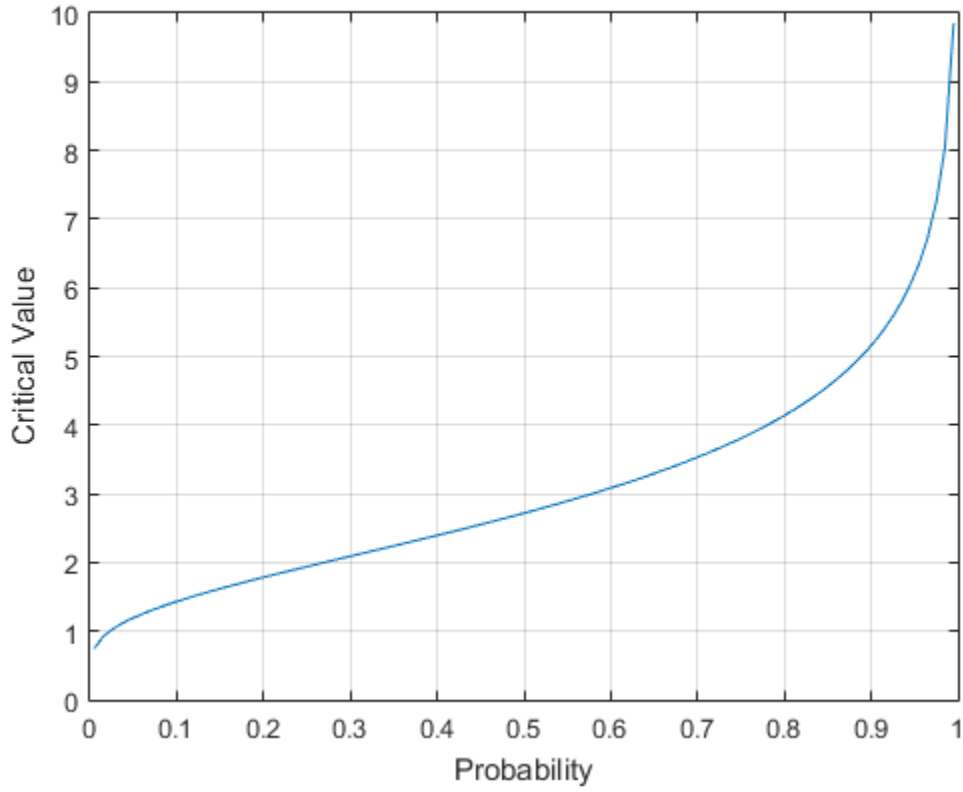
Compute the Lognormal Distribution Inverse cdf

Compute the inverse cdf of a lognormal distribution with `mu = 0` and `sigma = 0.5`.

```
p = (0.005:0.01:0.995);
crit = logninv(p,1,0.5);
```

Plot the inverse cdf.

```
figure;
plot(p,crit)
xlabel('Probability');
ylabel('Critical Value');
grid
```



More About

- "Lognormal Distribution" on page B-95

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. Hoboken, NJ: Wiley-Interscience, 2000. pp. 102–105.

See Also

`icdf` | `logncdf` | `lognpdf` | `lognstat` | `lognfit` | `lognlike` | `lognrnd`

lognlike

Lognormal negative log-likelihood

Syntax

```
nlogL = lognlike(params,data)
[nlogL,avar] = lognlike(params,data)
[...] = lognlike(params,data,censoring)
[...] = lognlike(params,data,censoring,freq)
```

Description

`nlogL = lognlike(params,data)` returns the negative log-likelihood of `data` for the lognormal distribution with parameters `params`. `params(1)` is the mean of the associated normal distribution, `mu`, and `params(2)` is the standard deviation of the associated normal distribution, `sigma`. The values of `mu` and `sigma` are scalars, and the output `nlogL` is a scalar.

`[nlogL,avar] = lognlike(params,data)` returns the inverse of Fisher's information matrix. If the input parameter value in `params` is the maximum likelihood estimate, `avar` is its asymptotic variance. `avar` is based on the observed Fisher's information, not the expected information.

`[...] = lognlike(params,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = lognlike(params,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

More About

- “Lognormal Distribution” on page B-95

See Also

`lognfit` | `lognpdf` | `logncdf` | `logninv` | `lognstat` | `lognrnd`

prob.LognormalDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Lognormal probability distribution object

Description

`prob.LognormalDistribution` is an object consisting of parameters, a model description, and sample data for a lognormal probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Lognormal')` creates a lognormal probability distribution object using the default parameter values.

`pd = makedist('Lognormal','mu',mu,'sigma',sigma)` creates a lognormal probability distribution object using the specified parameter values.

Input Arguments

`mu` — Log mean

`0` (default) | scalar value

Log mean for the lognormal distribution, specified as a scalar value. `mu` is the mean of the log of *x*, when *x* has a lognormal distribution.

Data Types: `single` | `double`

`sigma` — Log standard deviation

`1` (default) | nonnegative scalar value

Log standard deviation for the lognormal distribution, specified as a nonnegative scalar value. `sigma` is the standard deviation of the log of *x*, when *x* has a lognormal distribution.

Data Types: `single` | `double`

Properties

`mu` — Log mean

scalar value

Log mean for the lognormal distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Log standard deviation

nonnegative scalar value

Log standard deviation for the lognormal distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object

pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Lognormal Distribution

The lognormal distribution is closely related to the normal distribution. If x is distributed lognormally with parameters μ and σ, then $\log(x)$ is distributed normally with mean μ and standard deviation σ. The lognormal distribution is applicable when the quantity of interest must be positive, since $\log(x)$ exists only when x is positive.

The lognormal distribution uses the following parameters.

Parameter	Description	Support
`mu`	Log mean	$-\infty < \mu < \infty$
`sigma`	Log standard deviation	$\sigma \geq 0$

The probability density function (pdf) of the lognormal distribution is

$$f(x \mid \mu,\sigma) = \frac{1}{x\sigma\sqrt{2\pi}} \exp\left\{\frac{-(\ln x - \mu)^2}{2\sigma^2}\right\} \quad ; \quad x > 0 .$$

Examples

Create a Lognormal Distribution Object Using Default Parameters

Create a lognormal distribution object using the default parameter values.

```
pd = makedist('Lognormal')
```

```
pd =

  LognormalDistribution

  Lognormal distribution
       mu = 0
    sigma = 1
```

Create a Lognormal Distribution Object Using Specified Parameters

Create a lognormal distribution object by specifying the parameter values.

```
pd = makedist('Lognormal','mu',5,'sigma',2)
```

```
pd =

  LognormalDistribution
```

```
  Lognormal distribution
       mu = 5
    sigma = 2
```

Compute the mean of the lognormal distribution.

```
mean(pd)
```

```
ans =

   1.0966e+03
```

The mean of the lognormal distribution is not equal to the `mu` parameter.

Generate random numbers from the lognormal distribution and compute their log values.

```
rng(47);  % for reproducibility
x = random(pd,10000,1);
logx = log(x);
```

Compute the mean of the log values.

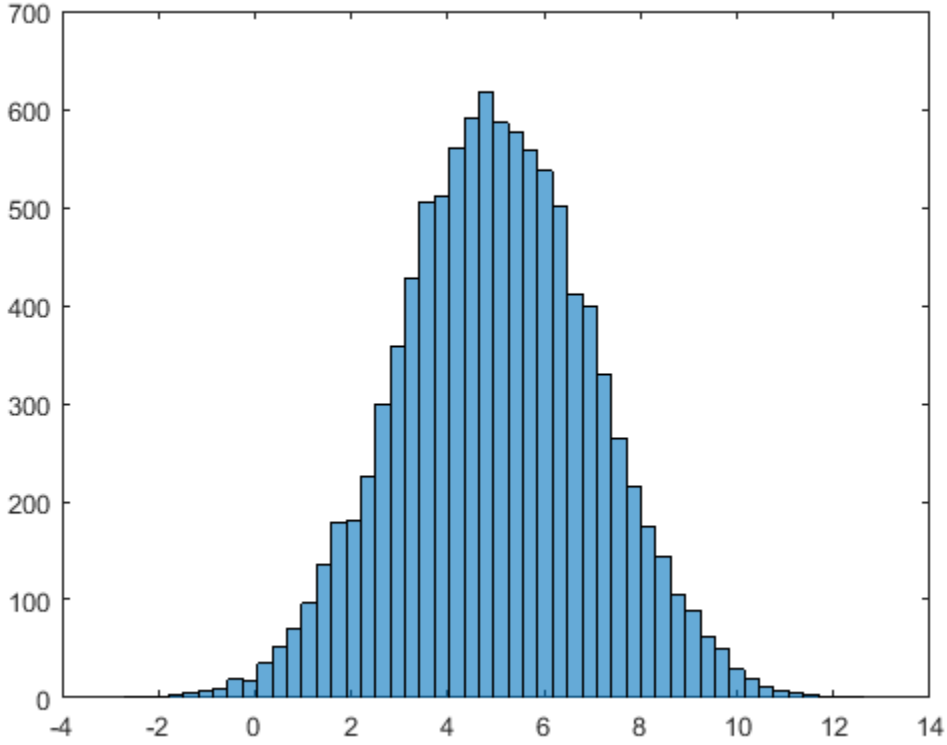
```
m = mean(logx)
```

```
m =

    4.9999
```

The mean of the log of `x` is equal to the `mu` parameter of `x`, since `x` has a lognormal distribution.

Plot `logx`.

```
histogram(logx,50)
```



The plot shows that the log values of `x` are normally distributed with a mean equal to 5 and a standard deviation equal to 2.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Lognormal Distribution"
- Class Attributes
- Property Attributes

lognpdf

Lognormal probability density function

Syntax

```
Y = lognpdf(X,mu,sigma)
```

Description

`Y = lognpdf(X,mu,sigma)` returns values at `X` of the lognormal pdf with distribution parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `X`, `mu`, or `sigma` is expanded to a constant array with the same dimensions as the other inputs.

The lognormal pdf is

$$y = f(x \mid \mu,\sigma) = \frac{1}{x\sigma\sqrt{2\pi}} e^{\frac{-(\ln x-\mu)^2}{2\sigma^2}}$$

The normal and lognormal distributions are closely related. If X is distributed lognormally with parameters μ and σ, then $\log(X)$ is distributed normally with mean μ and standard deviation σ.

The mean m and variance v of a lognormal random variable are functions of μ and σ that can be calculated with the `lognstat` function. They are:

$$m = \exp\left(\mu + \sigma^2 / 2\right)$$
$$v = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right)$$

So, a lognormal distribution with mean m and variance v has parameters

$$\mu = \log\left(m^2 / \sqrt{v + m^2} \right)$$
$$\sigma = \sqrt{\log\left(v / m^2 + 1 \right)}$$

If you do not know the population mean and variance, m and v, for the lognormal distribution, you can estimate μ and σ in the following way:

```
mu = mean(log(X))
sigma = std(log(X))
```

The lognormal distribution is applicable when the quantity of interest must be positive, since log(X) exists only when X is positive.

Examples

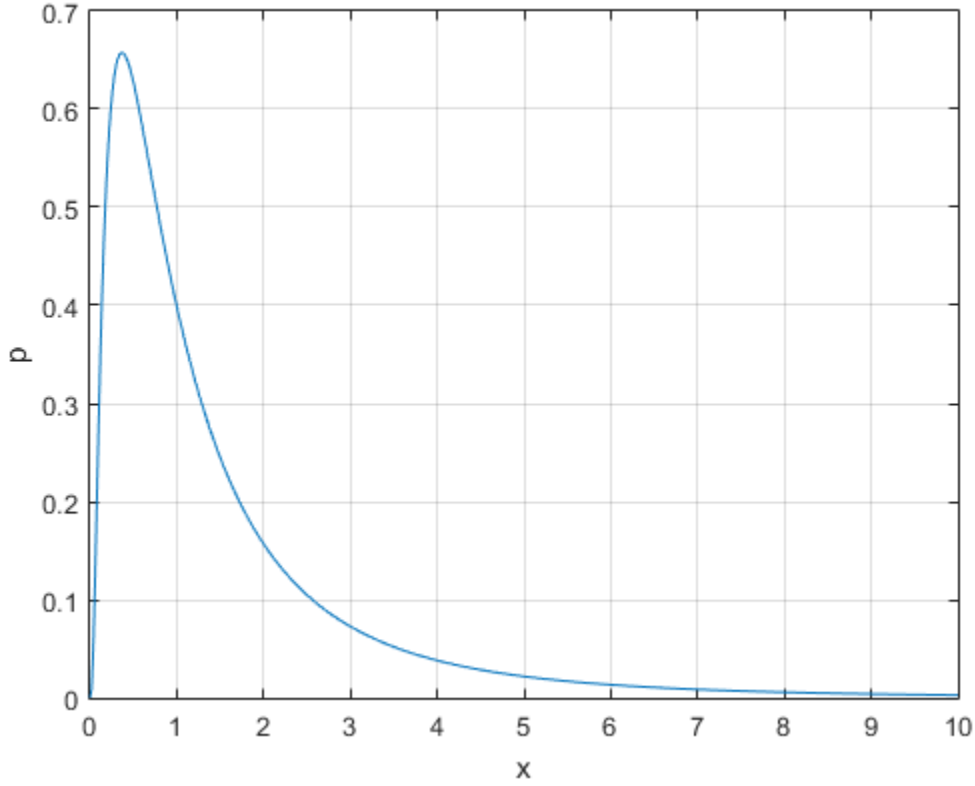
Compute the Lognormal Distribution pdf

Compute the pdf of a lognormal distribution with `mu = 0` and `sigma = 1`.

```
x = (0:0.02:10);
y = lognpdf(x,0,1);
```

Plot the pdf.

```
plot(x,y); grid;
xlabel('x'); ylabel('p')
```



More About

- "Lognormal Distribution" on page B-95

References

[1] Mood, A. M., F. A. Graybill, and D. C. Boes. *Introduction to the Theory of Statistics.* 3rd ed., New York: McGraw-Hill, 1974. pp. 540–541.

See Also

pdf | logncdf | logninv | lognstat | lognfit | lognlike | lognrnd

lognrnd

Lognormal random numbers

Syntax

```
R = lognrnd(mu,sigma)
R = lognrnd(mu,sigma,m,n,...)
R = lognrnd(mu,sigma,[m,n,...])
```

Description

`R = lognrnd(mu,sigma)` returns an array of random numbers generated from the lognormal distribution with parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

`R = lognrnd(mu,sigma,m,n,...)` or `R = lognrnd(mu,sigma,[m,n,...])` generates an `m`-by-`n`-by-... array. The `mu`, `sigma` parameters can each be scalars or arrays of the same size as `R`.

The normal and lognormal distributions are closely related. If X is distributed lognormally with parameters μ and σ, then $\log(X)$ is distributed normally with mean μ and standard deviation σ.

The mean m and variance v of a lognormal random variable are functions of μ and σ that can be calculated with the `lognstat` function. They are:

$$m = \exp\left(\mu + \sigma^2 / 2\right)$$
$$v = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right)$$

A lognormal distribution with mean m and variance v has parameters

$$\mu = \log\left(m^2 / \sqrt{v + m^2} \right)$$

$$\sigma = \sqrt{\log\left(v / m^2 + 1 \right)}$$

Examples

Generate one million lognormally distributed random numbers with mean 1 and variance 2:

```
m = 1;
v = 2;
mu = log((m^2)/sqrt(v+m^2));
sigma = sqrt(log(v/(m^2)+1));

[M,V]= lognstat(mu,sigma)
M =
     1
V =
    2.0000

X = lognrnd(mu,sigma,1,1e6);

MX = mean(X)
MX =
    0.9974
VX = var(X)
VX =
    1.9776
```

More About

- “Lognormal Distribution” on page B-95

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. Hoboken, NJ: Wiley-Interscience, 2000. pp. 102–105.

See Also

`random` | `lognpdf` | `logncdf` | `logninv` | `lognstat` | `lognfit` | `lognlike` | `normrnd`

lognstat

Lognormal mean and variance

Syntax

```
[M,V] = lognstat(mu,sigma)
```

Description

`[M,V] = lognstat(mu,sigma)` returns the mean of and variance of the lognormal distribution with parameters `mu` and `sigma`. `mu` and `sigma` are the mean and standard deviation, respectively, of the associated normal distribution. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

The normal and lognormal distributions are closely related. If X is distributed lognormally with parameters μ and σ, then $\log(X)$ is distributed normally with mean μ and standard deviation σ.

The mean m and variance v of a lognormal random variable are functions of μ and σ that can be calculated with the `lognstat` function. They are:

$$m = \exp\left(\mu + \sigma^2 / 2\right)$$
$$v = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right)$$

A lognormal distribution with mean m and variance v has parameters

$$\mu = \log\left(m^2 / \sqrt{v + m^2}\right)$$
$$\sigma = \sqrt{\log\left(v / m^2 + 1\right)}$$

Examples

Generate one million lognormally distributed random numbers with mean 1 and variance 2:

```
m = 1;
v = 2;
mu = log((m^2)/sqrt(v+m^2));
sigma = sqrt(log(v/(m^2)+1));

[M,V]= lognstat(mu,sigma)
M =
     1
V =
    2.0000

X = lognrnd(mu,sigma,1,1e6);

MX = mean(X)
MX =
    0.9974
VX = var(X)
VX =
    1.9776
```

More About

- “Lognormal Distribution” on page B-95

References

[1] Mood, A. M., F. A. Graybill, and D. C. Boes. *Introduction to the Theory of Statistics.* 3rd ed., New York: McGraw-Hill, 1974. pp. 540–541.

See Also

`lognpdf` | `logncdf` | `logninv` | `lognfit` | `lognlike` | `lognrnd`

logP

Class: CompactClassificationDiscriminant

Log unconditional probability density for discriminant analysis classifier

Syntax

```
lp = logP(obj,Xnew)
```

Description

`lp = logP(obj,Xnew)` returns the log of the unconditional probability density of each row of `Xnew`, computed using the discriminant analysis model `obj`.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

`Xnew`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `Xnew` must equal the number of predictors in `obj`.

Output Arguments

`lp`

Column vector with the same number of rows as `Xnew`. Each entry is the logarithm of the unconditional probability density of the corresponding row of `Xnew`.

Definitions

Unconditional Probability Density

The unconditional probability density of a point x of a discriminant analysis model is

$$P(x) = \sum_{k=1}^{K} P(x,k),$$

where $P(x,k)$ is the conditional density of the model at x for class k, when the total number of classes is K.

The conditional density $P(x,k)$ is
$P(x,k) = P(k)P(x \mid k)$,

where $P(k)$ is the prior probability of class k, and $P(x \mid k)$ is the conditional density of x given class k. The conditional density function of the multivariate normal with mean μ_k and covariance Σ_k at a point x is

$$P(x \mid k) = \frac{1}{\left(2\pi|\Sigma_k|\right)^{1/2}} \exp\left(-\frac{1}{2}(x-\mu_k)^T \Sigma_k^{-1}(x-\mu_k)\right),$$

where $|\Sigma_k|$ is the determinant of Σ_k, and Σ_k^{-1} is the inverse matrix.

Examples

Compute the Log Unconditional Probabiltiy Density of an Observation

Construct a discriminant analysis classifier for Fisher's iris data, and examine its prediction for an average measurement.

Load Fisher's iris data and construct a default discriminant analysis classifier.

```
load fisheriris
Mdl = fitcdiscr(meas,species);
```

Find the log probability of the discriminant model applied to an average iris.

```
logPAverage = logP(Mdl,mean(meas))

logPAverage =

   -1.7254
```

See Also

`CompactClassificationDiscriminant` | `fitcdiscr` | `mahal`

More About

- "Discriminant Analysis" on page 15-3

logP

Class: CompactClassificationNaiveBayes

Log unconditional probability density for naive Bayes classifier

Syntax

```
lp = logP(Mdl,X)
```

Description

`lp = logP(Mdl,X)` returns the log unconditional probability density of the observations (rows) in `X` using the naive Bayes model `Mdl`.

You can use `lp` to identify outliers in the training data.

Input Arguments

`Mdl` — Naive Bayes classifier

`ClassificationNaiveBayes` model | `CompactClassificationNaiveBayes` model

Naive Bayes classifier, specified as a `ClassificationNaiveBayes` model or `CompactClassificationNaiveBayes` model returned by `fitcnb` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained `Mdl`.

Data Types: `double` | `single`

Output Arguments

`lp` — Log of unconditional probability density

numeric column vector

Log of the unconditional probability density of the predictors, returned as a numeric column vector. `lp` has as many elements as rows in X, and each element is the log probability density of the corresponding row in `X`.

If any rows in X contain at least one `NaN`, then the corresponding element of `lp` is `NaN`.

Definitions

Unconditional Probability Density

The *unconditional probability density* of the predictors is its distribution marginalized over the classes.

In other words, the unconditional probability density is

$$P(X_1,..,X_P) = \sum_{k=1}^{K} P(X_1,..,X_P,Y=k) = \sum_{k=1}^{K} P(X_1,..,X_P \mid y=k)\pi(Y=k),$$

where $\pi(Y=k)$ is the class prior probability. The conditional distribution of the data given the class ($P(X_1,..,X_P \mid y=k)$) and the class prior probability distributions are training options (i.e., are specified when training the classifier).

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Examples

Compute Unconditional Probability Densities of Observations

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
```

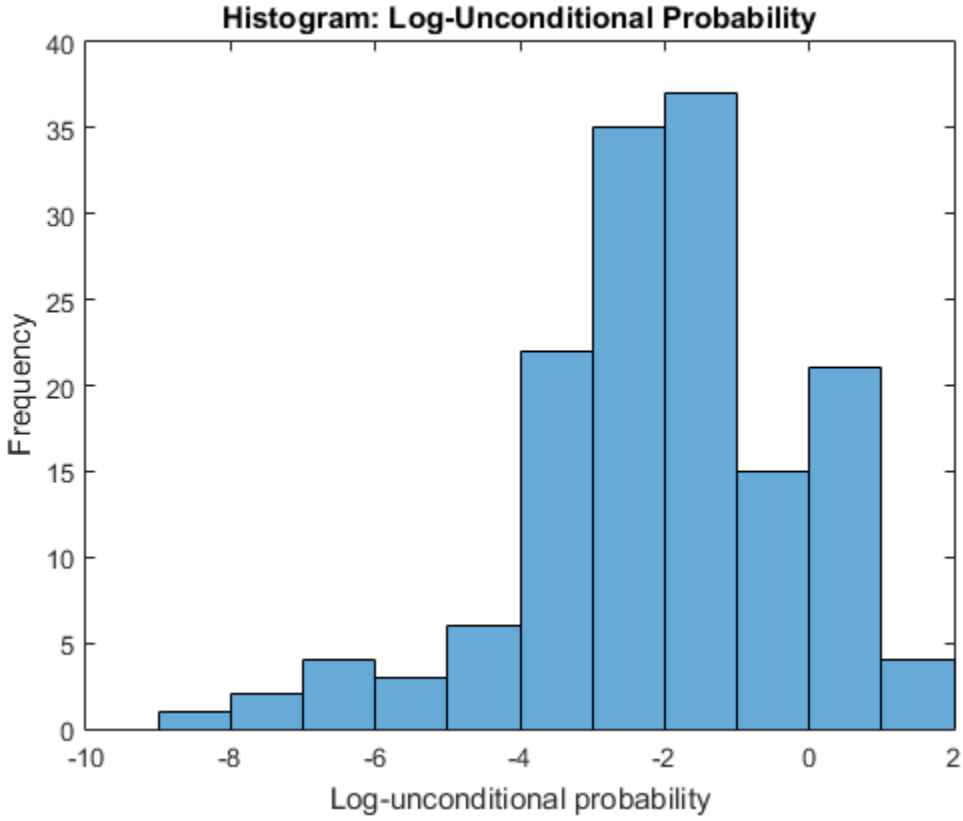
Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally normally distributed given its label.

```
Mdl = fitcnb(X,Y,'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier.

Compute the unconditional probability densities of the in-sample observations.

```
lp = logP(Mdl,X);
histogram(lp)
xlabel 'Log-unconditional probability'
ylabel 'Frequency'
title 'Histogram: Log-Unconditional Probability'
```



Identify indices of observations having log-unconditional probability less than -7.

```
idx = find(lp < -7)
```

```
idx =

    61
   118
   132
```

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `fitcnb` | `predict`

More About

- “Naive Bayes Classification” on page 15-31

loss

Class: ClassificationKNN

Loss of *k*-nearest neighbor classifier

Syntax

```
L = loss(mdl,X,Y)
L = loss(mdl,X,Y,Name,Value)
```

Description

`L = loss(mdl,X,Y)` returns a scalar representing how well `mdl` classifies the data in `X`, when `Y` contains the true classifications.

When computing the loss, `loss` normalizes the class probabilities in Y to the class probabilities used for training, stored in the `Prior` property of mdl.

`L = loss(mdl,X,Y,Name,Value)` returns the loss with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

`X` — Matrix of predictor values

matrix

Matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y` — Categorical variables
categorical array | cell array of strings | character array | logical vector | numeric vector

A categorical array, cell array of strings, character array, logical vector, or a numeric vector with the same number of rows as `X`. Each row of `Y` represents the classification of the corresponding row of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'lossfun '`

Function handle or string representing a loss function. The built-in loss functions are:

- `'binodeviance'` — See "Loss Functions" on page 22-2671.
- `'classiferror'` — Fraction of misclassified observations. See "Loss Functions" on page 22-2671.
- `'exponential'` — See "Loss Functions" on page 22-2671.
- `'hinge'` — See "Loss Functions" on page 22-2671.
- `'mincost'` — Smallest misclassification cost as given by the mdl`.Cost` matrix. See "Loss Functions" on page 22-2671.

You can write your own loss function using the syntax described in "Loss Functions" on page 22-2671.

Default: `'mincost'`

`'weights'`

Numeric vector of length `N`, where `N` is the number of rows of X. `weights` are nonnegative. `loss` normalizes the weights so that observation weights in each class sum to the prior probability of that class. When you supply `weights`, `loss` computes weighted classification loss.

Default: `ones(N,1)`

Output Arguments

`L`

Classification error, a scalar. The meaning of the error depends on the values in `weights` and `lossfun`. See "Classification Error" on page 22-2677.

Definitions

Classification Error

The default classification error is the fraction of data X that mdl misclassifies, where Y represents the true classifications.

The weighted classification error is the sum of weight i times the Boolean value that is `1` when mdl misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

  $$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

  $$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'classiferror'` — Predict the label with the largest posterior probability. The loss is then the fraction of misclassified observations.

- `'hinge'` — Classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

  where:

  - w_j is weight j.
  - For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
  - $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file in this form:

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in the classifier, represented in the `ClassNames` property.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in the `ClassNames` property.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST = ones(K) - eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.

- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

True Misclassification Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation.

You can set the true misclassification cost per class in the `Cost` name-value pair when you run `fitcknn`. `Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

Expected Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation. The third output of `predict` is the expected misclassification cost per observation.

Suppose you have `Nobs` observations that you want to classify with a trained classifier `mdl`. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row. The command

```
[label,score,cost] = predict(mdl,Xnew)
```

returns, among other outputs, a `cost` matrix of size `Nobs`-by-`K`. Each row of the `cost` matrix contains the expected (average) cost of classifying the observation into each of the `K` classes. `cost(n,k)` is

$$\sum_{i=1}^{K} \hat{P}(i \mid Xnew(n)) C(k \mid i),$$

where

- K is the number of classes.
- $\hat{P}(i \mid Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.

- $C(k|i)$ is the true misclassification cost of classifying an observation as k when its true class is i.

Examples

Loss Calculation

Construct a k-nearest neighbor classifier for the Fisher iris data, where $k = 5$.

Load the data.

```
load fisheriris
```

Construct a classifier for 5-nearest neighbors.

```
mdl = fitcknn(meas,species,'NumNeighbors',5);
```

Examine the loss of the classifier for a mean observation classified `'versicolor'`.

```
X = mean(meas);
Y = {'versicolor'};
L = loss(mdl,X,Y)
```

```
L =

     0
```

The classifier has no doubt that `'versicolor'` is the correct classification (all five nearest neighbors classify as `'versicolor'`).

- "Examine the Quality of a KNN Classifier" on page 16-29
- "Predict Classification Based on a KNN Classifier" on page 16-30
- "Modify a KNN Classifier" on page 16-30

See Also

`ClassificationKNN` | `edge` | `fitcknn` | `margin`

More About

- "Classification Using Nearest Neighbors" on page 16-8

loss

Class: CompactClassificationDiscriminant

Classification error

Syntax

```
L = loss(obj,X,Y)
L = loss(obj,X,Y,Name,Value)
```

Description

`L = loss(obj,X,Y)` returns a scalar representing how well `obj` classifies the data in `X`, when `Y` contains the true classifications.

When computing the loss, `loss` normalizes the class probabilities in Y to the class probabilities used for training, stored in the `Prior` property of obj.

`L = loss(obj,X,Y,Name,Value)` returns the loss with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `fitcdiscr`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

`Y`

Class labels, with the same data type as exists in `obj`. The number of elements of `Y` must equal the number of rows of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'lossfun '`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-2677.
- `'classiferror'` — Fraction of misclassified observations. See "Loss Functions" on page 22-2677.
- `'exponential'` — See "Loss Functions" on page 22-2677.
- `'hinge'` — See "Loss Functions" on page 22-2677.
- `'mincost'` — Smallest misclassification cost as given by the obj`.Cost` matrix. See "Loss Functions" on page 22-2677.

You can write your own loss function using the syntax described in "Loss Functions" on page 22-2677.

Default: `'mincost'`

`'weights'`

Numeric vector of length `N`, where `N` is the number of rows of X. `weights` are nonnegative. `loss` normalizes the weights so that observation weights in each class sum to the prior probability of that class. When you supply `weights`, `loss` computes weighted classification loss.

Default: `ones(N,1)`

Output Arguments

`L`

Classification error, a scalar. The meaning of the error depends on the values in `weights` and `lossfun`. See "Classification Error" on page 22-2677.

Definitions

Classification Error

The default classification error is the fraction of data X that obj misclassifies, where Y represents the true classifications.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when obj misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'classiferror'` — Predict the label with the largest posterior probability. The loss is then the fraction of misclassified observations.
- `'hinge'` — Classification error measure that has the form

$$L=\frac{\sum_{j=1}^{n} w_j \max\left\{0,1-y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file in this form:

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in the classifier, represented in the `ClassNames` property.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in the `ClassNames` property.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST = ones(K) - eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

Posterior Probability

The posterior probability that a point z belongs to class j is the product of the prior probability and the multivariate normal density. The density function of the multivariate normal with mean μ_j and covariance Σ_j at a point z is

$$P(x \mid k) = \frac{1}{\left(2\pi|\Sigma_k|\right)^{1/2}} \exp\left(-\frac{1}{2}(x-\mu_k)^T \Sigma_k^{-1}(x-\mu_k) \right),$$

where $|\Sigma_k|$ is the determinant of Σ_k, and Σ_k^{-1} is the inverse matrix.

Let $P(k)$ represent the prior probability of class k. Then the posterior probability that an observation x is of class k is

$$\hat{P}(k \mid x) = \frac{P(x \mid k)P(k)}{P(x)},$$

where $P(x)$ is a normalization constant, the sum over k of $P(x \mid k)P(k)$.

Prior Probability

The prior probability is one of three choices:

- `'uniform'` — The prior probability of class `k` is one over the total number of classes.
- `'empirical'` — The prior probability of class `k` is the number of training samples of class `k` divided by the total number of training samples.
- Custom — The prior probability of class `k` is the `k`th element of the `prior` vector. See `fitcdiscr`.

After creating a classifier `obj`, you can set the prior using dot notation:

```
obj.Prior = v;
```

where `v` is a vector of positive elements representing the frequency with which each element occurs. You do not need to retrain the classifier when you set a new prior.

Cost

The matrix of expected costs per observation is defined in “Cost” on page 15-8.

Examples

Compute the resubstituted classification error for the Fisher iris data:

```
load fisheriris
obj = fitcdiscr(meas,species);
L = loss(obj,meas,species)

L =
    0.0200
```

See Also

predict | ClassificationDiscriminant | fitcdiscr | edge | margin

How To

- “Discriminant Analysis” on page 15-3

loss

Class: CompactClassificationECOC

Classification loss for error-correcting output code multiclass classifiers

Syntax

```
L = loss(Mdl,X,Y)
L = loss(Mdl,X,Y,Name,Value)
```

Description

`L = loss(Mdl,X,Y)` returns the classification loss (`L`), a scalar representing how well the trained error-correcting output code (ECOC) multiclass classifer Mdl classifies the predictor data (X) as compared to the true class labels (Y). Each row of `X` and `Y` is an observation.

`L = loss(Mdl,X,Y,Name,Value)` returns the classification loss with additional options specified by one or more Name,Value pair arguments.

For example, specify a decoding scheme, classification loss function, or verbosity level.

Input Arguments

`Mdl` — ECOC multiclass classifier

`ClassificationECOC` model | `CompactClassificationECOC` model

ECOC multiclass classifier, specified as a `ClassificationECOC` or `CompactClassificationECOC` model. You can create a:

- `ClassificationECOC` model by training the ECOC classifier using `fitcecoc`
- `CompactClassificationECOC` model by passing a `ClassificationECOC` classifier to `compact`

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also called an instance or example), and each column corresponds to one variable (also known as a feature). The variables composing the columns of `X` should be the same as the variables that trained the `Mdl` classifier.

The length of `Y` and the number of rows of `X` must be equal.

If you trained `Mdl` specifying to standardize the predictor data, then the software standardizes the columns of `X` using the corresponding means and standard deviations that the software stored in `Mdl.BinaryLearner{j}.Mu` and `Mdl.BinaryLearner{j}.Sigma` for learner `j`.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `Mdl.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	$\{-1,1\}$	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	$[0,1]$	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `Mdl.CodingMatrix`.
  - `s` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.
  - L is the number of binary learners.

  For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`

- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'LossFun'` — Loss function

`'classiferror'` (default) | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or `'classiferror'`.

You can:

- Specify the built-in function `'classiferror'`. Subsequently, the loss function is classification error, i.e., the proportion of misclassified observations.
- Specify your own function using function handle notation.

Suppose that `n = size(X,1)` is the sample size and `k` is the number of classes. Your function must have the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

- The output argument `lossvalue` is a scalar.
- You choose the function name (*`lossfun`*).
- `C` is an `n`-by-`k` logical matrix with rows indicating which class the corresponding observation belongs. The column order corresponds to the class order in `Mdl.ClassNames`.

  Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q`, for each row. Set all other elements of row `p` to `0`.
- `S` is an `n`-by-`k` numeric matrix of negated loss values for classes. Each row corresponds to an observation. The column order corresponds to the class order in `Mdl.ClassNames`. `S` resembles the output argument `negLoss` of `predict`.
- `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes its elements to sum to `1`.
- `Cost` is a `k`-by-`k` numeric matrix of misclassification costs. For example, `Cost = ones(K) -eye(K)` specifies a cost of 0 for correct classification, and 1 for misclassification.

Specify your function using `'LossFun',@lossfun`.

Data Types: `function_handle | char`

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single | double`

`'Weights'` — Observation weights

`ones(size(X,1))` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector. `Weights` requires the same length as the number of rows of `X`, i.e., `size(X,1)`. The software normalizes `Weights` to sum up to the value of the prior probability in the respective class.

If you do not specify your own loss function (using LossFun), then the software normalizes `Weights` to sum up to the value of the prior probability in the respective class.

Output Arguments

`L` — Classification loss

scalar

Classification loss, returned as a scalar. `L` is a generalization or resubstitution quality measure. Its interpretation depends on the loss function and weighting scheme, but, in general, better classifiers yield smaller loss values.

Definitions

Classification Error

The *classification error* is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j e_j}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is the weight for observation j. The software renormalizes the weights to sum to 1.
- $e_j = 1$ if the predicted class of observation j differs from its true class, and 0 otherwise.

In other words, it is the proportion of observations that the classifier misclassifies.

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left|m_{kj}\right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Determine the Test Sample Loss of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers, and specify a 15% holdout sample. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'Holdout',0.15,'Learners',t,'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

Estimate the test-sample loss.

```
L = loss(CMdl,XTest,YTest)
```

```
L =

     0
```

The ECOC model correctly classifies all out-of-sample irises.

Determine ECOC Model Quality Using a Custom Loss

Suppose that it is interesting to know how well a model classifies a particular class. This example shows how to pass such a custom loss function to `loss`.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
n = numel(Y);           % Sample size
classOrder = unique(Y)  % Class order
K = numel(classOrder);  % Number of classes
rng(1) % For reproducibility
```

```
classOrder =

     setosa
     versicolor
     virginica
```

Train an ECOC model using SVM binary classifiers and specifying a 15% holdout sample. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'Holdout',0.15,'Learners',t,'ClassNames',classOrder);
```

```
CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

Compute the negated losses for the test-sample observations.

```
[~,negLoss] = predict(CMdl,XTest);
```

Create a function that takes the minimal loss for each observation, and then averages the minimal losses across all observations.

```
lossfun = @(C,S,~,~)mean(min(-negLoss,[],2));
```

Compute the test-sample custom loss.

```
loss(CMdl,XTest,YTest,'LossFun',lossfun)
```

```
ans =

    0.0033
```

The average, minimal, binary loss in the test sample is 0.0033.

- “Quick Start Parallel Computing for Statistics and Machine Learning Toolbox” on page 21-2

References

[1] Allwein, E., R. Schapire, and Y. Singer. “Reducing multiclass to binary: A unifying approach for margin classifiers.” *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. “On the decoding process in ternary error-correcting output codes.” *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. “Separability of ternary codes for sparse designs of error-correcting output codes.” *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q., X. Che, L. Zhang, and D. Yu. “Feature Evaluation and Selection Based on Neighborhood Soft Margin.” *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `CompactClassificationECOC` | `fitcecoc` | `predict` | `resubLoss`

More About

- “Reproducibility in Parallel Statistical Computations” on page 21-13
- “Concepts of Parallel Computing in Statistics and Machine Learning Toolbox” on page 21-7

loss

Class: CompactClassificationEnsemble

Classification error

Syntax

```
L = loss(ens,X,Y)
L = loss(ens,X,Y,Name,Value)
```

Description

`L = loss(ens,X,Y)` returns the classification error for ensemble ens computed using matrix of predictors `X` and true class labels `Y`.

When computing the loss, `loss` normalizes the class probabilities in Y to the class probabilities used for training, stored in the `Prior` property of ens.

`L = loss(ens,X,Y,Name,Value)` computes classification error with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

Classification ensemble created with `fitensemble`, or a compact classification ensemble created with `compact`.

`X`

Matrix of data to classify. Each row of `X` represents one observation, and each column represents one predictor. `X` must have the same number of columns as the data used to train ens. `X` should have the same number of rows as the number of elements in `Y`.

`Y`

Classification of X. `Y` should be of the same type as the classification used to train ens, and its number of elements should equal the number of rows of X.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `ens.NumTrained`. `loss` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'lossfun '`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-2694
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 22-2694
- `'hinge'` — See "Loss Functions" on page 22-2694.
- `'mincost'` — Smallest misclassification cost as given by the `obj.Cost` matrix. See "Loss Functions" on page 22-2694.

You can write your own loss function in the syntax described in "Loss Functions" on page 22-2694.

Default: `'classiferror'`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

`'UseObsForLearner'`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of X.
- `T` is the number of weak learners in ens.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of X.

Default: `true(N,T)`

`'weights'`

Vector of observation weights, with nonnegative entries. The length of `weights` must equal the number of rows in X. When you specify weights, `loss` normalizes the weights so that observation weights in each class sum to the prior probability of that class.

Default: `ones(size(X,1),1)`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Classification Error

The default classification error is the fraction of the data X that ens misclassifies, where Y are the true classifications.

Weighted classification error is the sum of weight *i* times the Boolean value that is `1` when tree misclassifies the *i*th row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'hinge'` — Classification error measure that has the form

$$L=\frac{\sum_{j=1}^{n} w_j \max\left\{0,1-y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

  where:

  - w_j is weight j.
  - For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
  - $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.
- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of ens`.X`.
- `K` is the number of classes in ens, represented in `ens.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `score` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@`*`lossfun`* as the value of the `lossfun` name-value pair.

Examples

Create a compact classification ensemble for the ionosphere data, and find the fraction of training data that the ensemble misclassifies:

```
load ionosphere
ada = fitensemble(X,Y,'AdaBoostM1',100,'tree');
adb = compact(ada);
L = loss(adb,X,Y)

L =
    0.0085
```

See Also

`loss` | `margin` | `predict` | `edge`

loss

Class: CompactClassificationNaiveBayes

Classification error for naive Bayes classifier

Syntax

```
L = loss(Mdl,X,Y)
L = loss(Mdl,X,Y,Name,Value)
```

Description

`L = loss(Mdl,X,Y)` returns the minimum misclassification cost loss (`L`), a scalar representing how well the trained naive Bayes classifer Mdl classifies the predictor data (X) as compared to the true class labels (Y).

`loss` normalizes the class probabilities in Y to the prior class probabilities `fitcnb` used for training, stored in the `Prior` property of `Mdl`.

`L = loss(Mdl,X,Y,Name,Value)` returns the classification loss with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`Mdl` — Naive Bayes classifier

`ClassificationNaiveBayes` model | `CompactClassificationNaiveBayes` model

Naive Bayes classifier, specified as a `ClassificationNaiveBayes` model or `CompactClassificationNaiveBayes` model returned by `fitcnb` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained `Mdl`.

The length of `Y` and the number of rows of `X` must be equal.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `Mdl.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun'` — Loss function

`'classiferror'` (default) | `'binodeviance'` | `'exponential'` | `'hinge'` | `'mincost'` | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or string.

- This table describes the built-in loss functions. Specify one using its corresponding string.

String	Loss Function
`'binodeviance'`	Binomial deviance
`'classiferror'`	Classification error
`'exponential'`	Exponential loss
`'hinge'`	Hinge loss
`'mincost'`	Minimum misclassification cost loss

- Specify your own function using function handle notation.

  Suppose that `n = size(X,1)` is the sample size and `k = size(Mdl.ClassNames,1)` is the number of classes. Your function must have the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

  - The output argument `lossvalue` is a scalar.
  - You choose the function name (`lossfun`).
  - `C` is an `n`-by-`k` logical matrix with rows indicating to which class the corresponding observation belongs. The column order corresponds to the class order in `Mdl.ClassNames`.

    Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q`, for each row. Set all other elements of row `p` to `0`.
  - `S` is an `n`-by-`k` numeric matrix of classification scores. The column order corresponds to the class order in `Mdl.ClassNames`. `S` is a matrix of posterior probabilities, similar to the output of `predict`.
  - `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes the weights to sum to the prior probability of their respective class. If `Mdl` is a compact model, then you must also supply the weights using the `'Weights'` name-value pair argument.
  - `Cost` is a `k`-by-`k` numeric matrix of misclassification costs. For example, `Cost = ones(K) - eye(K)` specifies a cost of `0` for correct classification, and `1` for misclassification.

  Specify your function using `'LossFun',@lossfun`.

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector.

The size of `Weights` must be equal to the number of rows of X. The software weighs the observations in each row of X with the corresponding weight in `Weights`.

If you do not specify your own loss function, then the software normalizes `Weights` to add up to `1`.

Data Types: `double`

Output Arguments

L — Classification loss

scalar

Classification loss, returned as a scalar. `L` is a generalization or resubstitution quality measure. Its interpretation depends on the loss function and weighting scheme, but, in general, better classifiers yield smaller loss values.

Definitions

Binomial Deviance

The *binomial deviance* (or *multinomial deviance* for number of classes $K > 3$) is a classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \log\left(1 + \exp\left(-2 y_j' f\left(X_j\right)\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

The binomial deviance has connections to the maximization of the binomial likelihood function. For details on binomial deviance, see [1].

Classification Error

The *classification error* is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j e_j}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is the weight for observation j. The software renormalizes the weights to sum to 1.
- $e_j = 1$ if the predicted class of observation j differs from its true class, and 0 otherwise.

In other words, it is the proportion of observations that the classifier misclassifies.

Exponential Loss

Exponential loss is a classification error measure that is similar to binomial deviance, and has the form

$$L = \frac{\sum_{j=1}^{n} w_j \exp\left(-y_j' f\left(X_j\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

Hinge Loss

Hinge loss is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

Hinge loss linearly penalizes for misclassified observations, and is related to the support vector machine (SVM) objective function used for optimization. For more details on hinge loss, see [1].

Minimum Misclassification Cost Loss

The *minimum misclassification cost loss* is the weighted average of the minimum expected misclassification costs for each observation.

In other words, the minimum misclassification cost is

$$L = \frac{\sum_{j=1}^{n} w_j c_j}{\sum_{j}^{n} w_j},$$

where:

- w_j is the weight of observation j.
- c_j is the minimum of the expected misclassification costs for observation j.

Misclassification Cost

A *misclassification cost* is the relative severity of a classifier labeling an observation into the wrong class.

There are two types of misclassification costs: true and expected. Let K be the number of classes.

- *True misclassification cost* — A K-by-K matrix, where element (i,j) indicates the misclassification cost of predicting an observation into class j if its true class is i. The software stores the misclassification cost in the property `Mdl.Cost`, and used in computations. By default, `Mdl.Cost(i,j)` = 1 if `i` ≠ `j`, and `Mdl.Cost(i,j)` = 0 if `i` = `j`. In other words, the cost is `0` for correct classification, and `1` for any incorrect classification.
- *Expected misclassification cost* — A K-dimensional vector, where element k is the weighted average misclassification cost of classifying an observation into class k, weighted by the class posterior probabilities. In other words,

$$c_k = \sum_{j=1}^{K} \hat{P}(Y = j \mid x_1,...,x_P)\texttt{Cost}_{jk}.$$

the software classifies observations to the class corresponding with the lowest expected misclassification cost.

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.
- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

$$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Examples

Determine Test Sample Minimum Cost Loss of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);      % For reproducibility
```

Train a naive Bayes classifier. Specify a 15% holdout sample for testing. It is good practice to specify the class order. Assume that each predictor is conditionally normally distributed given its label.

```
CVMdl = fitcnb(X,Y,'ClassNames',{'setosa','versicolor','virginica'},...
    'Holdout',0.15);
CMdl = CVMdl.Trained{1}; % Extract the trained, compact classifier
testInds = test(CVMdl.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds);
```

`CVMdl` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Determine how well the algorithm generalizes by estimating the test sample minimum cost loss.

```
L = loss(CMdl,XTest,YTest)
```

```
L =

    0.0476
```

The test sample average classification cost is approximately 0.05.

You might improve the classification error by specifying better predictor distributions when you train the classifier.

Determine the Test Sample Classification Error of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1); % For reproducibility
```

Train a naive Bayes classifier. Specify a 15% holdout sample for testing. It is good practice to specify the class order. Assume that each predictor is conditionally normally distributed given its label.

```
CVMdl = fitcnb(X,Y,'ClassNames',{'setosa','versicolor','virginica'},...
    'Holdout',0.15);
CMdl = CVMdl.Trained{1}; % Extract the trained, compact classifier
testInds = test(CVMdl.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds);
```

`CVMdl` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Determine how well the algorithm generalizes by estimating the test sample classification error.

```
L = loss(CMdl,XTest,YTest,'LossFun','classiferror')
```

```
L =

    0.0476
```

The classifier misclassified approximately 5% of the test sample observations.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, second edition. Springer, New York, 2008.

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `fitcnb` | `predict` | `resubLoss`

More About

- "Naive Bayes Classification" on page 15-31

loss

Class: CompactClassificationSVM

Classification error for support vector machine classifiers

Syntax

```
L = loss(SVMModel,X,Y)
L = loss(SVMModel,X,Y,Name,Value)
```

Description

`L = loss(SVMModel,X,Y)` returns the classification error (`L`), a scalar representing how well the trained support vector machine (SVM) classifer SVMModel classifies the predictor data (X) as compared to the true class labels (Y).

`loss` normalizes the class probabilities in Y to the prior class probabilities `fitcsvm` used for training, stored in the `Prior` property of `SVMModel`.

`L = loss(SVMModel,X,Y,Name,Value)` returns the classification error with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`SVMModel` — SVM classifier

`ClassificationSVM` classifier | `CompactClassificationSVM` classifier

SVM classifier, specified as a `ClassificationSVM` classifier or `CompactClassificationSVM` classifier returned by `fitcsvm` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained the `SVMModel` classifier.

The length of `Y` and the number of rows of `X` must be equal.

If you set `'Standardize',true` in `fitcsvm` to train `SVMModel`, then the software standardizes the columns of `X` using the corresponding means in `SVMModel.Mu` and standard deviations in `SVMModel.Sigma`.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `SVMModel.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun'` — Loss function

`'classiferror'` (default) | `'binodeviance'` | `'exponential'` | `'hinge'` | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or string.

- The following lists available loss functions. Specify one using its corresponding string.

Value	Loss Function
`'binodeviance'`	Binomial deviance
`'classiferror'`	Classification error

Value	Loss Function
`'exponential'`	Exponential loss
`'hinge'`	Hinge loss

- Specify your own function using function handle notation.

  Suppose that `n = size(X,1)` is the sample size and `K= size(SVMModel.ClassNames,1)` is the number of classes. Your function must have the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

  - The output argument `lossvalue` is a scalar.
  - You choose the function name (*`lossfun`*).
  - `C` is an `n`-by-`K` logical matrix with rows indicating which class the corresponding observation belongs. The column order corresponds to the class order in `SVMModel.ClassNames`.

    Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q`, for each row. Set all other elements of row `p` to `0`.
  - `S` is an `n`-by-`K` numeric matrix of classification scores. The column order corresponds to the class order in `SVMModel.ClassNames`. `S` is a matrix of classification scores, similar to the output of `predict`.
  - `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes them to sum to `1`.
  - `Cost` is a `K`-by-`K` numeric matrix of misclassification costs. For example, `Cost = ones(K) - eye(K)` specifies a cost of `0` for correct classification, and `1` for misclassification.

  Specify your function using `'LossFun',@lossfun`.

Data Types: `char` | `function_handle`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector.

The size of `Weights` must be equal to the number of rows of X. The software weighs the observations in each row of X with the corresponding weight in `Weights`.

If you do not specify your own loss function, then the software normalizes `Weights` to sum up to the value of the prior probability in the respective class.

Data Types: `double`

Output Arguments

`L` — Classification loss

scalar

Classification loss, returned as a scalar. `L` is a generalization or resubstitution quality measure. Its interpretation depends on the loss function and weighting scheme, but, in general, better classifiers yield smaller loss values.

Definitions

Binomial Deviance

The binomial deviance is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \log\left(1 + \exp\left(-2 y_j' f\left(X_j\right)\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j. The software renormalizes the weights to sum to 1.
- $y_j = \{-1,1\}$.
- $f(X_j)$ is the score for observation j.

The binomial deviance has connections to the maximization of the binomial likelihood function. For details on binomial deviance, see [1].

Classification Error

The *classification error* is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j e_j}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is the weight for observation j. The software renormalizes the weights to sum to 1.
- $e_j = 1$ if the predicted class of observation j differs from its true class, and 0 otherwise.

In other words, it is the proportion of observations that the classifier misclassifies.

Exponential Loss

A binary classification error measure that is similar to binomial deviance, and has the form

$$L = \frac{\sum_{j=1}^{n} w_j \exp\left(-y_j' f\left(X_j\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j. The software renormalizes the weights to sum to 1.
- $y_j = \{-1,1\}$.
- $f(X_j)$ is the score for observation j.

Hinge Loss

Hinge loss is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j. The software renormalizes the weights to sum to 1.
- y_j = {-1,1}.
- $f(X_j)$ is the score for observation j.

Hinge loss linearly penalizes for misclassified observations, and is related to the SVM objective function used for optimization. For more details on hinge loss, see [1].

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j, x) = x_j' x$ (the linear kernel), then the score function reduces to

$$f\left(x\right) = \left(x / s\right)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Examples

Determine the Test Sample Classification Error of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM classifier. Specify a 15% holdout sample for testing. It is good practice to specify the class order and standardize the data.

```
CVSVMModel = fitcsvm(X,Y,'Holdout',0.15,'ClassNames',{'b','g'},...
    'Standardize',true);
CompactSVMModel = CVSVMModel.Trained{1}; % Extract the trained, compact classifier
testInds = test(CVSVMModel.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVSVMModel` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Determine how well the algorithm generalizes by estimating the test sample classification error.

```
L = loss(CompactSVMModel,XTest,YTest)
```

```
L =

    0.0787
```

The SVM classifier misclassifies approximately 8% of the test sample radar returns.

Determine the Test Sample Hinge Loss of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

```
rng(1); % For reproducibility
```

Train an SVM classifier. Specify a 15% holdout sample for testing. It is good practice to specify the class order and standardize the data.

```
CVSVMModel = fitcsvm(X,Y,'Holdout',0.15,'ClassNames',{'b','g'},...
    'Standardize',true);
CompactSVMModel = CVSVMModel.Trained{1}; % Extract the trained, compact classifier
testInds = test(CVSVMModel.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVSVMModel` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Determine how well the algorithm generalizes by estimating the test sample hinge loss.

```
L = loss(CompactSVMModel,XTest,YTest,'LossFun','Hinge')
```

```
L =

    0.2998
```

The hinge loss is approximately 0.3. Classifiers with hinge losses close to 0 are desirable.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, second edition. Springer, New York, 2008.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `edge` | `fitcsvm` | `predict`

loss

Class: CompactClassificationTree

Classification error

Syntax

```
L = loss(tree,X,Y)
L = loss(tree,X,Y,Name,Value)
L = loss(tree,X,Y,'Subtrees',subtreevector)
[L,se] = loss(tree,X,Y,'Subtrees',subtreevector)
[L,se,NLeaf] = loss(tree,X,Y,'Subtrees',subtreevector)
[L,se,NLeaf,bestlevel] = loss(tree,X,Y,'Subtrees',subtreevector)
[L,...] = loss(tree,X,Y,'Subtrees',subtreevector,Name,Value)
```

Description

`L = loss(tree,X,Y)` returns a scalar representing how well `tree` classifies the data in `X`, when `Y` contains the true classifications.

When computing the loss, `loss` normalizes the class probabilities in Y to the class probabilities used for training, stored in the `Prior` property of tree.

`L = loss(tree,X,Y,Name,Value)` returns the loss with additional options specified by one or more Name,Value pair arguments.

`L = loss(tree,X,Y,'Subtrees',subtreevector)` returns a vector of classification errors for the trees in the pruning sequence `subtreevector`.

`[L,se] = loss(tree,X,Y,'Subtrees',subtreevector)` returns the vector of standard errors of the classification errors.

Note: `loss` returns `se` and further outputs only when the `LossFun` name-value pair is the default `'classiferror'`.

`[L,se,NLeaf] = loss(tree,X,Y,'Subtrees',subtreevector)` returns the vector of numbers of leaf nodes in the trees of the pruning sequence.

`[L,se,NLeaf,bestlevel] = loss(tree,X,Y,'Subtrees',subtreevector)` returns the best pruning level as defined in the `TreeSize` name-value pair. By default, `bestlevel` is the pruning level that gives loss within one standard deviation of minimal loss.

`[L,...] = loss(tree,X,Y,'Subtrees',subtreevector,Name,Value)` returns loss statistics with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

A classification tree or compact classification tree constructed by `fitctree` or `compact`.

`X`

Matrix of data to classify. Each row of `X` represents one observation, and each column represents one predictor. `X` must have the same number of columns as the data used to train tree. `X` should have the same number of rows as the number of elements in `Y`.

`Y`

Classification of X. `Y` should be of the same type as the classification used to train tree, and its number of elements should equal the number of rows of X.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun '`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-2719
- `'classiferror'` — Fraction of misclassified observations. See "Loss Functions" on page 22-2719.
- `'exponential'` — See "Loss Functions" on page 22-2719
- `'hinge'` — See "Loss Functions" on page 22-2719.
- `'mincost'` — Smallest misclassification cost as given by the tree`.Cost` matrix. See "Loss Functions" on page 22-2719.

You can write your own loss function in the syntax described in "Loss Functions" on page 22-2719.

Default: `'mincost'`

`'Weights'`

A numeric vector of length `N`, where `N` is the number of rows of X. `Weights` are nonnegative. `loss` normalizes the weights so that observation weights in each class sum to the prior probability of that class. When you supply `Weights`, `loss` computes weighted classification loss.

Default: `ones(N,1)`

Name,Value arguments associated with pruning subtrees:

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `CompactClassificationTree.loss` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`CompactClassificationTree.loss` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

`'TreeSize'`

One of the following strings:

- `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `Subtrees`).
- `'min'` — `loss` returns the element of `Subtrees` with smallest loss, usually the smallest element of `Subtrees`.

Output Arguments

`L`

Classification error, a vector the length of `Subtrees`. The meaning of the error depends on the values in `Weights` and `LossFun`; see “Classification Error” on page 22-2719.

`se`

Standard error of loss, a vector the length of `Subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `Subtrees`.

`bestlevel`

A scalar whose value depends on `TreeSize`:

- `TreeSize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `Subtrees`).

- `TreeSize` = `'min'` — `loss` returns the element of `Subtrees` with smallest loss, usually the smallest element of `Subtrees`.

Definitions

Classification Error

The default classification error is the fraction of data X that tree misclassifies, where Y represents the true classifications.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when tree misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'classiferror'` — Predict the label with the largest posterior probability. The loss is then the fraction of misclassified observations.
- `'hinge'` — Classification error measure that has the form

$$L=\frac{\sum_{j=1}^{n} w_j \max\left\{0,1-y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file in this form:

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in the classifier, represented in the `ClassNames` property.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in the `ClassNames` property.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST = ones(K) - eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

True Misclassification Cost

There are two costs associated with classification: the true misclassification cost per class, and the expected misclassification cost per observation.

You can set the true misclassification cost per class in the `Cost` name-value pair when you create the classifier using the `fitctree` method. `Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

Expected Misclassification Cost

There are two costs associated with classification: the true misclassification cost per class, and the expected misclassification cost per observation.

Suppose you have `Nobs` observations that you want to classify with a trained classifier. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row.

The expected cost matrix `CE` has size `Nobs`-by-`K`. Each row of `CE` contains the expected (average) cost of classifying the observation into each of the `K` classes. `CE(n,k)` is

$$\sum_{i=1}^{K} \hat{P}(i \mid Xnew(n)) C(k \mid i),$$

where

- K is the number of classes.
- $\hat{P}(i \mid Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.
- $C(k \mid i)$ is the true misclassification cost of classifying an observation as k when its true class is i.

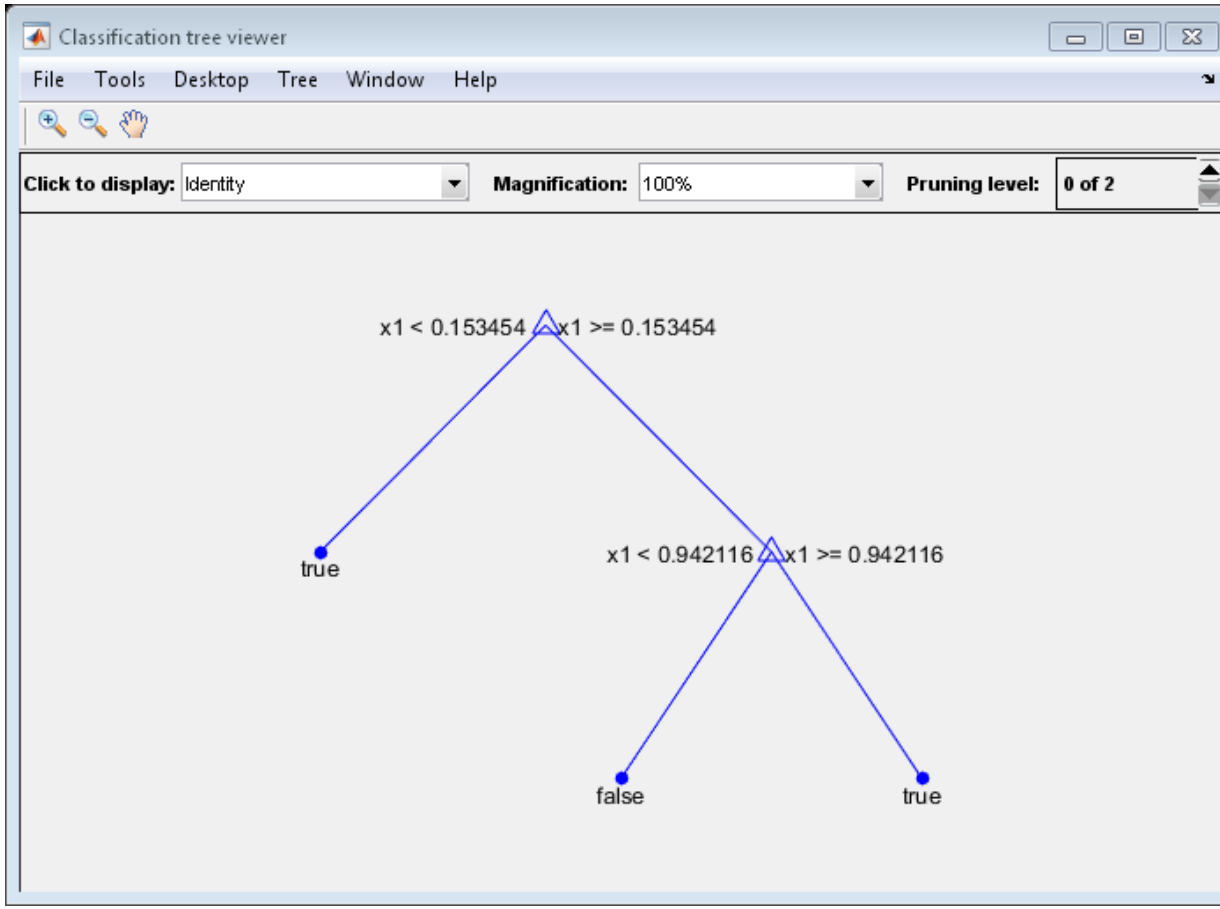
Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

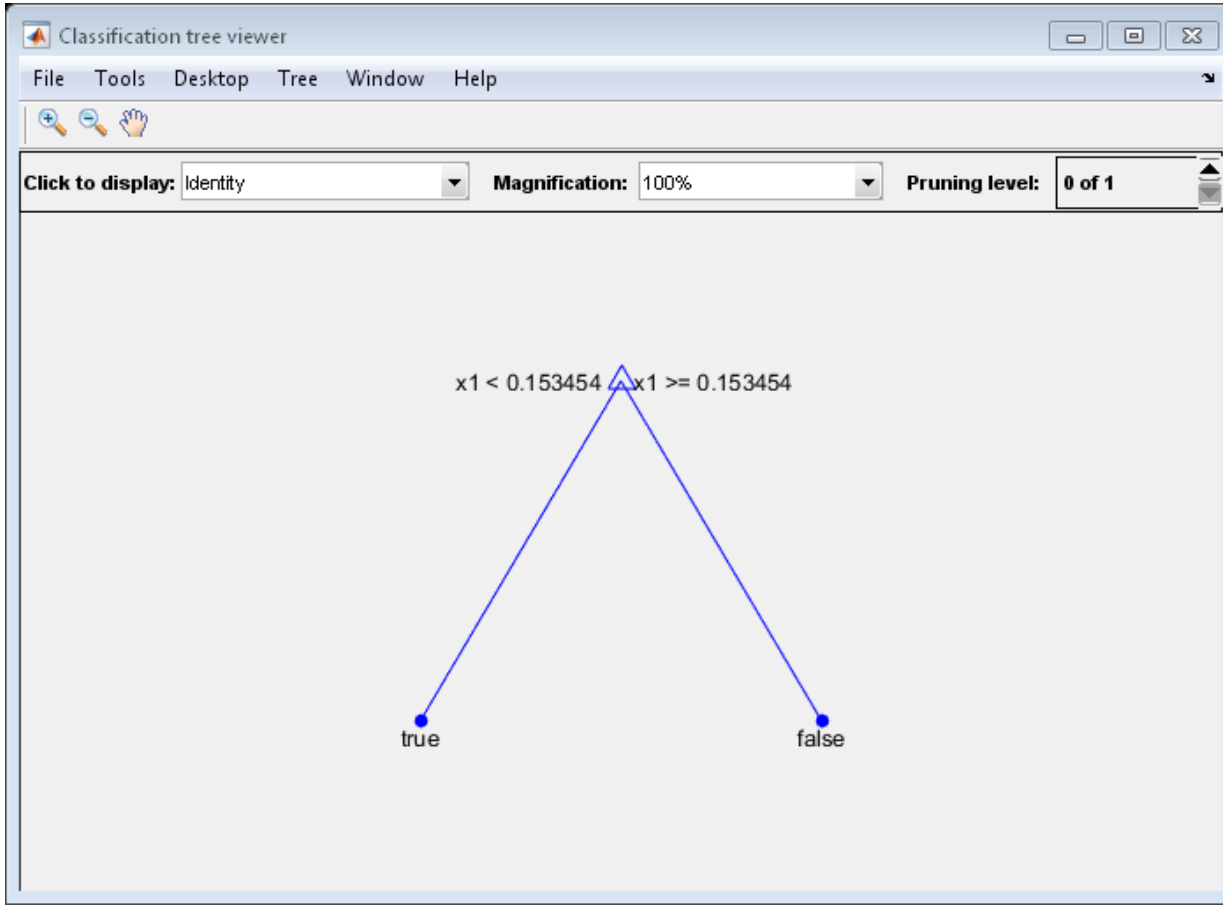
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Compute the In-sample Classification Error

Compute the resubstituted classification error for the `ionosphere` data set.

```
load ionosphere
tree = fitctree(X,Y);
L = loss(tree,X,Y)
```

```
L =

    0.0114
```

Examine the Classification Error for Each Subtree

Unpruned decision trees tend to overfit. One way to balance model complexity and out-of-sample performance is to prune a tree (or restrict its growth) so that in-sample and out-of-sample performance are satisfactory.

Load Fisher's iris data set. Partition the data into training (50%) and validation (50%) sets.

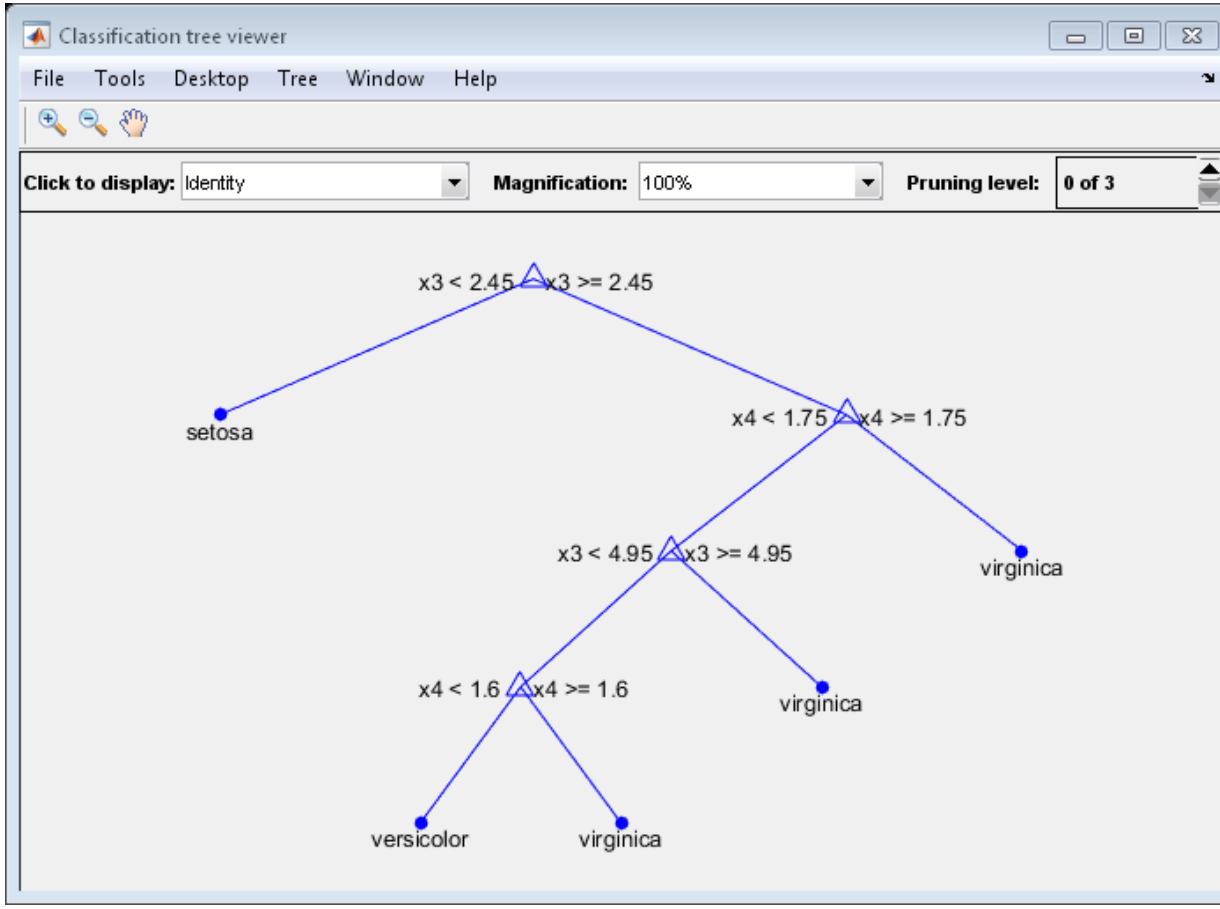
```
load fisheriris
n = size(meas,1);
rng(1) % For reproducibility
idxTrn = false(n,1);
idxTrn(randsample(n,round(0.5*n))) = true; % Training set logical indices
idxVal = idxTrn == false;                  % Validation set logical indices
```

Grow a classification tree using the training set.

```
Mdl = fitctree(meas(idxTrn,:),species(idxTrn));
```

View the classification tree.

```
view(Mdl,'Mode','graph');
```



The classification tree has four pruning levels. Level 0 is the full, unpruned tree (as displayed). Level 3 is just the root node (i.e., no splits).

Examine the training sample classification error for each subtree (or pruning level) excluding the highest level.

```
m = max(Mdl.PruneList) - 1;
trnLoss = resubLoss(Mdl,'SubTrees',0:m)
```

```
trnLoss =
```

```
    0.0267
    0.0533
    0.3067
```

- The full, unpruned tree misclassifies about 2.7% of the training observations.
- The tree pruned to level 1 misclassifies about 5.3% of the training observations.
- The tree pruned to level 2 (i.e., a stump) misclassifies about 30.6% of the training observations.

Examine the validation sample classification error at each level excluding the highest level.

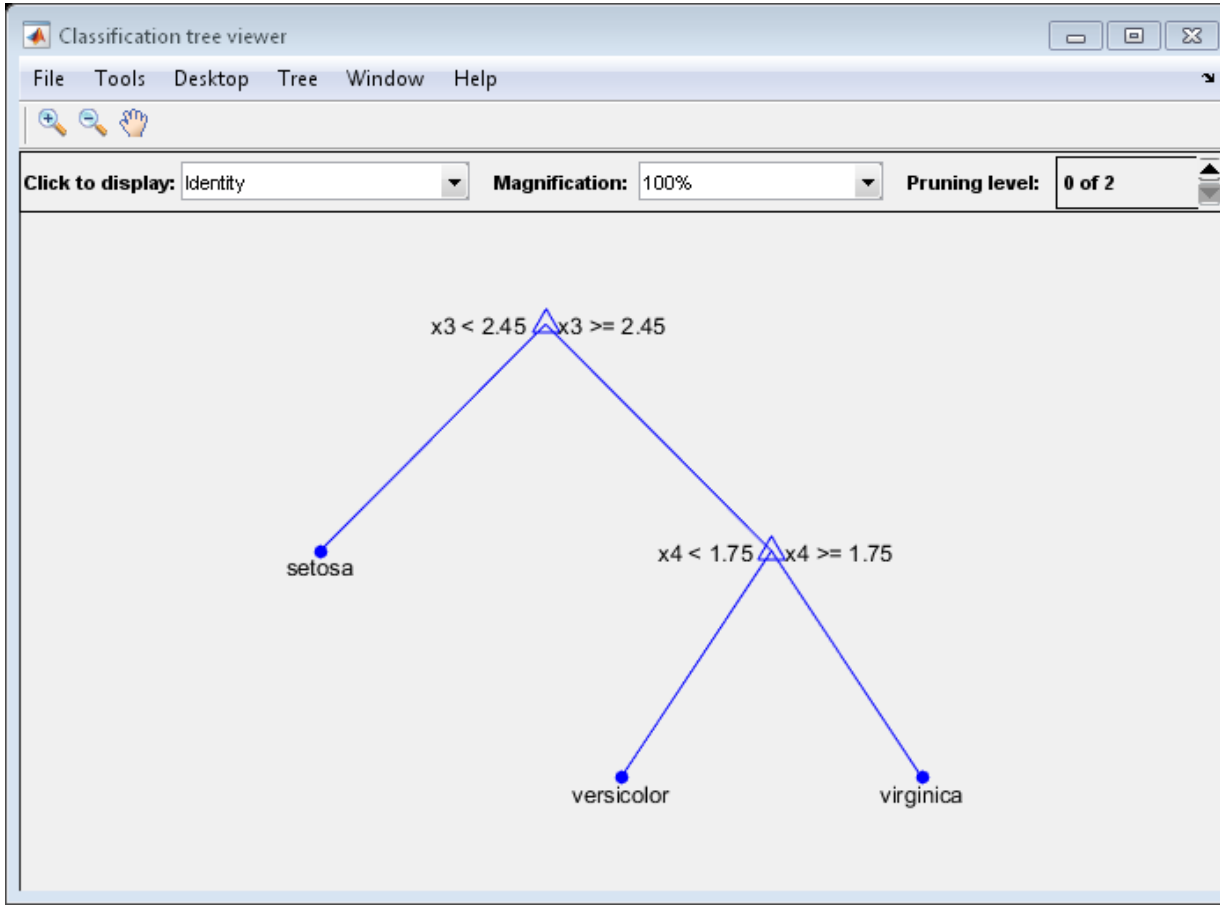
```
valLoss = loss(Mdl,meas(idxVal,:),species(idxVal),'SubTrees',0:m)
```

```
valLoss =

    0.0369
    0.0237
    0.3067
```

- The full, unpruned tree misclassifies about 3.7% of the validation observations.
- The tree pruned to level 1 misclassifies about 2.4% of the validation observations.
- The tree pruned to level 2 (i.e., a stump) misclassifies about 30.7% of the validation observations.

To balance model complexity and out-of-sample performance, consider pruning `Mdl` to level 1.

```
pruneMdl = prune(Mdl,'Level',1);
view(pruneMdl,'Mode','graph')
```



See Also

`margin` | `predict` | `fitctree` | `edge`

loss

Class: CompactRegressionEnsemble

Regression error

Syntax

```
L = loss(ens,X,Y)
L = loss(ens,X,Y,Name,Value)
```

Description

`L = loss(ens,X,Y)` returns the mean squared error between the predictions of `ens` to the data in `X`, compared to the true responses `Y`.

`L = loss(ens,X,Y,Name,Value)` computes the error in prediction with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`, or the `compact` method.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`NaN` values in `X` are taken to be missing values. Observations with all missing values for `X` are not used in the calculation of loss.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

`NaN` values in `Y` are taken to be missing values. Observations with missing values for `Y` are not used in the calculation of loss.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `ens.NumTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'lossfun'`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `loss` calls it as

```
fun(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length.

- `Y` is the observed response.
- `Yfit` is the predicted response.
- `W` is the observation weights.

The returned value `fun(Y,Yfit,W)` should be a scalar.

Default: `'mse'`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

`'UseObsForLearner'`

A logical matrix of size `N`-by-`NumTrained`, where `N` is the number of observations in `ens.X`, and `NumTrained` is the number of weak learners. When `UseObsForLearner(I,J)` is `true`, `predict` uses learner `J` in predicting observation `I`.

Default: `true(N,NumTrained)`

`'weights'`

Numeric vector of observation weights with the same number of elements as Y. The formula for `loss` with `weights` is in "Weighted Mean Squared Error" on page 22-2731.

Default: `ones(size(Y))`

Output Arguments

`L`

Weighted mean squared error of predictions. The formula for `loss` is in "Weighted Mean Squared Error" on page 22-2731.

Definitions

Weighted Mean Squared Error

Let n be the number of rows of data, x_j be the jth row of data, y_j be the true response to x_j, and let $f(x_j)$ be the response prediction of ens to x_j. Let w be the vector of weights (all one by default).

First the weights are divided by their sum so they add to one: $w \to w/\Sigma w$. The mean squared error L is

$$L = \sum_{j=1}^{n} w_j \left(f\left(x_j\right) - y_j \right)^2 .$$

Examples

Find the loss of an ensemble predictor of the `carsmall` data to find `MPG` as a function of engine displacement, horsepower, and vehicle weight:

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
L = loss(ens,X,MPG)

L =
    4.3904
```

See Also

`predict` | `fitensemble`

loss

Class: CompactRegressionTree

Regression error

Syntax

```
L = loss(tree,X,Y)
[L,se] = loss(tree,X,Y)
[L,se,NLeaf] = loss(tree,X,Y)
[L,se,NLeaf,bestlevel] = loss(tree,X,Y)
L = loss(tree,X,Y,Name,Value)
```

Description

`L = loss(tree,X,Y)` returns the mean squared error between the predictions of `tree` to the data in `X`, compared to the true responses `Y`.

`[L,se] = loss(tree,X,Y)` returns the standard error of the loss.

`[L,se,NLeaf] = loss(tree,X,Y)` returns the number of leaves (terminal nodes) in the tree.

`[L,se,NLeaf,bestlevel] = loss(tree,X,Y)` returns the optimal pruning level for `tree`.

`L = loss(tree,X,Y,Name,Value)` computes the error in prediction with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

Regression tree created with `fitrtree`, or the `compact` method.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun'`

Function handle for loss, or the string `'mse'` representing mean-squared error. If you pass a function handle `fun`, `loss` calls `fun` as:

```
fun(Y,Yfit,W)
```

- `Y` is the vector of true responses.
- `Yfit` is the vector of predicted responses.
- `W` is the observation weights. If you pass `W`, the elements are normalized to sum to `1`.

All the vectors have the same number of rows as Y.

Default: `'mse'`

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `CompactRegressionTree.loss` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`CompactRegressionTree.loss` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

`'TreeSize'`

A string, either:

- `'se'` — `loss` returns `bestlevel` that corresponds to the smallest tree whose mean squared error (MSE) is within one standard error of the minimum MSE.
- `'min'` — `loss` returns `bestlevel` that corresponds to the minimal MSE tree.

`'Weights'`

Numeric vector of observation weights with the same number of elements as Y.

Default: `ones(size(Y))`

Output Arguments

`L`

Classification error, a vector the length of `Subtrees`. The error for each tree is the mean squared error, weighted with `Weights`. If you include `LossFun`, `L` reflects the loss calculated with `LossFun`.

`se`

Standard error of loss, a vector the length of `Subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `Subtrees`.

`bestlevel`

A scalar whose value depends on `TreeSize`:

- `TreeSize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `Subtrees`).
- `TreeSize` = `'min'` — `loss` returns the element of `Subtrees` with smallest loss, usually the smallest element of `Subtrees`.

Definitions

Mean Squared Error

The mean squared error m of the predictions $f(X_n)$ with weight vector w is

$$m = \frac{\sum w_n \left(f(X_n) - Y_n\right)^2}{\sum w_n}.$$

Examples

Compute the In-Sample MSE

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
X = [Displacement Horsepower Weight];
```

Grow a regression tree using all observations.

```
tree = fitrtree(X,MPG);
```

Estimate the in-sample MSE.

```
L = loss(tree,X,MPG)
```

```
L =

    4.8952
```

Find the Pruning Level Yielding the Optimal In-sample Loss

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

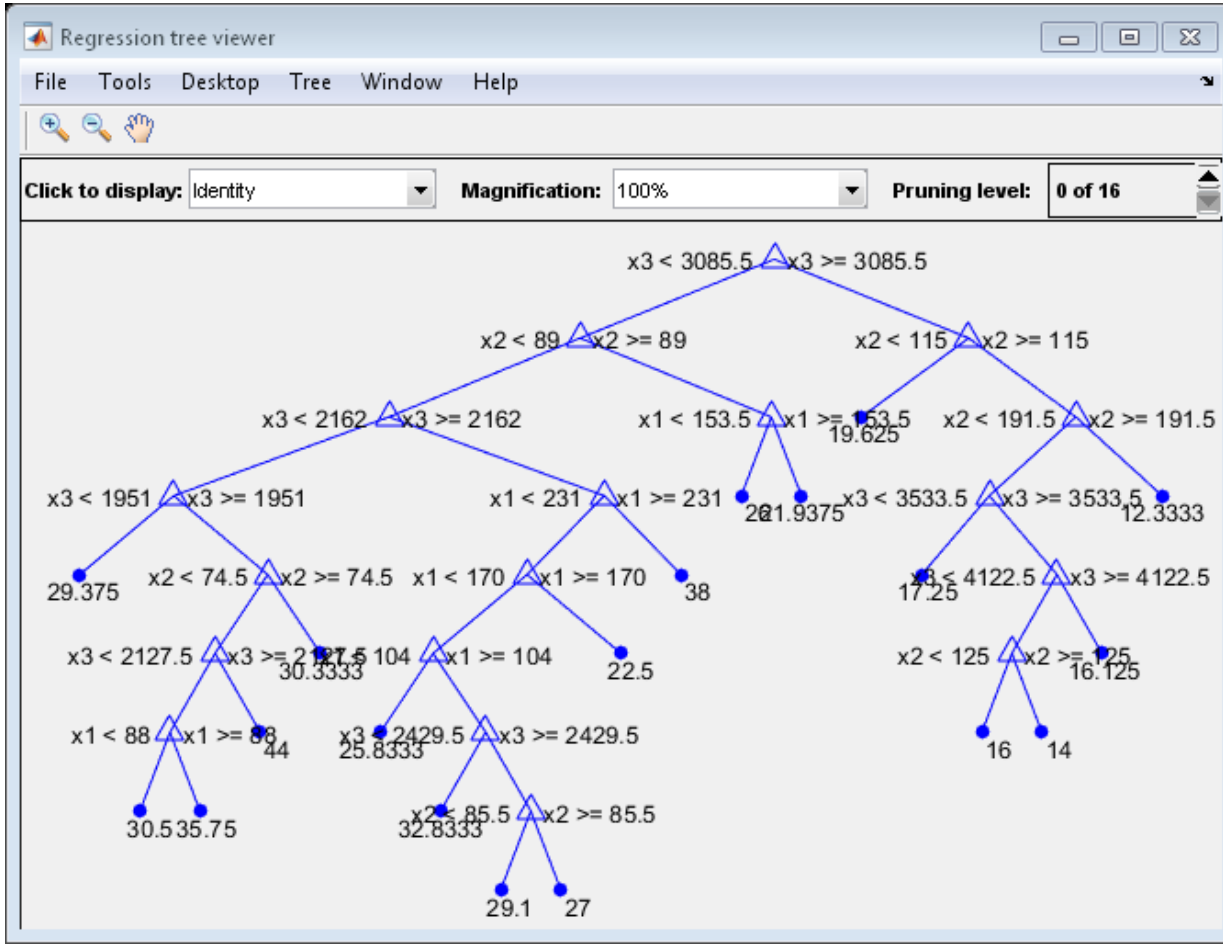
```
load carsmall
X = [Displacement Horsepower Weight];
```

Grow a regression tree using all observations.

```
Mdl = fitrtree(X,MPG);
```

View the regression tree.

```
view(Mdl,'Mode','graph');
```



Find the best pruning level that yields the optimal in-sample loss.

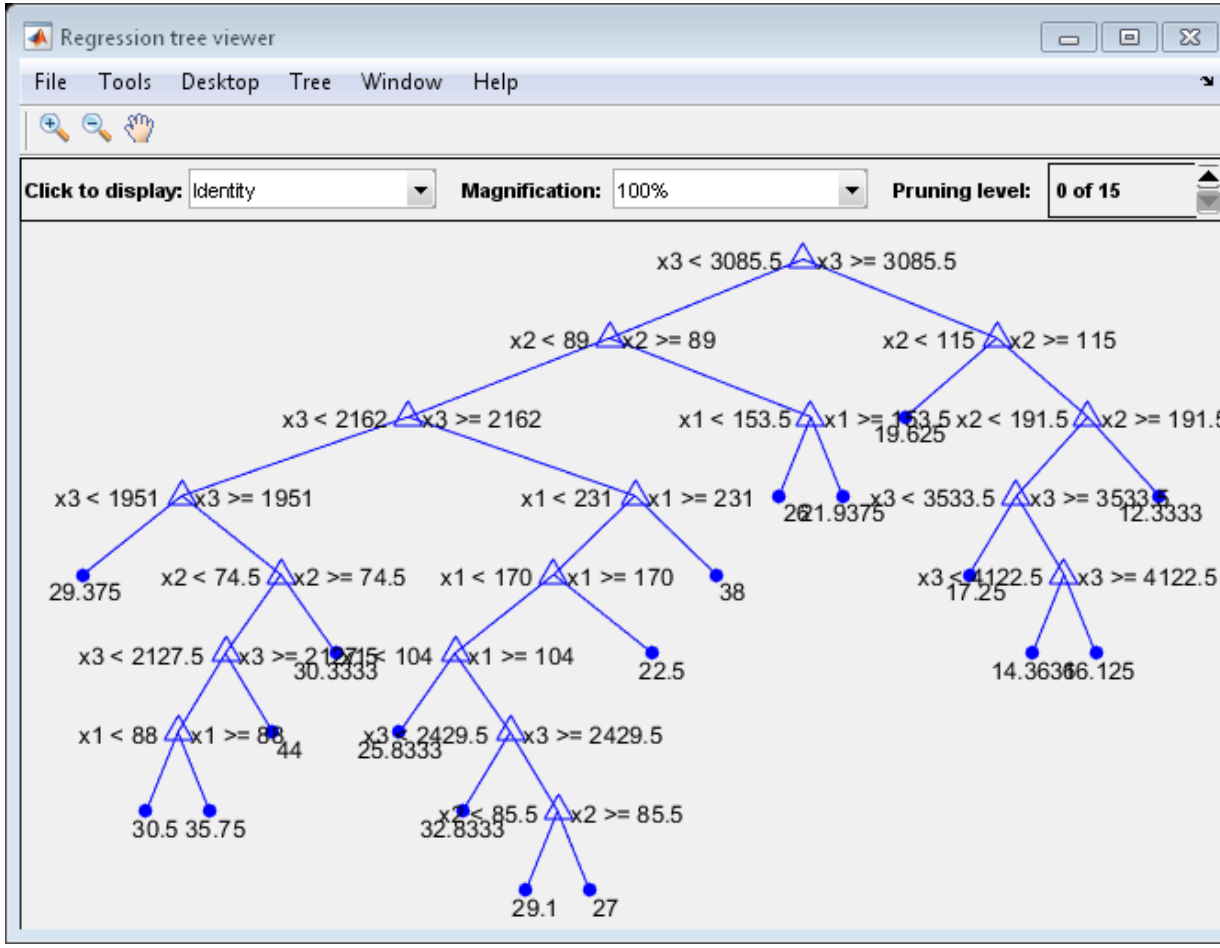
```
[L,se,NLeaf,bestLevel] = loss(Mdl,X,MPG,'Subtrees','all');
bestLevel
```

```
bestLevel =

     1
```

The best pruning level is level 1.

Prune the tree to level 1.

```
pruneMdl = prune(Mdl,'Level',bestLevel);
view(pruneMdl,'Mode','graph');
```



Examine the MSE for Each Subtree

Unpruned decision trees tend to overfit. One way to balance model complexity and out-of-sample performance is to prune a tree (or restrict its growth) so that in-sample and out-of-sample performance are satisfactory.

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
```

```
X = [Displacement Horsepower Weight];
Y = MPG;
```

Partition the data into training (50%) and validation (50%) sets.

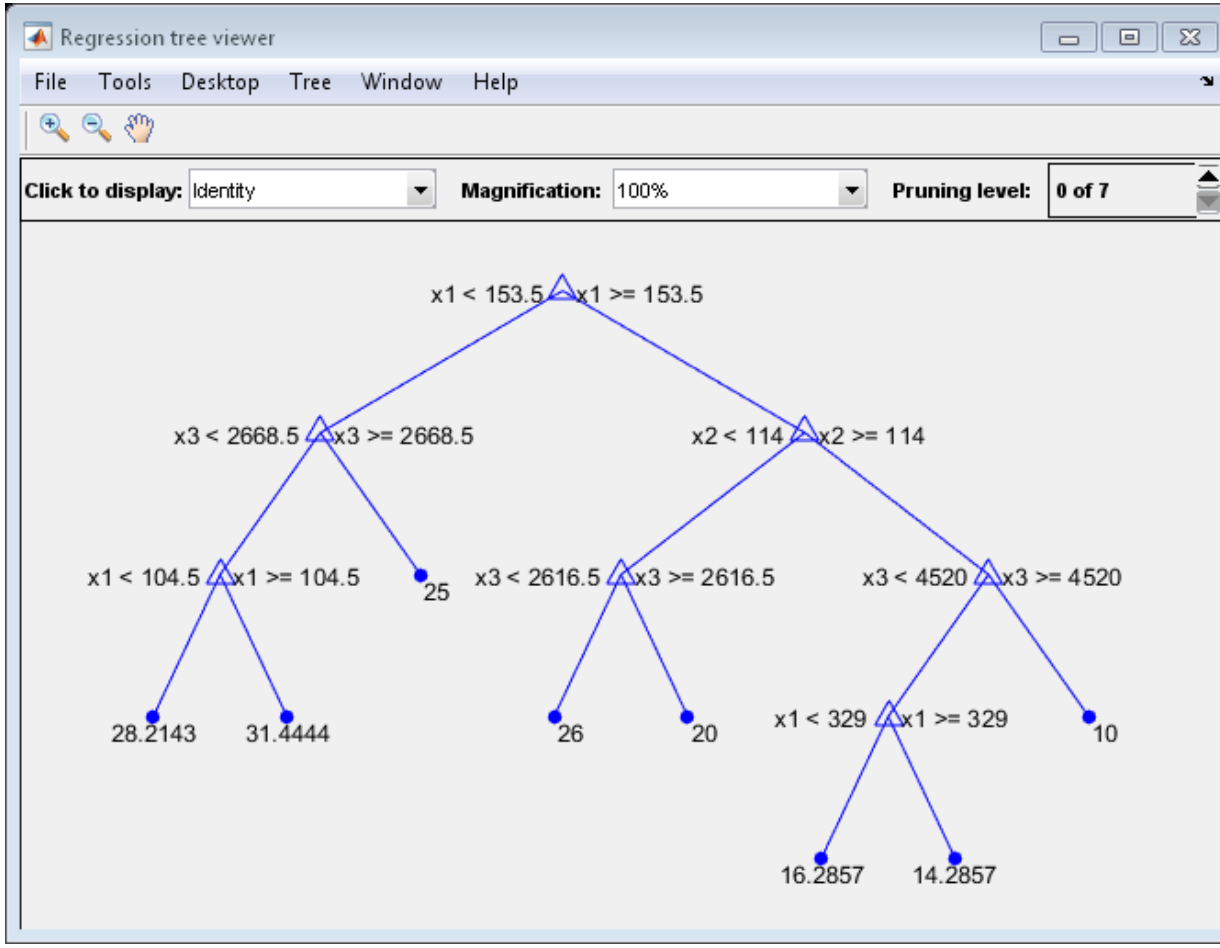
```
n = size(X,1);
rng(1) % For reproducibility
idxTrn = false(n,1);
idxTrn(randsample(n,round(0.5*n))) = true; % Training set logical indices
idxVal = idxTrn == false;                  % Validation set logical indices
```

Grow a regression tree using the training set.

```
Mdl = fitrtree(X(idxTrn,:),Y(idxTrn));
```

View the regression tree.

```
view(Mdl,'Mode','graph');
```



The regression tree has seven pruning levels. Level 0 is the full, unpruned tree (as displayed). Level 7 is just the root node (i.e., no splits).

Examine the training sample MSE for each subtree (or pruning level) excluding the highest level.

```
m = max(Mdl.PruneList) - 1;
trnLoss = resubLoss(Mdl,'SubTrees',0:m)
```

```
trnLoss =

    5.9789
    6.2768
    6.8316
    7.5209
    8.3951
   10.7452
   14.8445
```

- The MSE for the full, unpruned tree is about 6 units.
- The MSE for the tree pruned to level 1 is about 6.3 units.
- The MSE for the tree pruned to level 6 (i.e., a stump) is about 14.8 units.

Examine the validation sample MSE at each level excluding the highest level.

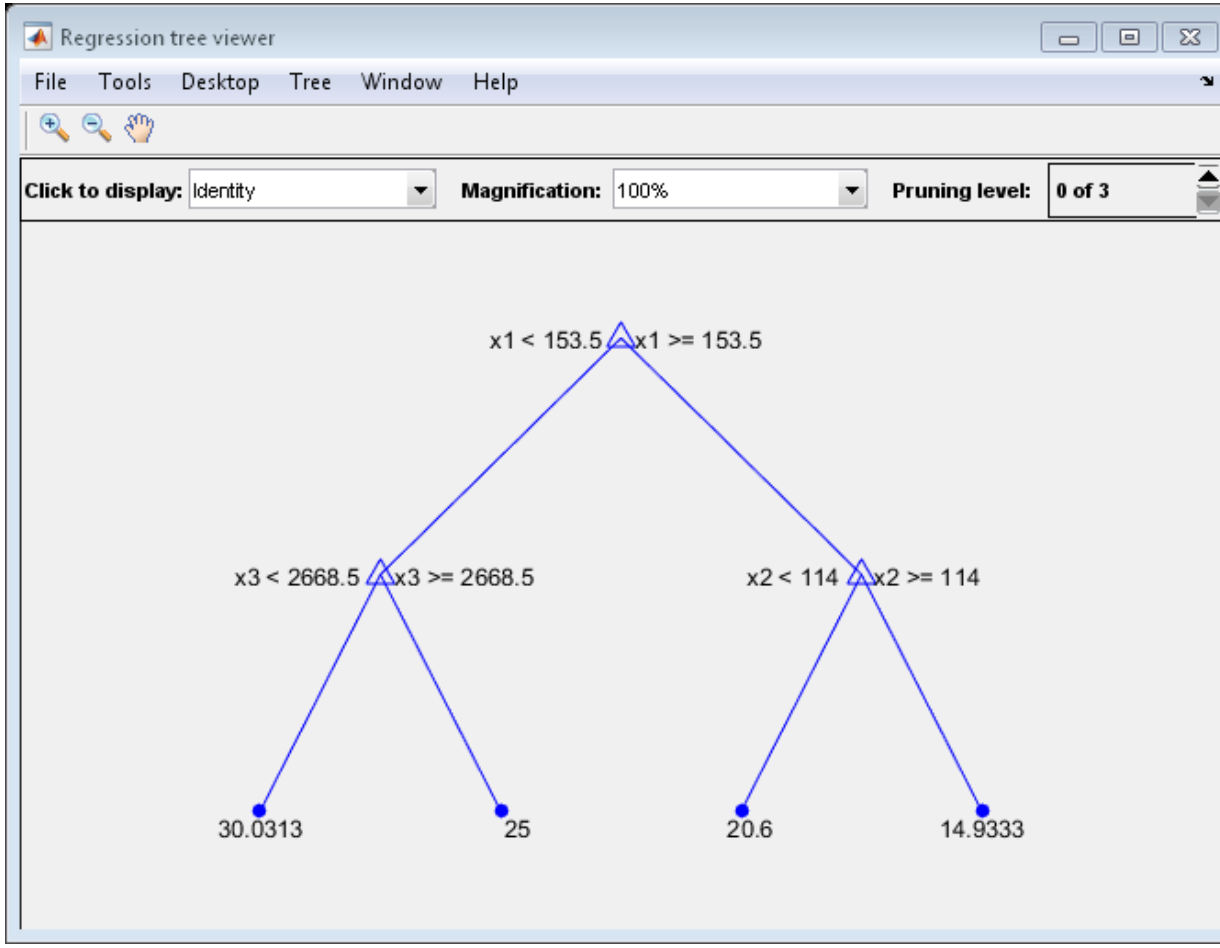
```
valLoss = loss(Mdl,X(idxVal,:),Y(idxVal),'SubTrees',0:m)
```

```
valLoss =

   32.1205
   31.5035
   32.0541
   30.8183
   26.3535
   30.0137
   38.4695
```

- The MSE for the full, unpruned tree (level 0) is about 32.1 units.
- The MSE for the tree pruned to level 4 is about 26.4 units.
- The MSE for the tree pruned to level 5 is about 30.0 units.
- The MSE for the tree pruned to level 6 (i.e., a stump) is about 38.5 units.

To balance model complexity and out-of-sample performance, consider pruning `Mdl` to level 4.

```
pruneMdl = prune(Mdl,'Level',4);
view(pruneMdl,'Mode','graph')
```



See Also

`predict` | `fitrtree`

lowerparams

Class: paretotails

Lower Pareto tails parameters

Syntax

```
params = lowerparams(obj)
```

Description

`params = lowerparams(obj)` returns the 2-element vector `params` of shape and scale parameters, respectively, of the lower tail of the Pareto tails object `obj`. `lowerparams` does not return a location parameter.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

lowerparams(obj)
ans =
   -0.1901    1.1898
upperparams(obj)
ans =
    0.3646    0.5103
```

See Also

`paretotails` | `upperparams`

lt

Class: qrandstream

Less than relation for handles

Syntax

```
h1 < h2
```

Description

`h1 < h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise < result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = lt(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `ge` | `gt` | `ne` | `eq` | `le`

lsline

Add least-squares line to scatter plot

Syntax

```
lsline
lsline(ax)
h = lsline( ___ )
```

Description

`lsline` superimposes a least-squares line on each scatter plot in the current axes. Scatter plots are produced by the MATLAB `scatter` and `plot` functions. Data points connected with solid, dashed, or dash-dot lines (`'-'`, `'--'`, or `'.-'`) are not considered to be scatter plots by `lsline`, and are ignored.

`lsline(ax)` superimposes a least-squares line on the scatter plot in axis `ax`.

`h = lsline( ___ )` returns a column vector of handles `h` to the least-squares lines, using any of the previous syntaxes.

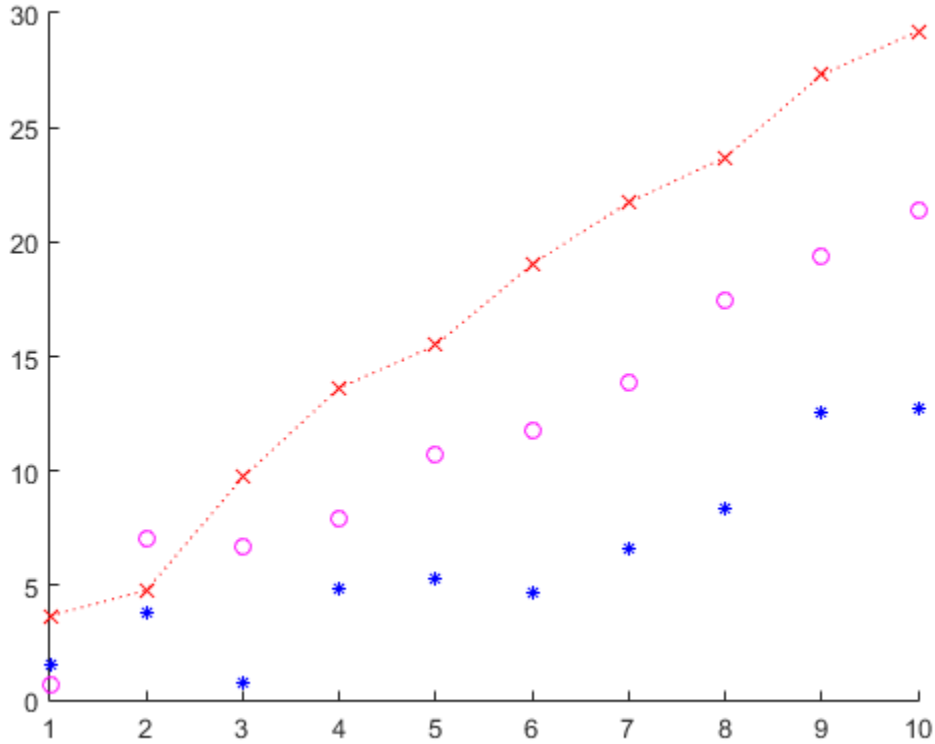
Examples

Plot a Least-Squares Line

Generate three sets of sample data and plot on the same figure.

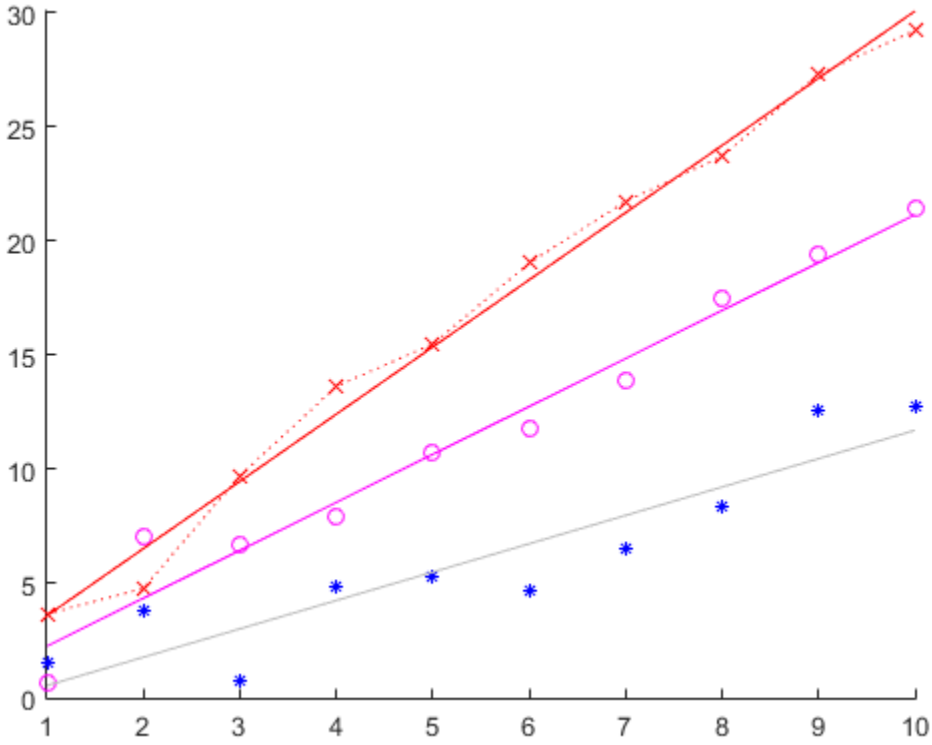
```
x = 1:10;
rng default;  % For reproducibility
figure;

y1 = x + randn(1,10);
scatter(x,y1,25,'b','*')
hold on
```

```
y2 = 2*x + randn(1,10);
plot(x,y2,'mo')

y3 = 3*x + randn(1,10);
plot(x,y3,'rx:')
```



Add a least-squares line for each set of sample data.

```
lsline
```



Specify Axes for Least-Squares and Reference Lines

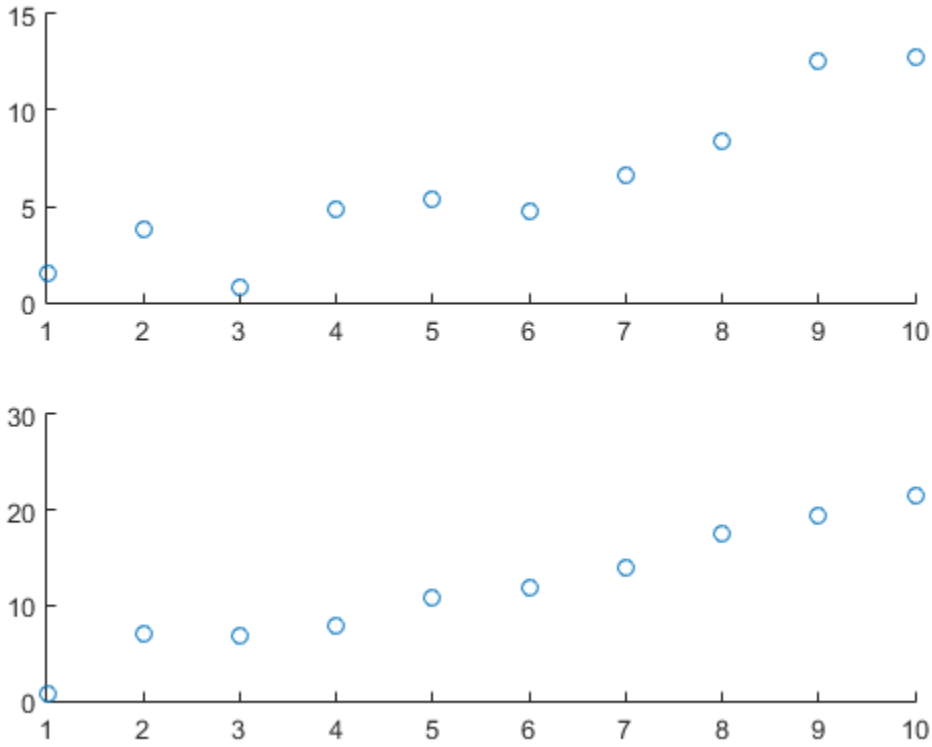
Define the x-variable and two different y-variables to use for the plots.

```
rng default  % For reproducibility
x = 1:10;
y1 = x + randn(1,10);
y2 = 2*x + randn(1,10);
```

Define `ax1` as the top half of the figure, and `ax2` as the bottom half of the figure. Create the first scatter plot on the top axis using `y1`, and the second scatter plot on the bottom axis using `y2`.

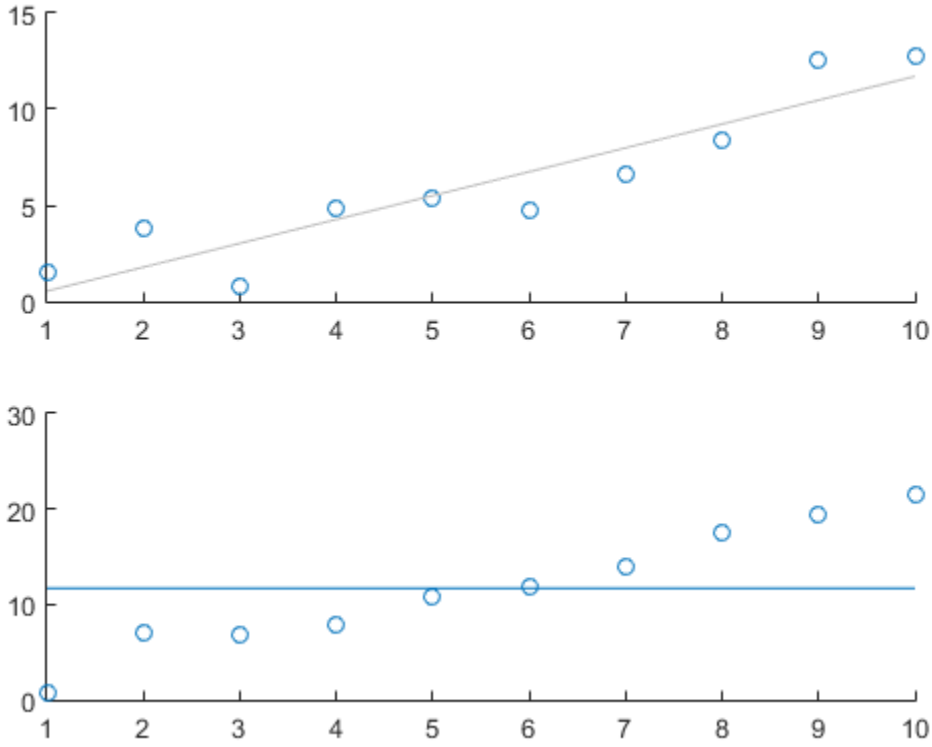
```
figure
```

```
ax1 = subplot(2,1,1);
ax2 = subplot(2,1,2);

scatter(ax1,x,y1)
scatter(ax2,x,y2)
```



Superimpose a least-squares line on the top plot, and a reference line at the mean of the `y2` values in the bottom plot.

```
lsline(ax1)

mu = mean(y2);
refline(ax2,[0 mu])
```



See Also

`scatter` | `plot` | `refline` | `refcurve` | `gline`

mad

Mean or median absolute deviation

Syntax

```
y = mad(X)
Y = mad(X,1)
Y = mad(X,0)
```

Description

`y = mad(X)` returns the mean absolute deviation of the values in `X`. For vector input, `y` is `mean(abs(X-mean(X)))`. For a matrix input, `y` is a row vector containing the mean absolute deviation of each column of `X`. For *N*-dimensional arrays, `mad` operates along the first nonsingleton dimension of `X`.

`Y = mad(X,1)` returns the median absolute deviation of the values in `X`. For vector input, `y` is `median(abs(X-median(X)))`. For a matrix input, `y` is a row vector containing the median absolute deviation of each column of `X`. For *N*-dimensional arrays, `mad` operates along the first nonsingleton dimension of `X`.

`Y = mad(X,0)` is the same as `mad(X)`, and returns the mean absolute deviation of the values in `X`.

`mad(X,flag,dim)` computes absolute deviations along the dimension `dim` of `X`. `flag` is `0` or `1` to indicate mean or median absolute deviation, respectively.

`mad` treats `NaNs` as missing values and removes them.

For normally distributed data, multiply `mad` by one of the following factors to obtain an estimate of the normal scale parameter σ:

- `sigma = 1.253*mad(X,0)` — For mean absolute deviation
- `sigma = 1.4826*mad(X,1)` — For median absolute deviation

Examples

The following compares the robustness of different scale estimates for normally distributed data in the presence of outliers:

```
x = normrnd(0,1,1,50);
xo = [x 10]; % Add outlier

r1 = std(xo)/std(x)
r1 =
    1.7385

r2 = mad(xo,0)/mad(x,0)
r2 =
    1.2306

r3 = mad(xo,1)/mad(x,1)
r3 =
    1.0602
```

References

[1] Mosteller, F., and J. Tukey. *Data Analysis and Regression*. Upper Saddle River, NJ: Addison-Wesley, 1977.

[2] Sachs, L. *Applied Statistics: A Handbook of Techniques*. New York: Springer-Verlag, 1984, p. 253.

See Also

`std` | `range` | `iqr`

mahal

Mahalanobis distance

Syntax

```
d = mahal(Y,X)
```

Description

`d = mahal(Y,X)` computes the Mahalanobis distance (in squared units) of each observation in `Y` from the reference sample in matrix `X`. If `Y` is n-by-m, where n is the number of observations and m is the dimension of the data, `d` is n-by-1. `X` and `Y` must have the same number of columns, but can have different numbers of rows. `X` must have more rows than columns.

For observation `I`, the Mahalanobis distance is defined by `d(I) = (Y(I,:)-mu)*inv(SIGMA)*(Y(I,:)-mu)'`, where `mu` and `SIGMA` are the sample mean and covariance of the data in `X`. `mahal` performs an equivalent, but more efficient, computation.

Examples

Compare Mahalanobis and Squared Euclidean Distances

Generate correlated bivariate data.

```
X = mvnrnd([0;0],[1 .9;.9 1],100);
```

Input observations.

```
Y = [1 1;1 -1;-1 1;-1 -1];
```

Compute the Mahalanobis distance of observations in `Y` from the reference sample in `X` .

```
d1 = mahal(Y,X)
```

```
d1 =

    0.6288
   19.3520
   21.1384
    0.9404
```

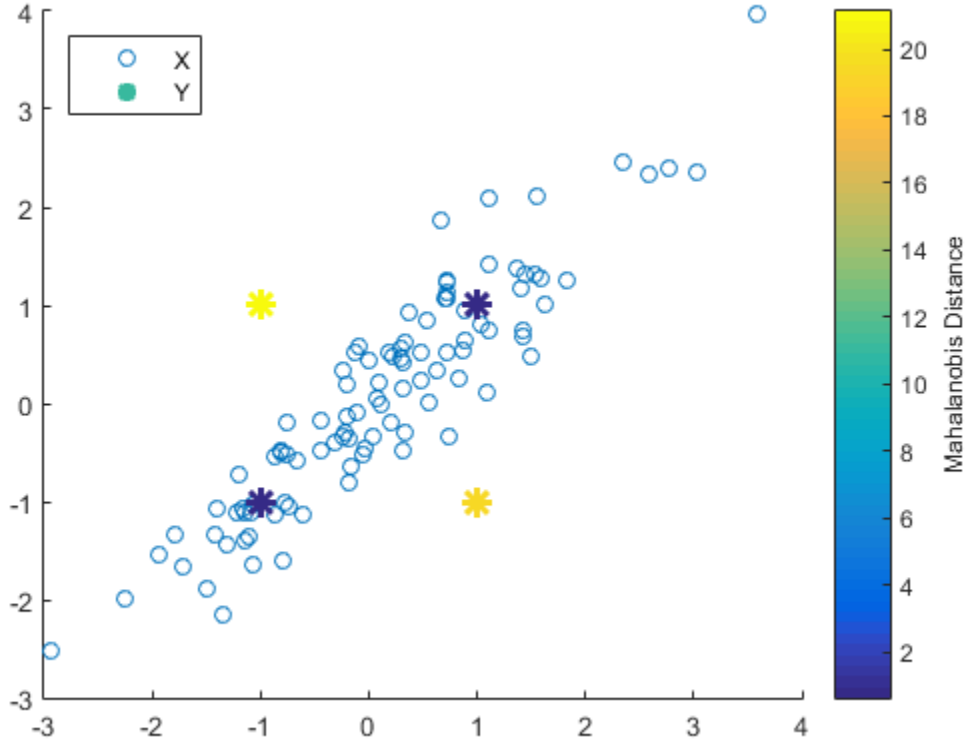
Compute their squared Euclidean distances from the mean of `X` .

```
d2 = sum((Y-repmat(mean(X),4,1)).^2, 2)
```

```
d2 =

    1.6170
    1.9334
    2.1094
    2.4258
```

Plot the observations with `Y` values colored according to the Mahalanobis distance.

```
scatter(X(:,1),X(:,2))
hold on
scatter(Y(:,1),Y(:,2),100,d1,'*','LineWidth',2)
hb = colorbar;
ylabel(hb,'Mahalanobis Distance')
legend('X','Y','Location','NW')
```



The observations in Y with equal coordinate values are much closer to X in Mahalanobis distance than observations with opposite coordinate values, even though all observations are approximately equidistant from the mean of X in Euclidean distance. The Mahalanobis distance, by considering the covariance of the data and the scales of the different variables, is useful for detecting outliers in such cases.

See Also

`pdist` | `mahal`

mahal

Class: CompactClassificationDiscriminant

Mahalanobis distance to class means

Syntax

```
M = mahal(obj,X)
M = mahal(obj,X,Name,Value)
```

Description

`M = mahal(obj,X)` returns the squared Mahalanobis distances from observations in `X` to the class means in `obj`.

`M = mahal(obj,X,Name,Value)` computes the squared Mahalanobis distance with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `fitcdiscr`.

`X`

Numeric matrix of size `n`-by-`p`, where `p` is the number of predictors in obj, and `n` is any positive integer. `mahal` computes the Mahalanobis distances from the rows of `X` to each of the `K` means of the classes in `obj`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'ClassLabels'`

Class labels consisting of `n` elements of obj`.Y`, where `n` is the number of rows of X.

Output Arguments

`M`

Size and meaning of output `M` depends on whether the `ClassLabels` name-value pair is present:

- No `ClassLabels` — `M` is a numeric matrix of size `n`-by-`K`, where `K` is the number of classes in obj, and `n` is the number of rows in X. `M(i,j)` is the squared Mahalanobis distance from the `i`th row of `X` to the mean of class `j`.
- `ClassLabels` exists — `M` is a column vector with `n` elements. `M(i)` is the squared Mahalanobis distance from the `i`th row of `X` to the mean for the class of the `i`th element of `ClassLabels`.

Definitions

Mahalanobis Distance

The Mahalanobis distance $d(x,y)$ between n-dimensional points x and y, with respect to a given n-by-n covariance matrix S, is

$$d(x,y) = \sqrt{(x-y)^T S^{-1} (x-y)}.$$

Examples

Find the Mahalanobis distances from the mean of the Fisher iris data to the class means, using distinct covariance matrices for each class:

```
load fisheriris
obj = fitcdiscr(meas,species,...
    'DiscrimType','quadratic');
mahadist = mahal(obj,mean(meas))

mahadist =
  220.0667    5.0254   30.5804
```

See Also

`CompactClassificationDiscriminant` | `fitcdiscr` | `mahal` | `gmdistribution`

How To

- “Discriminant Analysis” on page 15-3

mahal

Class: gmdistribution

Mahalanobis distance to component means

Syntax

```
D = mahal(obj,X)
```

Description

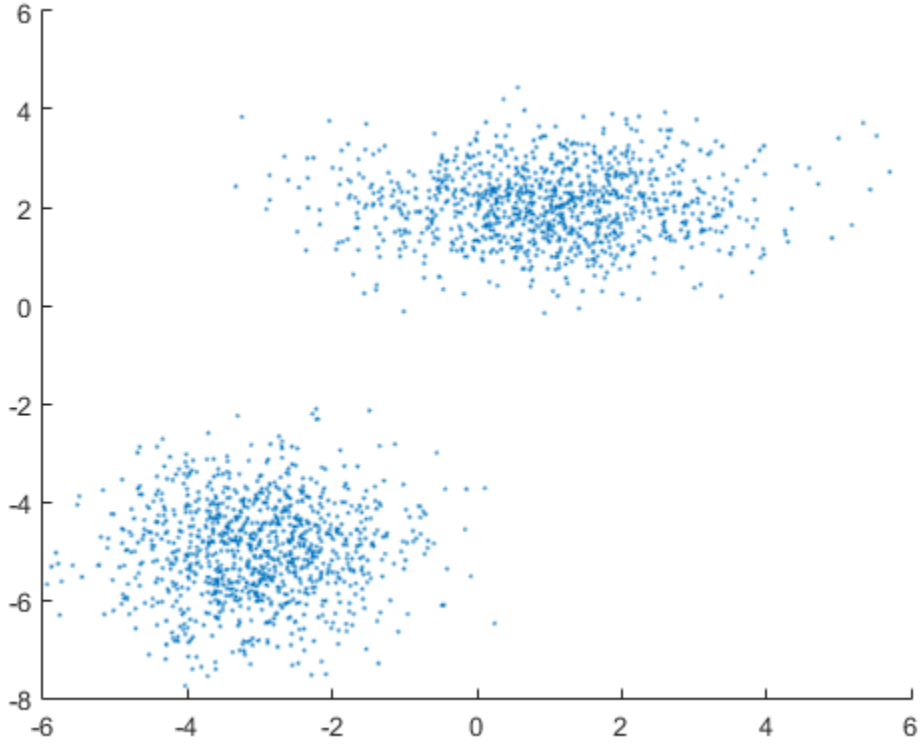
`D = mahal(obj,X)` computes the Mahalanobis distance (in squared units) of each observation in `X` to the mean of each of the k components of the Gaussian mixture distribution defined by `obj`. `obj` is an object created by `gmdistribution` or `fitgmdist`. `X` is an n-by-d matrix, where n is the number of observations and d is the dimension of the data. `D` is n-by-k, with `D(I,J)` the distance of observation `I` from the mean of component `J`.

Examples

Measure Mahalanobis Distances in Gaussian Mixture Data

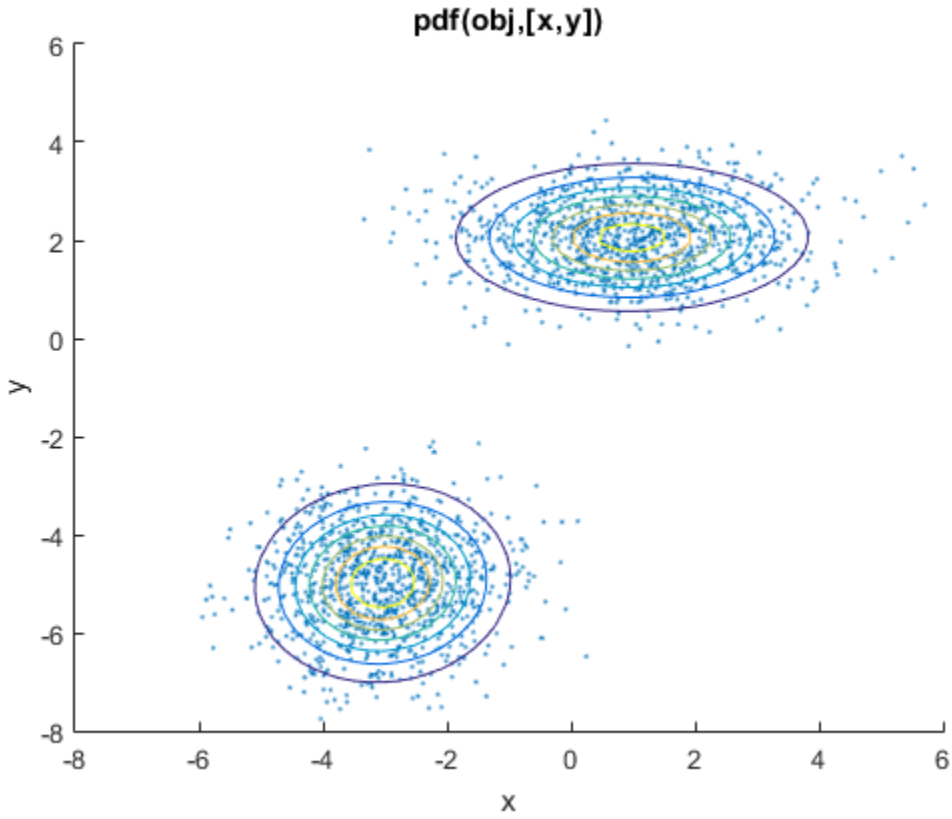
Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function.

```
MU1 = [1 2];
SIGMA1 = [2 0; 0 .5];
MU2 = [-3 -5];
SIGMA2 = [1 0; 0 1];
rng(1); % For reproducibility
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



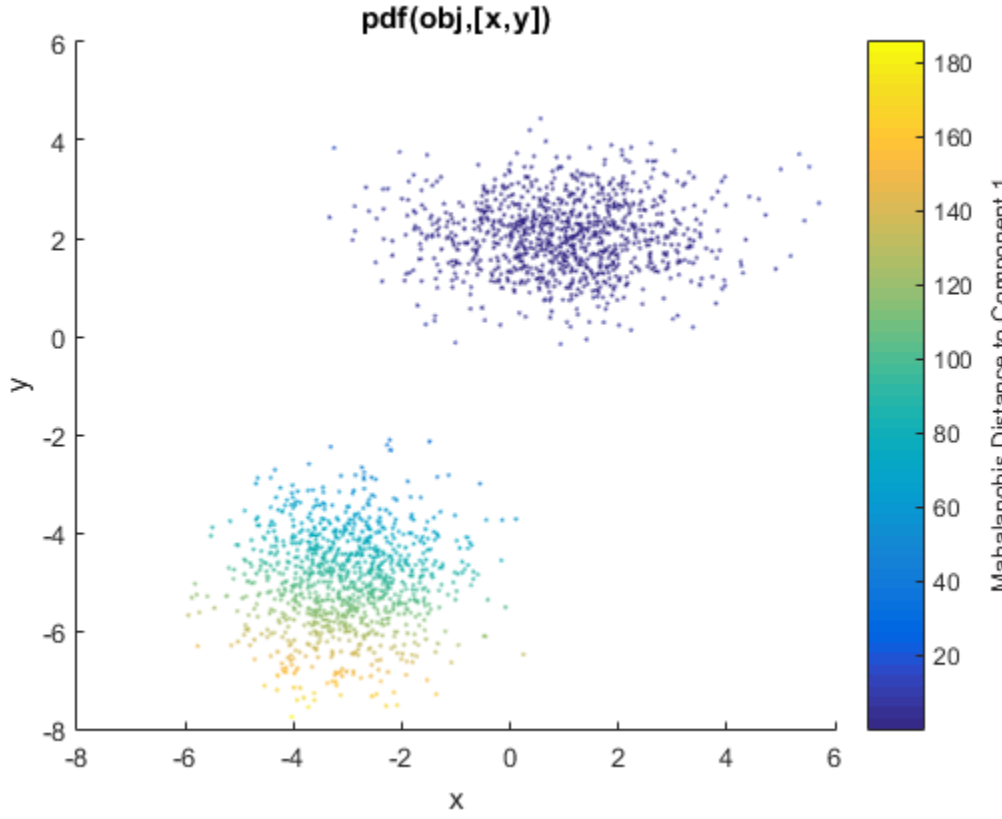
Fit a two-component Gaussian mixture model.

```
obj = fitgmdist(X,2);
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Compute the Mahalanobis distance of each point in `X` to the mean of each component of `obj`.

```
D = mahal(obj,X);

delete(h)
scatter(X(:,1),X(:,2),10,D(:,1),'.')
hb = colorbar;
ylabel(hb,'Mahalanobis Distance to Component 1')
```



See Also

`gmdistribution` | `posterior` | `cluster` | `mahal`

maineffectsplot

Main effects plot for grouped data

Syntax

```
maineffectsplot(Y,GROUP)
maineffectsplot(Y,GROUP,param1,val1,param2,val2,...)
[figh,AXESH] = maineffectsplot(...)
```

Description

`maineffectsplot(Y,GROUP)` displays main effects plots for the group means of matrix `Y` with groups defined by entries in the cell array `GROUP`. `Y` is a numeric matrix or vector. If `Y` is a matrix, the rows represent different observations and the columns represent replications of each observation. Each cell of `GROUP` must contain a grouping variable that can be a categorical variable, numeric vector, character matrix, or single-column cell array of strings. `GROUP` can also be a matrix whose columns represent different grouping variables. Each grouping variable must have the same number of rows as `Y`. The number of grouping variables must be greater than 1.

The display has one subplot per grouping variable, with each subplot showing the group means of `Y` as a function of one grouping variable.

`maineffectsplot(Y,GROUP,param1,val1,param2,val2,...)` specifies one or more of the following name/value pairs:

- `'varnames'` — Grouping variable names in a character matrix or a cell array of strings, one per grouping variable. Default names are `'X1'`, `'X2'`, ...
- `'statistic'` — String values that indicate whether the group mean or the group standard deviation should be plotted. Use `'mean'` or `'std'`. The default is `'mean'`. If the value is `'std'`, `Y` is required to have multiple columns.
- `'parent'` — A handle to the figure window for the plots. The default is the current figure window.

`[figh,AXESH] = maineffectsplot(...)` returns the handle `figh` to the figure window and an array of handles `AXESH` to the subplot axes.

Examples

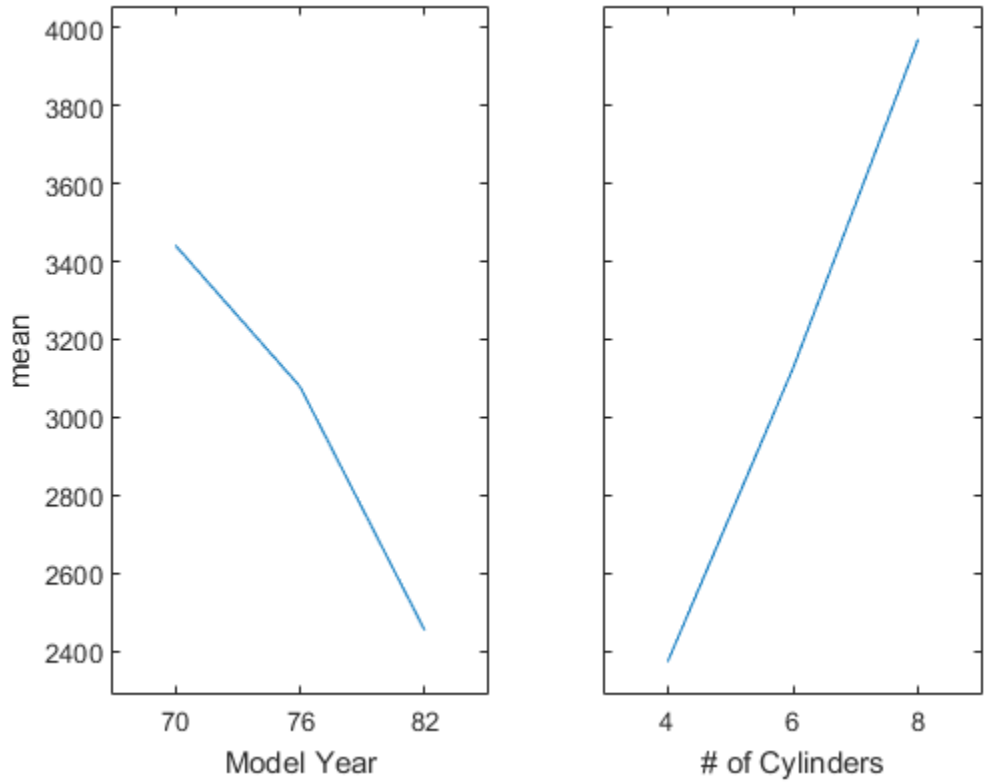
Main Effects Plot

Load the sample data.

```
load carsmall;
```

Display main effects plots for car weight with two grouping variables, model year and number of cylinders.

```
maineffectsplot(Weight,{Model_Year,Cylinders}, ...
                'varnames',{'Model Year','# of Cylinders'})
```



More About

- "Grouping Variables" on page 2-52

See Also

`interactionplot` | `multivarichart`

ClassificationDiscriminant.make

Class: ClassificationDiscriminant

Construct discriminant analysis classifier from parameters (to be removed)

Compatibility

`ClassificationDiscriminant.make` will be removed in a future release. Use `makecdiscr` instead.

Syntax

```
cobj = ClassificationDiscriminant.make(Mu,Sigma)
cobj = ClassificationDiscriminant.make(Mu,Sigma,Name,Value)
```

Description

`cobj = ClassificationDiscriminant.make(Mu,Sigma)` constructs a compact discriminant analysis classifier from the class means `Mu` and covariance matrix `Sigma`.

`cobj = ClassificationDiscriminant.make(Mu,Sigma,Name,Value)` constructs a compact classifier with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`Mu` — Class means

matrix of scalar values

Class means, specified as a `K`-by-`p` matrix of scalar values class means of size. `K` is the number of classes, and `p` is the number of predictors. Each row of `Mu` represents the mean of the multivariate normal distribution of the corresponding class. The class indices are in the ClassNames attribute.

`Sigma` — Within-class covariance
matrix of scalar values

Within-class covariance, specified as a matrix of scalar values.

- For a linear discriminant, `Sigma` is a symmetric, positive semidefinite matrix of size `p`-by-`p`, where `p` is the number of predictors.
- For a quadratic discriminant, `Sigma` is an array of size `p`-by-`p`-by-`K`, where `K` is the number of classes. For each `i`, `Sigma(:,:,i)` is a symmetric, positive semidefinite matrix.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'ClassNames'` — Class names
numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names as ordered in Mu, specified as the comma-separated pair consisting of `'ClassNames'` and an array containing grouping variables. Use any data type for a grouping variable, including numeric vector, categorical vector, logical vector, character array, or cell array of strings.

`ClassNames` names the classes, as ordered in `Mu`.

Default is `1:K`, where `K` is the number of classes (the number of rows of Mu).

Data Types: `single` | `double` | `logical` | `char` | `cell`

`'Cost'` — Cost of misclassification
square matrix | structure

Cost of misclassification, specified as the comma-separated pair consisting of `'Cost'` and a square matrix, where `Cost(i,j)` is the cost of classifying a point into class

`j` if its true class is `i`. Alternatively, `Cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Data Types: `single` | `double` | `struct`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

Data Types: `cell`

`'Prior'` — Prior probabilities

`'uniform'` (default) | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following.

- `'uniform'`, a string meaning all class prior probabilities are equal.
- A vector containing one scalar value for each class.
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as `ClassNames`.
  - `S.ClassProbs` containing a vector of corresponding probabilities.

Data Types: `single` | `double` | `struct`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable y.

Example: `'ResponseName','Response'`

Data Types: `char`

Output Arguments

`cobj` — Discriminant analysis classifier

discriminant analysis classifier object

Discriminant analysis classifier, returned as a discriminant analysis classifier object of class `CompactClassificationDiscriminant`. You can use the `predict` method to predict classification labels for new data.

Examples

Construct a Compact Linear Discriminant Analysis Classifier

Construct a compact linear discriminant analysis classifier from the means and covariances of the Fisher iris data.

```
load fisheriris
mu(1,:) = mean(meas(1:50,:));
mu(2,:) = mean(meas(51:100,:));
mu(3,:) = mean(meas(101:150,:));

mm1 = repmat(mu(1,:),50,1);
mm2 = repmat(mu(2,:),50,1);
mm3 = repmat(mu(3,:),50,1);
cc = meas;
cc(1:50,:) = cc(1:50,:) - mm1;
cc(51:100,:) = cc(51:100,:) - mm2;
cc(101:150,:) = cc(101:150,:) - mm3;
sigstar = cc' * cc / 147; % unbiased estimator of sigma
cpct = ClassificationDiscriminant.make(mu,sigstar,...
   'ClassNames',{'setosa','versicolor','virginica'})

cpct =
classreg.learning.classif.CompactClassificationDiscriminant:
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
       DiscrimType: 'linear'
                Mu: [3x4 double]
```

```
            Coeffs: [3x3 struct]
```

See Also

`compact` | `CompactClassificationDiscriminant` | `fitcdiscr` | `makecdiscr`

How To

- “Discriminant Analysis” on page 15-3

makecdiscr

Construct discriminant analysis classifier from parameters

Syntax

```
cobj = makecdiscr(Mu,Sigma)
cobj = makecdiscr(Mu,Sigma,Name,Value)
```

Description

`cobj = makecdiscr(Mu,Sigma)` constructs a compact discriminant analysis classifier from the class means `Mu` and covariance matrix `Sigma`.

`cobj = makecdiscr(Mu,Sigma,Name,Value)` constructs a compact classifier with additional options specified by one or more name-value pair arguments. For example, you can specify the cost of misclassification or the prior probabilities for each class.

Examples

Construct a Compact Linear Discriminant Analysis Classifier

Construct a compact linear discriminant analysis classifier from the means and covariances of the Fisher iris data.

```
load fisheriris
mu(1,:) = mean(meas(1:50,:));
mu(2,:) = mean(meas(51:100,:));
mu(3,:) = mean(meas(101:150,:));

mm1 = repmat(mu(1,:),50,1);
mm2 = repmat(mu(2,:),50,1);
mm3 = repmat(mu(3,:),50,1);
cc = meas;
cc(1:50,:) = cc(1:50,:) - mm1;
cc(51:100,:) = cc(51:100,:) - mm2;
cc(101:150,:) = cc(101:150,:) - mm3;
sigstar = cc' * cc / 147; % unbiased estimator of sigma
```

```
cpct = makecdiscr(mu,sigstar,...
   'ClassNames',{'setosa','versicolor','virginica'})

cpct =
classreg.learning.classif.CompactClassificationDiscriminant:
    PredictorNames: {'x1'  'x2'  'x3'  'x4'}
      ResponseName: 'Y'
        ClassNames: {'setosa'  'versicolor'  'virginica'}
    ScoreTransform: 'none'
       DiscrimType: 'linear'
                Mu: [3x4 double]
            Coeffs: [3x3 struct]
```

Input Arguments

`Mu` — Class means

matrix of scalar values

Class means, specified as a `K`-by-`p` matrix of scalar values class means of size. `K` is the number of classes, and `p` is the number of predictors. Each row of `Mu` represents the mean of the multivariate normal distribution of the corresponding class. The class indices are in the ClassNames attribute.

Data Types: `single` | `double`

`Sigma` — Within-class covariance

matrix of scalar values

Within-class covariance, specified as a matrix of scalar values.

- For a linear discriminant, `Sigma` is a symmetric, positive semidefinite matrix of size `p`-by-`p`, where `p` is the number of predictors.
- For a quadratic discriminant, `Sigma` is an array of size `p`-by-`p`-by-`K`, where `K` is the number of classes. For each `i`, `Sigma(:,:,i)` is a symmetric, positive semidefinite matrix.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'ClassNames',{'setosa' 'versicolor' 'virginica'}` specifies a discriminant analysis classifier that uses `'setosa'`, `'versicolor'`, and `'virginica'` as the grouping variables.

`'ClassNames'` — Class names

numeric vector | categorical vector | logical vector | character array | cell array of strings

Class names as ordered in `Mu`, specified as the comma-separated pair consisting of `'ClassNames'` and an array containing grouping variables. Use any data type for a grouping variable, including numeric vector, categorical vector, logical vector, character array, or cell array of strings.

The default is `1:K`, where `K` is the number of classes (the number of rows of Mu).

Example: `'ClassNames',{'setosa' 'versicolor' 'virginica'}`

Data Types: `single` | `double` | `logical` | `char` | `cell`

`'Cost'` — Cost of misclassification

square matrix | structure

Cost of misclassification, specified as the comma-separated pair consisting of `'Cost'` and a square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. Alternatively, `Cost` can be a structure `S` having two fields: `S.ClassNames` containing the group names as a variable of the same type as y, and `S.ClassificationCosts` containing the cost matrix.

The default is `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`.

Data Types: `single` | `double` | `struct`

`'PredictorNames'` — Predictor variable names

`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

Data Types: `cell`

`'Prior'` — Prior probabilities
`'uniform'` (default) | vector of scalar values | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and one of the following:

- `'uniform'`, a string meaning all class prior probabilities are equal
- A vector containing one scalar value for each class
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a variable of the same type as `ClassNames`
  - `S.ClassProbs` containing a vector of corresponding probabilities

Data Types: `single` | `double` | `struct`

`'ResponseName'` — Response variable name
`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable y.

Example: `'ResponseName','Response'`

Data Types: `char`

Output Arguments

`cobj` — Discriminant analysis classifier
discriminant analysis classifier object

Discriminant analysis classifier, returned as a discriminant analysis classifier object of class `CompactClassificationDiscriminant`. You can use the `predict` method to predict classification labels for new data.

More About

Tips

- You can change the discriminant type using dot notation after constructing cobj:

```
cobj.DiscrimType = 'discrimType'
```

where *discrimType* is one of `'linear'`, `'quadratic'`, `'diagLinear'`, `'diagQuadratic'`, `'pseudoLinear'`, or `'pseudoQuadratic'`. You can change between linear types or between quadratic types, but cannot change between a linear and a quadratic type.

- `cobj` is a linear classifier when `Sigma` is a matrix. `cobj` is a quadratic classifier when `Sigma` is a three-dimensional array.

- "Discriminant Analysis" on page 15-3

See Also

`compact` | `CompactClassificationDiscriminant` | `fitcdiscr` | `predict`

makedist

Create probability distribution object

Syntax

```
pd = makedist(distname)
pd = makedist(distname,Name,Value)
```

Description

`pd = makedist(distname)` creates a probability distribution object for the distribution `distname`, using the default parameter values.

`pd = makedist(distname,Name,Value)` creates a probability distribution object with one or more distribution parameter values specified by name-value pair arguments.

Examples

Create a Normal Distribution Object

Create a normal distribution object using the default parameter values.

```
pd = makedist('Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Compute the interquartile range of the distribution.

```
r = iqr(pd)
```

```
r =
```

```
    1.3490
```

Create a Gamma Distribution Object

Create a gamma distribution object using the default parameter values.

```
pd = makedist('Gamma')
```

```
pd =

  GammaDistribution

  Gamma distribution
    a = 1
    b = 1
```

Compute the mean of the gamma distribution.

```
mean = mean(pd)
```

```
mean =

     1
```

Specify Parameters for a Normal Distribution Object

Create a normal distribution object with parameter values `mu = 75` and `sigma = 10`.

```
pd = makedist('Normal','mu',75,'sigma',10)
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75
    sigma = 10
```

Specify Parameters for a Gamma Distribution Object

Create a gamma distribution object with the parameter value `a = 3` and the default value `b = 1`.

```
pd = makedist('Gamma','a',3)
```

```
pd =

  GammaDistribution

  Gamma distribution
    a = 3
    b = 1
```

Input Arguments

`distname` — Distribution name

string

Distribution name, specified as one of the following strings. The distribution specified by `distname` determines the class type of the returned probability distribution object.

Distribution Name	Description	Distribution Class
`'Beta'`	Beta distribution	`prob.BetaDistribution`
`'Binomial'`	Binomial distribution	`prob.BinomialDistribution`
`'BirnbaumSaunders'`	Birnbaum-Saunders distribution	`prob.BirnbaumSaundersDistributio`
`'Burr'`	Burr distribution	`prob.BurrDistribution`
`'Exponential'`	Exponential distribution	`prob.ExponentialDistribution`
`'ExtremeValue'`	Extreme Value distribution	`prob.ExtremeValueDistribution`
`'Gamma'`	Gamma distribution	`prob.GammaDistribution`
`'GeneralizedExtremeVal`	Generalized Extreme Value distribution	`prob.GeneralizedExtremeValueDist`
`'GeneralizedPareto'`	Generalized Pareto distribution	`prob.GeneralizedParetoDistributi`
`'InverseGaussian'`	Inverse Gaussian distribution	`prob.InverseGaussianDistribution`
`'Logistic'`	Logistic distribution	`prob.LogisticDistribution`
`'Loglogistic'`	Loglogistic distribution	`prob.LoglogisticDistribution`
`'Lognormal'`	Lognormal distribution	`prob.LognormalDistribution`

Distribution Name	Description	Distribution Class
'Multinomial'	Multinomial distribution	prob.MultinomialDistribution
'Nakagami'	Nakagami distribution	prob.NakagamiDistribution
'NegativeBinomial'	Negative Binomial distribution	prob.NegativeBinomialDistributio
'Normal'	Normal distribution	prob.NormalDistribution
'PiecewiseLinear'	Piecewise Linear distribution	prob.PiecewiseLinearDistribution
'Poisson'	Poisson distribution	prob.PoissonDistribution
'Rayleigh'	Rayleigh distribution	prob.RayleighDistribution
'Rician'	Rician distribution	prob.RicianDistribution
'tLocationScale'	*t* Location-Scale distribution	prob.tLocationScaleDistribution
'Triangular'	Triangular distribution	prob.TriangularDistribution
'Uniform'	Uniform distribution	prob.UniformDistribution
'Weibull'	Weibull distribution	prob.WeibullDistribution

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `makedist('Normal','mu',10)` specifies a normal distribution with parameter `mu` equal to 10, and parameter `sigma` equal to the default value of 1.

Beta Distribution

'a' — First shape parameter

1 (default) | nonnegative scalar value

Example: `'a',3`

Data Types: `single` | `double`

'b' — Second shape parameter

1 (default) | nonnegative scalar value

Example: `'b',5`

Data Types: `single` | `double`

Binomial Distribution

`'N'` — Number of trials
1 (default) | positive integer value

Example: `'N',25`

Data Types: `single` | `double`

`'p'` — Probability of success
`0.5` (default) | scalar value in the range [0,1]

Example: `'p',0.25`

Data Types: `single` | `double`

Birnbaum-Saunders Distribution

`'beta'` — Scale parameter
1 (default) | positive scalar value

Example: `'beta',2`

Data Types: `single` | `double`

`'gamma'` — Shape parameter
1 (default) | nonnegative scalar value

Example: `'gamma',0`

Data Types: `single` | `double`

Burr Distribution

`'alpha'` — Scale parameter
1 (default) | positive scalar value

Example: `'alpha',2`

Data Types: `single` | `double`

`'c'` — First shape parameter
1 (default) | positive scalar value

Example: `'c',2`

Data Types: `single` | `double`

`'k'` — Second shape parameter
1 (default) | positive scalar value

Example: `'k',5`

Data Types: `single` | `double`

Exponential Distribution

`'mu'` — Mean parameter
1 (default) | positive scalar value

Example: `'mu',5`

Data Types: `single` | `double`

Extreme Value Distribution

`'mu'` — Location parameter
0 (default) | scalar value

Example: `'mu',-2`

Data Types: `single` | `double`

`'sigma'` — Scale parameter
1 (default) | nonnegative scalar value

Example: `'sigma',2`

Data Types: `single` | `double`

Gamma Distribution

`'a'` — Shape parameter
1 (default) | positive scalar value

Example: `'a',2`

Data Types: `single` | `double`

`'b'` — Scale parameter
1 (default) | nonnegative scalar value

Example: `'b',0`

Data Types: `single` | `double`

Generalized Extreme Value Distribution

`'k'` — Shape parameter
0 (default) | scalar value

Example: `'k',0`

Data Types: `single` | `double`

`'sigma'` — Scale parameter
1 (default) | nonnegative scalar value

Example: `'sigma',2`

Data Types: `single` | `double`

`'mu'` — Location parameter
0 (default) | scalar value

Example: `'mu',1`

Data Types: `single` | `double`

Generalized Pareto Distribution

`'k'` — Shape parameter
1 (default) | scalar value

Example: `'k',0`

Data Types: `single` | `double`

`'sigma'` — Scale parameter
1 (default) | nonnegative scalar value

Example: `'sigma',2`

Data Types: `single` | `double`

`'theta'` — Location parameter
1 (default) | scalar value

Example: `'theta',2`

Data Types: `single` | `double`

Inverse Gaussian Distribution

`'mu'` — Scale parameter
1 (default) | positive scalar value

Example: `'mu',2`

Data Types: `single` | `double`

`'lambda'` — Shape parameter
1 (default) | positive scalar value

Example: `'lambda',4`

Data Types: `single` | `double`

Logistic Distribution

`'mu'` — Mean
0 (default) | scalar value

Example: `'mu',2`

Data Types: `single` | `double`

`'sigma'` — Scale parameter
1 (default) | nonnegative scalar value

Example: `'sigma',4`

Data Types: `single` | `double`

Loglogistic Distribution

`'mu'` — Log mean
0 (default) | scalar value

Example: `'mu',2`

Data Types: `single` | `double`

`'sigma'` — Log scale parameter
1 (default) | nonnegative scalar value

Example: `'sigma',4`

Data Types: `single` | `double`

Lognormal Distribution

`'mu'` — Log mean
0 (default) | scalar value

Example: `'mu',2`

Data Types: `single` | `double`

`'sigma'` — Log standard deviation
1 (default) | nonnegative scalar value

Example: `'sigma',2`

Data Types: `single` | `double`

Multinomial Distribution

`'probabilities'` — Outcome probabilities
`[0.500 0.500]` (default) | vector of scalar values in the range [0,1]

Example: `'probabilities',[0.1 0.2 0.5 0.2]`

Data Types: `single` | `double`

Nakagami Distribution

`'mu'` — Shape parameter
1 (default) | positive scalar value

Example: `'mu',5`

Data Types: `single` | `double`

`'omega'` — Scale parameter
1 (default) | positive scalar value

Example: `'omega',5`

Data Types: `single` | `double`

Negative Binomial Distribution

`'R'` — Number of successes
1 (default) | positive scalar value

Example: `'R',5`

Data Types: `single` | `double`

`'p'` — Probability of success

`0.5` (default) | scalar value in the range (0,1]

Example: `'p',0.1`

Data Types: `single` | `double`

Normal Distribution

`'mu'` — Mean

`0` (default) | scalar value

Example: `'mu',2`

Data Types: `single` | `double`

`'sigma'` — Standard deviation

`1` (default) | nonnegative scalar value

Example: `'sigma',2`

Data Types: `single` | `double`

Piecewise Linear Distribution

`'x'` — Data values

`1` (default) | vector of scalar values

Example: `'x',[1 2 3]`

Data Types: `single` | `double`

`'Fx'` — cdf values

`1` (default) | vector of scalar values

Example: `'Fx',[.2 .5 1]`

Data Types: `single` | `double`

Poisson Distribution

`'lambda'` — Mean

`1` (default) | nonnegative scalar value

Example: `'lambda',5`

Data Types: `single` | `double`

Rayleigh Distribution

`'b'` — Defining parameter

1 (default) | positive scalar value

Example: `'b',3`

Data Types: `single` | `double`

Rician Distribution

`'s'` — Noncentrality parameter

1 (default) | nonnegative scalar value

Example: `'s',0`

Data Types: `single` | `double`

`'sigma'` — Scale parameter

1 (default) | positive scalar value

Example: `'sigma',2`

Data Types: `single` | `double`

t Location-Scale Distribution

`'mu'` — Location parameter

0 (default) | scalar value

Example: `'mu',-2`

Data Types: `single` | `double`

`'sigma'` — Scale parameter

1 (default) | positive scalar value

Example: `'sigma',2`

Data Types: `single` | `double`

`'nu'` — Degrees of freedom

5 (default) | positive scalar value

Example: `'nu',20`

Data Types: `single` | `double`

Triangular Distribution

`'a'` — Lower limit
`0` (default) | scalar value

Example: `'a',-2`

Data Types: `single` | `double`

`'b'` — Peak location
`0.5` (default) | scalar value greater than or equal to `a`

Example: `'b',1`

Data Types: `single` | `double`

`'c'` — Upper limit
`1` (default) | scalar value greater than or equal to `b`

Example: `'c',5`

Data Types: `single` | `double`

Uniform Distribution

`'lower'` — Lower parameter
`0` (default) | scalar value

Example: `'lower',-4`

Data Types: `single` | `double`

`'upper'` — Upper parameter
`1` (default) | scalar value greater than `lower`

Example: `'upper',2`

Data Types: `single` | `double`

Weibull Distribution

`'a'` — Scale parameter
`1` (default) | positive scalar value

Example: `'a',2`

Data Types: `single` | `double`

`'b'` — Shape parameter

1 (default) | positive scalar value

Example: `'b',5`

Data Types: `single` | `double`

Output Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, returned as a probability distribution object of the type specified by distname.

Alternative Functionality

App

The Distribution Fitting app opens a graphical user interface for you to import data from the workspace and interactively fit a probability distribution to that data. You can then save the distribution to the workspace as a probability distribution object. Open the Distribution Fitting app using `dfittool`, or click Distribution Fitting on the Apps tab.

See Also

`dfittool` | `fitdist`

manova

Class: RepeatedMeasuresModel

Multivariate analysis of variance

Syntax

```
manovatbl = manova(rm)
manovatbl = manova(rm,Name,Value)
[manovatbl,A,C,D] = manova( ___ )
```

Description

`manovatbl = manova(rm)` returns the results of multivariate analysis of variance (manova) for the repeated measures model rm.

`manovatbl = manova(rm,Name,Value)` also returns manova results with additional options, specified by one or more Name,Value pair arguments.

`[manovatbl,A,C,D] = manova( ___ )` also returns arrays A, C, and D for the hypotheses tests of the form `A*B*C = D`, where `D` is zero.

Tips

- The multivariate response for each observation (subject) is the vector of repeated measures.
- To test a more general hypothesis `A*B*C = D`, use `coeftest`.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'WithinModel'` — Model specifying within-subjects hypothesis test

`'separatemeans'` (default) | model specification using formula

Model specifying the within-subjects hypothesis test, specified as one of the following:

- `'separatemeans'` — Compute a separate mean for each group, and test for equality among the means.
- Model specification — This is a model specification in the within-subject factors. Test each term in the model. In this case, `tbl` contains a separate manova for each term in the formula, with the multivariate response equal to the vector of coefficients of that term.
- An *r*-by-*nc* matrix, *C*, specifying *nc* contrasts among the *r* repeated measures. If *Y* represents the matrix of repeated measures you use in the repeated measures model `rm`, then the output `tbl` contains a separate manova for each column of *Y***C*.

Example: `'WithinModel','separatemeans'`

`'By'` — Single between-subjects factor

string

Single between-subjects factor, specified as the comma-separated pair consisting of `'By'` and a string. `manova` performs a separate test of the within-subjects model for each value of this factor.

For example, if you have a between-subjects factor, Drug, then you can specify that factor to perform manova as follows.

Example: `'By','Drug'`

Output Arguments

`manovatbl` — Results of multivariate analysis of variance

table

Results of multivariate analysis of variance for the repeated measures model rm, returned as a `table`.

`manova` uses these methods to measure the contributions of the model terms to the overall covariance:

- Wilks' Lambda
- Pillai's trace
- Hotelling-Lawley trace
- Roy's maximum root statistic

For details, see "Multivariate Analysis of Variance for Repeated Measures" on page 8-83.

`manova` returns the results for these tests for each group. manovatbl contains the following columns.

Column Name	Definition
`Within`	Within-subject terms
`Between`	Between-subject terms
`Statistic`	Name of the statistic computed
`Value`	Value of the corresponding statistic
`F`	*F*-statistic value
`RSquare`	Measure for variance explained
`df1`	Numerator degrees of freedom
`df2`	Denominator degrees of freedom
`pValue`	*p*-value for the corresponding *F*-statistic value

Data Types: `table`

`A` — Specification based on between-subjects model

matrix | cell array

Specification based on the between-subjects model, returned as a matrix or a cell array. It permits the hypothesis on the elements within given columns of `B` (within time hypothesis). If manovatbl contains multiple hypothesis tests, A might be a cell array.

Data Types: `single` | `double` | `cell`

`C` — Specification based on within-subjects model

matrix | cell array

Specification based on the within-subjects model, returned as a matrix or a cell array. It permits the hypotheses on the elements within given rows of `B` (between time hypotheses). If manovatbl contains multiple hypothesis tests, C might be a cell array.

Data Types: `single` | `double` | `cell`

`D` — Hypothesis value

0

Hypothesis value, returned as 0.

Examples

Perform Multivariate Analysis of Variance

Load the sample data.

```
load fisheriris
```

The column vector `species`consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = table([1 2 3 4]','VariableNames',{'Measurements'});
```

Fit a repeated measures model where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform multivariate analysis of variance.

```
manova(rm)
```

```
ans =

    Within       Between       Statistic       Value        F        RSquare    df1    df
    _______    ____________    _________    _________    ______    _______    ___    __

    Constant   (Intercept)     Pillai          0.99013    4847.5    0.99013    3      14
    Constant   (Intercept)     Wilks         0.0098724    4847.5    0.99013    3      14
    Constant   (Intercept)     Hotelling       100.29     4847.5    0.99013    3      14
    Constant   (Intercept)     Roy             100.29     4847.5    0.99013    3      14
    Constant   species         Pillai          0.96909    45.749    0.48455    6      29
    Constant   species         Wilks          0.041153    189.92    0.79714    6      29
    Constant   species         Hotelling       23.051    555.17    0.92016    6      28
    Constant   species         Roy              23.04    1121.3     0.9584    3      14
```

Perform multivariate anova separately for each species.

```
manova(rm,'By','species')
```

```
ans =

    Within          Between           Statistic      Value        F        RSquare    df
    _______    ___________________    _________    _________    ______    _______    __

    Constant   species=setosa         Pillai          0.9823    2682.7     0.9823    3
    Constant   species=setosa         Wilks         0.017698    2682.7     0.9823    3
    Constant   species=setosa         Hotelling       55.504    2682.7     0.9823    3
    Constant   species=setosa         Roy             55.504    2682.7     0.9823    3
    Constant   species=versicolor     Pillai            0.97    1562.8       0.97    3
    Constant   species=versicolor     Wilks         0.029999    1562.8       0.97    3
    Constant   species=versicolor     Hotelling       32.334    1562.8       0.97    3
    Constant   species=versicolor     Roy             32.334    1562.8       0.97    3
    Constant   species=virginica      Pillai         0.97261    1716.1    0.97261    3
    Constant   species=virginica      Wilks          0.027394    1716.1    0.97261    3
    Constant   species=virginica      Hotelling       35.505    1716.1    0.97261    3
    Constant   species=virginica      Roy             35.505    1716.1    0.97261    3
```

Return Arrays of the Hypothesis Test

Load the sample data.

```
load fisheriris
```

The column vector `species` consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform multivariate analysis of variance. Also return the arrays for constructing the hypothesis test.

```
[manovatbl,A,C,D] = manova(rm)
```

```
manovatbl =

    Within       Between      Statistic      Value        F       RSquare    df1    df
    _______    ___________    _________    _________    ______    _______    ___    __

    Constant   (Intercept)    Pillai         0.99013    4847.5    0.99013    3      14
    Constant   (Intercept)    Wilks        0.0098724    4847.5    0.99013    3      14
    Constant   (Intercept)    Hotelling      100.29     4847.5    0.99013    3      14
    Constant   (Intercept)    Roy            100.29     4847.5    0.99013    3      14
    Constant   species        Pillai         0.96909    45.749    0.48455    6      29
    Constant   species        Wilks         0.041153    189.92    0.79714    6      29
    Constant   species        Hotelling      23.051     555.17    0.92016    6      28
    Constant   species        Roy             23.04     1121.3     0.9584    3      14


A =

    [1x3 double]
    [2x3 double]


C =

     1     0     0
    -1     1     0
     0    -1     1
     0     0    -1
```

```
D =

     0
```

Index into matrix A.

```
A{1}

ans =

     1     0     0
```

```
A{2}

ans =

     0     1     0
     0     0     1
```

See Also

`anova` | `coeftest` | `fitrm` | `ranova`

More About

- "Model Specification for Repeated Measures Models" on page 8-77
- "Multivariate Analysis of Variance for Repeated Measures" on page 8-83

manova1

One-way multivariate analysis of variance

Syntax

```
d = manova1(X,group)
d = manova1(X,group,alpha)
[d,p] = manova1(...)
[d,p,stats] = manova1(...)
```

Description

`d = manova1(X,group)` performs a one-way Multivariate Analysis of Variance (MANOVA) for comparing the multivariate means of the columns of `X`, grouped by `group`. `X` is an m-by-n matrix of data values, and each row is a vector of measurements on n variables for a single observation. `group` is a grouping variable defined as a categorical variable, vector, string array, or cell array of strings. Two observations are in the same group if they have the same value in the `group` array. The observations in each group represent a sample from a population.

The function returns `d`, an estimate of the dimension of the space containing the group means. `manova1` tests the null hypothesis that the means of each group are the same n-dimensional multivariate vector, and that any difference observed in the sample `X` is due to random chance. If `d = 0`, there is no evidence to reject that hypothesis. If `d = 1`, then you can reject the null hypothesis at the 5% level, but you cannot reject the hypothesis that the multivariate means lie on the same line. Similarly, if `d = 2` the multivariate means may lie on the same plane in n-dimensional space, but not on the same line.

`d = manova1(X,group,alpha)` gives control of the significance level, `alpha`. The return value `d` will be the smallest dimension having `p > alpha`, where `p` is a p-value for testing whether the means lie in a space of that dimension.

`[d,p] = manova1(...)` also returns a `p`, a vector of p-values for testing whether the means lie in a space of dimension 0, 1, and so on. The largest possible dimension is either the dimension of the space, or one less than the number of groups. There is one element of `p` for each dimension up to, but not including, the largest.

If the ith p-value is near zero, this casts doubt on the hypothesis that the group means lie on a space of i-1 dimensions. The choice of a critical p-value to determine whether the result is judged statistically significant is left to the researcher and is specified by the value of the input argument `alpha`. It is common to declare a result significant if the p-value is less than 0.05 or 0.01.

`[d,p,stats] = manova1(...)` also returns `stats`, a structure containing additional MANOVA results. The structure contains the following fields.

Field	Contents
`W`	Within-groups sum of squares and cross-products matrix
`B`	Between-groups sum of squares and cross-products matrix
`T`	Total sum of squares and cross-products matrix
`dfW`	Degrees of freedom for `W`
`dfB`	Degrees of freedom for `B`
`dfT`	Degrees of freedom for `T`
`lambda`	Vector of values of Wilk's lambda test statistic for testing whether the means have dimension 0, 1, etc.
`chisq`	Transformation of `lambda` to an approximate chi-square distribution
`chisqdf`	Degrees of freedom for `chisq`
`eigenval`	Eigenvalues of W^1B
`eigenvec`	Eigenvectors of W^1B; these are the coefficients for the canonical variables `C`, and they are scaled so the within-group variance of the canonical variables is 1
`canon`	Canonical variables `C`, equal to `XC*eigenvec`, where `XC` is `X` with columns centered by subtracting their means
`mdist`	A vector of Mahalanobis distances from each point to the mean of its group
`gmdist`	A matrix of Mahalanobis distances between each pair of group means

The canonical variables `C` are linear combinations of the original variables, chosen to maximize the separation between groups. Specifically, `C(:,1)` is the linear combination of the `X` columns that has the maximum separation between groups. This means that among all possible linear combinations, it is the one with the most significant F statistic

in a one-way analysis of variance. `C(:,2)` has the maximum separation subject to it being orthogonal to `C(:,1)`, and so on.

You may find it useful to use the outputs from `manova1` along with other functions to supplement your analysis. For example, you may want to start with a grouped scatter plot matrix of the original variables using `gplotmatrix`. You can use `gscatter` to visualize the group separation using the first two canonical variables. You can use `manovacluster` to graph a dendrogram showing the clusters among the group means.

Assumptions

The MANOVA test makes the following assumptions about the data in `X`:

- The populations for each group are normally distributed.
- The variance-covariance matrix is the same for each population.
- All observations are mutually independent.

Examples

you can use `manova1` to determine whether there are differences in the averages of four car characteristics, among groups defined by the country where the cars were made.

```
load carbig
[d,p] = manova1([MPG Acceleration Weight Displacement],...
                Origin)
d =
   3
p =
     0
  0.0000
  0.0075
  0.1934
```

There are four dimensions in the input matrix, so the group means must lie in a four-dimensional space. `manova1` shows that you cannot reject the hypothesis that the means lie in a 3-D subspace.

More About

- “Grouping Variables” on page 2-52

References

[1] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

See Also

`anova1` | `canoncorr` | `gscatter` | `gplotmatrix` | `manovacluster`

manovacluster

Dendrogram of group mean clusters following MANOVA

Syntax

```
manovacluster(stats)
manovacluster(stats,method)
H = manovacluster(stats,method)
```

Description

`manovacluster(stats)` generates a dendrogram plot of the group means after a multivariate analysis of variance (MANOVA). `stats` is the output `stats` structure from `manova1`. The clusters are computed by applying the single linkage method to the matrix of Mahalanobis distances between group means.

See `dendrogram` for more information on the graphical output from this function. The dendrogram is most useful when the number of groups is large.

`manovacluster(stats,method)` uses the specified method in place of single linkage. *`method`* can be any of the following character strings that identify ways to create the cluster hierarchy. (See `linkage` for additional information.)

Method	Description
`'single'`	Shortest distance (default)
`'complete'`	Largest distance
`'average'`	Average distance
`'centroid'`	Centroid distance
`'ward'`	Incremental sum of squares

`H = manovacluster(stats,method)` returns a vector of handles to the lines in the figure.

Examples

Dendrogram of Group Means After MANOVA

Load the sample data.

```
load carbig
```

Define the variable matrix.

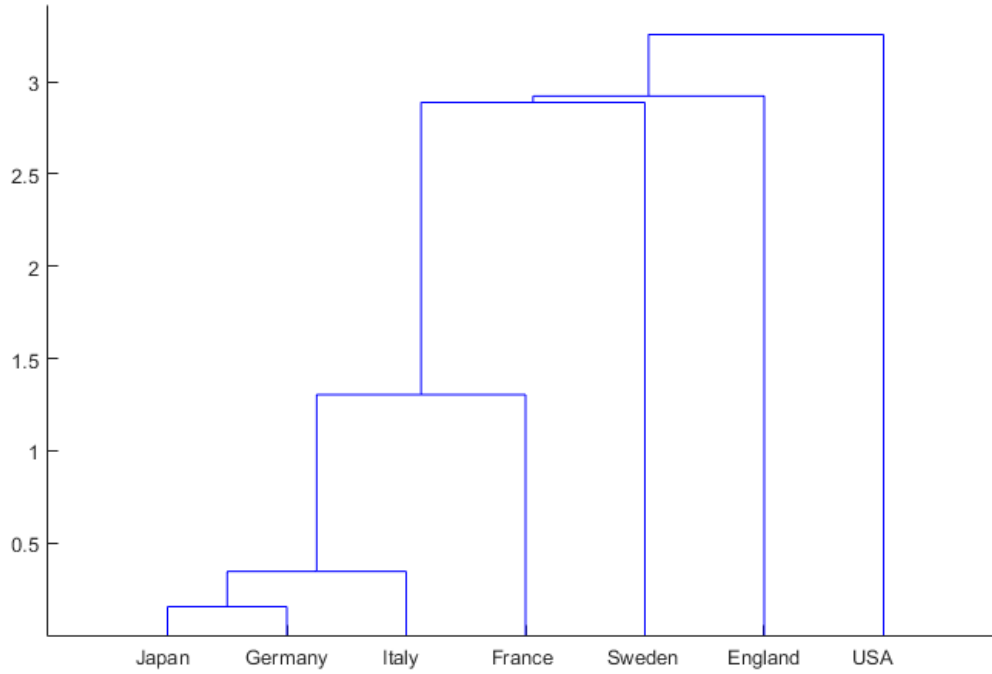
```
X = [MPG Acceleration Weight Displacement];
```

Perform one-way MANOVA to compare the means of MPG, Acceleration, Weight,and Displacement grouped by Origin.

```
[d,p,stats] = manova1(X,Origin);
```

Create a dendrogram plot of the group means.

```
manovacluster(stats)
```



See Also

`cluster` | `dendrogram` | `linkage` | `manova1`

margin

Class: ClassificationKNN

Margin of *k*-nearest neighbor classifier

Syntax

```
m = margin(mdl,X,Y)
```

Description

`m = margin(mdl,X,Y)` returns the classification margins for the matrix of predictors `X` and class labels `Y`. For the definition, see "Margin" on page 22-2805.

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

`X` — Matrix of predictor values

matrix

Matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

Y — Categorical variables

categorical array | cell array of strings | character array | logical vector | numeric vector

A categorical array, cell array of strings, character array, logical vector, or a numeric vector with the same number of rows as `X`. Each row of `Y` represents the classification of the corresponding row of `X`.

Output Arguments

m

Numeric column vector of length `size(X,1)`. Each entry in `m` represents the margin for the corresponding rows of X and (true class) Y, computed using mdl.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

Score

The *score* of a classification is the posterior probability of the classification. The posterior probability is the number of neighbors that have that classification, divided by the number of neighbors. For a more detailed definition that includes weights and prior probabilities, see "Posterior Probability" on page 22-3654.

Examples

Margin Calculation

Construct a k-nearest neighbor classifier for the Fisher iris data, where $k = 5$.

Load the data.

```
load fisheriris
```

Construct a classifier for 5-nearest neighbors.

```
mdl = fitcknn(meas,species,'NumNeighbors',5);
```

Examine the margin of the classifier for a mean observation classified `'versicolor'`.

```
X = mean(meas);
Y = {'versicolor'};
m = margin(mdl,X,Y)
```

```
m =

     1
```

The classifier has no doubt that `'versicolor'` is the correct classification (all five nearest neighbors classify as `'versicolor'`).

See Also

`ClassificationKNN` | `edge` | `fitcknn` | `loss`

More About

- “Classification Using Nearest Neighbors” on page 16-8

margin

Class: CompactClassificationDiscriminant

Classification margins

Syntax

```
m = margin(obj,X,Y)
```

Description

`m = margin(obj,X,Y)` returns the classification margins for the matrix of predictors `X` and class labels `Y`. For the definition, see "Definitions" on page 22-2808.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `fitcdiscr`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

`Y`

Class labels, with the same data type as exists in `obj`. The number of elements of `Y` must equal the number of rows of `X`.

Output Arguments

`m`

Numeric column vector of length `size(X,1)`. Each entry in `m` represents the margin for the corresponding rows of X and (true class) Y, computed using obj.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

The classification margin is a column vector with the same number of rows as in the matrix X. A high value of margin indicates a more reliable prediction than a low value.

Score (discriminant analysis)

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see "Posterior Probability" on page 15-7.

Examples

Compute the classification margin for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries:

```
load fisheriris
X = meas(:,1:2);
obj = fitcdiscr(X,species);
M = margin(obj,X,species);
M(end-10:end)

ans =
    0.6551
    0.4838
    0.6551
   -0.5127
    0.5659
    0.4611
    0.4949
    0.1024
    0.2787
   -0.1439
   -0.4444
```

The classifier trained on all the data is better:

```
obj = fitcdiscr(meas,species);
M = margin(obj,meas,species);
M(end-10:end)

ans =
    0.9983
    1.0000
    0.9991
    0.9978
    1.0000
    1.0000
    0.9999
    0.9882
    0.9937
    1.0000
    0.9649
```

See Also

`predict` | `ClassificationDiscriminant` | `fitcdiscr` | `edge` | `loss`

How To

- “Discriminant Analysis” on page 15-3

margin

Class: CompactClassificationECOC

Classification margins for error-correcting output code multiclass classifiers

Syntax

```
m = margin(Mdl,X,Y)
m = margin(Mdl,X,Y,Name,Value)
```

Description

`m = margin(Mdl,X,Y)` returns the classification margins (`m`) for the trained error-correcting output code (ECOC) multiclass classifier `Mdl` using the predictor data `X` and class labels `Y`. Each row of `X` and `Y` is an observation.

`m = margin(Mdl,X,Y,Name,Value)` returns the classification margins with additional options specified by one or more Name,Value pair arguments.

For example, specify a decoding scheme, binary learner loss function, or verbosity level.

Input Arguments

`Mdl` — ECOC multiclass classifier

`ClassificationECOC` model | `CompactClassificationECOC` model

ECOC multiclass classifier, specified as a `ClassificationECOC` or `CompactClassificationECOC` model. You can create a:

- `ClassificationECOC` model by training the ECOC classifier using `fitcecoc`
- `CompactClassificationECOC` model by passing a `ClassificationECOC` classifier to `compact`

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also called an instance or example), and each column corresponds to one variable (also known as a feature). The variables composing the columns of `X` should be the same as the variables that trained the `Mdl` classifier.

The length of `Y` and the number of rows of `X` must be equal.

If you trained `Mdl` specifying to standardize the predictor data, then the software standardizes the columns of `X` using the corresponding means and standard deviations that the software stored in `Mdl.BinaryLearner{j}.Mu` and `Mdl.BinaryLearner{j}.Sigma` for learner `j`.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `Mdl.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `Mdl.CodingMatrix`.
  - `s` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.
  - L is the number of binary learners.

  For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`

- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char | function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single` | `double`

Output Arguments

`m` — Classification margins

numeric column vector

Classification margins, returned as a numeric column vector.

`m` has the same length as `Y`. The software estimates each entry of `m` using the trained ECOC model Mdl, the corresponding row of X, and the true class label Y.

Definitions

Classification Margin

The *classification margins* are, for each observation, the difference between the negative loss for the positive class and maximal negative loss among the negative classes. If the margins are on the same scale, then they serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [4].

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left| m_{kj} \right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Estimate Test-Sample Classification Margins of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

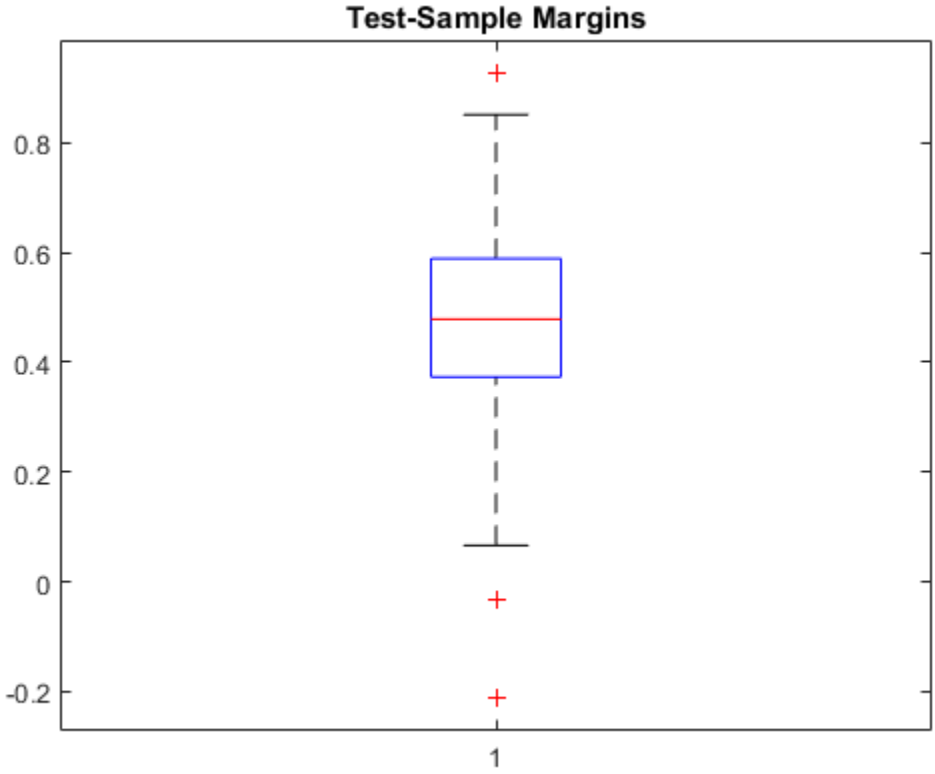
Train an ECOC model using SVM binary classifiers, and specify a 30% holdout sample. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'Holdout',0.30,'Learners',t,'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

Estimate the test-sample classification margins. Display the distribution of the margins using a boxplot.

```
m = margin(CMdl,XTest,YTest);

figure;
boxplot(m);
title 'Test-Sample Margins'
```



An observation margin is the positive-class, negated loss minus the maximum negative-class, negated loss. Classifiers that yield relatively large margins are desirable.

Select ECOC Model Features by Examining Test-Sample Margins

The classifier margins measure, for each observation, the difference between the positive-class, negated loss score and the maximal negative-class, negated loss. One way to perform feature selection is to compare test-sample margins from multiple models. Based solely on this criterion, the model with the highest margins is the best model.

Load Fisher's iris data set.

```
load fisheriris
```

```
X = meas;
Y = categorical(species);
classOrder = unique(Y); % Class order
rng(1); % For reproducibility
```

Partition the data set into training and test sets. Specify a 30% holdout sample for testing.

```
Partition = cvpartition(Y,'Holdout',0.30);
testInds = test(Partition); % Indices for the test set
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

Define these two data sets:

- `fullX` contains all four predictors.
- `partX` contains the sepal measurements.

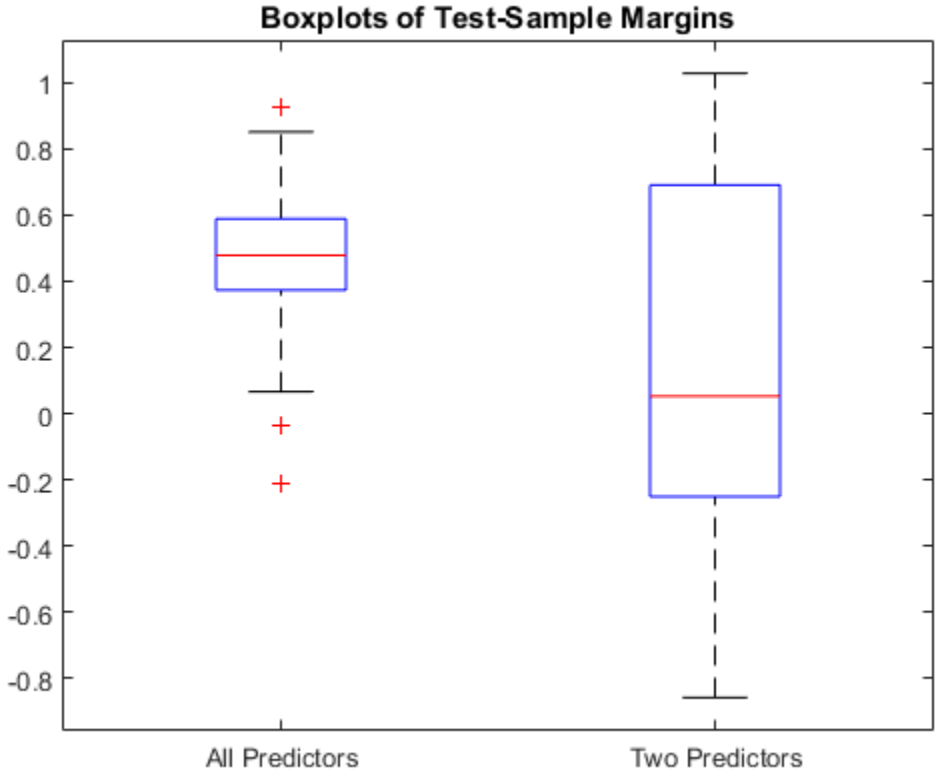
```
fullX = X;
partX = X(:,1:2);
```

Train an ECOC model using SVM binary classifiers for each predictor set, and specify the partition definition. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(fullX,Y,'CVPartition',Partition,'Learners',t,...
    'ClassNames',classOrder);
PCVMdl = fitcecoc(partX,Y,'CVPartition',Partition,'Learners',t,...
    'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};
PCMdl = PCVMdl.Trained{1};
```

Estimate the test-sample margins for each classifier. For each model, display the distribution of the margins using a boxplot.

```
fullMargins = margin(CMdl,XTest,YTest);
partMargins = margin(PCMdl,XTest(:,3:4),YTest);

figure;
boxplot([fullMargins partMargins],'Labels',{'All Predictors','Two Predictors'});
title('Boxplots of Test-Sample Margins')
```



The margin distribution of `CMdl` is situated higher, and with less variability than the margin distribution of `PCMdl`.

- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

Tip

To compare margins or edges of several classifiers, use template objects to specify a common score transform function among the classifiers when you train them using `fitcecoc`.

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q., X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `CompactClassificationECOC` | `edge` | `fitcecoc` | `predict` | `resubMargin`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

margin

Class: CompactClassificationEnsemble

Classification margins

Syntax

```
M = margin(ens,X,Y)
M = margin(ens,X,Y,Name,Value)
```

Description

`M = margin(ens,X,Y)` returns the classification margin for the predictions of `ens` on data `X`, when the true classifications are `Y`.

`M = margin(ens,X,Y,Name,Value)` calculates margin with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

Classification ensemble created with `fitensemble`, or a compact classification ensemble created with `compact`.

`X`

Matrix of data to classify. Each row of `X` represents one observation, and each column represents one predictor. `X` must have the same number of columns as the data used to train ens. `X` should have the same number of rows as the number of elements in `Y`.

`Y`

Classification of X. `Y` should be of the same type as the classification used to train ens, and its number of elements should equal the number of rows of X.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to ens`.NumTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'UseObsForLearner'`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of X.
- `T` is the number of weak learners in ens.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of X.

Default: `true(N,T)`

Output Arguments

`M`

A numeric column vector with the same number of rows as X. Each row of `M` gives the classification margin for that row of `X`.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix X.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the margin for classifying an average flower from the `Fisheriris` data as `'versicolor'`:

```
load fisheriris % X = meas, Y = species
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
flower = mean(meas);
predict(ens,flower)

ans =
    'versicolor'

margin(ens,mean(meas),'versicolor')

ans =
    3.2140
```

See Also

`predict` | `edge` | `loss`

margin

Class: CompactClassificationNaiveBayes

Classification margins for naive Bayes classifiers

Syntax

```
m = margin(Mdl,X,Y)
```

Description

`m = margin(Mdl,X,Y)` returns the classification margins (`m`) for the trained naive Bayes classifier `Mdl` using the predictor data `X` and class labels `Y`.

Input Arguments

`Mdl` — Naive Bayes classifier

`ClassificationNaiveBayes` model | `CompactClassificationNaiveBayes` model

Naive Bayes classifier, specified as a `ClassificationNaiveBayes` model or `CompactClassificationNaiveBayes` model returned by `fitcnb` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained `Mdl`.

The length of `Y` and the number of rows of `X` must be equal.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `Mdl.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Output Arguments

`m` — Classification margins

numeric vector

Classification margins, returned as a numeric vector.

`m` has the same length equal to `size(X,1)`. Each entry of `m` is the classification margin of the corresponding observation (row) of X and element of Y.

Definitions

Classification Edge

The *classification edge* is the weighted mean of the classification margins.

If you supply weights, then the software normalizes them to sum to the prior probability of their respective class. The software uses the normalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margin

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.
- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

  $$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Score

The naive Bayes *score* is the class posterior probability given the observation.

Examples

Estimate Test-Sample Classification Margins of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);
```

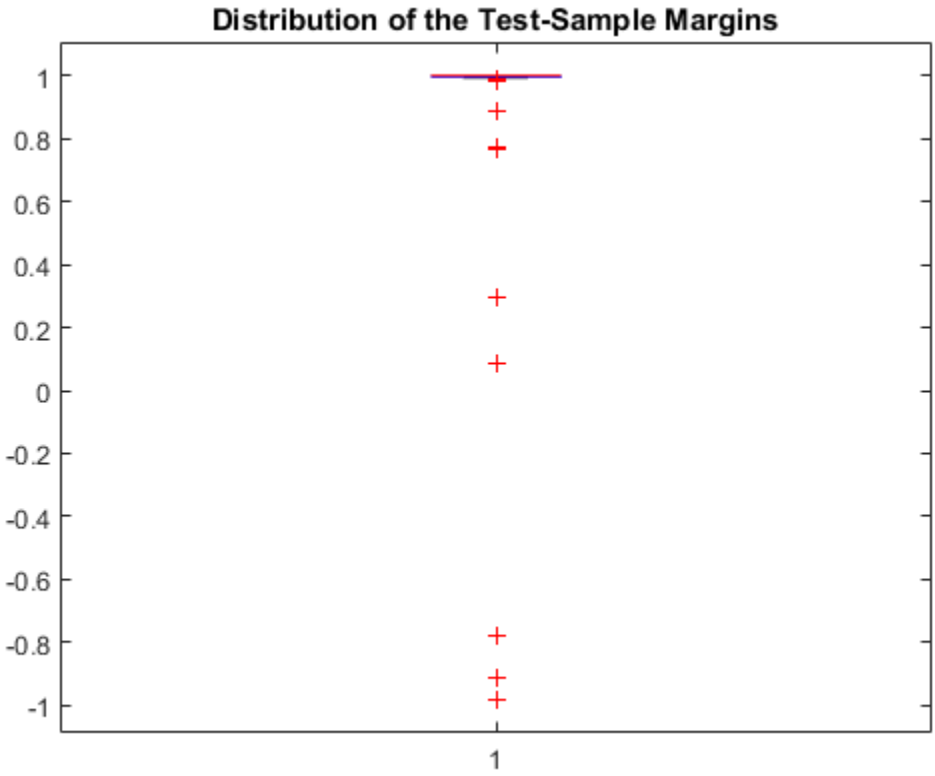
Train a naive Bayes classifier. Specify a 30% holdout sample for testing. It is good practice to specify the class order. Assume that each predictor is conditionally normally distributed given its label.

```
CVMdl = fitcnb(X,Y,'Holdout',0.30,...
    'ClassNames',{'setosa','versicolor','virginica'});
CMdl = CVMdl.Trained{1}; ...
    % Extract the trained, compact classifier
testInds = test(CVMdl.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds);
```

`CVMdl` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Estimate the test sample classification margins. Display the distribution of the margins using a boxplot.

```
m = margin(CMdl,XTest,YTest);

figure;
boxplot(m);
title 'Distribution of the Test-Sample Margins';
```



An observation margin is the observed true class score minus the maximum false class score among all scores in the respective class. Classifiers that yield relatively large margins are desirable.

Select Naive Bayes Classifier Features by Examining Test Sample Margins

The classifier margins measure, for each observation, the difference between the true class observed score and the maximal false class score for a particular class. One way to perform feature selection is to compare test sample margins from multiple models. Based solely on this criterion, the model with the highest margins is the best model.

Load Fisher's iris data set.

```
load fisheriris
```

```
X = meas;    % Predictors
Y = species; % Response
rng(1);
```

Partition the data set into training and test sets. Specify a 30% holdout sample for testing.

```
Partition = cvpartition(Y,'Holdout',0.30);
testInds = test(Partition); % Indices for the test set
XTest = X(testInds,:);
YTest = Y(testInds);
```

Partition defines the data set partition.

Define these two data sets:

- `fullX` contains all predictors.
- `partX` contains the last 2 predictors.

```
fullX = X;
partX = X(:,3:4);
```

Train naive Bayes classifiers for each predictor set. Specify the partition definition.

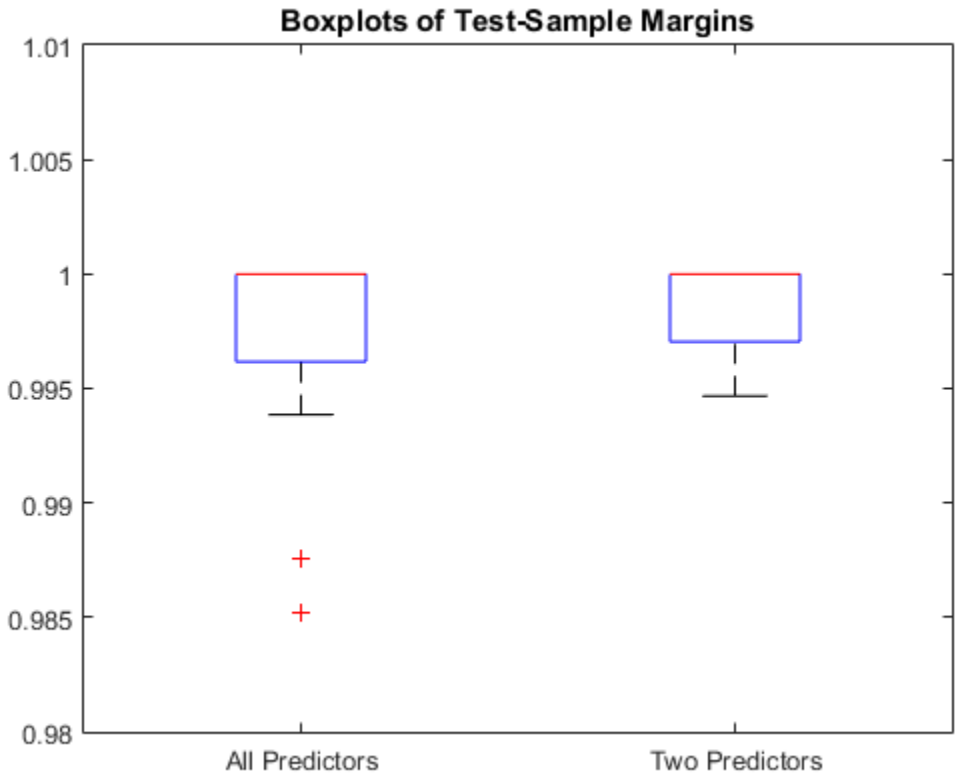
```
FCVMdl = fitcnb(fullX,Y,'CVPartition',Partition);
PCVMdl = fitcnb(partX,Y,'CVPartition',Partition);
FCMdl = FCVMdl.Trained{1};
PCMdl = PCVMdl.Trained{1};
```

`FullCVMdl` and `PartCVMdl` are `ClassificationPartitionedModel` classifiers. They contain the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Estimate the test sample margins for each classifier. Display the distributions of the margins for each model using boxplots.

```
fullM = margin(FCMdl,XTest,YTest);
partM = margin(PCMdl,XTest(:,3:4),YTest);

figure;
boxplot([fullM partM],'Labels',{'All Predictors','Two Predictors'})
h = gca;
h.YLim = [0.98 1.01]; % Modify axis to see boxes.
```

```
title 'Boxplots of Test-Sample Margins';
```



The margins have a similar distribution, but `PCMdl` is less complex.

References

[1] Hu, Q., X. Che, L. Zhang, and D. Yu. “Feature Evaluation and Selection Based on Neighborhood Soft Margin.” *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`| ClassificationNaiveBayes | CompactClassificationNaiveBayes | edge | fitcnb | loss | predict`

More About

- "Naive Bayes Classification" on page 15-31

margin

Class: CompactClassificationSVM

Classification margins for support vector machine classifiers

Syntax

```
m = margin(SVMModel,X,Y)
```

Description

`m = margin(SVMModel,X,Y)` returns the classification margins (`m`) for the trained support vector machine (SVM) classifier `SVMModel` using the predictor data `X` and class labels `Y`.

Input Arguments

`SVMModel` — SVM classifier

`ClassificationSVM` classifier | `CompactClassificationSVM` classifier

SVM classifier, specified as a `ClassificationSVM` classifier or `CompactClassificationSVM` classifier returned by `fitcsvm` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained the `SVMModel` classifier.

The length of `Y` and the number of rows of `X` must be equal.

If you set `'Standardize',true` in `fitcsvm` to train `SVMModel`, then the software standardizes the columns of `X` using the corresponding means in `SVMModel.Mu` and standard deviations in `SVMModel.Sigma`.

Data Types: `double` | `single`

`Y` — Class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings. `Y` must be the same as the data type of `SVMModel.ClassNames`.

The length of `Y` and the number of rows of `X` must be equal.

Output Arguments

`m` — Classification margins

numeric vector

Classification margins, returned as a numeric vector.

`m` has the same length as `Y`. The software estimates each entry of `m` using the trained SVM classifier SVMModel, the corresponding row of X, and the true class label Y.

Definitions

Classification Margin

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Classification Edge

The *edge* is the weighted mean of the *classification margins*.

The weights are the prior class probabilities. If you supply weights, then the software normalizes them to sum to the prior probabilities in the respective classes. The software uses the renormalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j, x) = x_j' x$ (the linear kernel), then the score function reduces to

$$f(x) = (x / s)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Examples

Estimate Test Sample Classification Margins of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM classifier. Specify a 15% holdout sample for testing. It is good practice to specify the class order and standardize the data.

```
CVSVMModel = fitcsvm(X,Y,'Holdout',0.15,'ClassNames',{'b','g'},...
    'Standardize',true);
CompactSVMModel = CVSVMModel.Trained{1}; ...
    % Extract the trained, compact classifier
testInds = test(CVSVMModel.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVSVMModel` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Estimate the test sample classification margins.

```
m = margin(CompactSVMModel,XTest,YTest);
m(10:20)
```

```
ans =

    3.5461
    5.5939
    4.9948
    4.5611
   -4.7963
    5.5127
   -2.8776
    1.8673
    9.4986
    9.5018
   20.9954
```

An observation margin is the observed true class score minus the maximum false class score among all scores in the respective class. Classifiers that yield relatively large margins are desirable.

Select SVM Classifier Features by Examining Test Sample Margins

The classifier margins measure, for each observation, the difference between the true class observed score and the maximal false class score for a particular class. One way to

perform feature selection is to compare test sample margins from multiple models. Based solely on this criterion, the model with the highest margins is the best model.

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Partition the data set into training and test sets. Specify a 15% holdout sample for testing.

```
Partition = cvpartition(Y,'Holdout',0.15);
testInds = test(Partition); % Indices for the test set
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

Partition defines the data set partition.

Define these two data sets:

- `fullX` contains all predictors (except the removed column of 0s).
- `partX` contains the last 20 predictors.

```
fullX = X;
partX = X(:,end-20:end);
```

Train SVM classifiers for each predictor set. Specify the partition definition.

```
FullCVSVMModel = fitcsvm(fullX,Y,'CVPartition',Partition);
PartCVSVMModel = fitcsvm(partX,Y,'CVPartition',Partition);
FCSVMModel = FullCVSVMModel.Trained{1};
PCSVMModel = PartCVSVMModel.Trained{1};
```

`FullCVSVMModel` and `PartCVSVMModel` are `ClassificationPartitionedModel` classifiers. They contain the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Estimate the test sample margins for each classifier.

```
fullM = margin(FCSVMModel,XTest,YTest);
partM = margin(PCSVMModel,XTest(:,end-20:end),YTest);
n = size(XTest,1);
p = sum(fullM < partM)/n
```

```
p =

    0.2500
```

Approximately 25% of the margins from the full model are less than those from the model with fewer predictors. This suggests that the model trained using all of the predictors is better.

Algorithms

For binary classification, the software defines the margin for observation j, m_j, as

$$m_j = 2y_j f(x_j),$$

where $y_j \in \{-1,1\}$, and $f(x_j)$ is the predicted score of observation j for the positive class. However, the literature commonly uses $m_j = y_j f(x_j)$ to define the margin.

References

[1] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[2] Hu, Q. X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `edge` | `fitcsvm` | `loss` | `predict`

margin

Class: CompactClassificationTree

Classification margins

Syntax

```
m = margin(tree,X,Y)
```

Description

`m = margin(tree,X,Y)` returns the classification margins for the matrix of predictors `X` and class labels `Y`. For the definition, see “Margin” on page 22-2839.

Input Arguments

`tree`

A classification tree created by `fitctree`, or a compact classification tree created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `tree`.

`Y`

Class labels, with the same data type as exists in `tree`.

Output Arguments

`m`

A numeric column vector of length `size(X,1)`. Each entry in `m` represents the margin for the corresponding rows of X and (true class) Y, computed using tree.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix X.

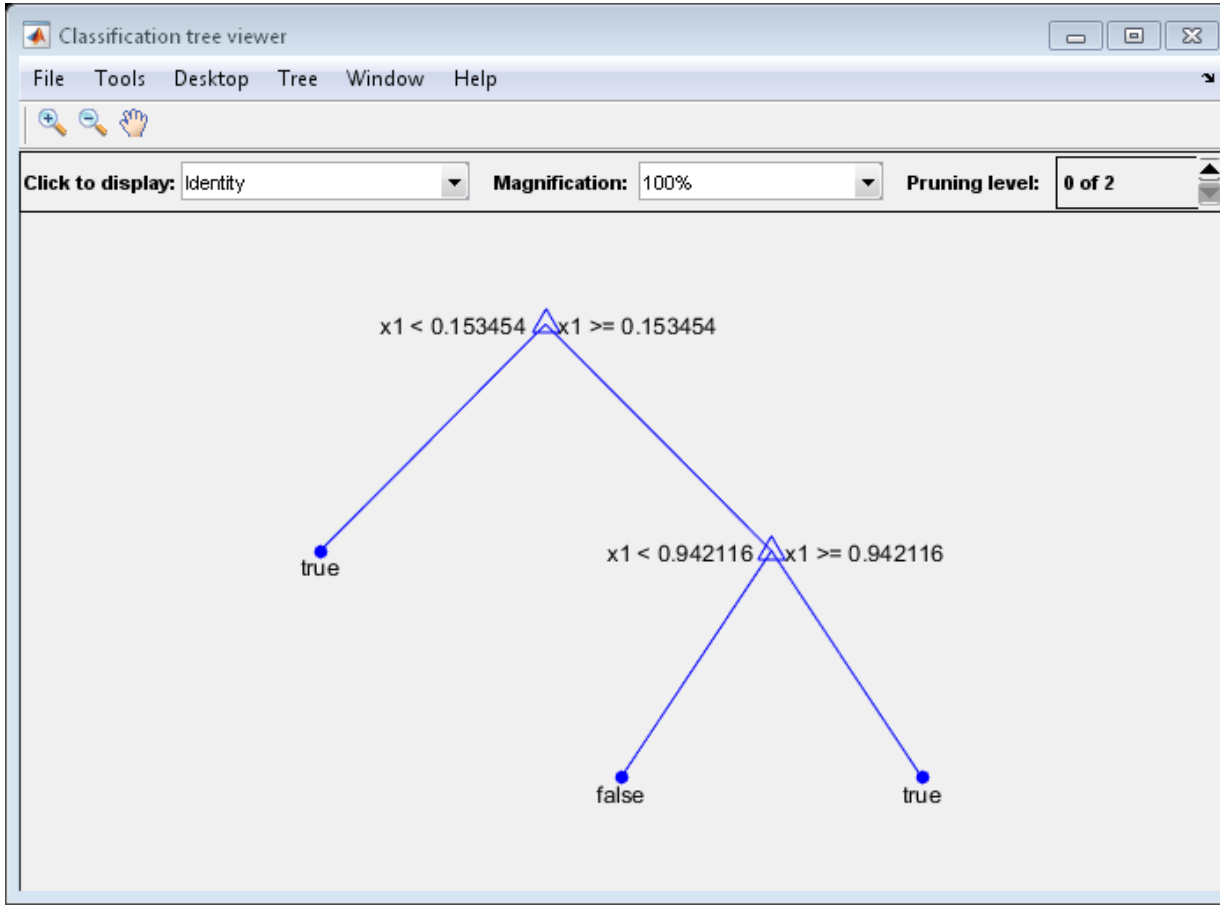
Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

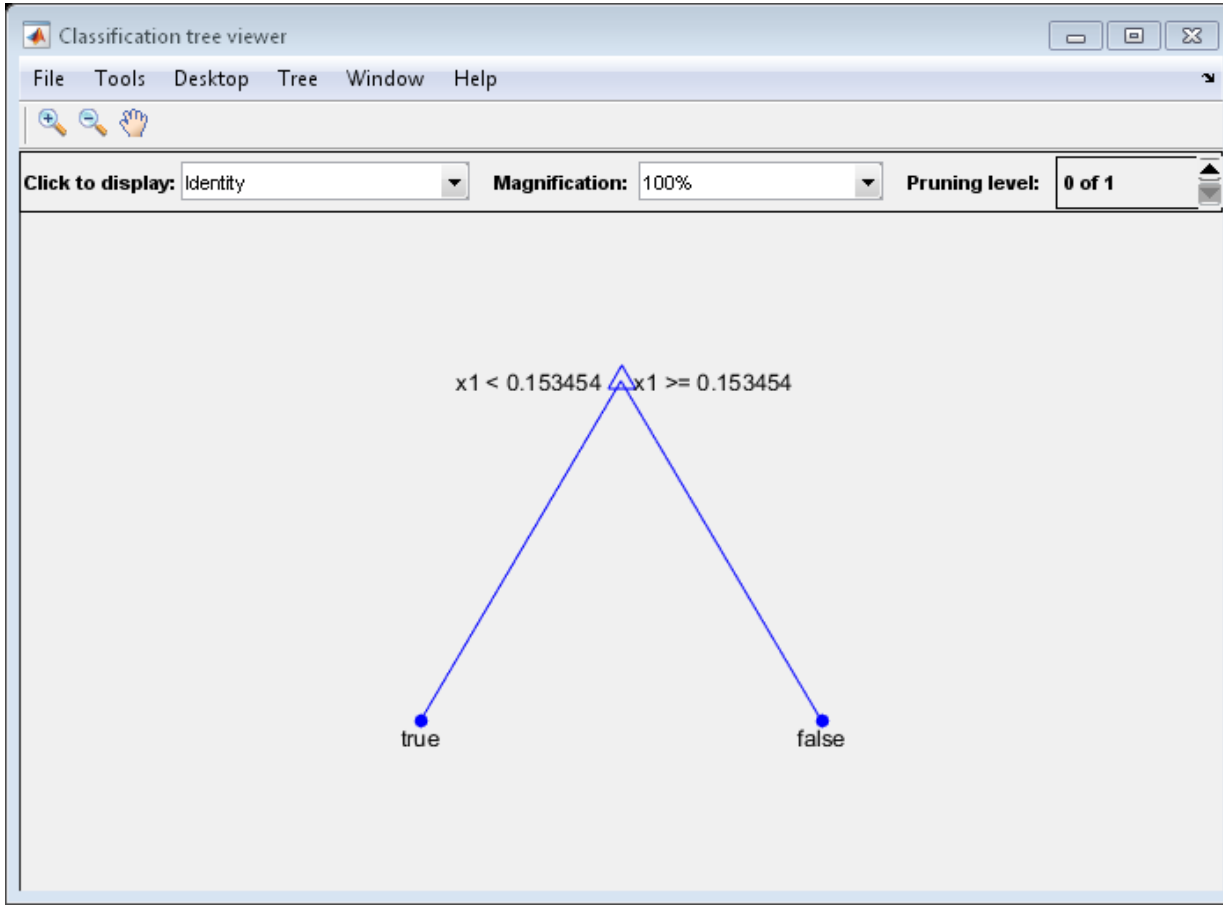
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Compute the classification margin for the Fisher iris data, trained on its first two columns of data, and view the last 10 entries.

```
load fisheriris
X = meas(:,1:2);
tree = fitctree(X,species);
M = margin(tree,X,species);
M(end-10:end)
```

```
ans =
    0.1111
    0.1111
    0.1111
   -0.2857
    0.6364
    0.6364
    0.1111
    0.7500
    1.0000
    0.6364
```

```
    0.2000
```

The classification tree trained on all the data is better.

```
tree = fitctree(meas,species);
M = margin(tree,meas,species);
M(end-10:end)
```

```
ans =
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
    0.9565
```

See Also

`predict` | `edge` | `loss` | `fitctree`

margin

Class: CompactTreeBagger

Classification margin

Syntax

```
mar = margin(B,X,Y)
mar = margin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = margin(B,X,Y)` computes the classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `mar` is a numeric array of size `Nobs`-by-`NTrees`, where `Nobs` is the number of rows of `X` and `Y`, and `NTrees` is the number of trees in the ensemble `B`. For observation `I` and tree `J`, `mar(I,J)` is the difference between the score for the true class and the largest score for other classes. This method is available for classification ensembles only.

`mar = margin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `margin` computes cumulative errors and `mar` is an `Nobs`-by-`NTrees` matrix, where the first column gives error from `trees(1)`, second column gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a `Nobs`-by-`NTrees` matrix, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `mar` a single column of length `Nobs` showing the cumulative margins for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes,

	where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`TreeBagger.margin`

margin

Class: TreeBagger

Classification margin

Syntax

```
mar = margin(B,X,Y)
mar = margin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = margin(B,X,Y)` computes the classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `mar` is a numeric array of size `Nobs`-by-`NTrees`, where `Nobs` is the number of rows of `X` and `Y`, and `NTrees` is the number of trees in the ensemble `B`. For observation `I` and tree `J`, `mar(I,J)` is the difference between the score for the true class and the largest score for other classes. This method is available for classification ensembles only.

`mar = margin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how the method computes errors. If set to `'cumulative'` (default), `margin` computes cumulative errors and `mar` is an `Nobs`-by-`NTrees` matrix, where the first column gives error from `trees(1)`, second column gives error from`trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a `Nobs`-by-`NTrees` matrix, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `mar` a single column of length `Nobs` showing the cumulative margins for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes,

	where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. The method uses these weights to combine output from the specified trees by taking a weighted average instead of the simple non-weighted majority vote. You cannot use this argument in the `'individual'` mode.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees should be used to make predictions for each observation. By default the method uses all trees for all observations.

See Also

`CompactTreeBagger.margin`

margmean

Class: RepeatedMeasuresModel

Estimate marginal means

Syntax

```
tbl = margmean(rm,vars)
tbl = margmean(rm,vars,'alpha',alpha)
```

Description

`tbl = margmean(rm,vars)` returns the estimated marginal means for the variables vars, in the table tbl.

`tbl = margmean(rm,vars,'alpha',alpha)` returns the 100*(1–`alpha`)% confidence intervals for the marginal means.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`vars` — Variables for which to compute the marginal means

string | cell array of strings

Variables for which to compute the marginal means, specified as a string representing the name of a between or within-subjects factor in rm, or a cell array of strings representing the names of multiple variables. Each between-subjects factor must be categorical.

For example, if you want to compute the marginal means for the variables Drug and Gender, then you can specify as follows.

Example: `{'Drug','Gender'}`

Data Types: `char` | `cell`

`alpha` — Confidence level

0.05 (default) | scalar value in the range of 0 to 1

Confidence level of the confidence intervals for population marginal means, specified as a scalar value in the range of 0 to 1. The confidence level is 100*(1–`alpha`)%.

For example, you can specify a 99% confidence level as follows.

Example: `'alpha',0.01`

Data Types: `double` | `single`

Output Arguments

`tbl` — Estimated marginal means

table

Estimated marginal means, returned as a table. tbl contains one row for each combination of the groups of the variables you specify in vars, one column for each variable, and the following columns.

Column name	Description
`Mean`	Estimated marginal means
`StdErr`	Standard errors of the estimates
`Lower`	Lower limit of a 95% confidence interval for the true population mean
`Upper`	Upper limit of a 95% confidence interval for the true population mean

Examples

Compute Marginal Means Grouped by Two Factors

Load the sample data.

```
load repeatedmeas
```

The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ to $y8$ as responses. The table `within` includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ to $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Compute the marginal means grouped by the between-subjects factor `Group` and the within-subject factor `Time`.

```
M = margmean(rm,{'Group' 'Time'})
```

```
M =

    Group    Time     Mean      StdErr     Lower       Upper
    _____    ____    _______    ______    ________    _______

    A        1         20.03    11.966     -4.7859     44.846
    A        2        5.8101    8.0942     -10.976     22.597
    A        3        20.694    5.1928      9.9247     31.463
    A        4        16.802    5.1693      6.0813     27.522
    A        5        13.157    6.2678     0.15862     26.156
    A        6       0.38527    5.8028     -11.649      12.42
    A        7        8.1398    6.4472     -5.2309      21.51
    A        8        11.057    7.6083     -4.7213     26.836
    B        1        23.768    11.816    -0.73653     48.273
    B        2        16.846    7.9927     0.26973     33.422
    B        3       -4.0888    5.1276     -14.723     6.5453
    B        4        2.0001    5.1045     -8.5858     12.586
    B        5        8.6458    6.1892     -4.1898     21.481
    B        6       -9.3054      5.73     -21.189      2.578
    B        7        8.8204    6.3663     -4.3825     22.023
    B        8        9.4889    7.5129     -6.0918      25.07
    C        1        19.951    12.236     -5.4261     45.327
    C        2         23.63    8.2771      6.4646     40.796
    C        3       -22.121    5.3101     -33.133    -11.109
    C        4       -14.307    5.2861      -25.27    -3.3443
    C        5       -20.138    6.4094      -33.43    -6.8456
    C        6       -28.583    5.9339     -40.889    -16.277
    C        7       -25.273    6.5928     -38.946      -11.6
    C        8       -21.836    7.7801     -37.971    -5.7009
```

Display the description for table M.

```
M.Properties.Description
```

```
ans =

Estimated marginal means
Means computed with Age=13.7, IQ=98.2667
```

Compute Estimated Marginal Means and Confidence Intervals

Load the sample data.

```
load fisheriris
```

The column vector, `species`, consists of iris flowers of three different species, setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers, the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Compute the marginal means grouped by the factor species.

```
margmean(rm,'species')
```

```
ans =

      species         Mean      StdErr     Lower     Upper
    ____________    ______    _________    ______    ______

    'setosa'        2.5355    0.042807     2.4509    2.6201
    'versicolor'     3.573    0.042807     3.4884    3.6576
    'virginica'      4.285    0.042807     4.2004    4.3696
```

`StdError` field shows the standard errors of the estimated marginal means. The `Lower` and `Upper` fields show the lower and upper bounds for the 95% confidence intervals

of the group marginal means, respectively. None of the confidence intervals overlap, which indicates that marginal means differ with species. You can also plot the estimated marginal means using the `plotprofile` method.

Compute the 99% confidence intervals for the marginal means.

```
margmean(rm,'species','alpha',0.01)
```

```
ans =

      species         Mean      StdErr     Lower     Upper
    _____________    ______    _________    ______    ______

    'setosa'         2.5355    0.042807    2.4238    2.6472
    'versicolor'      3.573    0.042807    3.4613    3.6847
    'virginica'       4.285    0.042807    4.1733    4.3967
```

See Also

`multcompare` | `fitrm` | `plotprofile`

mauchly

Class: RepeatedMeasuresModel

Mauchly's test for sphericity

Syntax

```
tbl = mauchly(rm)
tbl = mauchly(rm,C)
```

Description

`tbl = mauchly(rm)` returns the result of the Mauchly's test for sphericity for the repeated measures model rm.

It tests the null hypothesis that the sphericity assumption is true for the response variables in `rm`.

For more information, see "Mauchly's Test of Sphericity" on page 8-81.

`tbl = mauchly(rm,C)` returns the result of the Mauchly's test based on the contrast matrix C.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`C` — Contrasts

matrix

Contrasts, specified as a matrix. The default value of C is the Q factor in a QR decomposition of the matrix M, where M is defined so that Y*M is the difference between all successive pairs of columns of the repeated measures matrix Y.

Data Types: `single | double`

Output Arguments

`tbl` — Results of Mauchly's test of sphericity

table

Results of Mauchly's test for sphericity for the repeated measures model rm, returned as a `table`.

`tbl` contains the following columns.

Column Name	Definition
`W`	Value of Mauchly's *W* statistic
`ChiStat`	Chi-square statistic value
`DF`	Degrees of freedom of the Chi-square statistic
`pValue`	*p*-value corresponding to the Chi-square statistic

Data Types: `table`

Examples

Perform Mauchly's Test

Load the sample data.

```
load fisheriris
```

The column vector `species`consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform Mauchly's test to assess the sphericity assumption.

```
mauchly(rm)
```

```
ans =

       W        ChiStat     DF       pValue
    _______    ________    __    ___________

    0.55814     84.976     5     1.1102e-16
```

The small p-value (in the `pValue` field) indicates that the sphericity, hence the compound symmetry assumption, does not hold. You should use epsilon corrections to compute the p-values for a repeated measures anova. You can compute the epsilon corrections using the `epsilon` method and perform the repeated measures anova with the corrected p-values using the `ranova` method.

See Also

`epsilon` | `fitrm` | `ranova`

More About

- "Mauchly's Test of Sphericity" on page 8-81
- "Compound Symmetry Assumption and Epsilon Corrections" on page 8-79

mat2dataset

Convert matrix to dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds = mat2dataset(X)
ds = mat2dataset(X,Name,Value)
```

Description

`ds = mat2dataset(X)` converts a matrix to a `dataset` array.

`ds = mat2dataset(X,Name,Value)` performs the conversion using additional options specified by one or more Name,Value pair arguments.

Examples

Convert Matrix to Dataset Array

Convert a matrix to a dataset array using the default options.

Load sample data.

```
load('fisheriris')
X = meas;
size(X)

ans =
```

```
   150     4
```

Convert the matrix to a dataset array.

```
ds = mat2dataset(X);
size(ds)
```

```
ans =

   150     4
```

```
ds(1:5,:)
```

```
ans =

    X1     X2     X3     X4
    5.1    3.5    1.4    0.2
    4.9      3    1.4    0.2
    4.7    3.2    1.3    0.2
    4.6    3.1    1.5    0.2
      5    3.6    1.4    0.2
```

When you do not specify variable names, `mat2dataset` uses the matrix name and column numbers to create default variable names.

Convert Matrix to Dataset Array with Variable Names

Load sample data.

```
load('fisheriris')
X = meas;
size(X)
```

```
ans =

   150     4
```

Convert the matrix to a dataset array, providing a variable name for each of the four column of `X`.

```
ds = mat2dataset(X,'VarNames',{'SLength',...
'SWidth','PLength','PWidth'});
size(ds)
```

```
ans =
```

```
   150     4

ds(1:5,:)

ans =

    SWidth    SLength    PWidth    PLength
    5.1       3.5        1.4       0.2
    4.9         3        1.4       0.2
    4.7       3.2        1.3       0.2
    4.6       3.1        1.5       0.2
      5       3.6        1.4       0.2
```

Create a Dataset Array with Multicolumn Variables

Convert a matrix to a dataset array containing multicolumn variables.

Load sample data.

```
load('fisheriris')
X = meas;
size(X)

ans =

   150     4
```

Convert the matrix to a dataset array, combining the sepal measurements (the first two columns) into one variable named `SepalMeas`, and the petal measurements (third and fourth columns) into one variable names `PetalMeas`.

```
ds = mat2dataset(X,'NumCols',[2,2],...
'VarNames',{'SepalMeas','PetalMeas'});
ds(1:5,:)

ans =

    SepalMeas           PetalMeas
    5.1         3.5     1.4         0.2
    4.9           3     1.4         0.2
    4.7         3.2     1.3         0.2
    4.6         3.1     1.5         0.2
      5         3.6     1.4         0.2
```

The output dataset array has 150 observations and 2 variables.

```
size(ds)

ans =

   150     2
```

- "Create a Dataset Array from Workspace Variables" on page 2-63
- "Create a Dataset Array from a File" on page 2-69

Input Arguments

X — Input matrix

matrix

Input matrix to convert to a dataset array, specified as an *M*-by-*N* numeric matrix. Each column of `X` becomes a variable in the output *M*-by-*N* dataset array.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'NumCols',[1,1,2,1]` specifies that the 3rd and 4th columns of the input matrix should be combined into a single variable.

'VarNames' — Variable names for output dataset array

cell array of strings

Variable names for the output dataset array, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings. You must provide a variable name for each variable in ds. The names must be valid MATLAB identifiers, and must be unique.

Example: `'VarNames',{'myVar1','myVar2','myVar3'}`

'ObsNames' — Observation names for output dataset array

cell array of strings

Observation names for the output dataset array, specified as the comma-separated pair consisting of `'ObsNames'` and a cell array of strings. The names do not need to be valid MATLAB identifiers, but they must be unique.

`'NumCols'` — Number of columns for each variable

vector of nonnegative integers

Number of columns for each variable in ds, specified as the comma-separated pair consisting of `'NumCols'` and a vector of nonnegative integers. When the number of columns for a variable is greater than one, `mat2dataset` combines multiple columns in X into a single variable in `ds`. The vector you assign to `NumCols` must sum to `size(X,2)`.

For example, to convert a matrix with eight columns into a dataset array with five variables, specify a vector with five elements that sum to eight, such as `'NumCols', [1,1,3,1,2]`.

Output Arguments

`ds` — Output dataset array

dataset array

Output dataset array, returned by default with a variable for each column of X, and an observation for each row of `X`. If you specify NumCols, then the number of variables in `ds` is equal to the length of the specified vector of column numbers.

More About

- “Dataset Arrays” on page 2-132

See Also

`cell2dataset` | `dataset` | `struct2dataset`

mdscale

Nonclassical multidimensional scaling

Syntax

```
Y = mdscale(D,p)
[Y,stress] = mdscale(D,p)
[Y,stress,disparities] = mdscale(D,p)
[...] = mdscale(D,p,'Name',value)
```

Description

`Y = mdscale(D,p)` performs nonmetric multidimensional scaling on the n-by-n dissimilarity matrix `D`, and returns `Y`, a configuration of n points (rows) in `p` dimensions (columns). The Euclidean distances between points in `Y` approximate a monotonic transformation of the corresponding dissimilarities in `D`. By default, `mdscale` uses Kruskal's normalized stress1 criterion.

You can specify `D` as either a full n-by-n matrix, or in upper triangle form such as is output by `pdist`. A full dissimilarity matrix must be real and symmetric, and have zeros along the diagonal and non-negative elements everywhere else. A dissimilarity matrix in upper triangle form must have real, non-negative entries. `mdscale` treats `NaN`s in `D` as missing values, and ignores those elements. `Inf` is not accepted.

You can also specify `D` as a full similarity matrix, with ones along the diagonal and all other elements less than one. `mdscale` transforms a similarity matrix to a dissimilarity matrix in such a way that distances between the points returned in `Y` approximate `sqrt(1-D)`. To use a different transformation, transform the similarities prior to calling `mdscale`.

`[Y,stress] = mdscale(D,p)` returns the minimized stress, i.e., the stress evaluated at `Y`.

`[Y,stress,disparities] = mdscale(D,p)` returns the disparities, that is, the monotonic transformation of the dissimilarities `D`.

`[...] = mdscale(D,p,'Name',value)` specifies one or more optional parameter name/value pairs that control further details of `mdscale`. Specify *`Name`* in single quotes. Available parameters are

- `Criterion`— The goodness-of-fit criterion to minimize. This also determines the type of scaling, either non-metric or metric, that `mdscale` performs. Choices for non-metric scaling are:
  - `'stress'` — Stress normalized by the sum of squares of the inter-point distances, also known as stress1. This is the default.
  - `'sstress'` — Squared stress, normalized with the sum of 4th powers of the inter-point distances.

  Choices for metric scaling are:
  - `'metricstress'` — Stress, normalized with the sum of squares of the dissimilarities.
  - `'metricsstress'` — Squared stress, normalized with the sum of 4th powers of the dissimilarities.
  - `'sammon'` — Sammon's nonlinear mapping criterion. Off-diagonal dissimilarities must be strictly positive with this criterion.
  - `'strain'` — A criterion equivalent to that used in classical multidimensional scaling.
- `Weights` — A matrix or vector the same size as `D`, containing nonnegative dissimilarity weights. You can use these to weight the contribution of the corresponding elements of `D` in computing and minimizing stress. Elements of `D` corresponding to zero weights are effectively ignored.

  Note: When you specify weights as a full matrix, its diagonal elements are ignored and have no effect, since the corresponding diagonal elements of `D` do not enter into the stress calculation.
- `Start` — Method used to choose the initial configuration of points for Y. The choices are
  - `'cmdscale'` — Use the classical multidimensional scaling solution. This is the default. `'cmdscale'` is not valid when there are zero weights.
  - `'random'` — Choose locations randomly from an appropriately scaled p-dimensional normal distribution with uncorrelated coordinates.

  - An *n*-by-`p` matrix of initial locations, where n is the size of the matrix `D` and `p` is the number of columns of the output matrix `Y`. In this case, you can pass in `[]` for `p` and `mdscale` infers `p` from the second dimension of the matrix. You can also supply a 3-D array, implying a value for `'Replicates'` from the array's third dimension.
- `Replicates` — Number of times to repeat the scaling, each with a new initial configuration. The default is `1`.
- `Options` — Options for the iterative algorithm used to minimize the fitting criterion. Pass in an options structure created by `statset`. For example,

  ```
  opts = statset(param1,val1,param2,val2, ...);
  [...] = mdscale(...,'Options',opts)
  ```

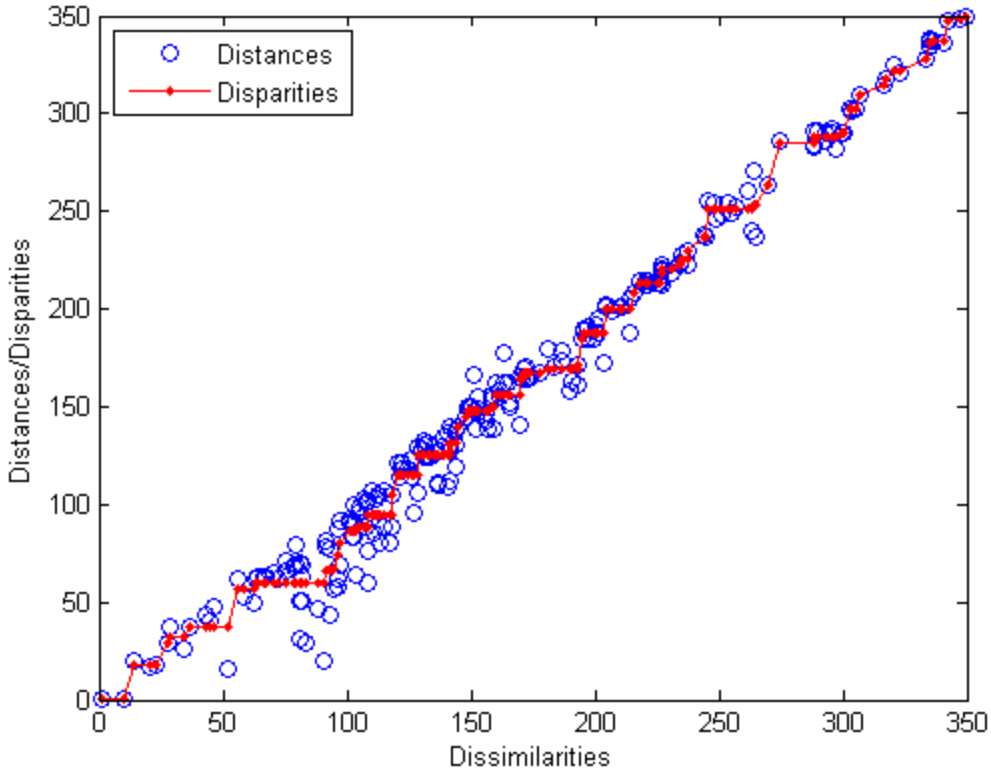
  The choices of `statset` parameters are

  - `'Display'` — Level of display output. The choices are `'off'` (the default), `'iter'`, and `'final'`.
  - `'MaxIter'` — Maximum number of iterations allowed. The default is `200`.
  - `'TolFun'` — Termination tolerance for the stress criterion and its gradient. The default is `1e-4`.
  - `'TolX'`— Termination tolerance for the configuration location step size. The default is `1e-4`.

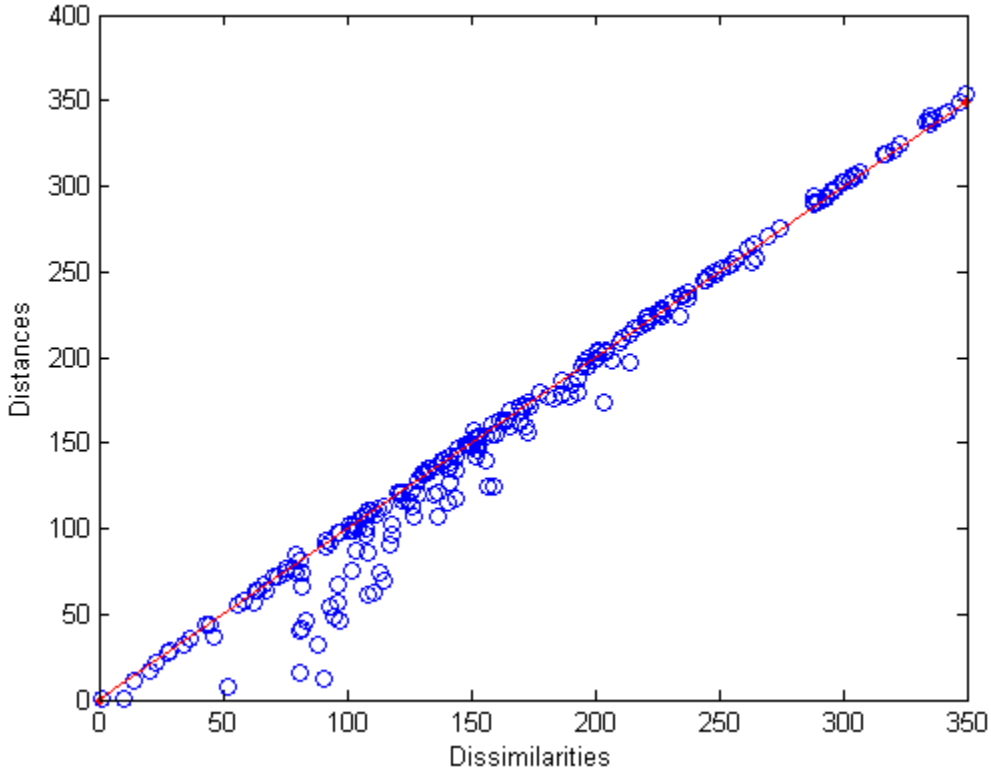
Examples

```
load cereal.mat
X = [Calories Protein Fat Sodium Fiber ...
     Carbo Sugars Shelf Potass Vitamins];

% Take a subset from a single manufacturer.
X = X(strcmp('K',cellstr(Mfg)),:);

% Create a dissimilarity matrix.
dissimilarities = pdist(X);

% Use non-metric scaling to recreate the data in 2D,
% and make a Shepard plot of the results.
[Y,stress,disparities] = mdscale(dissimilarities,2);
distances = pdist(Y);
```

```
[dum,ord] = sortrows([disparities(:) dissimilarities(:)]);
plot(dissimilarities,distances,'bo', ...
dissimilarities(ord),disparities(ord),'r.-');
xlabel('Dissimilarities'); ylabel('Distances/Disparities')
legend({'Distances' 'Disparities'},'Location','NW');
```




```
% Do metric scaling on the same dissimilarities.
figure
[Y,stress] = ...
mdscale(dissimilarities,2,'criterion','metricsstress');
distances = pdist(Y);
plot(dissimilarities,distances,'bo', ...
[0 max(dissimilarities)],[0 max(dissimilarities)],'r.-');
xlabel('Dissimilarities'); ylabel('Distances')
```



See Also

`cmdscale` | `pdist` | `statset`

mdsProx

Class: CompactTreeBagger

Multidimensional scaling of proximity matrix

Syntax

```
[SC,EIGEN] = mdsProx(B,X)
[SC,EIGEN] = mdsProx(B,X,'param1',val1,'param2',val2,...)
```

Description

`[SC,EIGEN] = mdsProx(B,X)` applies classical multidimensional scaling to the proximity matrix computed for the data in the matrix `X`, and returns scaled coordinates `SC` and eigenvalues `EIGEN` of the scaling transformation. The method applies multidimensional scaling to the matrix of distances defined as 1-`prox`, where `prox` is the proximity matrix returned by the `proximity` method.

You can supply the proximity matrix directly by using the `'data'` parameter.

`[SC,EIGEN] = mdsProx(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'data'`	Flag indicating how the method treats the `X` input argument. If set to `'predictors'` (default), `mdsProx` assumes `X` to be a matrix of predictors and used for computation of the proximity matrix. If set to `'proximity'`, the method treats `X` as a proximity matrix returned by the `proximity` method.
`'colors'`	If you supply this argument, `mdsProx` makes overlaid scatter plots of two scaled coordinates using specified colors for different classes. You must supply the colors as a string with one character for each color. If there are more classes in the data than characters in the supplied string, `mdsProx` only plots the first `C` classes, where `C` is the length of the string. For regression or if you do not provide the vector of true class labels, the method uses the first color for all observations in `X`.

`'labels'`	Vector of true class labels for a classification ensemble. True class labels can be either a numeric vector, character matrix, or cell array of strings. If supplied, this vector must have as many elements as there are observations (rows) in `X`. This argument has no effect unless you also supply the `'colors'` argument.
`'mdscoords'`	Indices of the two scaled coordinates to plot. By default, `mdsProx` makes a scatter plot of the first and second scaled coordinates which correspond to the two largest eigenvalues. You can specify any other two or three indices not exceeding the dimensionality of the scaled data. This argument has no effect unless you also supply the `'colors'` argument.

See Also

`cmdscale` | `TreeBagger.mdsProx` | `proximity`

mdsProx

Class: TreeBagger

Multidimensional scaling of proximity matrix

Syntax

```
[S,E] = mdsProx(B)
[S,E] = mdsProx(B,'param1',val1,'param2',val2,...)
```

Description

`[S,E] = mdsProx(B)` returns scaled coordinates, `S`, and eigenvalues, `E`, for the proximity matrix in the ensemble `B`. An earlier call to `fillProximities(B)` must create the proximity matrix.

`[S,E] = mdsProx(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'keep'`	Array of indices of observations in the training data to use for multidimensional scaling. By default, this argument is set to `'all'`. If you provide numeric or logical indices, the method uses only the subset of the training data specified by these indices to compute the scaled coordinates and eigenvalues.
`'colors'`	If you supply this argument, `mdsProx` makes overlaid scatter plots of two scaled coordinates using specified colors for different classes. You must supply the colors as a string with one character for each color. If there are more classes in the data than characters in the supplied string, `mdsProx` only plots the first `C` classes, where `C` is the length of the string. For regression or if you do not provide the vector of true class labels, the method uses the first color for all observations in `X`.
`'mdscoords'`	Indices of the two scaled coordinates to plot. By default, `mdsProx` makes a scatter plot of the first and second scaled coordinates which correspond to the two largest eigenvalues. You can specify any

other two or three indices not exceeding the dimensionality of the scaled data. This argument has no effect unless you also supply the `'colors'` argument.

See Also

`cmdscale` | `CompactTreeBagger.mdsProx` | `fillProximities`

mean

Mean of probability distribution

Syntax

```
m = mean(pd)
```

Description

`m = mean(pd)` returns the mean m of the probability distribution pd.

Examples

Mean of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Create a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the mean of the fitted distribution.

```
m = mean(pd)
```

```
m =
```

```
   75.0083
```

The mean of the normal distribution is equal to the parameter `mu`.

Mean of a Skewed Distribution

Create a Weibull probability distribution object.

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Compute the mean of the distribution.

```
mean = mean(pd)
```

```
mean =
    4.4311
```

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`m` — Mean

scalar value

Mean of the probability distribution, returned as a scalar value.

See Also

`dfittool` | `fitdist` | `makedist`

mean

Class: prob.KernelDistribution
Package: prob

Mean of probability distribution object

Syntax

```
m = mean(pd)
```

Description

`m = mean(pd)` returns the mean m of the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Fit a probability distribution object to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`m` — Mean

scalar value

Mean of the probability distribution, returned as a scalar value.

Examples

Mean of a Kernel Distribution

Load the sample data. Create a probability distribution object by fitting a kernel distribution to the miles per gallon (`MPG`) data.

```
load carsmall;
pd = fitdist(MPG,'Kernel')

pd =

  KernelDistribution

    Kernel = normal
    Bandwidth = 4.11428
    Support = unbounded
```

Compute the mean of the distribution.

```
mean(pd)

ans =

   23.7181
```

See Also

`dfittool` | `fitdist`

mean

Class: ProbDistUnivParam

Return mean of ProbDistUnivParam object

Syntax

```
M = mean(PD)
```

Description

`M = mean(PD)` returns *M*, the mean of the ProbDistUnivParam object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

M	The mean of the ProbDistUnivParam object *PD*.

See Also

`mean`

mean

Class: prob.ParametricTruncatableDistribution
Package: prob

Mean of probability distribution object

Syntax

```
m = mean(pd)
```

Description

`m = mean(pd)` returns the mean m of the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`.

Output Arguments

`m` — Mean

scalar value

Mean of the probability distribution, returned as a scalar value.

Examples

Mean of a Uniform Distribution

Create a uniform distribution object

```
pd = makedist('Uniform','lower',-3,'upper',5)

pd =

  UniformDistribution

  Uniform distribution
    Lower = -3
    Upper =  5
```

Compute the mean of the distribution.

```
m = mean(pd)

m =
     1
```

See Also

`makedist`

mean

Class: prob.ToolboxFittableParametricDistribution
Package: prob

Mean of probability distribution object

Syntax

```
m = mean(pd)
```

Description

`m = mean(pd)` returns the mean m of the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`m` — Mean

scalar value

Mean of the probability distribution, returned as a scalar value.

Examples

Mean of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Create a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the mean of the fitted distribution.

```
m = mean(pd)
```

```
m =

   75.0083
```

The mean of the normal distribution is equal to the parameter `mu`.

Mean of a Skewed Distribution

Create a Weibull probability distribution object.

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Compute the mean of the distribution.

```
mean = mean(pd)
```

```
mean =
    4.4311
```

See Also

`dfittool` | `fitdist` | `makedist`

meanMargin

Class: CompactTreeBagger

Mean classification margin

Syntax

```
mar = meanMargin(B,X,Y)
mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = meanMargin(B,X,Y)` computes average classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `meanMargin` averages the margins over all observations (rows) in `X` for each tree. `mar` is a matrix of size 1-by-`NTrees`, where `NTrees` is the number of trees in the ensemble `B`. This method is available for classification ensembles only.

`mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `meanMargin` computes errors. If set to `'cumulative'` (default), is a vector of length NTrees where the first element gives mean margin from `trees(1)`, second column gives mean margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a vector of length `NTrees`, where each element is a mean margin from each tree in the ensemble . If set to `'ensemble'`, `mar` is a scalar showing the cumulative mean margin for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'`

mode, the first element gives mean margin from `trees(1)`, the second element gives mean margin from `trees(1:2)` etc.

`'treeweights'` Vector of tree weights. This vector must have the same length as the `'trees'` vector. `meanMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`TreeBagger.meanMargin`

meanMargin

Class: TreeBagger

Mean classification margin

Syntax

```
mar = meanMargin(B,X,Y)
mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)
```

Description

`mar = meanMargin(B,X,Y)` computes average classification margins for predictors `X` given true response `Y`. The `Y` can be either a numeric vector, character matrix, cell array of strings, categorical vector or logical vector. `meanMargin` averages the margins over all observations (rows) in `X` for each tree. `mar` is a matrix of size 1-by-`NTrees`, where `NTrees` is the number of trees in the ensemble `B`. This method is available for classification ensembles only.

`mar = meanMargin(B,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `meanMargin` computes errors. If set to `'cumulative'` (default), is a vector of length NTrees where the first element gives mean margin from `trees(1)`, second column gives mean margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a vector of length `NTrees`, where each element is a mean margin from each tree in the ensemble . If set to `'ensemble'`, `mar` is a scalar showing the cumulative mean margin for the entire ensemble .
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'`

	mode, the first element gives mean margin from `trees(1)`, the second element gives mean margin from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. `meanMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.meanMargin`

meansurrvarassoc

Class: classregtree

Mean predictive measure of association for surrogate splits in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
MA = meansurrvarassoc(T)
MA = meansurrvarassoc(T,N)
```

Description

`MA = meansurrvarassoc(T)` returns a p-by-p matrix, `MA`, with predictive measures of association for p predictors. Element `MA`(i,j) is the predictive measure of association averaged over surrogate splits on predictor j for which predictor i is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor i and surrogate splits on predictor j and dividing by the total number of optimal splits on predictor i, including splits for which the predictive measure of association between predictors i and j is negative.

`MA = meansurrvarassoc(T,N)` takes an array `N` of node numbers and returns the predictive measure of association averaged over the specified nodes.

See Also

`classregtree` | `surrcuttype` | `surrcutpoint` | `surrcutvar` | `surrvarassoc` | `surrcutcategories` | `surrcutflip`

surrogateAssociation

Class: CompactClassificationTree

Mean predictive measure of association for surrogate splits in decision tree

Syntax

```
ma = surrogateAssociation(tree)
ma = surrogateAssociation(tree,N)
```

Description

`ma = surrogateAssociation(tree)` returns a matrix of predictive measures of association for the predictors in `tree`.

`ma = surrogateAssociation(tree,N)` returns a matrix of predictive measures of association averaged over the nodes in vector `N`.

Input Arguments

`tree`

A classification tree constructed with `fitctree`, or a compact regression tree constructed with `compact`.

`N`

Vector of node numbers in `tree`.

Output Arguments

`ma`

- `ma = surrogateAssociation(tree)` returns a `P`-by-`P` matrix, where `P` is the number of predictors in tree. `ma(i,j)` is the predictive measure of association

between the optimal split on variable `i` and a surrogate split on variable `j`. See "Predictive Measure of Association" on page 22-2887.

- `ma = surrogateAssociation(tree,N)` returns a `P`-by-`P` representing the predictive measure of association between variables averaged over nodes in the vector `N`. `N` contains node numbers from `1` to `max(tree.NumNodes)`.

Definitions

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j}>0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Find the mean predictive measure of association between the variables in the Fisher iris data:

```
load fisheriris
obj = fitctree(meas,species,'surrogate','on');
msva = surrogateAssociation(obj)

msva =
    1.0000         0         0         0
         0    1.0000         0         0
    0.4633    0.2500    1.0000    0.5000
    0.2065    0.1413    0.4022    1.0000
```

Find the mean predictive measure of association averaged over the odd-numbered nodes in `obj`:

```
N = 1:2:obj.NumNodes;
msva = surrogateAssociation(obj,N)

msva =
    1.0000         0         0         0
         0    1.0000         0         0
    0.7600    0.5000    1.0000    1.0000
    0.4130    0.2826    0.8043    1.0000
```

See Also

`ClassificationTree` | `fitctree`

surrogateAssociation

Class: CompactRegressionTree

Mean predictive measure of association for surrogate splits in decision tree

Syntax

```
ma = surrogateAssociation(tree)
ma = surrogateAssociation(tree,N)
```

Description

`ma = surrogateAssociation(tree)` returns a matrix of predictive measures of association for the predictors in `tree`.

`ma = surrogateAssociation(tree,N)` returns a matrix of predictive measures of association averaged over the nodes in vector `N`.

Input Arguments

`tree`

A regression tree constructed with `fitrtree`, or a compact regression tree constructed with `compact`.

`N`

Vector of node numbers in `tree`.

Output Arguments

`ma`

- `ma = surrogateAssociation(tree)` returns a `P`-by-`P` matrix, where `P` is the number of predictors in tree. `ma(i,j)` is the predictive measure of association

between the optimal split on variable `i` and a surrogate split on variable `j`. See "Predictive Measure of Association" on page 22-2890.

- `ma = surrogateAssociation(tree,N)` returns a `P`-by-`P` representing the predictive measure of association between variables averaged over nodes in the vector `N`. `N` contains node numbers from `1` to `max(tree.NumNodes)`.

Definitions

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Find the mean predictive measure of association between the `Displacement`, `Horsepower`, and `Weight` variables in the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
tree = fitrtree(X,MPG,'surrogate','on');
ma = surrogateAssociation(tree)

ma =
    1.0000    0.2708    0.3854
    0.4764    1.0000    0.4568
    0.3472    0.2326    1.0000
```

Find the mean predictive measure of association averaged over the odd-numbered nodes in `tree`:

```
N = 1:2:tree.NumNodes;
ma = surrogateAssociation(tree,N)

ma =
    1.0000    0.2500    0.3750
    0.5910    1.0000    0.5861
    0.5000    0.2361    1.0000
```

See Also

`prune` | `RegressionTree` | `fitrtree`

median

Median of probability distribution

Syntax

```
m = median(pd)
```

Description

`m = median(pd)` returns the median m for the probability distribution pd

Examples

Median of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Create a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the median of the fitted distribution.

```
m = median(pd)
```

```
m =

   75.0083
```

For a symmetrical distribution such as the normal distribution, the median will be equal to the mean, `mu`.

Median of a Skewed Distribution

Create a Weibull probability distribution object.

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Compute the median of the distribution.

```
m = median(pd)
```

```
m =
    4.1628
```

For a skewed distribution such as the Weibull distribution, the median and the mean may not be equal.

Calculate the mean of the Weibull distribution and compare it to the median.

```
mean = mean(pd)
```

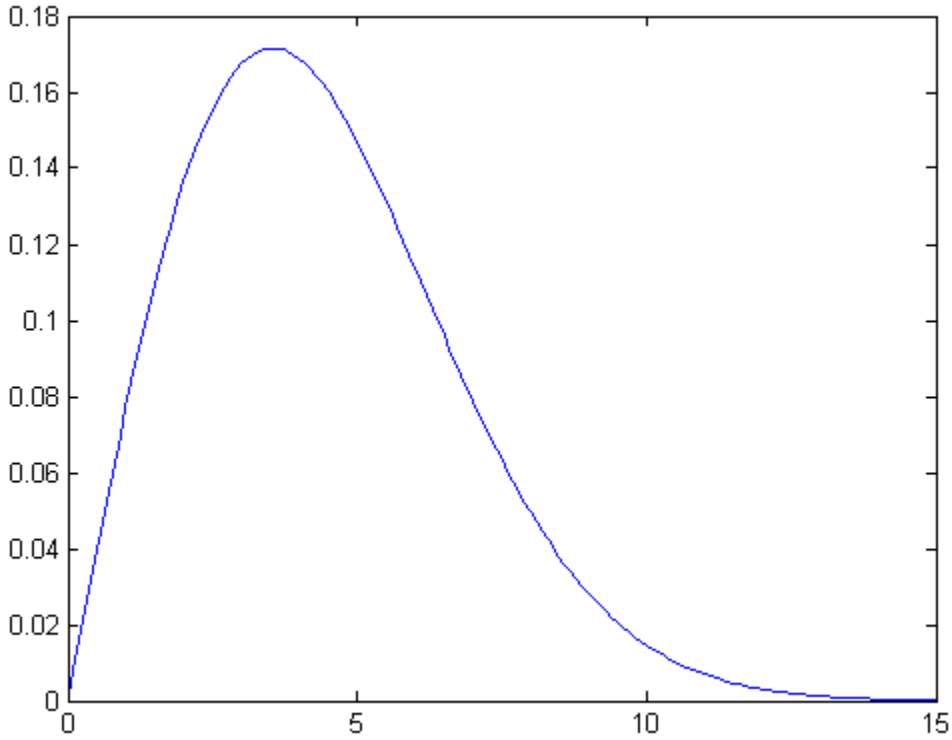
```
mean =
    4.4311
```

The mean of the distribution is greater than the median.

Plot the pdf to visualize the distribution.

```
x = [0:.1:15];
pdf = pdf(pd,x);
```

```
plot(x,pdf)
```



Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`m` — Median

scalar value

Median of the probability distribution, returned as a scalar value. The value of m is the 50th percentile of the probability distribution.

See Also

`dfittool` | `fitdist` | `makedist` | `mean` | `median`

median

Class: ProbDistUnivKernel

Return median of ProbDistUnivKernel object

Syntax

```
M = median(PD)
```

Description

`M = median(PD)` returns *M*, the median of the ProbDistUnivKernel object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivKernel`.

Output Arguments

M	The median of the ProbDistUnivKernel object *PD*.

See Also

`median`

median

Class: ProbDistUnivParam

Return median of ProbDistUnivParam object

Syntax

```
M = median(PD)
```

Description

`M = median(PD)` returns *M*, the median of the ProbDistUnivParam object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

M	The median of the ProbDistUnivParam object *PD*.

See Also

`median`

median

Class: prob.TruncatableDistribution
Package: prob

Median of probability distribution object

Syntax

```
m = median(pd)
```

Description

`m = median(pd)` returns the median m for the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`m` — Median

scalar value

Median of the probability distribution, returned as a scalar value. The value of m is the 50th percentile of the probability distribution.

Examples

Median of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Create a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the median of the fitted distribution.

```
m = median(pd)
```

```
m =

   75.0083
```

For a symmetrical distribution such as the normal distribution, the median will be equal to the mean, `mu`.

Median of a Skewed Distribution

Create a Weibull probability distribution object.

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution
```

```
  Weibull distribution
    A = 5
    B = 2
```

Compute the median of the distribution.

```
m = median(pd)
```

```
m =
    4.1628
```

For a skewed distribution such as the Weibull distribution, the median and the mean may not be equal.

Calculate the mean of the Weibull distribution and compare it to the median.

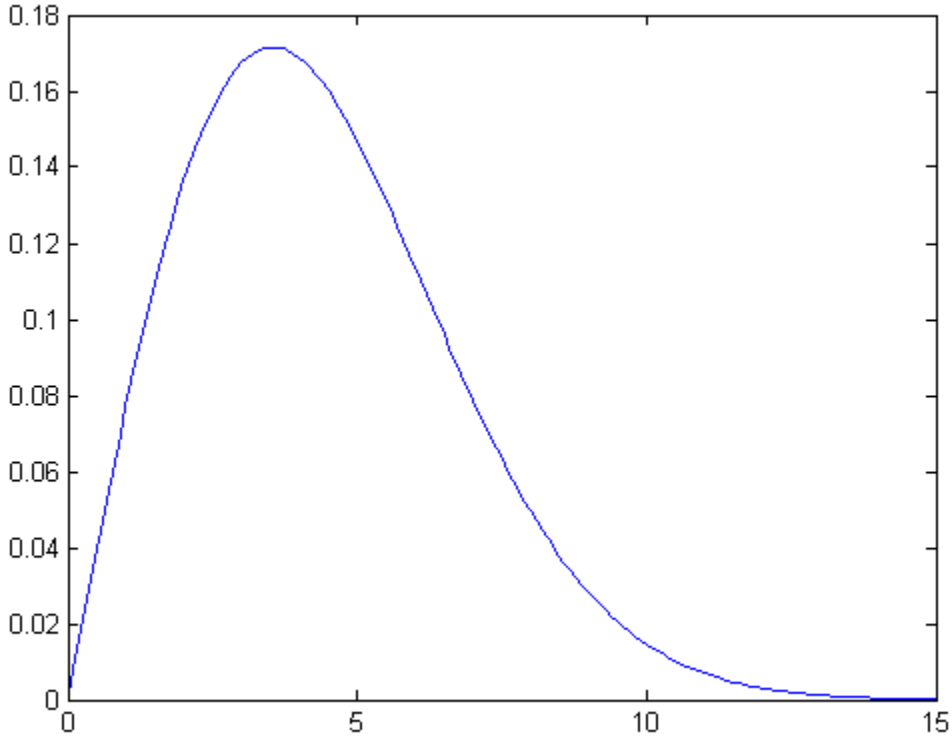
```
mean = mean(pd)
```

```
mean =
    4.4311
```

The mean of the distribution is greater than the median.

Plot the pdf to visualize the distribution.

```
x = [0:.1:15];
pdf = pdf(pd,x);
plot(x,pdf)
```



See Also

`dfittool` | `fitdist` | `makedist` | `mean` | `median`

MergeLeaves property

Class: TreeBagger

Flag to merge leaves that do not improve risk

Description

The `MergeLeaves` property is true if decision trees have their leaves with the same parent merged for splits that do not decrease the total risk, and false otherwise. The default value is false.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

mergelevels

Merge levels of nominal or ordinal arrays

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
B = mergelevels(A,oldlevels)
B = mergelevels(A,oldlevels,newlevel)
```

Description

`B = mergelevels(A,oldlevels)` merges two or more levels of A.

- If A is a `nominal` array, `mergelevels` uses the first label in oldlevels as the new level.
- If A is an `ordinal` array, the levels specified by oldlevels must be consecutive, and `mergelevels` uses the label corresponding to the lowest level in oldlevels as the label for the new level.

`B = mergelevels(A,oldlevels,newlevel)` merges two or more levels into the new level with label newlevel.

Examples

Create New Category From Merged Levels

Create a nominal array from string data in a cell array.

```
colors = nominal({'r','b','g';'g','r','b';'b','r','g'},...
```

```
                {'blue','green','red'})

colors =

     red        blue       green
     green      red        blue
     blue       red        green
```

Merge the elements of the `'red'` and `'blue'` levels into a new level labeled `'purple'`.

```
colors = mergelevels(colors,{'red','blue'},'purple')

colors =

     purple     purple     green
     green      purple     purple
     purple     purple     green
```

Display the levels of `colors`.

```
getlevels(colors)

ans =

     purple     green
```

- “Merge Category Levels” on page 2-19

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

`oldlevels` — Levels to merge

cell array of strings | 2-D character matrix

Levels to merge, specified as a cell array of strings or 2-D character matrix. For ordinal arrays, the levels in oldlevels must be consecutive.

Data Types: `char` | `cell`

`newlevel` — Level to create

string

Level to create from the merged levels, specified as a string that gives the label for the new level.

Data Types: `char`

Output Arguments

`B` — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, returned as a `nominal` or `ordinal` array object.

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`addlevels` | `droplevels` | `nominal` | `ordinal` | `reorderlevels`

Method property

Class: TreeBagger

Method used by trees (classification or regression)

Description

The `Method` property is `'classification'` for classification ensembles and `'regression'` for regression ensembles.

mhsample

Metropolis-Hastings sample

Syntax

```
smpl = mhsample(start,nsamples,'pdf',pdf,'proppdf',proppdf,
'proprnd',proprnd)
smpl = mhsample(...,'symmetric',sym)
smpl = mhsample(...,'burnin',K)
smpl = mhsample(...,'thin',m)
smpl = mhsample(...,'nchain',n)
[smpl,accept] = mhsample(...)
```

Description

`smpl = mhsample(start,nsamples,'pdf',pdf,'proppdf',proppdf, 'proprnd',proprnd)` draws `nsamples` random samples from a target stationary distribution `pdf` using the Metropolis-Hastings algorithm.

`start` is a row vector containing the start value of the Markov Chain, `nsamples` is an integer specifying the number of samples to be generated, and `pdf`, `proppdf`, and `proprnd` are function handles created using `@`. `proppdf` defines the proposal distribution density, and `proprnd` defines the random number generator for the proposal distribution. `pdf` and `proprnd` take one argument as an input with the same type and size as `start`. `proppdf` takes two arguments as inputs with the same type and size as `start`.

`smpl` is a column vector or matrix containing the samples. If the log density function is preferred, `'pdf'` and `'proppdf'` can be replaced with `'logpdf'` and `'logproppdf'`. The density functions used in Metropolis-Hastings algorithm are not necessarily normalized.

The proposal distribution $q(x,y)$ gives the probability density for choosing x as the next point when y is the current point. It is sometimes written as $q(x|y)$.

If the `proppdf` or `logproppdf` satisfies $q(x,y) = q(y,x)$, that is, the proposal distribution is symmetric, `mhsample` implements Random Walk Metropolis-Hastings sampling. If

the `proppdf` or `logproppdf` satisfies $q(x,y) = q(x)$, that is, the proposal distribution is independent of current values, `mhsample` implements Independent Metropolis-Hastings sampling.

`smpl = mhsample(...,'symmetric',sym)` draws `nsamples` random samples from a target stationary distribution `pdf` using the Metropolis-Hastings algorithm. `sym` is a logical value that indicates whether the proposal distribution is symmetric. The default value is false, which corresponds to the asymmetric proposal distribution. If `sym` is true, for example, the proposal distribution is symmetric, `proppdf` and `logproppdf` are optional.

`smpl = mhsample(...,'burnin',K)` generates a Markov chain with values between the starting point and the k^{th} point omitted in the generated sequence. Values beyond the k^{th} point are kept. `k` is a nonnegative integer with default value of `0`.

`smpl = mhsample(...,'thin',m)` generates a Markov chain with `m-1` out of `m` values omitted in the generated sequence. `m` is a positive integer with default value of `1`.

`smpl = mhsample(...,'nchain',n)` generates `n` Markov chains using the Metropolis-Hastings algorithm. `n` is a positive integer with a default value of 1. `smpl` is a matrix containing the samples. The last dimension contains the indices for individual chains.

`[smpl,accept] = mhsample(...)` also returns `accept`, the acceptance rate of the proposed distribution. `accept` is a scalar if a single chain is generated and is a vector if multiple chains are generated.

Examples

Estimate Moments Using Independent Metropolis-Hastings Sampling

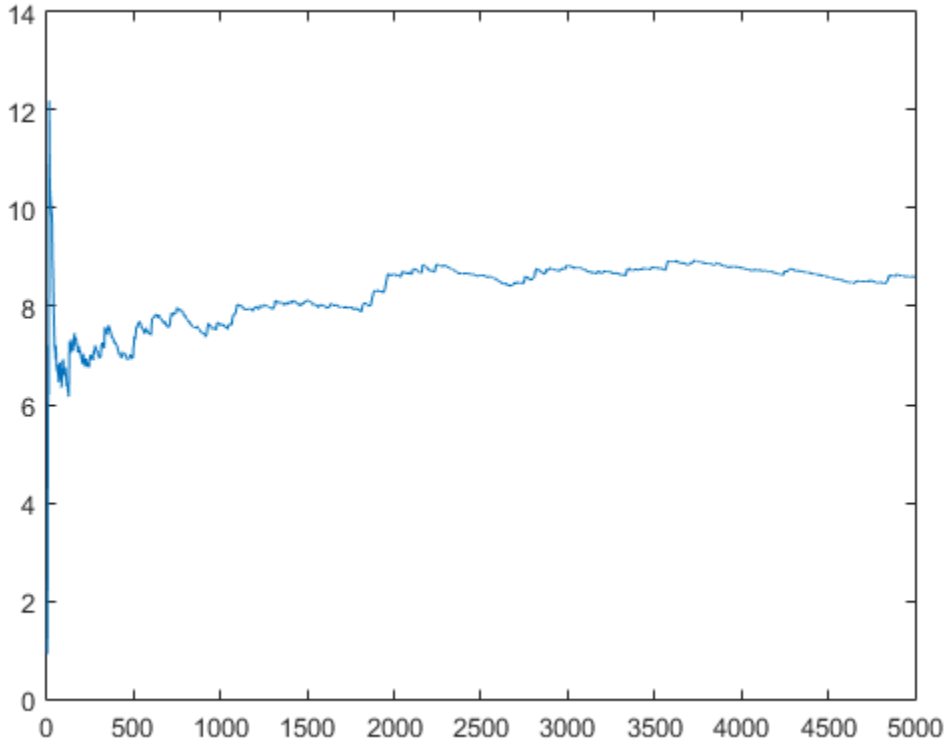
Use Independent Metropolis-Hastings sampling to estimate the second order moment of a Gamma distribution.

```
rng default;  % For reproducibility
alpha = 2.43;
beta = 1;
pdf = @(x)gampdf(x,alpha,beta); % Target distribution
proppdf = @(x,y)gampdf(x,floor(alpha),floor(alpha)/alpha);
proprnd = @(x)sum(...
              exprnd(floor(alpha)/alpha,floor(alpha),1));
```

```
nsamples = 5000;
smpl = mhsample(1,nsamples,'pdf',pdf,'proprnd',proprnd,...
                'proppdf',proppdf);
```

Plot the results.

```
xxhat = cumsum(smpl.^2)./(1:nsamples)';
figure;
plot(1:nsamples,xxhat)
```



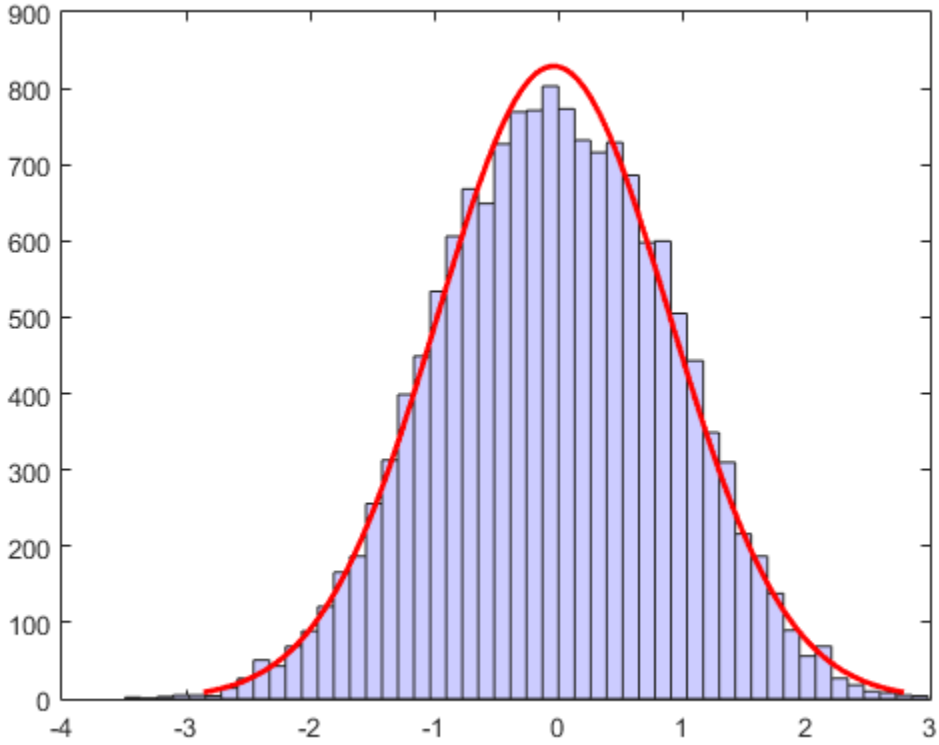
Random Walk Metropolis-Hastings Sampling

Use Random Walk Metropolis-Hastings sampling to generate sample data from a standard normal distribution.

```
rng default  % For reproducibility
delta = .5;
pdf = @(x) normpdf(x);
proppdf = @(x,y) unifpdf(y-x,-delta,delta);
proprnd = @(x) x + rand*2*delta - delta;
nsamples = 15000;
x = mhsample(1,nsamples,'pdf',pdf,'proprnd',proprnd,'symmetric',1);
```

Plot the sample data.

```
figure;
h = histfit(x,50);
h(1).FaceColor = [.8 .8 1];
```



- “Using the Metropolis-Hastings Algorithm” on page 6-14

See Also

`rand` | `slicesample`

MinLeaf property

Class: TreeBagger

Minimum number of observations per tree leaf

Description

The `MinLeaf` property specifies the minimum number of observations per tree leaf. The default values are 1 for classification and 5 for regression. For `fitctree` or `fitrtree` training, the `'minparent'` value is set to `2*MinLeaf`.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

mle

Maximum likelihood estimates

Syntax

```
phat = mle(data)
phat = mle(data,'distribution',dist)

phat = mle(data,'pdf',pdf,'start',start)
phat = mle(data,'pdf',pdf,'start',start,'cdf',cdf)

phat = mle(data,'logpdf',logpdf,'start',start)
phat = mle(data,'logpdf',logpdf,'start',start,'logsf',logsf)

phat = mle(data,'nloglf',nloglf,'start',start)

phat = mle(___,Name,Value)
[phat,pci] = mle(___)
```

Description

`phat = mle(data)` returns maximum likelihood estimates (MLEs) for the parameters of a normal distribution, using the sample data in the vector `data`.

`phat = mle(data,'distribution',dist)` returns parameter estimates for a distribution specified by `dist`.

`phat = mle(data,'pdf',pdf,'start',start)` returns parameter estimates for a custom distribution specified by the probability density function `pdf`. You must also specify the initial parameter values, `start`.

`phat = mle(data,'pdf',pdf,'start',start,'cdf',cdf)` returns parameter estimates for a custom distribution specified by the probability density function `pdf` and custom cumulative distribution function `cdf`.

`phat = mle(data,'logpdf',logpdf,'start',start)` returns parameter estimates for a custom distribution specified by the log probability density function `logpdf`. You must also specify the initial parameter values, `start`.

`phat = mle(data,'logpdf',logpdf,'start',start,'logsf',logsf)` returns parameter estimates for a custom distribution specified by the log probability density function `logpdf` and custom log survival function `logsf`.

`phat = mle(data,'nloglf',nloglf,'start',start)` returns parameter estimates for the custom distribution specified by the negative loglikelihood function `nloglf`. You must also specify the initial parameter values, `start`.

`phat = mle(___,Name,Value)` also returns the parameter estimates with additional options specified by one or more name-value pair arguments. You can use any of the input arguments in the previous syntaxes.

`[phat,pci] = mle(___)` also returns the 95% confidence intervals for the parameters.

Examples

Estimate Parameters of Burr Distribution

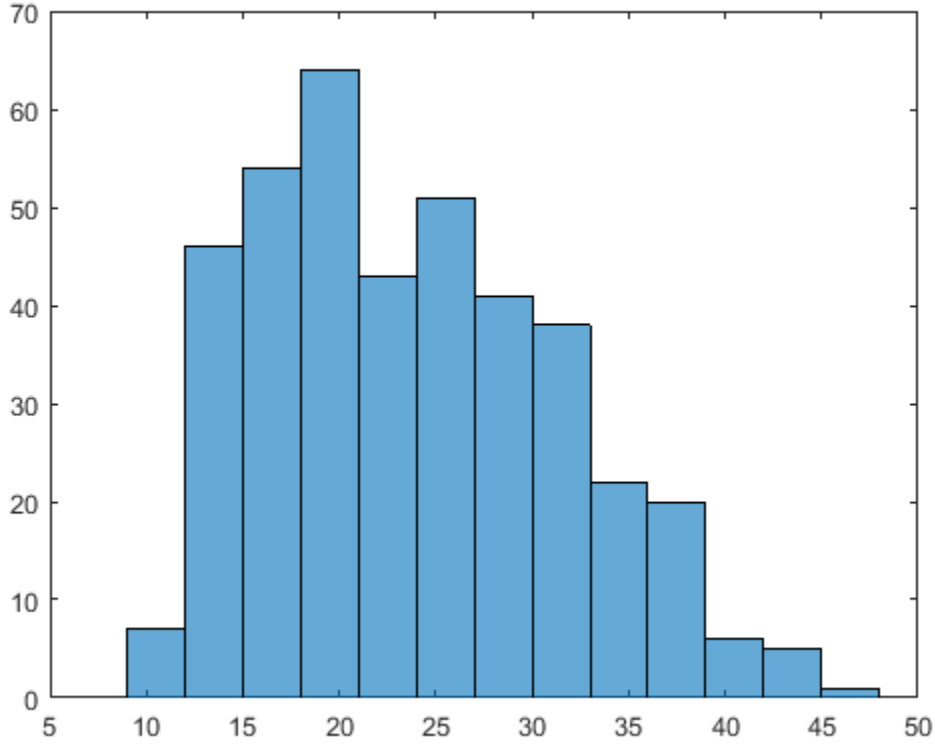
Load the sample data.

```
load carbig
```

The variable `MPG` has the miles per gallon for different models of cars.

Draw a histogram of `MPG` data.

```
histogram(MPG)
```



The distribution is somewhat right skewed. A symmetric distribution, such as normal distribution, might not be a good fit.

Estimate the parameters of the Burr Type XII distribution for the `MPG` data.

```
phat = mle(MPG,'distribution','burr')
```

```
phat =

   34.6447    3.7898    3.5722
```

The maximum likelihood estimates for the scale parameter α is 34.6447. The estimates for the two shape parameters c and k of the Burr Type XII distribution are 3.7898 and 3.5722, respectively.

Fit Custom Distribution to Censored Data

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load readmissiontimes
```

The data includes `ReadmissionTime`, which has readmission times for 100 patients. The column vector `Censored` has the censorship information for each patient, where 1 indicates a censored observation, and 0 indicates the exact readmission time is observed. This is simulated data.

Define a custom probability density and cumulative distribution function.

```
custpdf = @(data,lambda) lambda*exp(-lambda*data);
custcdf = @(data,lambda) 1-exp(-lambda*data);
```

Estimate the parameter, `lambda`, of the custom distribution for the censored sample data.

```
phat = mle(ReadmissionTime,'pdf',custpdf,...
'cdf',custcdf,'start',0.05,'Censoring',Censored)
phat
```

```
phat =

    0.1096
```

Estimate Parameters of a Noncentral Chi-Square Distribution

Generate sample data of size 1000 from a noncentral chi-square distribution with degrees of freedom 8 and noncentrality parameter 3.

```
rng('default') % for reproducibility
x = ncx2rnd(8,3,1000,1);
```

Estimate the parameters of the noncentral chi-square distribution from the sample data. To do this, custom define the noncentral chi-square pdf using the pdf input argument.

```
[phat,pci] = mle(x,'pdf',@(x,v,d)ncx2pdf(x,v,d),'start',[1,1])

phat =

    8.1052    2.6693


pci =

    7.1121    1.6025
    9.0983    3.7362
```

The estimate for the degrees of freedom is 8.1052 and the noncentrality parameter is 2.6693. The 95% confidence interval for the degrees of freedom is (7.0983,9.0983) and the noncentrality parameter is (1.6025,3.7362). The confidence intervals include the true parameter values of 8 and 3, respectively.

Fit Custom Log pdf and Survival Function

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load readmissiontimes
```

The data includes `ReadmissionTime`, which has readmission times for 100 patients. The column vector `Censored` has the censorship information for each patient, where 1 indicates a censored observation, and 0 indicates the exact readmission time is observed. This is simulated data.

Define a custom log probability density and survival function.

```
custlogpdf = @(data,lambda,k) log(k)-k*log(lambda)...
             +(k-1)*log(data)-(data/lambda).^k;
custlogsf = @(data,lambda,k) -(data/lambda).^k;
```

Estimate the parameters, `lambda` and `k`, of the custom distribution for the censored sample data.

```
phat = mle(ReadmissionTime,'logpdf',custlogpdf,...
'logsf',custlogsf,'start',[1,0.75],'Censoring',Censored)

phat =
```

```
    9.2090    1.4223
```

The scale and shape parameters of the custom-defined distribution are 9.2090 and 1.4223, respectively.

Fit Custom Log Negative Likelihood Function

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load readmissiontimes
```

The data includes `ReadmissionTime`, which has readmission times for 100 patients. This is simulated data.

Define a negative log likelihood function.

```
custnloglf = @(lambda,data,cens,freq) -length(data)*log(lambda)...
+ nansum(lambda*data);
```

Estimate the parameters of the defined distribution.

```
phat = mle(ReadmissionTime,'nloglf',custnloglf,'start',0.05)
```

```
phat =

    0.1462
```

Estimate Probability of Success

Generate 100 random observations from a binomial distribution with the number of trials, $n = 20$, and the probability of success, $p = 0.75$.

```
data = binornd(20,0.75,100,1);
```

Estimate the probability of success and 95% confidence limits using the simulated sample data.

```
[phat,pci] = mle(data,'distribution','binomial',...
                 'alpha',.05,'ntrials',20)
```

```
phat =
    0.7370
```

```
pci =
    0.7171
    0.7562
```

The estimate of probability of success is 0.737 and the lower and upper limits of the 95% confidence interval are 0.7171 and 0.7562. This interval covers the true value used to simulate the data.

Fit a Distribution with Known Parameter

Generate sample data of size 1000 from a noncentral chi-square distribution with degrees of freedom 10 and noncentrality parameter 5.

```
rng('default') % for reproducibility
x = ncx2rnd(10,5,1000,1);
```

Suppose the noncentrality parameter is fixed at the value 5. Estimate the degrees of freedom of the noncentral chi-square distribution from the sample data. To do this, custom define the noncentral chi-square pdf using the pdf input argument.

```
[phat,pci] = mle(x,'pdf',@(x,v,d)ncx2pdf(x,v,5),'start',1)
```

```
phat =

    9.9307


pci =

    9.5626
   10.2989
```

The estimate for the noncentrality parameter is 9.9307, with a 95% confidence interval of 9.5626 and 10.2989. The confidence interval includes the true parameter value of 10.

Fit Rician Distribution with Known Scale Parameter

Generate sample data of size 1000 from a Rician distribution with noncentrality parameter of 8 and scale parameter of 5. First create the Rician distribution.

```
r = makedist('Rician','s',8,'sigma',5);
```

Now, generate sample data from the distribution you created above.

```
rng('default');
x = random(r,1000,1);
```

Suppose the scale parameter is known, and estimate the noncentrality parameter from sample data. To do this using `mle`, you must custom define the Rician probability density function.

```
[phat,pci] = mle(x,'pdf',@(x,s,sigma) pdf('rician',x,s,5),'start',10)
```

```
phat =

    7.8953


pci =

    7.5405
    8.2501
```

The estimate for the noncentrality parameter is 7.8953, with a 95% confidence interval of 7.5404 and 8.2501. The confidence interval includes the true parameter value of 8.

Fit a Distribution with Additional Parameter

Add a scale parameter to the chi-square distribution for adapting to the scale of data and fit it. First, generate sample data of size 1000 from a chi-square distribution with degrees of freedom 5, and scale it by the factor of 100.

```
rng('default') % for reproducibility
x = 100*chi2rnd(5,1000,1);
```

Estimate the degrees of freedom and the scaling factor. To do this, custom define the chi-square probability density function using the pdf input argument. The density function requires a 1/*s* factor for data scaled by *s*.

```
[phat,pci] = mle(x,'pdf',@(x,v,s)chi2pdf(x/s,v)/s,'start',[1,200])
```

```
phat =

    5.1079   99.1681


pci =

    4.6862   90.1215
    5.5297  108.2146
```

The estimate for the degrees of freedom is 5.1079 and the scale is 99.1681. The 95% confidence interval for the degrees of freedom is (4.6862,5.5279) and the scale parameter

is (90.1215,108.2146). The confidence intervals include the true parameter values of 5 and 100, respectively.

Input Arguments

`data` — Sample data

vector

Sample data `mle` uses to estimate the distribution parameters, specified as a vector.

Data Types: `single` | `double`

`dist` — Distribution type

`'normal'` (default) | string

Distribution type to estimate parameters for, specified as one of the following.

`dist`	Description	Parameter 1	Parameter 2	Parameter 3
`'bernoulli'`	"Bernoulli Distribution" on page B-2	`p`: probability of success for each trial	—	—
`'beta'` or `'Beta'`	"Beta Distribution" on page B-4	`a`	`b`	—
`'bino'` or `'Binomial'`	"Binomial Distribution" on page B-9	`n`: number of trials	`p`: probability of success for each trial	—
`'birnbaumsaunder`	"Birnbaum-Saunders Distribution" on page B-13	β: scale	γ: shape	—
`'burr'` or `'Burr'`	"Burr Type XII Distribution" on page B-15	α: scale	`c`: first shape	`k`: second shape
`'Discrete Uniform'` or `'unid'`	"Uniform Distribution (Discrete)" on page B-169	`N`: maximum observable value	—	—
`'exp'` or `'Exponential'`	"Exponential Distribution" on page B-35	μ: mean	—	—

dist	Description	Parameter 1	Parameter 2	Parameter 3
'ev' or 'Extreme Value'	"Extreme Value Distribution" on page B-39	μ: location	σ: scale	—
'gam' or 'Gamma'	"Gamma Distribution" on page B-48	a: shape	b: scale	—
'gev' or 'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-54	k: shape	σ: scale	μ: location
'gp' or 'Generalized Pareto'	"Generalized Pareto Distribution" on page B-60	k: tail index (shape)	σ: scale	θ: threshold
'geo' or 'Geometric'	"Geometric Distribution" on page B-65	p: probability	—	—
'inversegaussian'	"Inverse Gaussian Distribution" on page B-77	μ: scale	λ: shape	—
'logistic'	"Logistic Distribution" on page B-91	μ: location	σ: scale	—
'loglogistic'	"Loglogistic Distribution" on page B-93	μ: log location	σ: log scale	—
'logn' or 'Lognormal'	"Lognormal Distribution" on page B-95	μ: log location	σ: log scale	—
'nakagami'	"Nakagami Distribution" on page B-113	μ: shape	ω: scale	—
'nbin' or 'Negative Binomial'	"Negative Binomial Distribution" on page B-115	r: number of successes	p: probability of success in a single trial	—
'norm' or 'Normal'	"Normal Distribution" on page B-130	μ: location (mean)	σ: scale (standard deviation)	—
'poiss' or 'Poisson'	"Poisson Distribution" on page B-138	λ: mean	—	—

dist	Description	Parameter 1	Parameter 2	Parameter 3
'rayl' or 'Rayleigh'	"Rayleigh Distribution" on page B-141	b: scale	—	—
'rician'	"Rician Distribution" on page B-144	s: noncentrality	σ: scale	—
'tlocationscale'	"t Location-Scale Distribution" on page B-154	μ: location	σ: scale	ν: degrees of freedom
'unif' or 'Uniform'	"Uniform Distribution (Continuous)" on page B-163	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'wbl' or 'Weibull'	"Weibull Distribution" on page B-172	a: scale	b: shape	—

Example: 'rician'

pdf — Custom probability density function

function handle

Custom probability distribution function, specified as a function handle created using @.

This custom function accepts the vector data and one or more individual distribution parameters as input parameters, and returns a vector of probability density values.

For example, if the name of the custom probability density function is newpdf, then you can specify the function handle in mle as follows.

Example: @newpdf

Data Types: function_handle

cdf — Custom cumulative distribution function

function handle

Custom cumulative distribution function, specified as a function handle created using @.

This custom function accepts the vector data and one or more individual distribution parameters as input parameters, and returns a vector of cumulative probability values.

You must define `cdf` with `pdf` if data is censored and you use the `'censoring'` name-value pair argument. If `'censoring'` is not present, you do not have to specify `cdf` while using `pdf`.

For example, if the name of the custom cumulative distribution function is `newcdf`, then you can specify the function handle in `mle` as follows.

Example: `@newcdf`

Data Types: `function_handle`

`logpdf` — Custom log probability density function

function handle

Custom log probability density function, specified as a function handle created using `@`.

This custom function accepts the vector `data` and one or more individual distribution parameters as input parameters, and returns a vector of log probability values.

For example, if the name of the custom log probability density function is `customlogpdf`, then you can specify the function handle in `mle` as follows.

Example: `@customlogpdf`

Data Types: `function_handle`

`logsf` — Custom log survival function

function handle

Custom log survival function, specified as a function handle created using `@`.

This custom function accepts the vector `data` and one or more individual distribution parameters as input parameters, and returns a vector of log survival probability values.

You must define `logsf` with `logpdf` if data is censored and you use the `'censoring'` name-value pair argument. If `'censoring'` is not present, you do not have to specify `logsf` while using `logpdf`.

For example, if the name of the custom log survival function is `logsurvival`, then you can specify the function handle in `mle` as follows.

Example: `@logsurvival`

Data Types: `function_handle`

`nloglf` — Custom negative loglikelihood function

function handle

Custom negative loglikelihood function, specified as a function handle created using `@`.

This custom function accepts the following input arguments.

`params`	Vector of distribution parameter values. `mle` detects the number of parameters from the number of elements in start.
`data`	Vector of data.
`cens`	Boolean vector of censored values.
`freq`	Vector of integer data frequencies.

`nloglf` must accept all four arguments even if you do not use the `'censoring'` or `'frequency'` name-value pair arguments. You can write `'nloglf'` to ignore `cens` and `freq` arguments in that case.

`nloglf` returns a scalar negative loglikelihood value and optionally, a negative loglikelihood gradient vector (see the `'GradObj'` field in `'options'`).

If the name of the custom negative log likelihood function is `negloglik`, then you can specify the function handle in `mle` as follows.

Example: `@negloglik`

Data Types: `function_handle`

`start` — Initial parameter values

scalar | vector

Initial parameter values for the custom functions, specified as a scalar value or a vector of scalar values.

Use `start` when you fit custom distributions, that is, when you use pdf and cdf, logpdf and logsf, or nloglf input arguments.

Example: `0.05`

Example: `[100,2]`

Data Types: `single | double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'censoring',Cens,'alpha',0.01,'options',Opt` specifies that `mle` estimates the parameters for the distribution of censored data specified by array `Cens`, computes the 99% confidence limits for the parameter estimates, and uses the algorithm control parameters specified by the structure `Opt`.

`'censoring'` — Indicator for censoring

array of 0s (default) | array of 0s and 1s

Indicator for censoring, specified as the comma-separated pair consisting of `'censoring'` and a Boolean array of the same size as data. Use 1 for observations that are right censored and 0 for observations that are fully observed. The default is all observations are fully observed.

For example, if the censored data information is in the binary array called `Censored`, then you can specify the censored data as follows.

Example: `'censoring',Censored`

`mle` supports censoring for the following distributions:

Birnbaum-Saunders	Logistic
Burr	Lognormal
Exponential	Nakagami
Extreme Value	Normal
Gamma	Rician
Inverse Gaussian	t Location-Scale
Kernel	Weibull
Log-Logistic	

Data Types: `logical`

`'frequency'` — Frequency of observations

array of 1s (default) | vector of nonnegative integer counts

Frequency of observations, specified as the comma-separated pair consisting of `'frequency'` and an array containing nonnegative integer counts, which is the same size as `data`. The default is one observation per element of `data`.

For example, if the observation frequencies are stored in an array named `Freq`, you can specify the frequencies as follows.

Example: `'frequency',Freq`

Data Types: `single | double`

`'alpha'` — Confidence level

0.05 (default) | scalar value in the range (0,1)

Confidence level for the confidence interval of parameter estimates, `pci`, specified as the comma-separated pair consisting of `'alpha'` and a scalar value in the range (0,1). The confidence level of `pci` is `100(1-alpha)`% . The default is `0.05` for 95% confidence.

For example, for 99% confidence limits, you can specify the confidence level as follows.

Example: `'alpha',0.01`

Data Types: `single | double`

`'ntrials'` — Number of trials

scalar value | vector

Number of trials for the corresponding element of `data`, specified as the comma-separated pair consisting of `'ntrials'` and a scalar or a vector of the same size as `data`.

Applies only to binomial distribution.

Example: `'ntrials',total`

Data Types: `single | double`

`'options'` — Fitting algorithm control parameters

structure

Fitting algorithm control parameters, specified as the comma-separated pair consisting of `'options'` and a structure returned by `statset`.

Not applicable to all distributions.

Use the `'options'` name-value pair argument to control details of the maximum likelihood optimization when fitting a custom distribution. For parameter names and

default values, type `statset('mlecustom')`. You can set the options under a new name and use that in the name-value pair argument. `mle` interprets the following `statset` parameters for custom distribution fitting.

Parameter	Value
`'GradObj'`	Default is `'off'`. `'on'` or `'off'`, indicating whether or not `fmincon` can expect the custom function provided with the `nloglf` input argument to return the gradient vector of the negative log-likelihood as a second output. `mle` ignores `'GradObj'` when using `fminsearch`.
`'DerivStep'`	Default is `eps^(1/3)`. The relative difference, specified as a scalar or a vector the same size as `start`, used in finite difference derivative approximations when using `fmincon`, and `'GradObj'` is `'off'`. `mle` ignores `'DerivStep'` when using `fminsearch`.
`'FunValCheck'`	Default is `'on'`. `'on'` or `'off'`, indicating whether or not `mle` should check the values returned by the custom distribution functions for validity. A poor choice of starting point can sometimes cause these functions to return `NaN`s, infinite values, or out-of-range values if they are written without suitable error checking.
`'TolBnd'`	Default is `1e-6`. An offset for upper and lower bounds when using `fmincon`. `mle` treats upper and lower bounds as strict inequalities, that is, open bounds. With `fmincon`, this is approximated by creating closed bounds inset from the specified upper and lower bounds by `TolBnd`.

Example: `'options',statset('mlecustom')`

Data Types: `struct`

`'lowerbound'` — Lower bounds for distribution parameters

– ∞ (default) | vector

Lower bounds for distribution parameters, specified as the comma-separated pair consisting of `'lowerbound'` and a vector the same size as start.

This name-value pair argument is valid only when you use the `pdf` and `cdf`, `logpdf` and `logcdf`, or `nloglf` input arguments.

Example: `'lowerbound',0`

Data Types: `single` | `double`

`'upperbound'` — Upper bounds for distribution parameters

∞ (default) | vector

Upper bounds for distribution parameters, specified as the comma-separated pair consisting of `'upperbound'` and a vector the same size as start.

This name-value pair argument is valid only when you use the pdf and cdf, logpdf and logsf, or nloglf input arguments.

Example: `'upperbound',1`

Data Types: `single` | `double`

`'optimfun'` — Optimization function

`'fminsearch'` (default) | `'fmincon'`

Optimization function `mle` uses in maximizing the likelihood, specified as the comma-separated pair consisting of `'optimfun'` and either `'fminsearch'` or `'fmincon'`.

Default is `'fminsearch'`.

You can only specify `'fmincon'` if Optimization Toolbox is available.

The `'optimfun'` name-value pair argument is valid only when you fit custom distributions, that is, when you use the pdf and cdf, logpdf and logsf, or nloglf input arguments.

Example: `'optimfun','fmincon'`

Output Arguments

`phat` — Parameter estimates

scalar value | row vector

Parameter estimates, returned as a scalar value or a row vector.

`pci` — Confidence intervals for parameter estimates

2-by-*k* matrix

Confidence intervals for parameter estimates, returned as a column vector or a matrix depending on the number of parameters, hence the size of phat.

`pci` is a 2-by-*k* matrix, where *k* is the number of parameters `mle` estimates. The first and second rows of the `pci` show the upper and lower confidence limits, respectively.

More About

Survival Function

The survival function is the probability of survival as a function of time. It is also called the survivor function. It gives the probability that the survival time of an individual exceeds a certain value. Since the cumulative distribution function, $F(t)$, is the probability that the survival time is less than or equal to a given point in time, the survival function for a continuous distribution, $S(t)$, is the complement of the cumulative distribution function: $S(t) = 1 - F(t)$.

Tips

When you supply distribution functions, `mle` computes the parameter estimates using an iterative maximization algorithm. With some models and data, a poor choice of starting point can cause `mle` to converge to a local optimum that is not the global maximizer, or to fail to converge entirely. Even in cases for which the log-likelihood is well-behaved near the global maximum, the choice of starting point is often crucial to convergence of the algorithm. In particular, if the initial parameter values are far from the MLEs, underflow in the distribution functions can lead to infinite log-likelihoods.

- "What Is Survival Analysis?" on page 12-2

See Also

`fitdist` | `mlecov` | `statset`

mlecov

Asymptotic covariance of maximum likelihood estimators

Syntax

```
acov = mlecov(params,data,'pdf',pdf)
acov = mlecov(params,data,'pdf',pdf,'cdf',cdf)

acov = mlecov(params,data,'logpdf',logpdf)
acov = mlecov(params,data,'logpdf',logpdf,'logsf',logsf)

acov = mlecov(params,data,'nloglf',nloglf)

acov = mlecov(___,Name,Value)
```

Description

`acov = mlecov(params,data,'pdf',pdf)` returns an approximation to the asymptotic covariance matrix of the maximum likelihood estimators of the parameters for a distribution specified by the custom probability density function `pdf`.

`mlecov` computes a finite difference approximation to the Hessian of the log-likelihood at the maximum likelihood estimates `params`, given the observed `data`, and returns the negative inverse of that Hessian.

`acov = mlecov(params,data,'pdf',pdf,'cdf',cdf)` returns an approximation to the asymptotic covariance matrix of the maximum likelihood estimators of the parameters for a distribution specified by the custom probability density function `pdf` and cumulative distribution function `cdf`.

`acov = mlecov(params,data,'logpdf',logpdf)` returns an approximation to the asymptotic covariance matrix of the maximum likelihood estimators of the parameters for a distribution specified by the custom log probability density function `logpdf`.

`acov = mlecov(params,data,'logpdf',logpdf,'logsf',logsf)` returns an approximation to the asymptotic covariance matrix of the maximum likelihood estimators of the parameters for a distribution specified by the custom log probability density function `logpdf` and custom log survival function `logsf`.

`acov = mlecov(params,data,'nloglf',nloglf)` returns an approximation to the asymptotic covariance matrix of the maximum likelihood estimators of the parameters for a distribution specified by the custom negative loglikelihood function `nloglf`.

`acov = mlecov(___,Name,Value)` also returns an approximation to the asymptotic covariance matrix of the maximum likelihood estimators of the parameters with additional options specified by one or more name-value pair arguments. You can use any of the input arguments in the previous syntaxes.

Examples

Custom Probability Density Function

Load the sample data.

```
load carbig
```

The vector `Weight` shows the weights of 406 cars.

In the MATLAB Editor, create a function that returns the probability density function (pdf) of a lognormal distribution. Save the file in your current working folder as `lognormpdf.m`.

```
function newpdf = lognormpdf(data,mu,sigma)
newpdf = exp((-(log(data)-mu).^2)/(2*sigma^2))./(data*sigma*sqrt(2*pi));
```

Estimate the parameters, `mu` and `sigma`, of the custom-defined distribution.

```
phat = mle(Weight,'pdf',@lognormpdf,'start',[4.5 0.3])
```

```
phat =

    7.9600    0.2804
```

Compute the approximate covariance matrix of the parameter estimates.

```
acov = mlecov(phat,Weight,'pdf',@lognormpdf)
```

```
acov =

   1.0e-03 *

    0.1937   -0.0000
```

```
   -0.0000    0.0968
```

Estimate the standard errors of estimates.

```
se = sqrt(diag(acov))
```

```
se =

    0.0139
    0.0098
```

The standard error of the estimates of mu and sigma are 0.0139 and 0.0098, respectively.

Custom Log Probability Density Function

In the MATLAB Editor, create a function that returns the log probability density function of a beta distribution. Save the file in your current working folder as `betalogpdf.m`.

```
function logpdf = betalogpdf(x,a,b)
logpdf = (a-1)*log(x)+(b-1)*log(1-x)-betaln(a,b);
```

Generate sample data from a beta distribution with parameters 1.23 and 3.45 and estimate the parameters using the simulated data.

```
rng('default')
x = betarnd(1.23,3.45,25,1);
phat = mle(x,'dist','beta')
```

```
phat =

    1.1213    2.7182
```

Compute the approximate covariance matrix of the parameter estimates.

```
acov = mlecov(phat,x,'logpdf',@betalogpdf)
```

```
acov =

    0.0810    0.1646
    0.1646    0.6074
```

Custom Log pdf and Survival Function

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load readmissiontimes
```

The sample data includes `ReadmissionTime`, which has readmission times for 100 patients. The column vector `Censored` has the censorship information for each patient, where 1 indicates a censored observation, and 0 indicates the exact readmission time is observed. This is simulated data.

Define a custom log probability density and survival function.

```
custlogpdf = @(data,lambda,k) log(k)-k*log(lambda)...
             +(k-1)*log(data)-(data/lambda).^k;
custlogsf = @(data,lambda,k) -(data/lambda).^k;
```

Estimate the parameters, `lambda` and `k`, of the custom distribution for the censored sample data.

```
phat = mle(ReadmissionTime,'logpdf',custlogpdf,...
'logsf',custlogsf,'start',[1,0.75],'Censoring',Censored)
```

```
phat =

    9.2090    1.4223
```

The scale and shape parameters of the custom-defined distribution are 9.2090 and 1.4223, respectively.

Compute the approximate covariance matrix of the parameter estimates.

```
acov = mlecov(phat,ReadmissionTime,...
'logpdf',custlogpdf,'logsf',custlogsf,'Censoring',Censored)
```

```
acov =

    0.5653    0.0102
    0.0102    0.0163
```

Custom Log Negative Likelihood Function

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load readmissiontimes
```

The sample data includes `ReadmissionTime`, which has readmission times for 100 patients. This is simulated data.

Define a negative log likelihood function.

```
custnloglf = @(lambda,data,cens,freq) -length(data)*log(lambda)...
+ nansum(lambda*data);
```

Estimate the parameters of the defined distribution.

```
phat = mle(ReadmissionTime,'nloglf',custnloglf,'start',0.05)
```

```
phat =

    0.1462
```

Compute the variance of the parameter estimate.

```
acov = mlecov(phat,ReadmissionTime,'nloglf',custnloglf)
```

```
acov =

   2.1374e-04
```

Compute the standard error.

```
sqrt(acov)
```

```
ans =

    0.0146
```

Input Arguments

`params` — Parameter estimates

scalar value | vector

Parameter estimates, specified as a scalar value or vector of scalar values. These parameter estimates must be maximum likelihood estimates. For example, you can specify parameter estimates returned by `mle`.

Data Types: `single | double`

`data` — Sample data

vector

Sample data `mle` uses to estimate the distribution parameters, specified as a vector.

Data Types: `single | double`

`pdf` — Custom probability density function

function handle

Custom probability distribution function, specified as a function handle created using `@`.

This custom function accepts the vector `data` and one or more individual distribution parameters as input parameters, and returns a vector of probability density values.

For example, if the name of the custom probability density function is `newpdf`, then you can specify the function handle in `mlecov` as follows.

Example: `@newpdf`

Data Types: `function_handle`

`cdf` — Custom cumulative distribution function

function handle

Custom cumulative distribution function, specified as a function handle created using `@`.

This custom function accepts the vector `data` and one or more individual distribution parameters as input parameters, and returns a vector of cumulative probability values.

You must define `cdf` with `pdf` if data is censored and you use the `'censoring'` name-value pair argument. If `'censoring'` is not present, you do not have to specify `cdf` while using `pdf`.

For example, if the name of the custom cumulative distribution function is `newcdf`, then you can specify the function handle in `mlecov` as follows.

Example: `@newcdf`

Data Types: `function_handle`

`logpdf` — Custom log probability density function

function handle

Custom log probability density function, specified as a function handle created using `@`.

This custom function accepts the vector `data` and one or more individual distribution parameters as input parameters, and returns a vector of log probability values.

For example, if the name of the custom log probability density function is `customlogpdf`, then you can specify the function handle in `mlecov` as follows.

Example: `@customlogpdf`

Data Types: `function_handle`

`logsf` — Custom log survival function

function handle

Custom log survival function, specified as a function handle created using `@`.

This custom function accepts the vector `data` and one or more individual distribution parameters as input parameters, and returns a vector of log survival probability values.

You must define `logsf` with `logpdf` if data is censored and you use the `'censoring'` name-value pair argument. If `'censoring'` is not present, you do not have to specify `logsf` while using `logpdf`.

For example, if the name of the custom log survival function is `logsurvival`, then you can specify the function handle in `mlecov` as follows.

Example: `@logsurvival`

Data Types: `function_handle`

`nloglf` — Custom negative loglikelihood function

function handle

Custom negative loglikelihood function, specified as a function handle created using `@`.

This custom function accepts the following input arguments.

`params`	Vector of distribution parameter values

`data`	Vector of data
`cens`	Boolean vector of censored values
`freq`	Vector of integer data frequencies

`nloglf` must accept all four arguments even if you do not use the `'censoring'` or `'frequency'` name-value pair arguments. You can write `'nloglf'` to ignore `cens` and `freq` arguments in that case.

`nloglf` returns a scalar negative loglikelihood value and optionally, a negative loglikelihood gradient vector (see the `'GradObj'` field in `'options'`).

If the name of the custom negative log likelihood function is `negloglik`, then you can specify the function handle in `mlecov` as follows.

Example: `@negloglik`

Data Types: `function_handle`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'censoring',cens,'options',opt` specifies that `mlecov` reads the censored data information from the vector `cens` and performs according to the new options structure `opt`.

`'censoring'` — Indicator for censoring

array of 0s (default) | array of 0s and 1s

Indicator for censoring, specified as the comma-separated pair consisting of `'censoring'` and a Boolean array of the same size as data. Use 1 for observations that are right censored and 0 for observations that are fully observed. The default is all observations are fully observed.

For censored data, you must use cdf with pdf, or logsf with logpdf, or nloglf must be defined to account for censoring.

For example, if the censored data information is in the binary array called `Censored`, then you can specify the censored data as follows.

Example: `'censoring',Censored`

Data Types: `logical`

`'frequency'` — Frequency of observations

array of 1s (default) | vector of nonnegative integer counts

Frequency of observations, specified as the comma-separated pair consisting of `'frequency'` and an array containing nonnegative integer counts, which is the same size as `data`. The default is one observation per element of `data`.

For example, if the observation frequencies are stored in an array named `Freq`, you can specify the frequencies as follows.

Example: `'frequency',Freq`

Data Types: `single | double`

`'options'` — Numerical options

structure

Numerical options for the finite difference Hessian calculation, specified as the comma-separated pair consisting of `'options'` and a structure returned by `statset`.

You can set the options under a new name and use it in the name-value pair argument. The applicable `statset` parameters are as follows.

Parameter	Value
`'GradObj'`	Default is `'off'`. `'on'` or `'off'`, indicating whether or not the function provided with the `nloglf` input argument can return the gradient vector of the negative log-likelihood as a second output.
`'DerivStep'`	Default is `eps^(1/4)`. Relative step size used in finite difference for Hessian calculations. It can be a scalar, or the same size as `params`. A smaller value than the default might be appropriate if `'GradObj'` is `'on'`.

Example: `'options',statset('mlecov')`

Data Types: `struct`

Output Arguments

`acov` — Approximation to asymptotic covariance matrix
p-by-*p* matrix

Approximation to asymptotic covariance matrix, returned as a *p*-by-*p* matrix, where *p* is the number of parameters in params.

More About

Survival Function

The survival function is the probability of survival as a function of time. It is also called the survivor function. It gives the probability that the survival time of an individual exceeds a certain value. Since the cumulative distribution function, $F(t)$, is the probability that the survival time is less than or equal to a given point in time, the survival function for a continuous distribution, $S(t)$, is the complement of the cumulative distribution function: $S(t) = 1 - F(t)$.

- "What Is Survival Analysis?" on page 12-2

See Also

`mle`

mnpdf

Multinomial probability density function

Syntax

```
Y = mnpdf(X,PROB)
```

Description

`Y = mnpdf(X,PROB)` returns the pdf for the multinomial distribution with probabilities `PROB`, evaluated at each row of `X`. `X` and `PROB` are m-by-k matrices or 1-by-k vectors, where k is the number of multinomial bins or categories. Each row of `PROB` must sum to one, and the sample sizes for each observation (rows of `X`) are given by the row sums `sum(X,2)`. `Y` is an m-by-k matrix, and `mnpdf` computes each row of `Y` using the corresponding rows of the inputs, or replicates them if needed.

Examples

Compute the Multinomial Distribution pdf

Compute the pdf of a multinomial distribution with a sample size of `n = 10`. The probabilities are `p = 1/2` for outcome 1, `p = 1/3` for outcome 2, and `p = 1/6` for outcome 3.

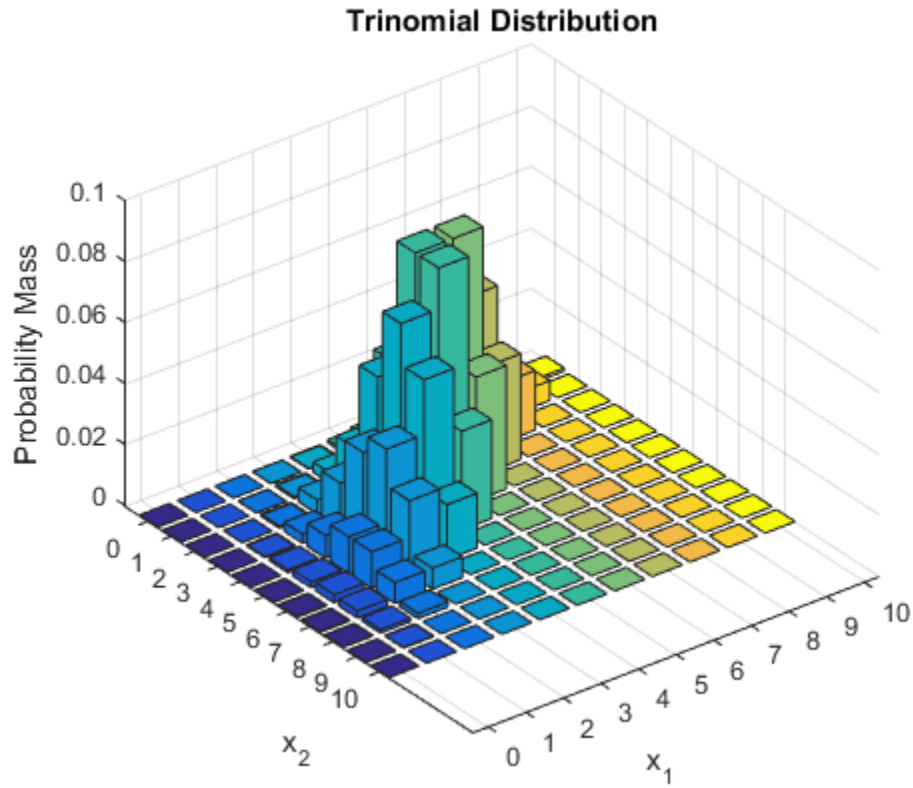
```
p = [1/2 1/3 1/6];
n = 10;
x1 = 0:n;
x2 = 0:n;
[X1,X2] = meshgrid(x1,x2);
X3 = n-(X1+X2);
```

Compute the pdf of the distribution.

```
Y = mnpdf([X1(:),X2(:),X3(:)],repmat(p,(n+1)^2,1));
```

Plot the pdf on a 3-dimensional figure.

```
Y = reshape(Y,n+1,n+1);
bar3(Y)
h = gca;
h.XTickLabel = [0:n];
h.YTickLabel = [0:n];
xlabel('x_1')
ylabel('x_2')
zlabel('Probability Mass')
title('Trinomial Distribution')
```



Note that the visualization does not show `x3`, which is determined by the constraint `x1 + x2 + x3 = n`.

More About

- "Multinomial Distribution" on page B-98

See Also

`mnrnd`

mnrfit

Multinomial logistic regression

Syntax

```
B = mnrfit(X,Y)
B = mnrfit(X,Y,Name,Value)
[B,dev,stats] = mnrfit( ___ )
```

Description

`B = mnrfit(X,Y)` returns a matrix, `B`, of coefficient estimates for a multinomial logistic regression of the nominal responses in `Y` on the predictors in `X`.

`B = mnrfit(X,Y,Name,Value)` returns a matrix, `B`, of coefficient estimates for a multinomial model fit with additional options specified by one or more `Name,Value` pair arguments.

For example, you can fit a nominal, an ordinal, or a hierarchical model, or change the link function.

`[B,dev,stats] = mnrfit( ___ )` also returns the deviance of the fit, `dev`, and the structure `stats` for any of the previous input arguments. `stats` contains model statistics such as degrees of freedom, standard errors for coefficient estimates, and residuals.

Examples

Multinomial Regression for Nominal Responses

Fit a multinomial regression for nominal outcomes and interpret the results.

Load the sample data.

```
load fisheriris
```

The column vector, `species`, consists of iris flowers of three different species, setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers, the length and width of sepals and petals in centimeters, respectively.

Define the nominal response variable using a categorical array.

```
sp = categorical(species);
```

Fit a multinomial regression model to predict the species using the measurements.

```
[B,dev,stats] = mnrfit(meas,sp);
B
```

```
B =

   13.3860   15.4492
    2.4623    1.8196
    5.2948    2.5700
   -7.4916   -4.3714
   -8.9322   -7.6467
```

This is a nominal model for the response category relative risks, with separate slopes on all four predictors, that is, each category of `meas`. The first row of `B` contains the intercept terms for the relative risk of the first two response categories, setosa and versicolor versus the reference category, virginica. The last four rows contain the slopes for the models for the first two categories. `mnrfit` accepts the third category as the reference category.

The models for the relative risk of an iris flower being a setosa versus a virginica, and the relative risk of an iris flower being a versicolor species versus a virginica species are respectively

$$\ln\left(\frac{\pi_{setosa}}{\pi_{virginica}}\right) = 13.38 + 2.46X_1 + 5.29X_2 - 7.49X_3 - 8.93X_4$$

and

$$\ln\left(\frac{\pi_{versicolor}}{\pi_{virginica}}\right) = 15.45 + 1.82X_1 + 2.57X_2 - 4.37X_3 - 7.65X_4$$

The coefficients express the effects of the predictor variables on the relative risk or the log odds of being in one category versus the reference category.

For example, the estimated coefficient 2.46 indicates that the probability of being species 1 (setosa) compared to the probability of being species 3 (virginica) (the relative risk of being a setosa versus a virginica) increases exp(2.46) times for each unit increase in X_1, the first measurement, given all else equal.

In terms of log odds, you can say that the relative log odds of being a setosa versus a virginica increases 2.46 times with a one-unit increase in X_1 given all else is equal.

Check the statistical significance of the model coefficients.

```
stats.p
```

```
ans =

    0.2457    0.0031
    0.4543    0.1048
    0.0773    0.0815
    0.0258    0.0007
    0.1856    0.0002
```

The p-value of 0.0258 indicates that the third measure is significant on the relative risk of being a setosa versus a virginica (species 1 compared to species 3). The p-values of 0.0007 and 0.0002 indicate that the third and fourth measures are significant on the relative risk of being a versicolor versus a virginica (species 2 compared to species 3).

Request the standard errors of coefficient estimates.

```
stats.se
```

```
ans =

   11.5316    5.2201
    3.2905    1.1218
    2.9976    1.4753
    3.3609    1.2869
    6.7474    2.0846
```

Calculate the 95% confidence limits for the coefficients.

```
LL = stats.beta - 1.96.*stats.se;
```

```
UL = stats.beta + 1.96.*stats.se;
```

Display the confidence intervals for the coefficients of the model for the relative risk of being a setosa versus a virginica (the first column of coefficients in B).

```
[LL(:,1) UL(:,1)]
```

```
ans =

   -9.2160   35.9880
   -3.9869    8.9116
   -0.5805   11.1701
  -14.0790   -0.9043
  -22.1570    4.2926
```

Find the confidence intervals for the coefficients of the model for the relative risk of being a versicolor versus a virginica (the second column of coefficients in B).

```
[LL(:,2) UL(:,2)]
```

```
ans =

    5.2177   25.6807
   -0.3791    4.0184
   -0.3216    5.4615
   -6.8938   -1.8490
  -11.7324   -3.5610
```

Multinomial Regression for Ordinal Responses

Fit a multinomial regression model for categorical responses with natural ordering among categories.

Load the sample data and define the predictor variables.

```
load carbig
X = [Acceleration Displacement Horsepower Weight];
```

The predictor variables are the acceleration, engine displacement, horsepower, and weight of the cars. The response variable is miles per gallon (mpg).

Create an ordinal response variable categorizing `MPG` into four levels from 9 to 48 mpg by labeling the response values in the range 9-19 as 1, 20-29 as 2, 30-39 as 3, and 40-48 as 4.

```
miles = ordinal(MPG,{'1','2','3','4'},[],[9,19,29,39,48]);
```

Fit an ordinal response model for the response variable `miles`.

```
[B,dev,stats] = mnrfit(X,miles,'model','ordinal');
B
```

```
B =

  -16.6895
  -11.7208
   -8.0606
    0.1048
    0.0103
    0.0645
    0.0017
```

The first three elements of `B` are the intercept terms for the models, and the last four elements of `B` are the coefficients of the covariates, assumed common across all categories. This model corresponds to *parallel regression*, which is also called the *proportional odds* model, where there is a different intercept but common slopes among categories. You can specify this using the `'interactions','off'` name-value pair argument, which is the default for ordinal models.

```
[B(1:3)'; repmat(B(4:end),1,3)]
```

```
ans =

  -16.6895  -11.7208   -8.0606
    0.1048    0.1048    0.1048
    0.0103    0.0103    0.0103
    0.0645    0.0645    0.0645
    0.0017    0.0017    0.0017
```

The link function in the model is logit (`'link','logit'`), which is the default for an ordinal model. The coefficients express the relative risk or log odds of the mpg of a car being less than or equal to one value versus greater than that value.

The proportional odds model in this example is

$$\ln\left(\frac{P(mpg\leq 19)}{P(mpg>19)}\right) = -16.6895 + 0.1048X_A + 0.0103X_D + 0.0645X_H + 0.0017X_W$$

$$\ln\left(\frac{P(mpg\leq 29)}{P(mpg>29)}\right) = -11.7208 + 0.1048X_A + 0.0103X_D + 0.0645X_H + 0.0017X_W$$

$$\ln\left(\frac{P(mpg\leq 39)}{P(mpg>39)}\right) = -8.0606 + 0.1048X_A + 0.0103X_D + 0.0645X_H + 0.0017X_W$$

For example, the coefficient estimate of 0.1048 indicates that a unit change in acceleration would impact the odds of the mpg of a car being less than or equal to 19 versus more than 19, or being less than or equal to 29 versus greater than 29, or being less than or equal to 39 versus greater than 39, by a factor of exp(0.01048) given all else is equal.

Assess the significance of the coefficients.

```
stats.p
```

```
ans =

    0.0000
    0.0000
    0.0000
    0.1899
    0.0350
    0.0000
    0.0118
```

The p-values of 0.035, 0.0000, and 0.0118 for engine displacement, horsepower, and weight of a car, respectively, indicate that these factors are significant on the odds of mpg of a car being less than or equal to a certain value versus being greater than that value.

Hierarchical Multinomial Regression Model

Fit a hierarchical multinomial regression model.

Navigate to the folder containing sample data.

```
cd(matlabroot)
```

```
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load smoking
```

The data set `smoking` contains five variables: sex, age, weight, and systolic and diastolic blood pressure. Sex is a binary variable where 1 indicates female patients, and 0 indicates male patients.

Define the response variable.

```
Y = categorical(smoking.Smoker);
```

The data in `Smoker` has four categories:

- 0: Nonsmoker, 0 cigarettes a day
- 1: Smoker, 1–5 cigarettes a day
- 2: Smoker, 6–10 cigarettes a day
- 3: Smoker, 11 or more cigarettes a day

Define the predictor variables.

```
X = [smoking.Sex smoking.Age smoking.Weight...
    smoking.SystolicBP smoking.DiastolicBP];
```

Fit a hierarchical multinomial model.

```
[B,dev,stats] = mnrfit(X,Y,'model','hierarchical');
B
```

```
B =

   43.8148    5.9571   44.0712
    1.8709   -0.0230    0.0662
    0.0188    0.0625    0.1335
    0.0046   -0.0072   -0.0130
   -0.2170    0.0416   -0.0324
   -0.2273   -0.1449   -0.4824
```

The first column of `B` includes the intercept and the coefficient estimates for the model of the relative risk of being a nonsmoker versus a smoker. The second column includes the parameter estimates for modeling the log odds of smoking 1–5 cigarettes a day versus

more than five cigarettes a day given that a person is a smoker. Finally, the third column includes the parameter estimates for modeling the log odds of a person smoking 6–10 cigarettes a day versus more than 10 cigarettes a day given he/she smokes more than 5 cigarettes a day.

The coefficients differ across categories. You can specify this using the `'interactions','on'` name-value pair argument, which is the default for hierarchical models. So, the model in this example is

$$\ln\left(\frac{P(y=0)}{P(y>0)}\right)=43.8148+1.8709X_S+0.0188X_A+0.0046X_W-0.2170X_{SBP}-0.2273X_{DBP}$$

$$\ln\left(\frac{P(1\le y\le 5)}{P(y>5)}\right)=5.9571-0.0230X_S+0.0625X_A+0.0072X_W+0.0416X_{SBP}-0.1449X_{DBP}$$

$$\ln\left(\frac{P(6\le y\le 10)}{P(y>10)}\right)=44.0712+0.0662X_S+0.1335X_A-0.0130X_W-0.0324X_{SBP}-0.4824X_{DBP}$$

For example, the coefficient estimate of 1.8709 indicates that the likelihood of being a smoker versus a nonsmoker increases by exp(1.8709) = 6.49 times as the gender changes from female to male given everything else held constant.

Assess the statistical significance of the terms.

```
stats.p
```

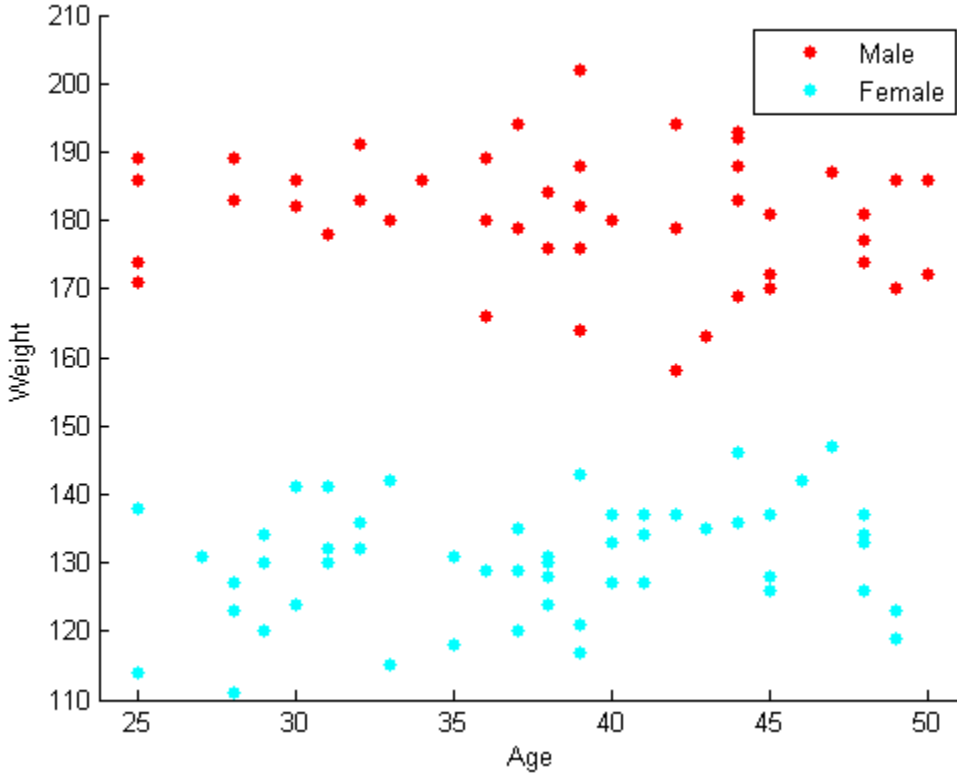
```
ans =

    0.0000    0.5363    0.2149
    0.3549    0.9912    0.9835
    0.6850    0.2676    0.2313
    0.9032    0.8523    0.8514
    0.0009    0.5187    0.8165
    0.0004    0.0483    0.0545
```

Sex, age, or weight don't appear significant on any level. The *p*-values of 0.0009 and 0.0004 indicate that both types of blood pressure are significant on the relative risk of a person being a smoker versus a nonsmoker. The *p*-value of 0.0483 shows that only

diastolic blood pressure is significant on the odds of a person smoking 0–5 cigarettes a day versus more than 5 cigarettes a day. Similarly, the *p*-value of 0.0545 indicates that diastolic blood pressure is significant on the odds of a person smoking 6–10 cigarettes a day versus more than 10 cigarettes a day.

Check if any nonsignificant factors are correlated to each other. Draw a scatterplot of age versus weight grouped by sex.

```
figure()
gscatter(smoking.Age,smoking.Weight,smoking.Sex)
legend('Male','Female')
xlabel('Age')
ylabel('Weight')
```



The range of weight of an individual seems to differ according to gender. Age does not seem to have any obvious correlation with sex or weight. Age is insignificant and weight seems to be correlated with sex, so you can eliminate both and reconstruct the model.

Eliminate age and weight from the model and fit a hierarchical model with sex, systolic blood pressure, and diastolic blood pressure as the predictor variables.

```
X = double([smoking.Sex smoking.SystolicBP...
smoking.DiastolicBP]);
[B,dev,stats] = mnrfit(X,Y,'model','hierarchical');
B
```

```
B =

    44.8456    5.3230   25.0248
    1.6045    0.2330    0.4982
   -0.2161    0.0497    0.0179
   -0.2222   -0.1358   -0.3092
```

Here, a coefficient estimate of 1.6045 indicates that the likelihood of being a nonsmoker versus a smoker increases by exp(1.6045) = 4.97 times as sex changes from male to female. A unit increase in the systolic blood pressure indicates an exp(–.2161) = 0.8056 decrease in the likelihood of being a nonsmoker versus a smoker. Similarly, a unit increase in the diastolic blood pressure indicates an exp(–.2222) = 0.8007 decrease in the relative rate of being a nonsmoker versus being a smoker.

Assess the statistical significance of the terms.

```
stats.p
```

```
ans =

    0.0000    0.4715    0.2325
    0.0210    0.7488    0.6362
    0.0010    0.4107    0.8899
    0.0003    0.0483    0.0718
```

The *p*-values of 0.0210, 0.0010, and 0.0003 indicate that the terms sex and both types of blood pressure are significant on the relative risk of a person being a nonsmoker versus a smoker, given the other terms in the model. Based on the *p*-value of 0.0483, diastolic blood pressure appears significant on the relative risk of a person smoking 1–5 cigarettes versus more than 5 cigarettes a day, given that this person is a smoker. Because none of the *p*-values on the third column are less than 0.05, you can say that none of the

variables are statistically significant on the relative risk of a person smoking from 6–10 cigarettes versus more than 10 cigarettes, given that this person smokes more than 5 cigarettes a day.

Input Arguments

X — Observations on predictor variables

n-by-*p* matrix

Observations on predictor variables, specified as an *n*-by-*p* matrix. `X` contains *n* observations for *p* predictors.

Note: `mnrfit` automatically includes a constant term (intercept) in all models. Do not include a column of 1s in `X`.

Data Types: `single` | `double`

Y — Response values

n-by-*k* matrix | *n*-by-1 column vector

Response values, specified as a column vector or a matrix. `Y` can be one of the following:

- An *n*-by-*k* matrix, where *Y*(*i*,*j*) is the number of outcomes of the multinomial category *j* for the predictor combinations given by *X*(*i*,:). In this case, the number of observations are made at each predictor combination.
- An *n*-by-1 column vector of scalar integers from 1 to *k* indicating the value of the response for each observation. In this case, all sample sizes are 1.
- An *n*-by-1 categorical array indicating the nominal or ordinal value of the response for each observation. In this case, all sample sizes are 1.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Model','ordinal','Link','probit'` specifies an ordinal model with a probit link function.

`'Model'` — Type of model to fit

`'nominal'` (default) | `'ordinal'` | `'hierarchical'`

Type of model to fit, specified as the comma-separated pair consisting of `'Model'` and one of the following.

`'nominal'`	Default. There is no ordering among the response categories.
`'ordinal'`	There is a natural ordering among the response categories.
`'hierarchical'`	The choice of response category is sequential/nested.

Example: `'Model','ordinal'`

`'Interactions'` — Indicator for interaction between multinomial categories and coefficients

`'on'` | `'off'`

Indicator for an interaction between the multinomial categories and coefficients, specified as the comma-separated pair consisting of `'Interactions'` and one of the following.

`'on'`	Default for nominal and hierarchical models. Fit a model with different coefficients across categories.
`'off'`	Default for ordinal models. Fit a model with a common set of coefficients for the predictor variables, across all multinomial categories. This is often described as *parallel regression* or the *proportional odds model*.

In all cases, the model has different intercepts across categories. The choice of `'Interactions'` determines the dimensions of the output array B.

Example: `'Interactions','off'`

Data Types: `logical`

`'Link'` — Link function

`'logit'` (default) | `'probit'` | `'comploglog'` | `'loglog'`

Link function to use for ordinal and hierarchical models, specified as the comma-separated pair consisting of `'Link'` and one of the following.

`'logit'`	Default. $f(\gamma) = \ln(\gamma/(1-\gamma))$
`'probit'`	$f(\gamma) = \Phi^{-1}(\gamma)$ — error term is normally distributed with variance 1
`'comploglog'`	Complementary log-log $f(\gamma) = \ln(-\ln(1-\gamma))$
`'loglog'`	$f(\gamma) = \ln(-\ln(\gamma))$

The link function defines the relationship between response probabilities and the linear combination of predictors, $X\beta$. The link functions might be functions of cumulative or conditional probabilities based on whether the model is for an ordinal or a sequential/nested response. For example, for an ordinal model, γ represents the cumulative probability of being in categories 1 to j and the model with a logit link function as follows:

$$\ln\left(\frac{\gamma}{1-\gamma}\right) = \ln\left(\frac{\pi_1+\pi_2+\cdots+\pi_j}{\pi_{j+1}+\cdots+\pi_k}\right) = \beta_{0j} + \beta_1 X_1 + \beta_2 X_2 + \cdots + \beta_p X_p,$$

where k represents the last category.

You cannot specify the `'Link'` parameter for nominal models; these always use a multinomial logit link,

$$\ln\left(\frac{\pi_j}{\pi_r}\right) = \beta_{j0} + \beta_{j1} X_{j1} + \beta_{j2} X_{j2} + \cdots + \beta_{jp} X_{jp}, \quad j = 1, \ldots, k-1,$$

where π stands for a categorical probability, and r corresponds to the reference category. `mnrfit` uses the last category as the reference category for nominal models.

Example: `'Link','loglog'`

`'EstDisp'` — Indicator for estimating dispersion parameter

`'off'` (default) | `'on'`

Indicator for estimating a dispersion parameter, specified as the comma-separated pair consisting of `'EstDisp'` and one of the following.

`'off'`	Default. Use the theoretical dispersion value of 1.
`'on'`	Estimate a dispersion parameter for the multinomial distribution in computing standard errors.

Example: `'EstDisp','on'`

Output Arguments

`B` — Coefficient estimates

vector | matrix

Coefficient estimates for a multinomial logistic regression of the responses in Y, returned as a vector or a matrix.

- If `'Interaction'` is `'off'`, then `B` is a $k - 1 + p$ vector. The first $k - 1$ rows of `B` correspond to the intercept terms, one for each $k - 1$ multinomial categories, and the remaining p rows correspond to the predictor coefficients, which are common for all of the first $k - 1$ categories.
- If `'Interaction'` is `'on'`, then `B` is a $(p + 1)$-by-$(k - 1)$ matrix. Each column of `B` corresponds to the estimated intercept term and predictor coefficients, one for each of the first $k - 1$ multinomial categories.

The estimates for the kth category are taken to be zero as `mnrfit` takes the last category as the reference category.

`dev` — Deviance of the fit

scalar value

Deviance of the fit, returned as a scalar value. It is twice the difference between the maximum achievable log likelihood and that attained under the fitted model. This corresponds to the sum of deviance residuals,

$$dev = 2 * \sum_{i}^{n} \sum_{j}^{k} y_{ij} * \log\left(\frac{y_{ij}}{\pi_{ij} * m_i}\right) = \sum_{i}^{n} rd_i,$$

where rd_i are the deviance residuals. For deviance residuals see stats.

`stats` — Model statistics

structure

Model statistics, returned as a structure that contains the following fields.

`beta`	The coefficient estimates. These are the same as `B`.
`dfe`	Degrees of freedom for error • If `'Interactions'` is `'off'`, then degrees of freedom is $n*(k-1)-(k-1+p)$. • If `'Interactions'` is `'on'`, then degrees of freedom is $(n-p+1)*(k-1)$.
`sfit`	Estimated dispersion parameter.
`s`	Theoretical or estimated dispersion parameter. • If `'Estdisp'` is `'off'`, then `s` is the theoretical dispersion parameter, 1. • If `'Estdisp'` is `'on'`, then `s` is equal to the estimated dispersion parameter, `sfit`.
`estdisp`	Indicator for a theoretical or estimated dispersion parameter.
`se`	Standard errors of coefficient estimates, `B`.
`coeffcorr`	Estimated correlation matrix for `B`.
`covb`	Estimated covariance matrix for `B`.
`t`	t statistics for `B`.
`p`	p-values for `B`.
`resid`	Raw residuals. Observed minus fitted values, $$r_{ij} = y_{ij} - \hat{\pi}_{ij} * m_i, \quad \begin{cases} i = 1,\cdots,n \\ j = 1,\cdots,k \end{cases},$$ where π_{ij} is the categorical, cumulative or conditional probability, and m_i is the corresponding sample size.
`residp`	Pearson residuals, which are the raw residuals scaled by the estimated standard deviation:

	$$rp_{ij} = \frac{r_{ij}}{\hat{\sigma}_{ij}} = \frac{y_{ij} - \hat{\pi}_{ij} * m_i}{\sqrt{\hat{\pi}_{ij} * \left(1 - \hat{\pi}_{ij}\right) * m_i}}, \quad \begin{cases} i = 1, \cdots, n \\ j = 1, \cdots, k \end{cases},$$ where π_{ij} is the categorical, cumulative, or conditional probability, and m_i is the corresponding sample size.
`residd`	Deviance residuals: $$rd_i = 2 * \sum_j^k y_{ij} * \log\left(\frac{y_{ij}}{\pi_{ij} * m_i}\right), \quad i = 1, \cdots, n.$$ where π_{ij} is the categorical, cumulative, or conditional probability, and m_i is the corresponding sample size.

More About

Algorithms

`mnrfit` treats `NaN`s in either `X` or `Y` as missing values, and ignores them.

- "Multinomial Distribution" on page B-98
- "Multinomial Models for Nominal Responses" on page 10-2
- "Multinomial Models for Ordinal Responses" on page 10-5
- "Hierarchical Multinomial Models" on page 10-9

References

[1] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

[2] Long, J. S. *Regression Models for Categorical and Limited Dependent Variables*. Sage Publications, 1997.

[3] Dobson, A. J., and A. G. Barnett. *An Introduction to Generalized Linear Models*. Chapman and Hall/CRC. Taylor & Francis Group, 2008.

See Also

`fitglm` | `glmfit` | `glmval` | `mnrval`

mnrnd

Multinomial random numbers

Syntax

```
r = mnrnd(n,p)
R = mnrnd(n,p,m)
R = mnrnd(N,P)
```

Description

`r = mnrnd(n,p)` returns random values `r` from the multinomial distribution with parameters `n` and `p`. `n` is a positive integer specifying the number of trials (sample size) for each multinomial outcome. `p` is a 1-by-*k* vector of multinomial probabilities, where *k* is the number of multinomial bins or categories. `p` must sum to one. (If `p` does not sum to one, `r` consists entirely of `NaN` values.) `r` is a 1-by-*k* vector, containing counts for each of the *k* multinomial bins.

`R = mnrnd(n,p,m)` returns `m` random vectors from the multinomial distribution with parameters `n` and `p`. `R` is a `m`-by-*k* matrix, where *k* is the number of multinomial bins or categories. Each row of `R` corresponds to one multinomial outcome.

`R = mnrnd(N,P)` generates outcomes from different multinomial distributions. `P` is a *m*-by-*k* matrix, where *k* is the number of multinomial bins or categories and each of the *m* rows contains a different set of multinomial probabilities. Each row of `P` must sum to one. (If any row of `P` does not sum to one, the corresponding row of `R` consists entirely of `NaN` values.) `N` is a *m*-by-1 vector of positive integers or a single positive integer (replicated by `mnrnd` to a *m*-by-1 vector). `R` is a `m`-by-*k* matrix. Each row of `R` is generated using the corresponding rows of `N` and `P`.

Examples

Generate 2 random vectors with the same probabilities:

```
n = 1e3;
```

```
p = [0.2,0.3,0.5];
R = mnrnd(n,p,2)
R =
   215   282   503
   194   303   503
```

Generate 2 random vectors with different probabilities:

```
n = 1e3;
P = [0.2, 0.3, 0.5; ...
     0.3, 0.4, 0.3;];
R = mnrnd(n,P)
R =
   186   290   524
   290   389   321
```

More About

- "Multinomial Distribution" on page B-98

See Also

`mnpdf`

mnrval

Multinomial logistic regression values

Syntax

```
pihat = mnrval(B,X)
[pihat,dlow,dhi] = mnrval(B,X,stats)
[pihat,dlow,dhi] = mnrval(B,X,stats,Name,Value)

yhat = mnrval(B,X,ssize)
[yhat,dlow,dhi] = mnrval(B,X,ssize,stats)
[yhat,dlow,dhi] = mnrval(B,X,ssize,stats,Name,Value)
```

Description

`pihat = mnrval(B,X)` returns the predicted probabilities for the multinomial logistic regression model with predictors, `X`, and the coefficient estimates, `B`.

`pihat` is an n-by-k matrix of predicted probabilities for each multinomial category. `B` is the vector or matrix that contains the coefficient estimates returned by `mnrfit`. And `X` is an n-by-p matrix which contains n observations for p predictors.

Note: `mnrval` automatically includes a constant term in all models. Do not enter a column of 1s in `X`.

`[pihat,dlow,dhi] = mnrval(B,X,stats)` also returns 95% error bounds on the predicted probabilities, `pihat`, using the statistics in the structure, `stats`, returned by `mnrfit`.

The lower and upper confidence bounds for `pihat` are `pihat` minus `dlow` and `pihat` plus `dhi`, respectively. Confidence bounds are nonsimultaneous and only apply to the fitted curve, not to new observations.

`[pihat,dlow,dhi] = mnrval(B,X,stats,Name,Value)` returns the predicted probabilities and 95% error bounds on the predicted probabilities `pihat`, with additional options specified by one or more `Name,Value` pair arguments.

For example, you can specify the model type, link function, and the type of probabilities to return.

`yhat = mnrval(B,X,ssize)` returns the predicted category counts for sample sizes, `ssize`.

`[yhat,dlow,dhi] = mnrval(B,X,ssize,stats)` also computes 95% error bounds on the predicted counts `yhat`, using the statistics in the structure, `stats`, returned by `mnrfit`.

The lower and upper confidence bounds for `yhat` are `yhat` minus `dlo` and `yhat` plus `dhi`, respectively. Confidence bounds are nonsimultaneous and they apply to the fitted curve, not to new observations.

`[yhat,dlow,dhi] = mnrval(B,X,ssize,stats,Name,Value)` returns the predicted category counts and 95% error bounds on the predicted counts `yhat`, with additional options specified by one or more `Name,Value` pair arguments.

For example, you can specify the model type, link function, and the type of predicted counts to return.

Examples

Estimate Category Probabilities for Nominal Responses

Fit a multinomial regression for nominal outcomes and estimate the category probabilities.

Load the sample data.

```
load('fisheriris.mat')
```

The column vector, `species`, consists of iris flowers of three different species, setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers, the length and width of sepals and petals in centimeters, respectively.

Define the nominal response variable.

```
sp = nominal(species);
sp = double(sp);
```

Now in `sp`, 1, 2, and 3 indicate the species setosa, versicolor, and virginica, respectively.

Fit a nominal model to estimate the species using the flower measurements as the predictor variables.

```
[B,dev,stats] = mnrfit(meas,sp);
```

Estimate the probability of being a certain kind of species for an iris flower having the measurements (6.2, 3.7, 5.8, 0.2).

```
x = [6.2, 3.7, 5.8, 0.2];
pihat = mnrval(B,x);
pihat
```

```
pihat =

    0.0017    0.9982    0.0001
```

The probability of an iris flower having the measurements (6.2, 3.7, 5.8, 0.2) being a setosa is 0.0017, a versicolor is 0.9982, and a virginica is 0.0001.

Estimate Upper and Lower Error Bounds for Probability Estimates of Ordinal Responses

Fit a multinomial regression model for categorical responses with natural ordering among categories. Then estimate the upper and lower confidence bounds for the category probability estimates.

Load the sample data and define the predictor variables.

```
load('carbig.mat')
X = [Acceleration Displacement Horsepower Weight];
```

The predictor variables are the acceleration, engine displacement, horsepower, and the weight of the cars. The response variable is miles per gallon (`MPG`).

Create an ordinal response variable categorizing `MPG` into four levels from 9 to 48 mpg.

```
miles = ordinal(MPG,{'1','2','3','4'},[],[9,19,29,39,48]);
miles = double(miles);
```

Now in miles, 1 indicates the cars with miles per gallon from 9 to 19, and 2 indicates the cars with miles per gallon from 20 to 29. Similarly, 3 and 4 indicate the cars with miles per gallon from 30 to 39 and 40 to 48, respectively.

Fit a multinomial regression model for the response variable `miles`. For an ordinal model, the default `'link'` is `logit` and the default `'interactions'` is `'off'`.

```
[B,dev,stats] = mnrfit(X,miles,'model','ordinal');
```

Compute the probability estimates and 95% error bounds for probability confidence intervals for miles per gallon of a car with $x = (12, 113, 110, 2670)$.

```
x = [12,113,110,2670];
[pihat,dlow,hi] = mnrval(B,x,stats,'model','ordinal');
pihat
```

```
pihat =

   0.0615    0.8426    0.0932    0.0027
```

Calculate the confidence bounds for the category probability estimates.

```
LL = pihat - dlow;
UL = pihat + hi;
[LL;UL]
```

```
ans =

    0.0073    0.7829    0.0283   -0.0003
    0.1157    0.9022    0.1580    0.0057
```

Estimate Category Counts and Error Bounds for Nominal Responses

Fit a multinomial regression for nominal outcomes and estimate the category counts.

Load the sample data.

```
load('fisheriris.mat')
```

The column vector, `species`, consists of iris flowers of three different species, setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers, the length and width of sepals and petals in centimeters, respectively.

Define the nominal response variable.

```
sp = nominal(species);
sp = double(sp);
```

Now in `sp`, 1, 2, and 3 indicate the species setosa, versicolor, and virginica, respectively.

Fit a nominal model to estimate the species based on the flower measurements.

```
[B,dev,stats] = mnrfit(meas,sp);
```

Estimate the number in each species category for a sample of 100 iris flowers all with the measurements (6.2, 3.7, 5.8, 0.2).

```
x = [6.2,3.7,5.8,0.2];
yhat = mnrval(B,x,18)
```

```
yhat =

    0.0314   17.9671    0.0016
```

Estimate the error bounds for the counts.

```
[yhat,dlow,hi] = mnrval(B,x,18,stats,'model','nominal');
```

Calculate the confidence bounds for the category probability estimates.

```
LL = yhat - dlow;
UL = yhat + hi;
[LL;UL]
```

```
ans =

   -0.7084   17.2272   -0.0115
    0.7711   18.7069    0.0146
```

Plot the Count Estimates

Create sample data with one predictor variable and a categorical response variable with three categories.

```
x = [-3 -2 -1 0 1 2 3]';
Y = [1 11 13; 2 9 14; 6 14 5; 5 10 10;...
   5 14 6; 7 13 5; 8 11 6];
[Y x]
```

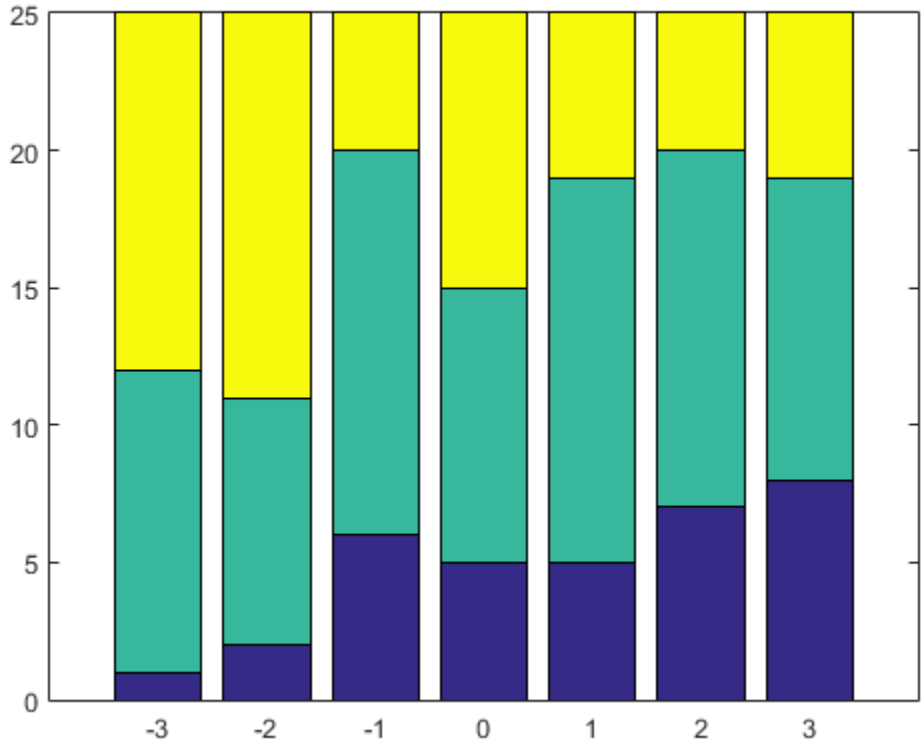
```
ans =

     1    11    13    -3
     2     9    14    -2
     6    14     5    -1
     5    10    10     0
     5    14     6     1
     7    13     5     2
```

```
     8    11     6     3
```

There are observations on seven different values of the predictor variable `x` . The response variable `Y` has three categories and the data shows how many of the 25 individuals are in each category of `Y` for each observation of `x`. For example, when `x` is -3, 1 of 25 individuals is observed in category 1, 11 observed in category 2, and 13 observed in category 3. Similarly, when `x` is 1, 5 of the individuals are observed in category 1, 14 are observed in category 2, and 6 are observed in category 3.

Plot the number in each category versus the `x` values, on a stacked bar graph.

```
bar(x,Y,'stacked');
ylim([0 25]);
```



Fit a nominal model for the individual response category probabilities, with separate slopes on the single predictor variable, `x`, for each category.

```
betaHatNom = mnrfit(x,Y,'model','nominal',...
    'interactions','on')
```

```
betaHatNom =

   -0.6028    0.3832
    0.4068    0.1948
```

The first row of `betaHatOrd` contains the intercept terms for the first two response categories. The second row contains the slopes. `mnrfit` accepts the third category as the reference category and hence assumes the coefficients for the third category are zero.

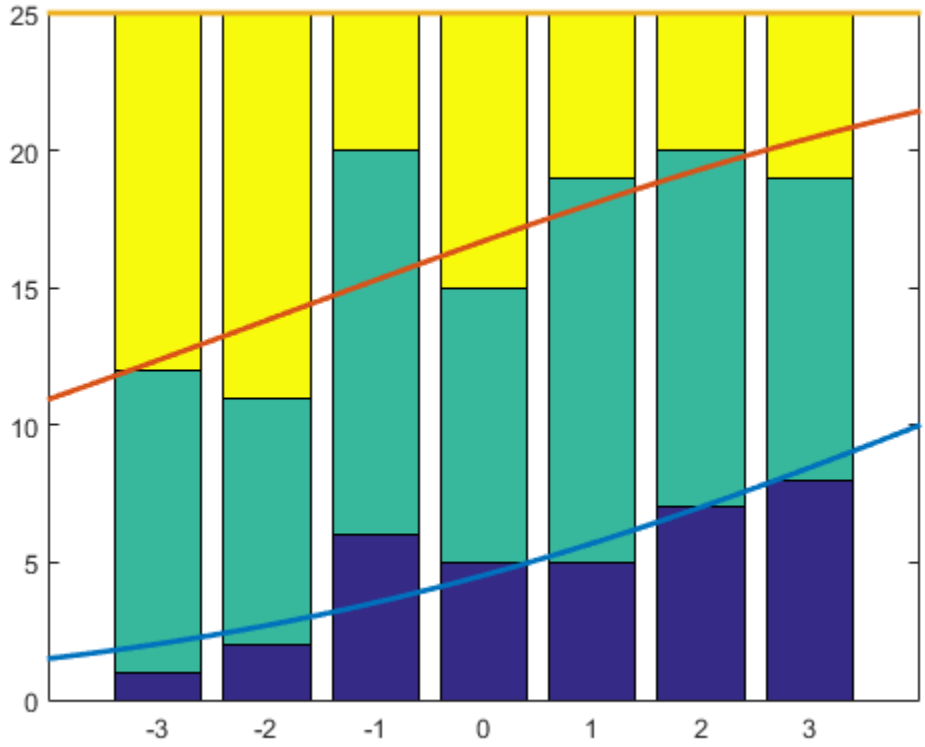
Compute the predicted probabilities for the three response categories.

```
xx = linspace(-4,4)';
piHatNom = mnrval(betaHatNom,xx,'model','nominal',...
    'interactions','on');
```

The probability of being in the third category is simply 1 - P(y = 1) - P(y = 2).

Plot the estimated cumulative number in each category on the bar graph.

```
line(xx,cumsum(25*piHatNom,2),'LineWidth',2);
```



The cumulative probability for the third category is always 1.

Now, fit a "parallel" ordinal model for the cumulative response category probabilities, with a common slope on the single predictor variable, `x`, across all categories:

```
betaHatOrd = mnrfit(x,Y,'model','ordinal',...
    'interactions','off')
```

```
betaHatOrd =

   -1.5001
    0.7266
    0.2642
```

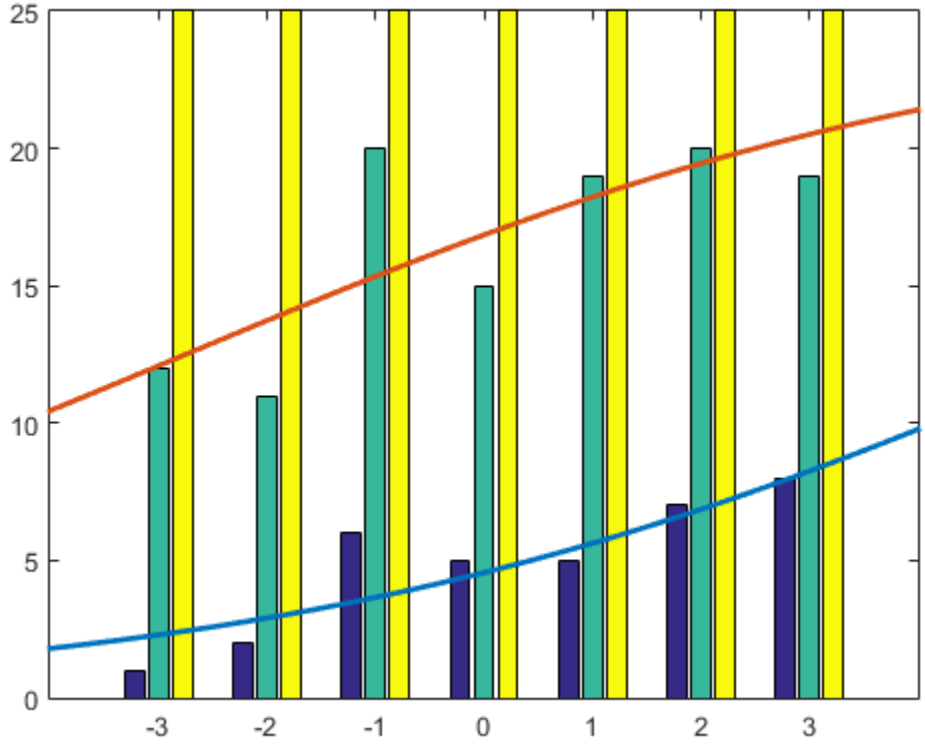
The first two elements of `betaHatOrd` are the intercept terms for the first two response categories. The last element of `betaHatOrd` is the common slope.

Compute the predicted cumulative probabilities for the first two response categories. The cumulative probability for the third category is always 1.

```
piHatOrd = mnrval(betaHatOrd,xx,'type','cumulative',...
    'model','ordinal','interactions','off');
```

Plot the estimated cumulative number on the bar graph of the observed cumulative number.

```
figure()
bar(x,cumsum(Y,2),'grouped');
ylim([0 25]);
line(xx,25*piHatOrd,'LineWidth',2);
```



Input Arguments

B — Coefficient estimates

vector or matrix returned by `mnrfit`

Coefficient estimates for the multinomial logistic regression model, specified as a vector or matrix returned by `mnrfit`. It is a vector or matrix depending on the model and interactions.

Example: `B = mnrfit(X,y); pihat = mnrval(B,X)`

Data Types: `single | double`

X — Sample data

matrix

Sample data on predictors, specified as an n-by-p. `X` contains n observations for p predictors.

Note: `mnrval` automatically includes a constant term in all models. Do not enter a column of 1s in `X`.

Example: `pihat = mnrval(B,X)`

Data Types: `single | double`

stats — Model statistics

structure returned by `mnrfit`

Model statistics, specified as a structure returned by `mnrfit`. You must use the `stats` input argument in `mnrval` to compute the lower and upper error bounds on the category probabilities and counts.

Example: `[B,dev,stats] = mnrfit(X,y);[pihat,dlo,dhi] = mnrval(B,X,stats)`

ssize — Sample sizes

column vector of positive integers

Sample sizes to return the number of items in response categories for each combination of the predictor variables, specified as an n-by-1 column vector of positive integers.

For example, for a response variable having three categories, if an observation of the number of individuals in each category is y_1, y_2, and y_3, respectively, then the sample size, m, for that observation is $m = y_1 + y_2 + y_3$.

If the sample sizes for n observations are in vector `sample`, then you can enter the sample sizes as follows.

Example: `yhat = mnrval(B,X,sample)`

Data Types: `single | double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'model','ordinal','link','probit','type','cumulative'` specifies that `mnrval` returns the estimates for cumulative probabilities for an ordinal model with a probit link function.

`'model'` — Type of multinomial model

`'nominal'` (default) | `'ordinal'` | `'hierarchical'`

Type of multinomial model fit by `mnrfit`, specified as the comma-separated pair consisting of `'model'` and one of the following.

`'nominal'`	Default. Specify when there is no ordering among the response categories.
`'ordinal'`	Specify when there is a natural ordering among the response categories.
`'hierarchica`	Specify when the choice of response category is sequential.

Example: `'model','ordinal'`

`'interactions'` — Indicator for interaction between multinomial categories and coefficients

`'on'` | `'off'`

Indicator for an interaction between the multinomial categories and coefficients in the model fit by `mnrfit`, specified as the comma-separated pair consisting of `'interactions'` and one of the following.

`'on'`	Default for nominal and hierarchical models. Specify to fit a model with different intercepts and coefficients across categories.
`'off'`	Default for ordinal models. Specify to fit a model with different intercepts, but a common set of coefficients for the predictor variables, across all multinomial categories. This is often described as *parallel regression* or *proportional odds model*.

Example: `'interactions','off'`

Data Types: `logical`

`'link'` — Link function

`'logit'` (default) | `'probit'` | `'comploglog'` | `'loglog'`

Link function `mnrfit` uses for ordinal and hierarchical models, specified as the comma-separated pair consisting of `'link'` and one of the following.

`'logit'`	Default. $f(\gamma) = \ln(\gamma/(1-\gamma))$
`'probit'`	$f(\gamma) = \Phi^{-1}(\gamma)$ — error term is normally distributed with variance 1
`'comploglog'`	Complementary log-log $f(\gamma) = \ln(-\ln(1-\gamma))$
`'loglog'`	$f(\gamma) = \ln(-\ln(\gamma))$

The link function defines the relationship between response probabilities and the linear combination of predictors, $X\beta$.

γ might be cumulative or conditional probabilities based on whether the model is for an ordinal or a sequential/nested response.

You cannot specify the `'link'` parameter for nominal models; these always use a multinomial logit link,

$$\ln\left(\frac{\pi_j}{\pi_r}\right) = \beta_{j0} + \beta_{j1}X_{j1} + \beta_{j2}X_{j2} + \cdots + \beta_{jp}X_{jp}, \quad j = 1, \ldots, k-1,$$

where π stands for a categorical probability, and r corresponds to the reference category, k is the total number of response categories, p is the number of predictor variables. `mnrfit` uses the last category as the reference category for nominal models.

Example: `'link','loglog'`

`'type'` — Type of probabilities or counts to estimate

`'category'` (default) | `'cumulative'` | `'conditional'`

Type of probabilities or counts to estimate, specified as the comma-separated pair including `'type'` and one of the following.

`'category'`	Default. Specify to return predictions and error bounds for the probabilities (or counts) of the k multinomial categories.
`'cumulative'`	Specify to return predictions and confidence bounds for the cumulative probabilities (or counts) of the first k – 1 multinomial categories, as an n-by-(k – 1) matrix. The predicted cumulative probability for the kth category is always 1.
`'conditional'`	Specify to return predictions and error bounds in terms of the first k – 1 conditional category probabilities (counts), i.e., the probability (count) for category j, given an outcome in category j or higher. When `'type'` is `'conditional'`, and you supply the sample size argument `ssize`, the predicted counts at each row of `X` are conditioned on the corresponding element of `ssize`, across all categories.

Example: `'type','cumulative'`

`'confidence'` — Confidence level

0.95 (default) | Scalar value in the range (0,1)

Confidence level for the error bounds, specified as the comma-separated pair consisting of `'confidence'` and a scalar value in the range (0,1).

For example, for 99% error bounds, you can specify the confidence as follows:

Example: `'confidence',0.99`

Data Types: `single | double`

Output Arguments

`pihat` — Probability estimates

n-by-(k – 1) matrix

Probability estimates for each multinomial category, returned as an n-by-(k – 1) matrix, where n is the number of observations, and k is the number of response categories.

`yhat` — Count estimates

n-by-k– 1 matrix

Count estimates for the number in each response category, returned as an n-by-k – 1 matrix, where n is the number of observations, and k is the number of response categories.

`dlow` — Lower error bound

column vector

Lower error bound to compute the lower confidence bound for pihat or yhat, returned as a column vector.

The lower confidence bound for `pihat` is `pihat` minus `dlow`. Similarly, the lower confidence bound for `yhat` is `yhat` minus `dlow`. Confidence bounds are nonsimultaneous and only apply to the fitted curve, not to new observations.

`dhi` — Upper error bound

column vector

Upper error bound to compute the upper confidence bound for pihat or yhat, returned as a column vector.

The upper confidence bound for `pihat` is `pihat` plus `dhi`. Similarly, the upper confidence bound for `yhat` is `yhat` plus `dhi`. Confidence bounds are nonsimultaneous and only apply to the fitted curve, not to new observations.

More About

- "Multinomial Models for Nominal Responses" on page 10-2
- "Multinomial Models for Ordinal Responses" on page 10-5
- "Hierarchical Multinomial Models" on page 10-9

References

[1] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

See Also

`fitglm` | `glmfit` | `glmval` | `mnrfit`

moment

Central moments

Syntax

```
m = moment(X,order)
moment(X,order,dim)
```

Description

`m = moment(X,order)` returns the central sample moment of `X` specified by the positive integer `order`. For vectors, `moment(x,order)` returns the central moment of the specified order for the elements of `x`. For matrices, `moment(X,order)` returns central moment of the specified order for each column. For N-dimensional arrays, `moment` operates along the first nonsingleton dimension of `X`.

`moment(X,order,dim)` takes the moment along dimension `dim` of `X`.

Examples

```
X = randn([6 5])
X =
  1.1650  0.0591  1.2460 -1.2704 -0.0562
  0.6268  1.7971 -0.6390  0.9846  0.5135
  0.0751  0.2641  0.5774 -0.0449  0.3967
  0.3516  0.8717 -0.3600 -0.7989  0.7562
 -0.6965 -1.4462 -0.1356 -0.7652  0.4005
  1.6961 -0.7012 -1.3493  0.8617 -1.3414

m = moment(X,3)
m =
  -0.0282  0.0571  0.1253  0.1460  -0.4486
```

More About

Tips

Note that the central first moment is zero, and the second central moment is the variance computed using a divisor of n rather than $n – 1$, where n is the length of the vector `x` or the number of rows in the matrix `X`.

The central moment of order k of a distribution is defined as

$$m_k = E(x - \mu)^k$$

where $E(x)$ is the expected value of x.

See Also

`kurtosis` | `mean` | `skewness` | `std` | `var`

mu property

Class: gmdistribution

Input matrix of means `mu`

Description

Input matrix of means `mu`.

multcompare

Multiple comparison test

Syntax

```
c = multcompare(stats)
c = multcompare(stats,Name,Value)
[c,m] = multcompare( ___ )
[c,m,h] = multcompare( ___ )
[c,m,h,gnames] = multcompare( ___ )
```

Description

`c = multcompare(stats)` returns a matrix c of the pairwise comparison results from a multiple comparison test using the information contained in the stats structure. `multcompare` also displays an interactive graph of the estimates and comparison intervals. Each group mean is represented by a symbol, and the interval is represented by a line extending out from the symbol. Two group means are significantly different if their intervals are disjoint; they are not significantly different if their intervals overlap. If you use your mouse to select any group, then the graph will highlight all other groups that are significantly different, if any.

`c = multcompare(stats,Name,Value)` returns a matrix of pairwise comparison results, c, using additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the confidence interval, or the type of critical value to use in the multiple comparison.

`[c,m] = multcompare( ___ )` also returns a matrix, m, which contains estimated values of the means (or whatever statistics are being compared) for each group and the corresponding standard errors. You can use any of the previous syntaxes.

`[c,m,h] = multcompare( ___ )` also returns a handle, h, to the comparison graph.

`[c,m,h,gnames] = multcompare( ___ )` also returns a cell array, `gnames`, which contains the names of the groups.

Examples

Multiple Comparison of Group Means

Load the sample data.

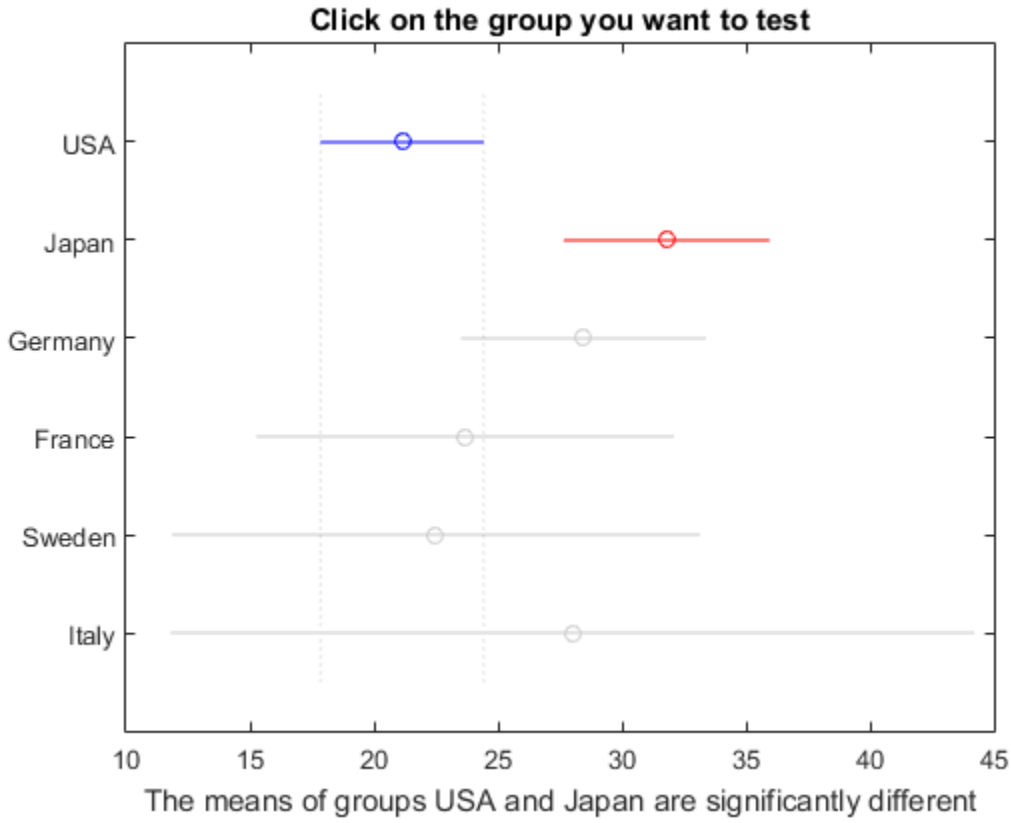
```
load carsmall
```

Perform a one-way analysis of variance (ANOVA) to see if there is any difference between the mileage of the cars by origin.

```
[p,t,stats] = anova1(MPG,Origin,'off');
```

Perform a multiple comparison of the group means.

```
[c,m,h,nms] = multcompare(stats);
```



`multcompare` displays the estimates with comparison intervals around them. You can click the graphs of each country to compare its mean to those of other countries.

Now display the mean estimates and the standard errors with the corresponding group names.

```
[nms num2cell(m)]
```

```
ans =

    'USA'        [21.1328]    [0.8814]
    'Japan'      [31.8000]    [1.8206]
    'Germany'    [28.4444]    [2.3504]
```

```
    'France'     [23.6667]    [4.0711]
    'Sweden'     [22.5000]    [4.9860]
    'Italy'      [     28]    [7.0513]
```

Multiple Comparisons for Two-Way ANOVA

Load the sample data.

```
load popcorn
popcorn
```

```
popcorn =

    5.5000    4.5000    3.5000
    5.5000    4.5000    4.0000
    6.0000    4.0000    3.0000
    6.5000    5.0000    4.0000
    7.0000    5.5000    5.0000
    7.0000    5.0000    4.5000
```

The data is from a study of popcorn brands and popper types (Hogg 1987). The columns of the matrix `popcorn` are brands (Gourmet, National, and Generic). The rows are popper types oil and air. In the study, researchers popped a batch of each brand three times with each popper. The values are the yield in cups of popped popcorn.

Perform a two-way ANOVA. Also compute the statistics that you need to perform a multiple comparison test on the main effects.

```
[~,~,stats] = anova2(popcorn,3,'off')
```

```
stats =

      source: 'anova2'
     sigmasq: 0.1389
    colmeans: [6.2500 4.7500 4]
        coln: 6
    rowmeans: [4.5000 5.5000]
        rown: 9
       inter: 1
        pval: 0.7462
```

```
          df: 12
```

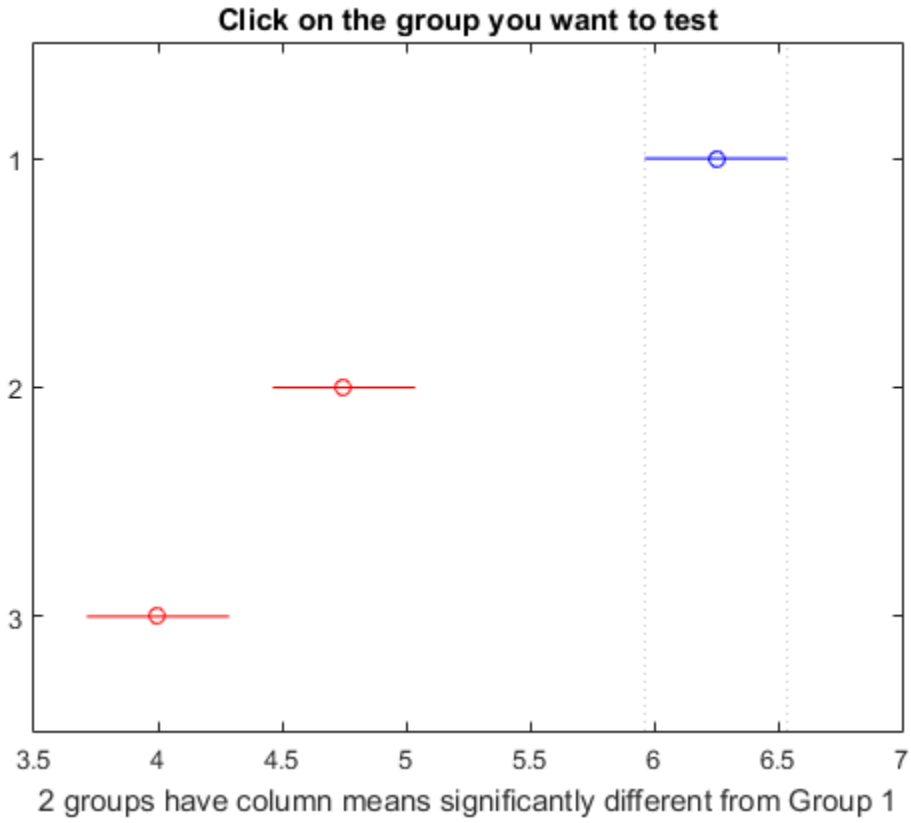
The `stats` structure includes

- The mean squared error (`sigmasq`)
- The estimates of the mean yield for each popcorn brand (`colmeans`)
- The number of observations for each popcorn brand (`coln`)
- The estimate of the mean yield for each popper type (`rowmeans`)
- The number of observations for each popper type (`rown`)
- The number of interactions (`inter`)
- The *p*-value that shows the significance level of the interaction term (`pval`)
- The error degrees of freedom (`df`).

Perform a multiple comparison test to see if the popcorn yield differs between pairs of popcorn brands (columns).

```
c = multcompare(stats)
```

```
Note: Your model includes an interaction term.  A test of main effects can be
difficult to interpret when the model includes interactions.

c =

    1.0000    2.0000    0.9260    1.5000    2.0740    0.0000
    1.0000    3.0000    1.6760    2.2500    2.8240    0.0000
    2.0000    3.0000    0.1760    0.7500    1.3240    0.0116
```



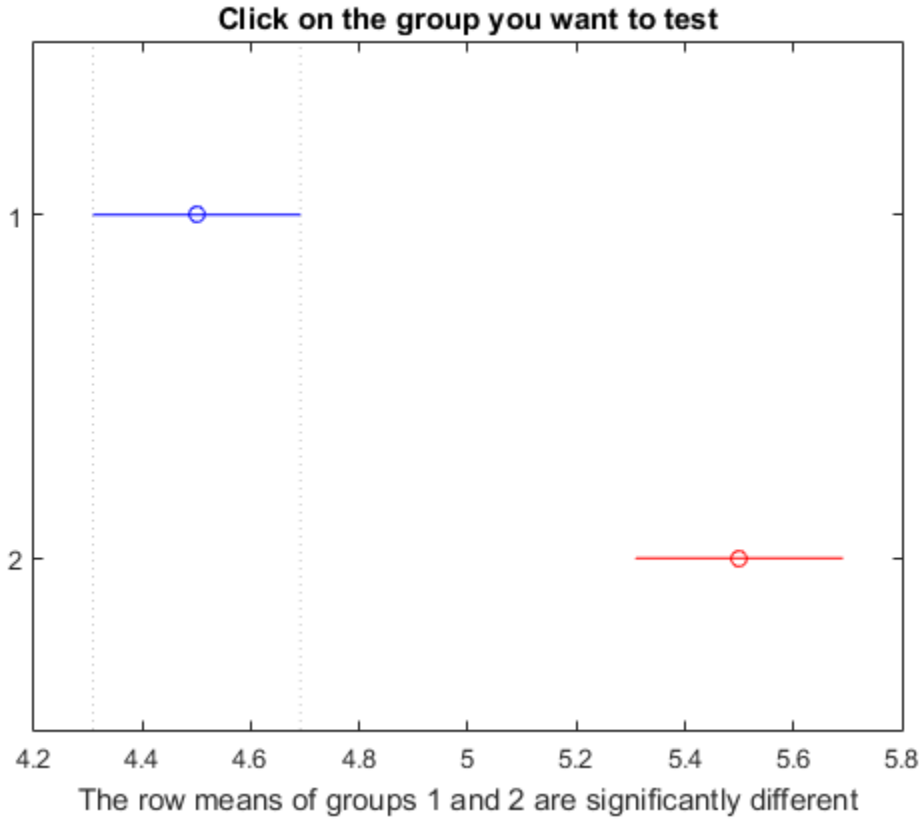
The first two columns of `c` show the groups that are compared. The fourth column shows the difference between the estimated group means. The third and fifth columns show the lower and upper limits for 95% confidence intervals for the true mean difference. The sixth column contains the *p*-value for a hypothesis test that the corresponding mean difference is equal to zero. All *p*-values (0, 0, and 0.0116) are very small, which indicates that the popcorn yield differs across all three brands.

The figure shows the multiple comparison of the means. By default, the group 1 mean is highlighted and the comparison interval is in blue. Because the comparison intervals for the other two groups do not intersect with the intervals for the group 1 mean, they are highlighted in red. This lack of intersection indicates that both means are different than group 1 mean. Select other group means to confirm that all group means are significantly different from each other.

Perform a multiple comparison test to see the popcorn yield differs between the two popper types (rows).

```
c = multcompare(stats,'Estimate','row')
```

```
Note: Your model includes an interaction term.  A test of main effects can be
difficult to interpret when the model includes interactions.

c =

    1.0000    2.0000   -1.3828   -1.0000   -0.6172    0.0001
```



The small *p*-value of 0.0001 indicates that the popcorn yield differs between the two popper types (air and oil). The figure shows the same results. The disjoint comparison intervals indicate that the group means are significantly different from each other.

Multiple Comparisons for Three-Way ANOVA

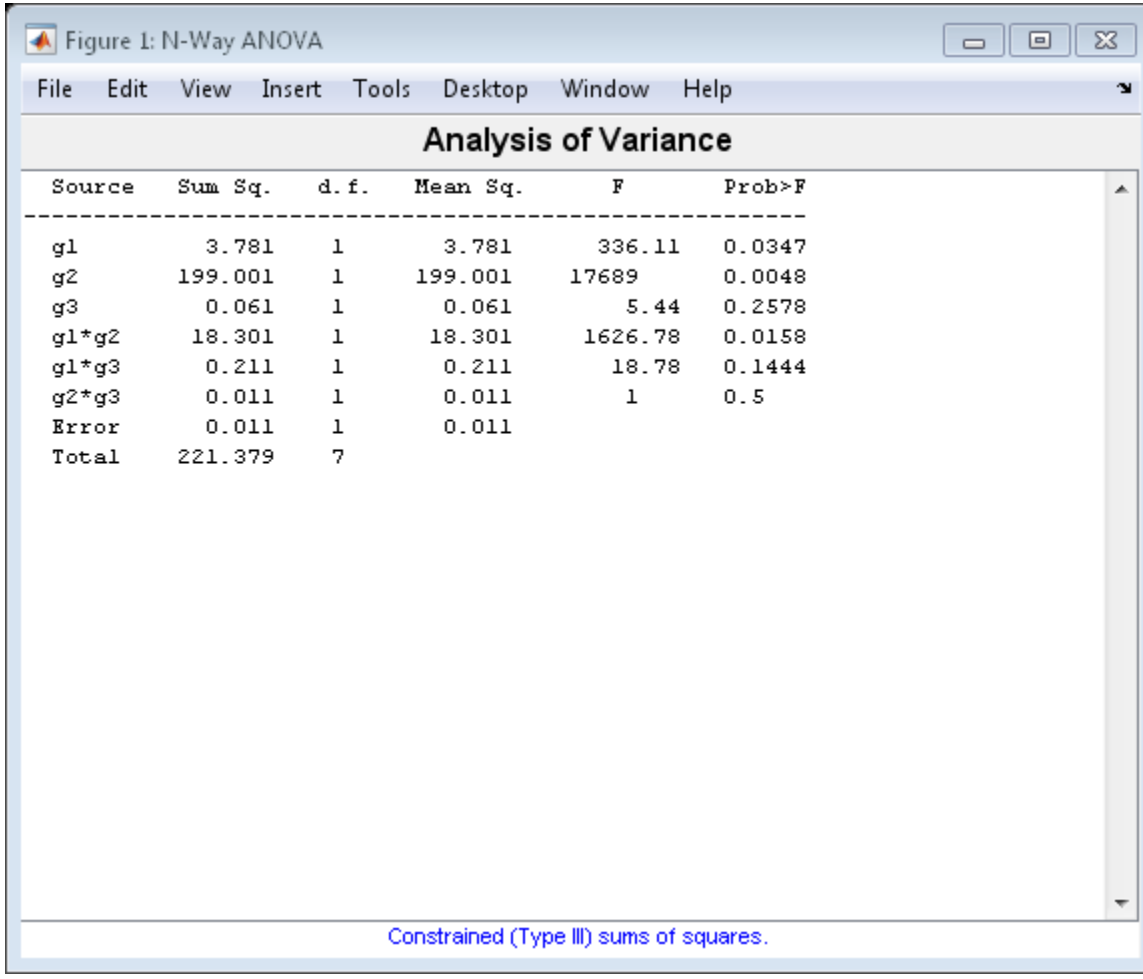
Load the sample data.

```
y = [52.7 57.5 45.9 44.5 53.0 57.0 45.9 44.0]';
g1 = [1 2 1 2 1 2 1 2];
g2 = {'hi';'hi';'lo';'lo';'hi';'hi';'lo';'lo'};
g3 = {'may';'may';'may';'may';'june';'june';'june';'june'};
```

`y` is the response vector and `g1`, `g2`, and `g3` are the grouping variables (factors). Each factor has two levels, and every observation in `y` is identified by a combination of factor levels. For example, observation `y(1)` is associated with level 1 of factor `g1`, level `'hi'` of factor `g2`, and level `'may'` of factor `g3`. Similarly, observation `y(6)` is associated with level 2 of factor `g1`, level `'hi'` of factor `g2`, and level `'june'` of factor `g3`.

Test if the response is the same for all factor levels. Also compute the statistics required for multiple comparison tests.

```
[~,~,stats] = anovan(y,{g1 g2 g3},'model','interaction',...
    'varnames',{'g1','g2','g3'});
```

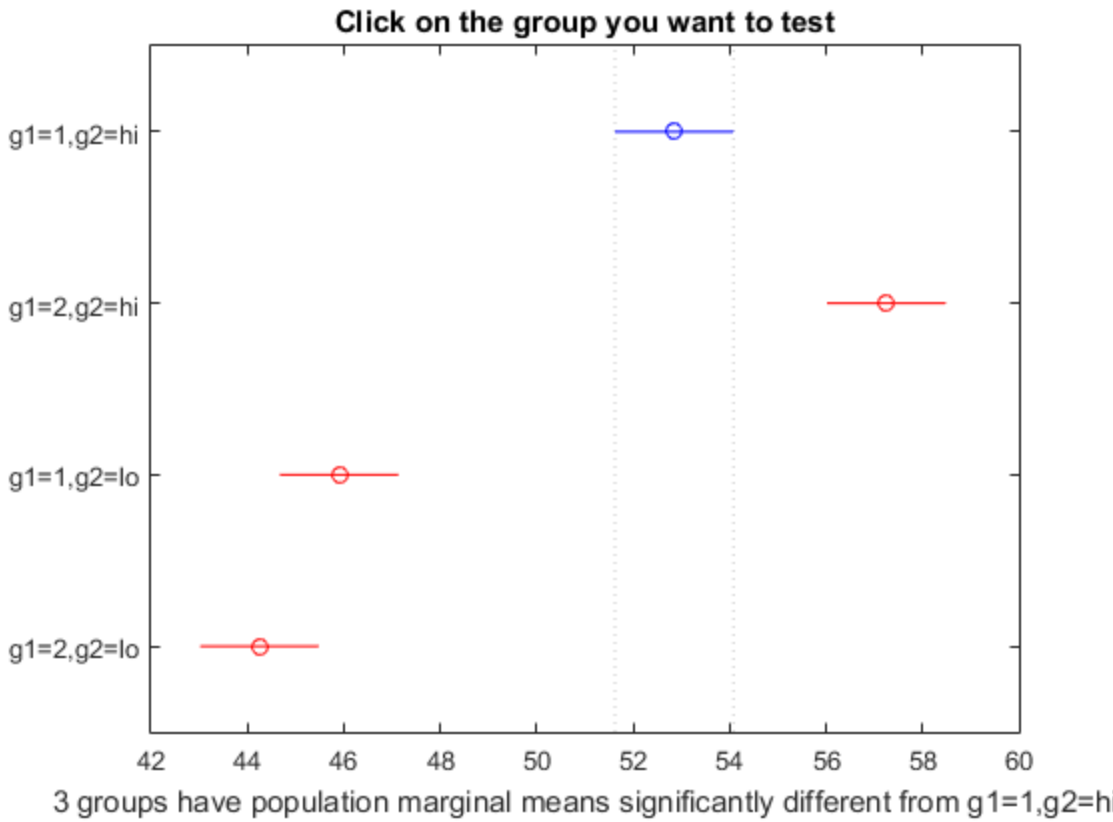


The p-value of 0.2578 indicates that the mean responses for levels `'may'` and `'june'` of factor `g3` are not significantly different. The p-value of 0.0347 indicates that the mean responses for levels `1` and `2` of factor `g1` are significantly different. Similarly, the p-value of 0.0048 indicates that the mean responses for levels `'hi'` and `'lo'` of factor `g2` are significantly different.

Perform multiple comparison tests to find out which groups of the factors `g1` and `g2` are significantly different.

```
results = multcompare(stats,'Dimension',[1 2])
```

```
results =

    1.0000    2.0000   -6.8604   -4.4000   -1.9396    0.0280
    1.0000    3.0000    4.4896    6.9500    9.4104    0.0177
    1.0000    4.0000    6.1396    8.6000   11.0604    0.0143
    2.0000    3.0000    8.8896   11.3500   13.8104    0.0108
    2.0000    4.0000   10.5396   13.0000   15.4604    0.0095
    3.0000    4.0000   -0.8104    1.6500    4.1104    0.0745
```



multcompare compares the combinations of groups (levels) of the two grouping variables, `g1` and `g2`. In the `results` matrix, the number 1 corresponds to the combination of level `1` of `g1` and level `hi` of `g2`, the number 2 corresponds to the combination of level `2` of `g1` and level `hi` of `g2`. Similarly, the number 3 corresponds to the combination of level `1` of `g1` and level `lo` of `g2`, and the number 4 corresponds to the combination of level `2` of `g1` and level `lo` of `g2`. The last column of the matrix contains the *p*-values.

For example, the first row of the matrix shows that the combination of level `1` of `g1` and level `hi` of `g2` has the same mean response values as the combination of level `2` of `g1` and level `hi` of `g2`. The *p*-value corresponding to this test is 0.0280, which indicates that the mean responses are significantly different. You can also see this result in the figure. The blue bar shows the comparison interval for the mean response for the combination of level `1` of `g1` and level `hi` of `g2`. The red bars are the comparison intervals for the mean response for other group combinations. None of the red bars overlap with the blue bar, which means the mean response for the combination of level `1` of `g1` and level `hi` of `g2` is significantly different from the mean response for other group combinations.

You can test the other groups by clicking on the corresponding comparison interval for the group. The bar you click on turns to blue. The bars for the groups that are significantly different are red. The bars for the groups that are not significantly different are gray. For example, if you click on the comparison interval for the combination of level `1` of `g1` and level `lo` of `g2`, the comparison interval for the combination of level `2` of `g1` and level `lo` of `g2` overlaps, and is therefore gray. Conversely, the other comparison intervals are red, indicating significant difference.

Input Arguments

`stats` — Test data

structure

Test data, specified as a structure. You can create a structure using one of the following functions:

- `anova1` — One-way analysis of variance.
- `anova2` — Two-way analysis of variance.
- `anovan` — *N*-way analysis of variance.
- `aoctool` — Interactive analysis of covariance tool.
- `friedman` — Friedman's test.

- `kruskalwallis` — Kruskal-Wallis test.

`multcompare` does not support multiple comparisons using `anovan` output for a model that includes random or nested effects. The calculations for a random effects model produce a warning that all effects are treated as fixed. Nested models are not accepted.

Data Types: `struct`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alpha',0.01,'CType','bonferroni','Display','off'` computes the Bonferroni critical values, conducts the hypothesis tests at the 1% significance level, and omits the interactive display.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the multiple comparison test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1). The value specified for `'Alpha'` determines the $100 \times (1 - \alpha)$ confidence levels of the intervals returned in the matrix c and in the figure.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'CType'` — Type of critical value

`'tukey-kramer'` (default) | `'hsd'` | `'lsd'` | `'bonferroni'` | `'dunn-sidak'` | `'scheffe'`

Type of critical value to use for the multiple comparison, specified as the comma-separated pair consisting of `'CType'` and one of the following.

Value	Description
`'tukey-kramer'` or `'hsd'`	Tukey's honest significant difference criterion
`'bonferroni'`	Bonferroni method

Value	Description
'dunn-sidak'	Dunn and Sidák's approach
'lsd'	Fisher's least significant difference procedure
'scheffe'	Scheffé's S procedure

Example: 'CType','bonferroni'

'Display' — Display toggle

'on' (default) | 'off'

Display toggle, specified as the comma-separated pair consisting of 'Display' and either 'on' or 'off'. If you specify 'on', then multcompare displays a graph of the estimates and their comparison intervals. If you specify 'off', then multcompare omits the graph.

Example: 'Display','off'

'Dimension' — Dimension over which to calculate marginal means

1 (default) | positive integer value | vector of positive integer values

A vector specifying the dimension or dimensions over which to calculate the population marginal means, specified as a positive integer value, or a vector of such values. Use the 'Dimension' name-value pair only if you create the input structure stats using the function anovan.

For example, if you specify 'Dimension' as 1, then multcompare compares the means for each value of the first grouping variable, adjusted by removing effects of the other grouping variables as if the design were balanced. If you specify 'Dimension'as [1,3], then multcompare computes the population marginal means for each combination of the first and third grouping variables, removing effects of the second grouping variable. If you fit a singular model, some cell means may not be estimable and any population marginal means that depend on those cell means will have the value NaN.

Population marginal means are described by Milliken and Johnson (1992) and by Searle, Speed, and Milliken (1980). The idea behind population marginal means is to remove any effect of an unbalanced design by fixing the values of the factors specified by 'Dimension', and averaging out the effects of other factors as if each factor combination occurred the same number of times. The definition of population marginal means does not depend on the number of observations at each factor combination. For designed experiments where the number of observations at each factor combination has no meaning, population marginal means can be easier to interpret than simple means

ignoring other factors. For surveys and other studies where the number of observations at each combination does have meaning, population marginal means may be harder to interpret.

Example: `'Dimension',[1,3]`

Data Types: `single` | `double`

`'Estimate'` — Estimates to be compared

`'column'` (default) | `'row'` | `'slope'` | `'intercept'` | `'pmm'`

Estimates to be compared, specified as the comma-separated pair consisting of `'Estimate'` and an allowable value. The allowable values for `'Estimate'` depend on the function used to generate the input structure stats, according to the following table.

Source	Values
`anova1`	None. This name-value pair is ignored, and `multcompare` always compares the group means.
`anova2`	Either `'column'` to compare column means, or `'row'` to compare row means.
`anovan`	None. This name-value pair is ignored, and `multcompare` always compares the population marginal means as specified by the `'Dimension'` name-value pair argument.
`aoctool`	Either `'slope'`, `'intercept'`, or `'pmm'` to compare slopes, intercepts, or population marginal means, respectively. If the analysis of covariance model did not include separate slopes, then `'slope'` is not allowed. If it did not include separate intercepts, then no comparisons are possible.
`friedman`	None. This name-value pair is ignored, and `multcompare` always compares the average column ranks.
`kruskalwallis`	None. This name-value pair is ignored, and `multcompare` always compares the average group ranks.

Example: `'Estimate','row'`

Output Arguments

`c` — Matrix of multiple comparison results

matrix of scalar values

Matrix of multiple comparison results, returned as an p-by-6 matrix of scalar values, where p is the number of pairs of groups. Each row of the matrix contains the result of one paired comparison test. Columns 1 and 2 contain the indices of the two samples being compared. Column 3 contains the lower confidence interval, column 4 contains the estimate, and column 5 contains the upper confidence interval. Column 6 contains the p-value for the hypothesis test that the corresponding mean difference is not equal to 0.

For example, suppose one row contains the following entries.

```
2.0000   5.0000   1.9442   8.2206   14.4971 0.0432
```

These numbers indicate that the mean of group 2 minus the mean of group 5 is estimated to be 8.2206, and a 95% confidence interval for the true difference of the means is [1.9442, 14.4971]. The p-value for the corresponding hypothesis test that the difference of the means of groups 2 and 5 is significantly different from zero is 0.0432.

In this example the confidence interval does not contain 0, so the difference is significant at the 5% significance level. If the confidence interval did contain 0, the difference would not be significant. The p-value of 0.0432 also indicates that the difference of the means of groups 2 and 5 is significantly different from 0.

`m` — Matrix of estimates

matrix of scalar values

Matrix of the estimates, returned as a matrix of scalar values. The first column of `m` contains the estimated values of the means (or whatever statistics are being compared) for each group, and the second column contains their standard errors.

`h` — Handle to the figure

handle

Handle to the figure containing the interactive graph, returned as a handle. The title of this graph contains instructions for interacting with the graph, and the x-axis label contains information about which means are significantly different from the selected mean. If you plan to use this graph for presentation, you may want to omit the title and the x-axis label. You can remove them using interactive features of the graph window, or you can use the following commands.

```
title('')
xlabel('')
```

`gnames` — Group names

cell array of strings

Group names, returned as a cell array of strings. Each row of gnames contains the name of a group.

More About

Multiple Comparison Tests

Analysis of variance compares the means of several groups to test the hypothesis that they are all equal, against the general alternative that they are not all equal. Sometimes this alternative may be too general. You may need information about which pairs of means are significantly different, and which are not. A *multiple comparison test* can provide this information.

When you perform a simple *t*-test of one group mean against another, you specify a significance level that determines the cutoff value of the *t*-statistic. For example, you can specify the value `alpha = 0.05` to insure that when there is no real difference, you will incorrectly find a significant difference no more than 5% of the time. When there are many group means, there are also many pairs to compare. If you applied an ordinary *t*-test in this situation, the `alpha` value would apply to each comparison, so the chance of incorrectly finding a significant difference would increase with the number of comparisons. Multiple comparison procedures are designed to provide an upper bound on the probability that *any* comparison will be incorrectly found significant.

References

[1] Hochberg, Y., and A. C. Tamhane. *Multiple Comparison Procedures*. Hoboken, NJ: John Wiley & Sons, 1987.

[2] Milliken, G. A., and D. E. Johnson. *Analysis of Messy Data, Volume I: Designed Experiments*. Boca Raton, FL: Chapman & Hall/CRC Press, 1992.

[3] Searle, S. R., F. M. Speed, and G. A. Milliken. "Population marginal means in the linear model: an alternative to least-squares means." *American Statistician*. 1980, pp. 216–221.

See Also

`anova1` | `anova2` | `anovan` | `aoctool` | `friedman` | `kruskalwallis`

multcompare

Class: RepeatedMeasuresModel

Multiple comparison of estimated marginal means

Syntax

```
tbl = multcompare(rm,var)
tbl = multcompare(rm,var,Name,Value)
```

Description

`tbl = multcompare(rm,var)` returns multiple comparisons of the estimated marginal means based on the variable var in the repeated measures model rm.

`tbl = multcompare(rm,var,Name,Value)` returns multiple comparisons of the estimated marginal means with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the comparison type or which variable to group by.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`var` — Variables for which to compute marginal means

string

Variables for which to compute the marginal means, specified as a string representing the name of a between- or within-subjects factor in rm. If `var` is a between-subjects factor, it must be categorical.

Data Types: `char` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range of 0 through 1

Confidence level of the confidence intervals for population marginal means, specified as the comma-separated pair consisting of `'alpha'` and a scalar value in the range of 0 through 1. The confidence level is 100*(1–`alpha`)%.

Example: `'alpha',0.01`

Data Types: `double | single`

`'By'` — Factor to perform comparisons by

string

Factor to do the comparisons by, specified as the comma-separated pair consisting of `'By'` and a string. The comparison between levels of var occurs separately for each value of the factor you specify.

If you have more then one between-subjects factors, *A*, *B*, and *C*, and if you want to do the comparisons of *A* levels separately for each level of *C*, then specify *A* as the `var` argument and specify *C* using the `'By'` argument as follows.

Example: `'By',C`

Data Types: `char`

`'ComparisonType'` — Type of critical value to use

`'tukey-kramer'` (default) | `'dunn-sidak'` | `'bonferroni'` | `'scheffe'` | `'lsd'`

Type of critical value to use, specified as the comma-separated pair consisting of `'ComparisonType'` and one of the following.

Comparison Type	Definition
`'tukey-kramer'`	Default. Also called Tukey's Honest Significant Difference procedure. It is based on the Studentized range

Comparison Type	Definition
	distribution. According to the unproven Tukey-Kramer conjecture, it is also accurate for problems where the quantities being compared are correlated, as in analysis of covariance with unbalanced covariate values.
`'dunn-sidak'`	Use critical values from the *t* distribution, after an adjustment for multiple comparisons that was proposed by Dunn and proved accurate by Sidák. The critical value is $$\left|t\right| = \frac{\left|\bar{y}_i - \bar{y}_j\right|}{\sqrt{MSE\left(\frac{1}{n_i} + \frac{1}{n_j}\right)}} > t_{1-\eta/2,v},$$ where $$\eta = 1 - \left(1-\alpha\right)^{1/\binom{k}{2}}$$ and *ng* is the number of groups (marginal means). This procedure is similar to, but less conservative than, the Bonferroni procedure.

Comparison Type	Definition
`'bonferroni'`	Use critical values from the t distribution, after a Bonferroni adjustment to compensate for multiple comparisons. The critical value is $t_{\alpha/2\binom{ng}{2},v}$, where ng is the number of groups (marginal means), and v is the error degrees of freedom. This procedure is conservative, but usually less so than the Scheffé procedure.
`'scheffe'`	Use critical values from Scheffé's S procedure, derived from the Fdistribution. The critical value is $\sqrt{(ng-1)F_{\alpha,ng-1,v}}$, where ng is the number of groups (marginal means), and v is the error degrees of freedom. This procedure provides a simultaneous confidence level for comparisons of all linear combinations of the means, and it is conservative for comparisons of simple differences of pairs.
`'lsd'`	Least significant difference. This option uses plain t-tests. The critical value is $t_{\alpha/2,v}$, where v is the error degrees of freedom. It provides no protection against the multiple comparison problem.

Example: `'ComparisonType','dunn-sidak'`

Output Arguments

`tbl` — Results of multiple comparison

table

Results of multiple comparisons of estimated marginal means, returned as a table. tbl has the following columns.

Column Name	Description
`Difference`	Estimated difference between the corresponding two marginal means
`StdErr`	Standard error of the estimated difference between the corresponding two marginal means
`pValue`	*p*-value for a test that the difference between the corresponding two marginal means is 0
`Lower`	Lower limit of simultaneous 95% confidence intervals for the true difference
`Upper`	Upper limit of simultaneous 95% confidence intervals for the true difference

Examples

Multiple Comparison of Estimated Marginal Means

Load the sample data.

```
load fisheriris
```

The column vector `species`consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform a multiple comparison of the estimated marginal means of species.

```
tbl = multcompare(rm,'species')
```

```
tbl =

     species_1       species_2      Difference     StdErr       pValue       Lower
    ____________    ____________    __________    ________    __________    ________

    'setosa'        'versicolor'    -1.0375       0.060539    9.5606e-10     -1.1794
    'setosa'        'virginica'     -1.7495       0.060539    9.5606e-10     -1.8914
    'versicolor'    'setosa'         1.0375       0.060539    9.5606e-10     0.89562
    'versicolor'    'virginica'      -0.712       0.060539    9.5606e-10    -0.85388
    'virginica'     'setosa'         1.7495       0.060539    9.5606e-10      1.6076
    'virginica'     'versicolor'      0.712       0.060539    9.5606e-10     0.57012
```

The small p-values (in the `pValue` field) indicate that the estimated marginal means for the three species significantly differ from each other.

Perform Multiple Comparisons with Specified Options

Load the sample data.

```
load repeatedmeas
```

The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ through $y8$ as responses. The table `within` includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ through $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
R = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Perform a multiple comparison of the estimated marginal means based on the variable `Group`.

```
T = multcompare(R,'Group')
```

```
T =

    Group_1    Group_2    Difference    StdErr      pValue        Lower       Upper
```

A	B	4.9875	5.6271	0.65436	-9.1482	19.123
A	C	23.094	5.9261	0.0021493	8.2074	37.981
B	A	-4.9875	5.6271	0.65436	-19.123	9.1482
B	C	18.107	5.8223	0.013588	3.4805	32.732
C	A	-23.094	5.9261	0.0021493	-37.981	-8.2074
C	B	-18.107	5.8223	0.013588	-32.732	-3.4805

The small *p*-value of 0.0021493 indicates that there is significant difference between the marginal means of groups A and C. The *p*-values of 0.65436 indicates that the difference between the marginal means for groups A and B is not significantly different from 0.

`multcompare` uses the Tukey-Kramer test statistic by default. Change the comparison type to the Scheffe procedure.

```
T = multcompare(R,'Group','ComparisonType','Scheffe')
```

```
T =
```

Group_1	Group_2	Difference	StdErr	pValue	Lower	Upper
A	B	4.9875	5.6271	0.67981	-9.7795	19.755
A	C	23.094	5.9261	0.0031072	7.5426	38.646
B	A	-4.9875	5.6271	0.67981	-19.755	9.7795
B	C	18.107	5.8223	0.018169	2.8273	33.386
C	A	-23.094	5.9261	0.0031072	-38.646	-7.5426
C	B	-18.107	5.8223	0.018169	-33.386	-2.8273

The Scheffe test produces larger *p*-values, but similar conclusions.

Perform multiple comparisons of estimated marginal means based on the variable `Group` for each gender separately.

```
T = multcompare(R,'Group','By','Gender')
```

```
T =
```

Gender	Group_1	Group_2	Difference	StdErr	pValue	Lower	
Female	A	B	4.1883	8.0177	0.86128	-15.953	
Female	A	C	24.565	8.2083	0.017697	3.9449	
Female	B	A	-4.1883	8.0177	0.86128	-24.329	

```
Female    B          C           20.376       8.1101     0.049957     0.0033459
Female    C          A          -24.565       8.2083     0.017697       -45.184
Female    C          B          -20.376       8.1101     0.049957       -40.749    -(
Male      A          B           5.7868       7.9498      0.74977       -14.183
Male      A          C            21.624      8.1829     0.038022        1.0676
Male      B          A          -5.7868       7.9498      0.74977       -25.757
Male      B          C           15.837       8.0511      0.14414       -4.3881
Male      C          A          -21.624       8.1829     0.038022       -42.179
Male      C          B          -15.837       8.0511      0.14414       -36.062
```

The results indicate that the difference between marginal means for groups A and B is not significant from 0 for either gender (corresponding p-values are 0.86128 for females and 0.74977 for males). The difference between marginal means for groups A and C is significant for both genders (corresponding p-values are 0.017697 for females and 0.038022 for males). While the difference between marginal means for groups B and C is significantly different from 0 for females (p-value is 0.049957), it is not significantly different from 0 for males (p-value is 0.14414).

References

[1] G. A. Milliken, and Johnson, D. E. *Analysis of Messy Data. Volume I: Designed Experiments*. New York, NY: Chapman & Hall, 1992.

See Also

`fitrm` | `margmean` | `plotprofile`

prob.MultinomialDistribution class

Package: prob
Superclasses: prob.ParametricTruncatableDistribution

Multinomial probability distribution object

Description

`prob.MultinomialDistribution` is an object consisting of parameters and a model description for a multinomial probability distribution. Create a probability distribution object with specified parameters using `makedist`.

Construction

`pd = makedist('Multinomial')` creates a multinomial probability distribution object using the default parameter values.

`pd = makedist('Multinomial','Probabilities',probabilities)` creates a multinomial distribution object using the specified parameter value.

Input Arguments

`probabilities` — outcome probabilities
`[0.500 0.500]` (default) | vector of scalar values in the range `[0,1]`

Outcome probabilities, specified as a vector of scalar values in the range `[0,1]`. Each vector element is the probability that a multinomial trial has a particular corresponding outcome. The values in `probabilities` must sum to 1.

Data Types: `single` | `double`

Properties

`probabilities` — outcome probabilities
vector of scalar values in the range `[0,1]`

Outcome probabilities for the multinomial distribution, stored as a vector of scalar values in the range `[0,1]`. The values in `probabilities` must sum to 1.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Multinomial Distribution

The multinomial distribution is a generalization of the binomial distribution. While the binomial distribution gives the probability of the number of "successes" in n independent trials of a two-outcome process, the multinomial distribution gives the probability of each combination of outcomes in n independent trials of a k-outcome process. The probability of each outcome in any one trial is given by the fixed probabilities p_1, ..., p_k.

The multinomial distribution uses the following parameters.

Parameter	Description	Support
`probabilities`	Outcome probabilities	$0 \le probabilities(i) \le 1$; $\sum_{all(i)} probabilities(i) = 1$

The probability density function (pdf) is

$$f(x \mid n, p) = \frac{n!}{x_1! \ldots x_k!} {p_1}^{x_1} \cdots {p_k}^{x_k} \quad ; \quad \sum_1^k x_i = n \, , \, \sum_1^k p_i = 1 \, ,$$

where $x = (x_1,...,x_k)$ gives the number of each k outcome in n trials of a process with fixed probabilities $p = (p_1,...,p_k)$ of individual outcomes in any one trial.

Examples

Create a Multinomial Distribution Object Using Default Parameters

Create a multinomial distribution object using the default parameter values.

```
pd = makedist('Multinomial')
```

```
pd =

  MultinomialDistribution

  Probabilities:
    0.5000    0.5000
```

Create a Multinomial Distribution Object Using Specified Parameters

Create a multinomial distribution object for a distribution with three possible outcomes. Outcome 1 has a probability of 1/2, outcome 2 has a probability of 1/3, and outcome 3 has a probability of 1/6.

```
pd = makedist('Multinomial','probabilities',[1/2 1/3 1/6])
```

```
pd =

  MultinomialDistribution

  Probabilities:
    0.5000    0.3333    0.1667
```

Generate a random outcome from the distribution.

```
rng('default');  % for reproducibility
r = random(pd)
```

```
r =

     2
```

The result of this trial is outcome 2. By default, the number of trials in each experiment, n, equals 1.

Generate random outcomes from the distribution when the number of trials in each experiment, n, equals 1, and the experiment is repeated ten times.

```
rng('default');  % for reproducibility
```

```
r = random(pd,10,1)

r =

     2
     3
     1
     3
     2
     1
     1
     2
     3
     3
```

Each element in the array is the outcome of an individual experiment that contains one trial.

Generate random outcomes from the distribution when the number of trials in each experiment, n, equals 5, and the experiment is repeated ten times.

```
rng('default');  % for reproducibility
r = random(pd,10,5)

r =

     2     1     2     2     1
     3     3     1     1     1
     1     3     3     1     2
     3     1     3     1     2
     2     2     2     1     1
     1     1     2     2     1
     1     1     2     2     1
     2     3     1     1     2
     3     2     2     3     2
     3     3     1     1     2
```

Each element in the resulting matrix is the outcome of one trial. The columns correspond to the five trials in each experiment, and the rows correspond to the ten experiments. For example, in the first experiment (corresponding to the first row), 2 of the 5 trials resulted in outcome 1, and 3 of the 5 trials resulted in outcome 2.

See Also

`makedist`

More About

- "Multinomial Distribution"
- Class Attributes
- Property Attributes

multivarichart

Multivari chart for grouped data

Syntax

```
multivarichart(y,GROUP)
multivarichart(Y)
multivarichart(...,param1,val1,param2,val2,...)
[charthandle,AXESH] = multivarichart(...)
```

Description

`multivarichart(y,GROUP)` displays the multivari chart for the vector `y` grouped by entries in the cell array `GROUP`. Each cell of `GROUP` must contain a grouping variable that can be a categorical variable, numeric vector, character matrix, or single-column cell array of strings. `GROUP` can also be a matrix whose columns represent different grouping variables. Each grouping variable must have the same number of elements as `y`. The number of grouping variables must be 2, 3, or 4.

Each subplot of the plot matrix contains a multivari chart for the first and second grouping variables. The *x*-axis in each subplot indicates values of the first grouping variable. The legend at the bottom of the figure window indicates values of the second grouping variable. The subplot at position (*i*,*j*) is the multivari chart for the subset of `y` at the *i*th level of the third grouping variable and the *j*th level of the fourth grouping variable. If the third or fourth grouping variable is absent, it is considered to have only one level.

`multivarichart(Y)` displays the multivari chart for a matrix `Y`. The data in different columns represent changes in one factor. The data in different rows represent changes in another factor.

`multivarichart(...,param1,val1,param2,val2,...)` specifies one or more of the following name/value pairs:

- `'varnames'` — Grouping variable names in a character matrix or a cell array of strings, one per grouping variable. Default names are `'X1'`, `'X2'`, ...

- `'plotorder'` — A string with the value `'sorted'` or a vector containing a permutation of the integers from 1 to the number of grouping variables.

  If `'plotorder'` is a string with value `'sorted'`, the grouping variables are rearranged in descending order according to the number of levels in each variable.

  If `'plotorder'` is a vector, it indicates the order in which each grouping variable should be plotted. For example, `[2,3,1,4]` indicates that the second grouping variable should be used as the *x*-axis of each subplot, the third grouping variable should be used as the legend, the first grouping variable should be used as the columns of the plot, and the fourth grouping variable should be used as the rows of the plot.

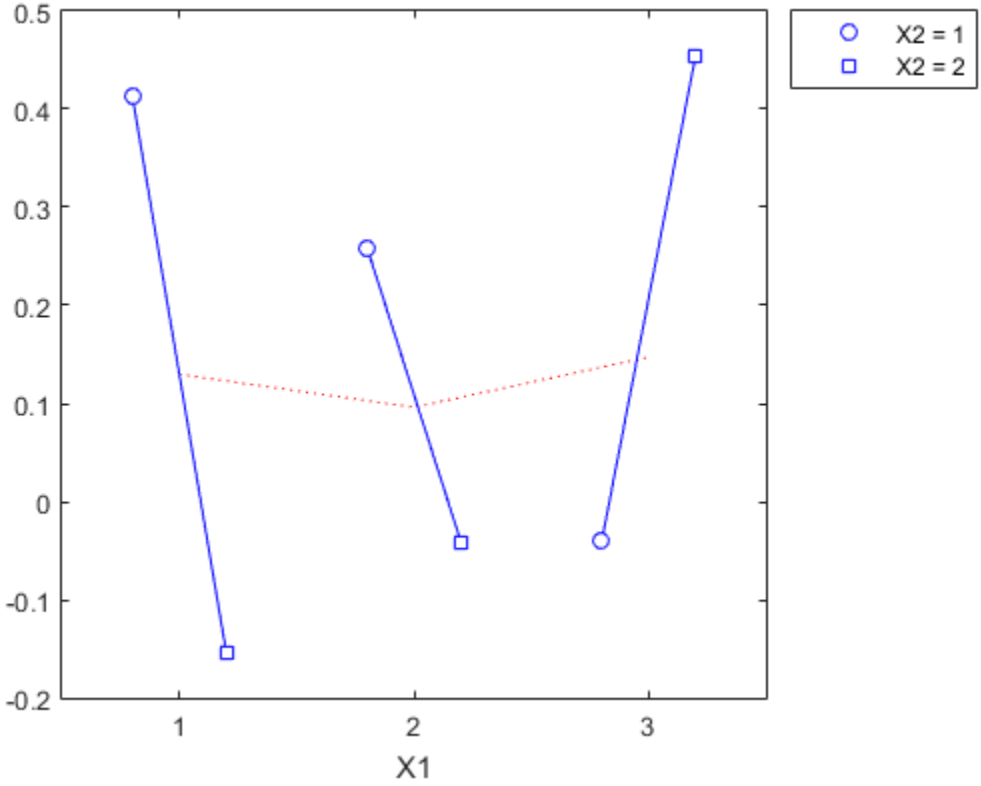
`[charthandle,AXESH] = multivarichart(...)` returns a handle `charthandle` to the figure window and a matrix `AXESH` of handles to the subplot axes.

Examples

Multivari Chart for Grouped Data

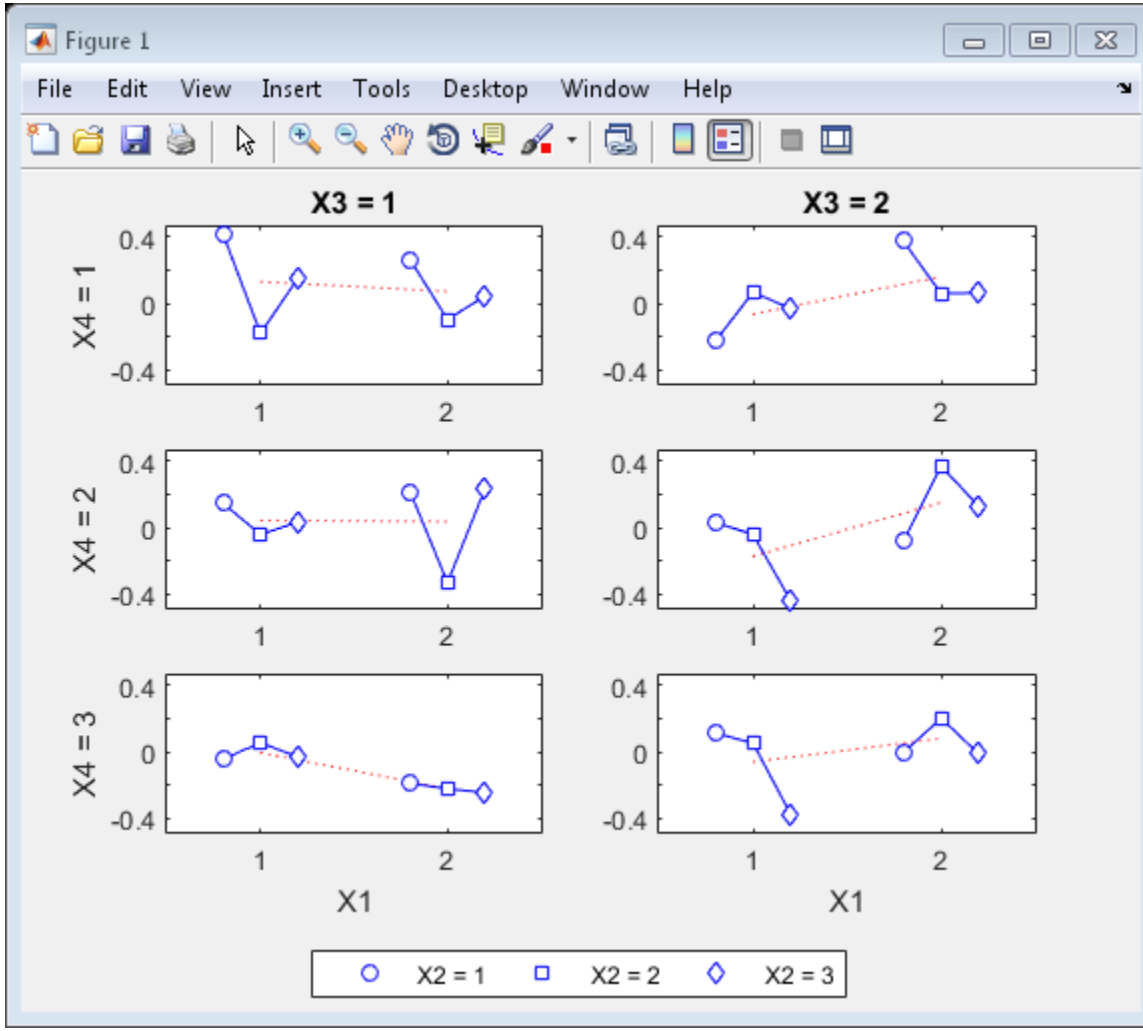
Display a multivari chart for data with two grouping variables.

```
rng default; % For reproducibility
y = randn(100,1); % Randomly generate response
group = [ceil(3*rand(100,1)) ceil(2*rand(100,1))];
multivarichart(y,group)
```



Display a multivari chart for data with four grouping variables.

```
y = randn(1000,1); % Randomly generate response
group = {ceil(2*rand(1000,1)),ceil(3*rand(1000,1)), ...
         ceil(2*rand(1000,1)),ceil(3*rand(1000,1))};
multivarichart(y,group)
```



More About

- "Grouping Variables" on page 2-52

See Also

`maineffectsplot` | `interactionplot`

mvncdf

Multivariate normal cumulative distribution function

Syntax

```
y = mvncdf(X)
y = mvncdf(X,mu,SIGMA)
y = mvncdf(xl,xu,mu,SIGMA)
[y,err] = mvncdf(...)
[...] = mvncdf(...,options)
```

Description

`y = mvncdf(X)` returns the cumulative probability of the multivariate normal distribution with zero mean and identity covariance matrix, evaluated at each row of `X`. Rows of the n-by-d matrix `X` correspond to observations or points, and columns correspond to variables or coordinates. `y` is an n-by-`1` vector.

`y = mvncdf(X,mu,SIGMA)` returns the cumulative probability of the multivariate normal distribution with mean `mu` and covariance `SIGMA`, evaluated at each row of `X`. `mu` is a `1`-by-d vector, and `SIGMA` is a d-by-d symmetric, positive definite matrix. `mu` can also be a scalar value, which `mvncdf` replicates to match the size of `X`. If the covariance matrix is diagonal, containing variances along the diagonal and zero covariances off the diagonal, `SIGMA` may also be specified as a `1`-by-d vector containing just the diagonal. Pass in the empty matrix `[]` for `mu` to use as its default value when you want to only specify `SIGMA`.

The multivariate normal cumulative probability at `X` is defined as the probability that a random vector `V`, distributed as multivariate normal, will fall within the semi-infinite rectangle with upper limits defined by `X`, for example, $\texttt{Pr\{V(1)} \le \texttt{X(1),V(2)} \le \texttt{X(2),...,V(}d\texttt{)} \le \texttt{X(}d\texttt{)\}}$.

`y = mvncdf(xl,xu,mu,SIGMA)` returns the multivariate normal cumulative probability evaluated over the rectangle with lower and upper limits defined by `xl` and `xu`, respectively.

`[y,err] = mvncdf(...)` returns an estimate of the error in `y`. For bivariate and trivariate distributions, `mvncdf` uses adaptive quadrature on a transformation of the t density, based on methods developed by Drezner and Wesolowsky and by Genz, as described in the references. The default absolute error tolerance for these cases is `1e-8`. For four or more dimensions, `mvncdf` uses a quasi-Monte Carlo integration algorithm based on methods developed by Genz and Bretz, as described in the references. The default absolute error tolerance for these cases is `1e-4`.

`[...] = mvncdf(...,options)` specifies control parameters for the numerical integration used to compute `y`. This argument can be created by a call to `statset`. Choices of `statset` parameters:

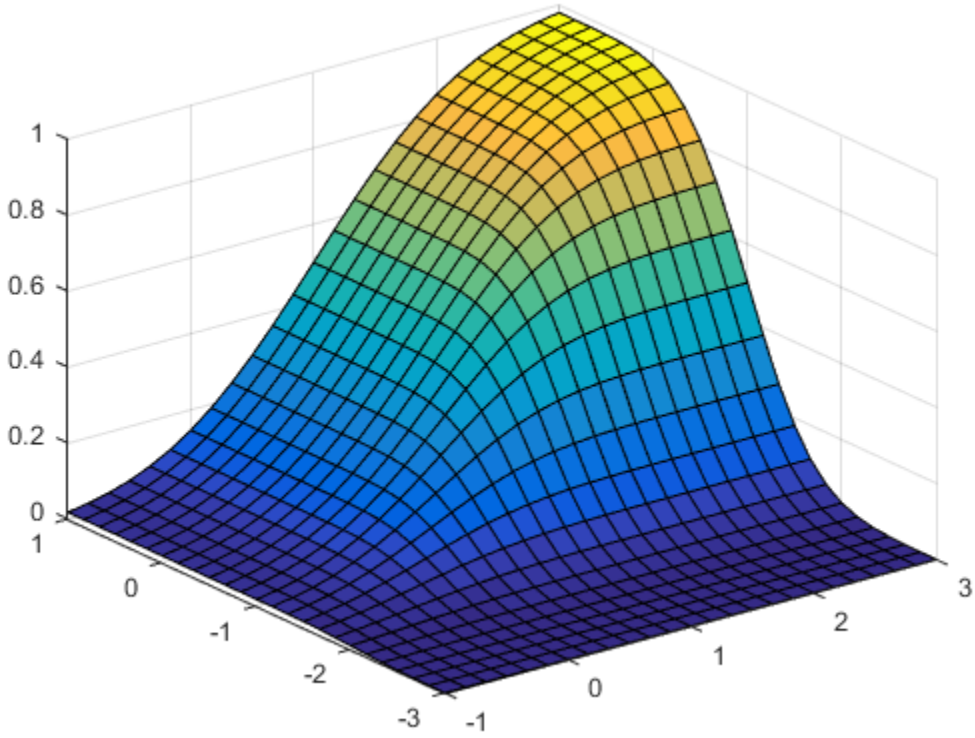
- `'TolFun'` — Maximum absolute error tolerance. Default is `1e-8` when $d < 4$, or `1e-4` when $d \geq 4$.
- `'MaxFunEvals'` — Maximum number of integrand evaluations allowed when $d \geq 4$. Default is `1e7`. `'MaxFunEvals'` is ignored when $d < 4$.
- `'Display'` — Level of display output. Choices are `'off'` (the default), `'iter'`, and `'final'`. `'Display'` is ignored when $d < 4$.

Examples

Compute the Multivariate Normal cdf

Compute and plot the cdf of a multivariate normal distribution with parameters `mu = [1 -1]` and `SIGMA = [.9 .4; .4 .3]`.

```
mu = [1 -1];
SIGMA = [.9 .4; .4 .3];
figure;
[X1,X2] = meshgrid(linspace(-1,3,25)',linspace(-3,1,25)');
X = [X1(:) X2(:)];
p = mvncdf(X,mu,SIGMA);
surf(X1,X2,reshape(p,25,25));
```



More About

- "Multivariate Normal Distribution" on page B-101

References

[1] Drezner, Z. "Computation of the Trivariate Normal Integral." *Mathematics of Computation*. Vol. 63, 1994, pp. 289–294.

[2] Drezner, Z., and G. O. Wesolowsky. "On the Computation of the Bivariate Normal Integral." *Journal of Statistical Computation and Simulation*. Vol. 35, 1989, pp. 101–107.

[3] Genz, A. "Numerical Computation of Rectangular Bivariate and Trivariate Normal and t Probabilities." *Statistics and Computing*. Vol. 14, No. 3, 2004, pp. 251–260.

[4] Genz, A., and F. Bretz. "Numerical Computation of Multivariate t Probabilities with Application to Power Calculation of Multiple Contrasts." *Journal of Statistical Computation and Simulation*. Vol. 63, 1999, pp. 361–378.

[5] Genz, A., and F. Bretz. "Comparison of Methods for the Computation of Multivariate t Probabilities." *Journal of Computational and Graphical Statistics*. Vol. 11, No. 4, 2002, pp. 950–971.

See Also

`mvnpdf` | `mvnrnd`

mvnpdf

Multivariate normal probability density function

Syntax

```
y = mvnpdf(X)
y = mvnpdf(X,MU)
y = mvnpdf(X,MU,SIGMA)
```

Description

`y = mvnpdf(X)` returns the n-by-`1` vector `y`, containing the probability density of the multivariate normal distribution with zero mean and identity covariance matrix, evaluated at each row of the n-by-d matrix `X`. Rows of `X` correspond to observations and columns correspond to variables or coordinates.

`y = mvnpdf(X,MU)` returns the density of the multivariate normal distribution with mean `mu` and identity covariance matrix, evaluated at each row of `X`. `MU` is a `1`-by-d vector, or an n-by-d matrix. If `MU` is a matrix, the density is evaluated for each row of `X` with the corresponding row of `MU`. `MU` can also be a scalar value, which `mvnpdf` replicates to match the size of `X`.

`y = mvnpdf(X,MU,SIGMA)` returns the density of the multivariate normal distribution with mean `MU` and covariance `SIGMA`, evaluated at each row of `X`. `SIGMA` is a d-by-d matrix, or a d-by-d-by-n array, in which case the density is evaluated for each row of `X` with the corresponding page of `SIGMA`, i.e., `mvnpdf` computes `y(i)` using `X(i,:)` and `SIGMA(:,:,i)`. If the covariance matrix is diagonal, containing variances along the diagonal and zero covariances off the diagonal, `SIGMA` may also be specified as a `1`-by-d vector or a 1-by-d-by-n array, containing just the diagonal. Specify `[]` for `MU` to use its default value when you want to specify only `SIGMA`.

If `X` is a 1-by-d vector, `mvnpdf` replicates it to match the leading dimension of `mu` or the trailing dimension of `SIGMA`.

Examples

```
mu = [1 -1];
```

```
SIGMA = [.9 .4; .4 .3];
X = mvnrnd(mu,SIGMA,10);
p = mvnpdf(X,mu,SIGMA);
```

More About

- "Multivariate Normal Distribution" on page B-101

See Also

`mvncdf` | `mvnrnd` | `normpdf`

mvregress

Multivariate linear regression

Syntax

```
beta = mvregress(X,Y)
beta = mvregress(X,Y,Name,Value)
[beta,Sigma] = mvregress( ___ )
[beta,Sigma,E,CovB,logL] = mvregress( ___ )
```

Description

`beta = mvregress(X,Y)` returns the estimated coefficients for a multivariate normal regression of the *d*-dimensional responses in Y on the design matrices in X.

`beta = mvregress(X,Y,Name,Value)` returns the estimated coefficients using additional options specified by one or more name-value pair arguments. For example, you can specify the estimation algorithm, initial estimate values, or maximum number of iterations for the regression.

`[beta,Sigma] = mvregress( ___ )` also returns the estimated *d*-by-*d* variance-covariance matrix of Y, using any of the input arguments from the previous syntaxes.

`[beta,Sigma,E,CovB,logL] = mvregress( ___ )` also returns a matrix of residuals `E`, estimated variance-covariance matrix of the regression coefficients `CovB`, and the value of the log likelihood objective function after the last iteration `logL`.

Examples

Multivariate Regression Model for Panel Data with Different Intercepts

Fit a multivariate regression model to panel data, assuming different intercepts and common slopes.

Load the sample data.

```
load('flu')
```

The dataset array `flu` contains national CDC flu estimates, and nine separate regional estimates based on Google query data.

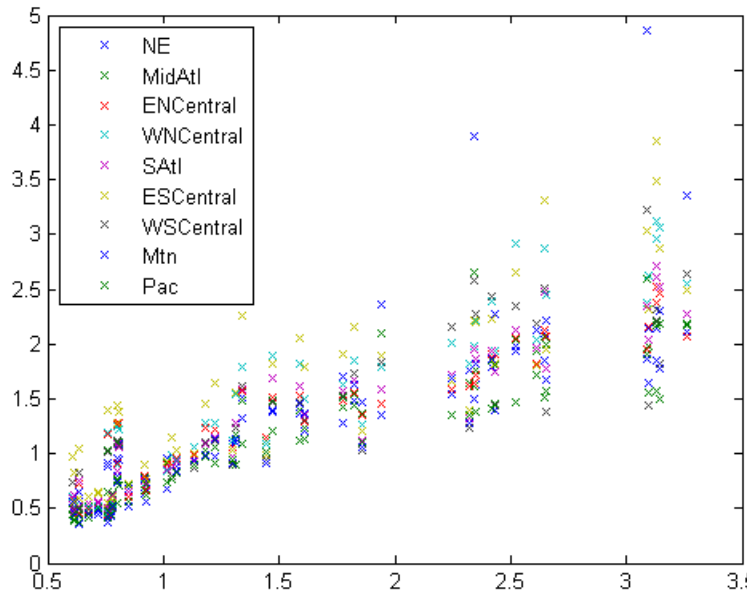
Extract the response and predictor data.

```
Y = double(flu(:,2:end-1));
[n,d] = size(Y);
x = flu.WtdILI;
```

The responses in `Y` are the nine regional flu estimates. Observations exist for every week over a one-year period, so $n = 52$. The dimension of the responses corresponds to the regions, so $d = 9$. The predictors in `x` are the weekly national flu estimates.

Plot the flu data, grouped by region.

```
figure;
regions = flu.Properties.VarNames(2:end-1);
plot(x,Y,'x')
legend(regions,'Location','NorthWest')
```



Fit the multivariate regression model

$$y_{ij} = \alpha_j + \beta x_{ij} + \varepsilon_{ij},\ i = 1,\ldots,n;\ j = 1,\ldots,d,$$

with between-region concurrent correlation

$$COV(\varepsilon_{ij},\varepsilon_{ij'}) = \sigma_{jj'},\ j = 1,\ldots,d.$$

There are $K = 10$ regression coefficients to estimate: nine intercept terms and a common slope. The input argument `X` should be an n-element cell array of d-by-K design matrices.

```
X = cell(n,1);
for i=1:n
  X{i} = [eye(d) repmat(x(i),d,1)];
end
[beta,Sigma] = mvregress(X,Y);
```

`beta` contains estimates of the K-dimensional coefficient vector

$$(\alpha_1,\alpha_2,\ldots,\alpha_9,\beta)'.$$

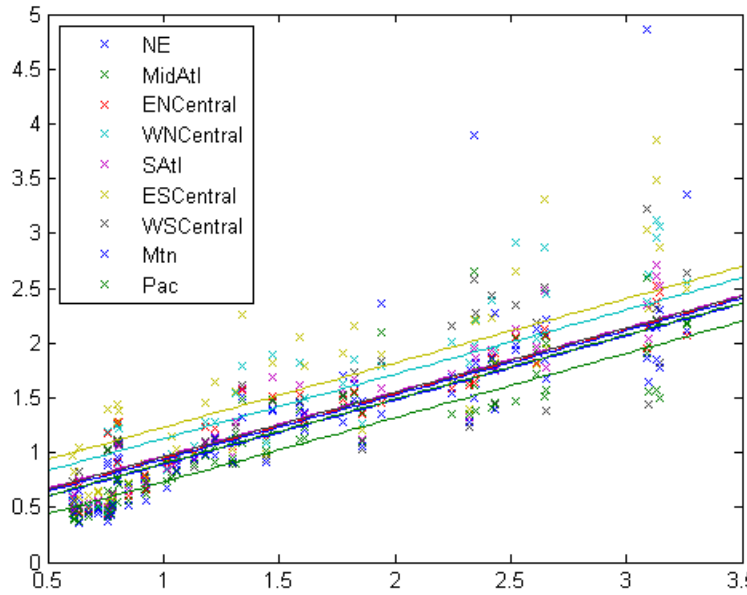
`Sigma` contains estimates of the d-by-d variance-covariance matrix for the between-region concurrent correlations

$$\begin{pmatrix} \sigma_{11} & \cdots & \sigma_{1,9} \\ \vdots & \ddots & \vdots \\ \sigma_{9,1} & \cdots & \sigma_{9,9} \end{pmatrix}.$$

Plot the fitted regression model.

```
B = [beta(1:d)';repmat(beta(end),1,d)];
xx = linspace(.5,3.5)';
fits = [ones(size(xx)),xx]*B;

figure;
h = plot(x,Y,'x',xx,fits,'-');
```

```
for i = 1:d
 set(h(d+i),'color',get(h(i),'color'));
end
legend(regions,'Location','NorthWest');
```



The plot shows that each regression line has a different intercept but the same slope. Upon visual inspection, some regression lines appear to fit the data better than others.

Multivariate Regression for Panel Data with Different Slopes

Fit a multivariate regression model to panel data using least squares, assuming different intercepts and slopes.

Load the sample data.

```
load('flu');
```

The dataset array `flu` contains national CDC flu estimates, and nine separate regional estimates based on Google queries.

Extract the response and predictor data.

```
Y = double(flu(:,2:end-1));
[n,d] = size(Y);
x = flu.WtdILI;
```

The responses in `Y` are the nine regional flu estimates. Observations exist for every week over a one-year period, so $n = 52$. The dimension of the responses corresponds to the regions, so $d = 9$. The predictors in `x` are the weekly national flu estimates.

Fit the multivariate regression model

$$y_{ij} = \alpha_j + \beta_j x_{ij} + \varepsilon_{ij},\ i = 1,\ldots,n;\ j = 1,\ldots,d,$$

with between-region concurrent correlation

$$COV(\varepsilon_{ij},\varepsilon_{ij'}) = \sigma_{jj'},\ j = 1,\ldots,d.$$

There are $K = 18$ regression coefficients to estimate: nine intercept terms, and nine slope terms. `X` is an n-element cell array of d-by-K design matrices.

```
X = cell(n,1);
for i=1:n
  X{i} = [eye(d) x(i)*eye(d)];
end
[beta,Sigma] = mvregress(X,Y,'algorithm','cwls');
```

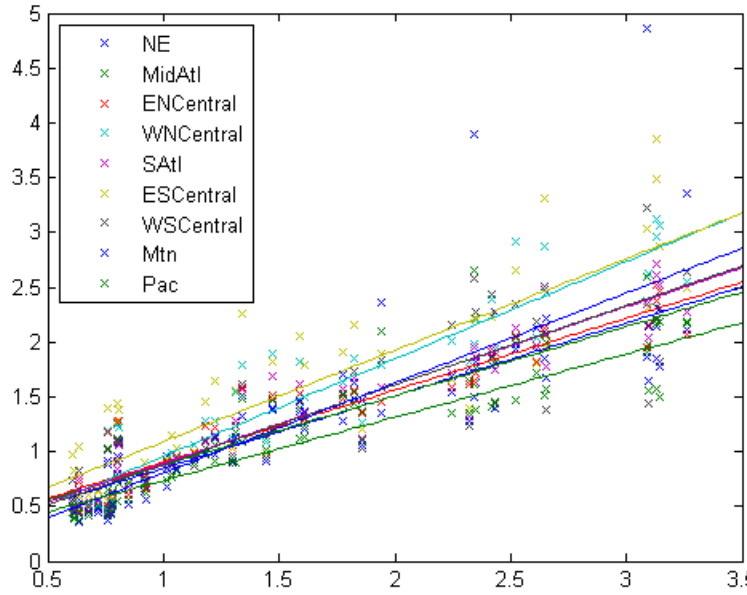
`beta` contains estimates of the K-dimensional coefficient vector,

$$(\alpha_1,\alpha_2,\ldots,\alpha_9,\beta_1,\beta_2,\ldots,\beta_9)'.$$

Plot the fitted regression model.

```
B = [beta(1:d)';beta(d+1:end)'];
xx = linspace(.5,3.5)';
fits = [ones(size(xx)),xx]*B;

figure;
h = plot(x,Y,'x',xx,fits,'-');
for i = 1:d
```

```
 set(h(d+i),'color',get(h(i),'color'));
end

regions = flu.Properties.VarNames(2:end-1);
legend(regions,'Location','NorthWest');
```



The plot shows that each regression line has a different intercept and slope.

Multivariate Regression With a Single Design Matrix

Fit a multivariate regression model using a single n-by-P design matrix for all response dimensions.

Load the sample data.

```
load('flu');
```

The dataset array `flu` contains national CDC flu estimates, and nine separate regional estimates based on Google queries.

Extract the response and predictor data.

```
Y = double(flu(:,2:end-1));
[n,d] = size(Y);
x = flu.WtdILI;
```

The responses in `Y` are the nine regional flu estimates. Observations exist for every week over a one-year period, so $n = 52$. The dimension of the responses corresponds to the regions, so $d = 9$. The predictors in `x` are the weekly national flu estimates.

Create an n-by-P design matrix `X`. Add a column of ones to include a constant term in the regression.

```
X = [ones(size(x)),x];
```

Fit the multivariate regression model

$$y_{ij} = \alpha_j + \beta_j x_{ij} + \varepsilon_{ij},\ i = 1,\ldots,n;\ j = 1,\ldots,d,$$

with between-region concurrent correlation

$$COV(\varepsilon_{ij}, \varepsilon_{ij'}) = \sigma_{jj'},\ j = 1,\ldots,d.$$

There are 18 regression coefficients to estimate: nine intercept terms, and nine slope terms.

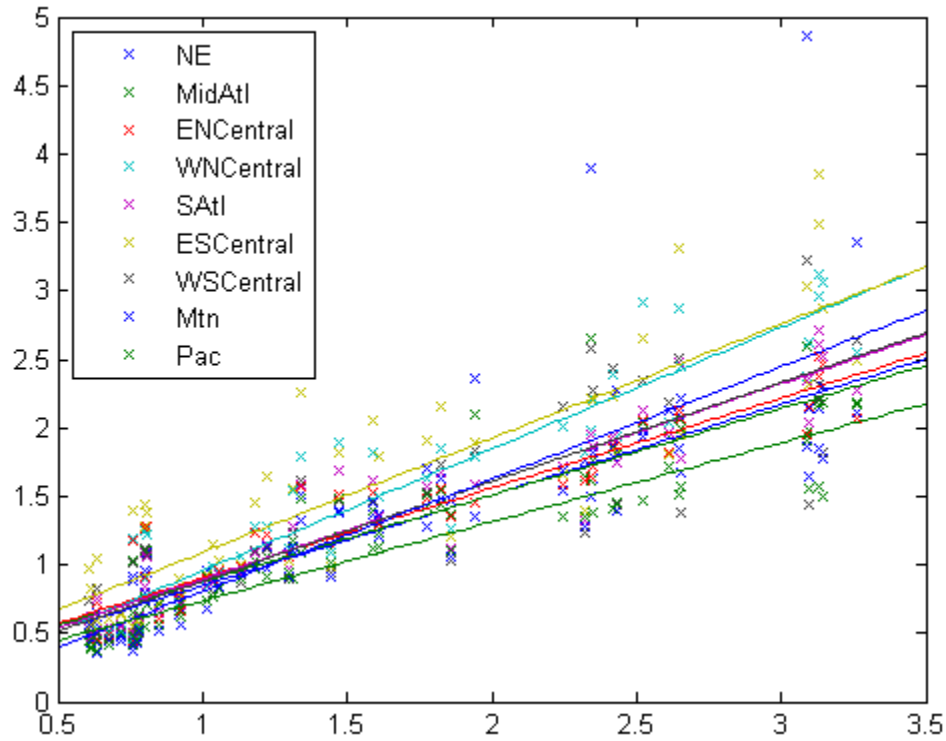
```
[beta,Sigma,E,CovB,logL] = mvregress(X,Y);
```

`beta` contains estimates of the P-by-d coefficient matrix. `Sigma` contains estimates of the d-by-d variance-covariance matrix for the between-region concurrent correlations. `E` is a matrix of the residuals. `CovB` is the estimated variance-covariance matrix of the regression coefficients. `logL` is the value of the log likelihood objective function after the last iteration.

Plot the fitted regression model.

```
B = beta;
xx = linspace(.5,3.5)';
fits = [ones(size(xx)),xx]*B;
```

```
figure;
h = plot(x,Y,'x', xx,fits,'-');
for i = 1:d
    set(h(d+i),'color',get(h(i),'color'));
end

regions = flu.Properties.VarNames(2:end-1);
legend(regions,'Location','NorthWest');
```



The plot shows that each regression line has a different intercept and slope.

- “Set Up Multivariate Regression Problems” on page 13-15
- “Multivariate General Linear Model” on page 13-29

- "Fixed Effects Panel Model with Concurrent Correlation" on page 13-34
- "Longitudinal Analysis" on page 13-42

Input Arguments

`X` — Design matrices

matrix | cell array of matrices

Design matrices for the multivariate regression, specified as a matrix or cell array of matrices. n is the number of observations in the data, K is the number of regression coefficients to estimate, p is the number of predictor variables, and d is the number of dimensions in the response variable matrix Y.

- If $d = 1$, then specify `X` as a single n-by-K design matrix.
- If $d > 1$ and all d dimensions have the same design matrix, then you can specify `X` as a single n-by-p design matrix (not in a cell array).
- If $d > 1$ and all n observations have the same design matrix, then you can specify `X` as a cell array containing a single d-by-K design matrix.
- If $d > 1$ and all n observations do not have the same design matrix, then specify X as a cell array of length n containing d-by-K design matrices.

To include a constant term in the regression model, each design matrix should contain a column of ones.

`mvregress` treats `NaN` values in X as missing values, and ignores rows in X with missing values.

Data Types: `single` | `double` | `cell`

`Y` — Response variables

matrix

Response variables, specified as an n-by-d matrix. n is the number of observations in the data, and d is the number of dimensions in the response. When $d = 1$, `mvregress` treats the values in `Y` like n independent response values.

`mvregress` treats `NaN` values in Y as missing values, and handles them according to the estimation algorithm specified using the name-value pair argument algorithm.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'algorithm','cwls','covar0',C` specifies covariance-weighted least squares estimation using the covariance matrix `C`.

`'algorithm'` — Estimation algorithm

`'mvn' | 'ecm' | 'cwls'`

Estimation algorithm, specified as the comma-separated pair consisting of `'algorithm'` and one of the following.

`'mvn'`	Ordinary multivariate normal maximum likelihood estimation.
`'ecm'`	Maximum likelihood estimation via the ECM algorithm.
`'cwls'`	Covariance-weighted least squares estimation.

The default algorithm depends on the presence of missing data.

- For complete data, the default is `'mvn'`.
- If there are any missing responses (indicated by `NaN`), the default is `'ecm'`, provided the sample size is sufficient to estimate all parameters. Otherwise, the default algorithm is `'cwls'`.

Note: If algorithm has the value `'mvn'`, then `mvregress` removes observations with missing response values before estimation.

Example: `'algorithm','ecm'`

`'beta0'` — Initial estimates for regression coefficients

vector

Initial estimates for the regression coefficients, specified as the comma-separated pair consisting of `'beta0'` and a vector with K elements. The default value is a vector of 0s.

The `beta0` argument is not used if the estimation algorithm is `'mvn'`.

`'covar0'` — Initial estimate for variance-covariance matrix

matrix

Initial estimate for the variance-covariance matrix, Sigma, specified as the comma-separated pair consisting of `'covar0'` and a symmetric, positive definite, d-by-d matrix. The default value is the identity matrix.

If the estimation algorithm is `'cwls'`, then `mvregress` uses `covar0` as the weighting matrix at each iteration, without changing it.

`'covtype'` — Type of variance-covariance matrix

`'full'` (default) | `'diagonal'`

Type of variance-covariance matrix to estimate for Y, specified as the comma-separated pair consisting of `'covtype'` and one of the following.

`'full'`	Estimate all $d(d + 1)/2$ variance-covariance elements.
`'diagonal'`	Estimate only the d diagonal elements of the variance-covariance matrix.

Example: `'covtype','diagonal'`

`'maxiter'` — Maximum number of iterations

100 (default) | positive integer

Maximum number of iterations for the estimation algorithm, specified as the comma-separated pair consisting of `'maxiter'` and a positive integer.

Iterations continue until estimates are within the convergence tolerances tolbeta and tolobj, or the maximum number of iterations specified by maxiter is reached. If both tolbeta and tolobj are 0, then `mvregress` performs `maxiter` iterations with no convergence tests.

Example: `'maxiter',50`

`'outputfcn'` — Function to evaluate each iteration

function handle

Function to evaluate at each iteration, specified as the comma-separated pair consisting of `'outputfcn'` and a function handle. The function must return a logical `true` or `false`. At each iteration, `mvregress` evaluates the function. If the result is `true`, iterations stop. Otherwise, iterations continue. For example, you could specify a function that plots or displays current iteration results, and returns `true` if you close the figure.

The function must accept three input arguments, in this order:

- Vector of current coefficient estimates
- Structure containing these three fields:

`Covar`	Current value of the variance-covariance matrix
`iteration`	Current iteration number
`fval`	Current value of the loglikelihood objective function

- Text string that takes these three values:

`'init'`	When the function is called during initialization
`'iter'`	When the function is called after an iteration
`'done'`	When the function is called after completion

`'tolbeta'` — Convergence tolerance for regression coefficients

`sqrt(eps)` (default) | positive scalar value

Convergence tolerance for regression coefficients, specified as the comma-separated pair consisting of `'tolbeta'` and a positive scalar value.

Let $\mathbf{b}^t$ denote the estimate of the coefficient vector at iteration t, and τ_β be the tolerance specified by `tolbeta`. The convergence criterion for regression coefficient estimation is

$$\left\|\mathbf{b}^t - \mathbf{b}^{t-1}\right\| < \tau_\beta \sqrt{K}\left(1 + \left\|\mathbf{b}^t\right\|\right),$$

where K is the length of $\mathbf{b}^t$ and $\|\mathbf{v}\|$ is the norm of a vector $\mathbf{v}$.

Iterations continue until estimates are within the convergence tolerances tolbeta and tolobj, or the maximum number of iterations specified by maxiter is reached. If

both tolbeta and tolobj are 0, then `mvregress` performs `maxiter` iterations with no convergence tests.

Example: `'tolbeta',1e-5`

`'tolobj'` — Convergence tolerance for loglikelihood objective function

`eps^(3/4)` (default) | positive scalar value

Convergence tolerance for the loglikelihood objective function, specified as the comma-separated pair consisting of `'tolobj'` and a positive scalar value.

Let L^t denote the value of the loglikelihood objective function at iteration t, and τ_ℓ be the tolerance specified by `tolobj`. The convergence criterion for the objective function is

$$\left|L^t - L^{t-1}\right| < \tau_\ell \left(1 + \left|L^t\right|\right).$$

Iterations continue until estimates are within the convergence tolerances tolbeta and tolobj, or the maximum number of iterations specified by maxiter is reached. If both tolbeta and tolobj are 0, then `mvregress` performs `maxiter` iterations with no convergence tests.

Example: `'tolobj',1e-5`

`'varformat'` — Format for parameter estimate variance-covariance matrix

`'beta'` (default) | `'full'`

Format for the parameter estimate variance-covariance matrix, CovB, specified as the comma-separated pair consisting of `'varformat'` and one of the following.

`'beta'`	Return the variance-covariance matrix for only the regression coefficient estimates, beta.
`'full'`	Return the variance-covariance matrix for both the regression coefficient estimates, beta, and the variance-covariance matrix estimate, Sigma.

Example: `'varformat','full'`

`'vartype'` — Type of variance-covariance matrix for parameter estimates

`'hessian'` (default) | `'fisher'`

Type of variance-covariance matrix for parameter estimates, specified as the comma-separated pair consisting of `'vartype'` and either `'hessian'` or `'fisher'`.

- If the value is `'hessian'`, then `mvregress` uses the Hessian, or observed information, matrix to compute CovB.
- If the value is `'fisher'`, then `mvregress` uses the complete-data Fisher, or expected information, matrix to compute CovB.

The `'hessian'` method takes into account the increase uncertainties due to missing data, while the `'fisher'` method does not.

Example: `'vartype','fisher'`

Output Arguments

`beta` — Estimated regression coefficients

column vector | matrix

Estimated regression coefficients, returned as a column vector or matrix.

- If you specify X as a single n-by-K design matrix, then `mvregress` returns beta as a column vector of length K. For example, if X is a 20-by-5 design matrix, then beta is a 5-by-1 column vector.
- If you specify X as a cell array containing one or more d-by-K design matrices, then `mvregress` returns beta as a column vector of length K. For example, if X is a cell array containing 2-by-10 design matrices, then beta is a 10-by-1 column vector.
- If you specify X as a single n-by-p design matrix (not in a cell array), and Y has dimension $d > 1$, then `mvregress` returns beta as a p-by-d matrix. For example, if X is a 20-by-5 design matrix, and Y has two dimensions such that $d = 2$, then beta is a 5-by-2 matrix, and the fitted Y values are X × beta.

`Sigma` — Estimated variance-covariance matrix

square matrix

Estimated variance-covariance matrix for the responses in Y, returned as a d-by-d square matrix.

Note: The estimated variance-covariance matrix, `Sigma`, is not the sample covariance matrix of the residual matrix, E.

`E` — Residuals

matrix

Residuals for the fitted regression model, returned as an n-by-d matrix.

If algorithm has the value `'ecm'` or `'cwls'`, then `mvregress` computes the residual values corresponding to missing values in Y as the difference between the conditionally imputed values and the fitted values.

Note: If algorithm has the value `'mvn'`, then `mvregress` removes observations with missing response values before estimation.

`CovB` — Parameter estimate variance-covariance matrix

square matrix

Parameter estimate variance-covariance matrix, returned as a square matrix.

- If varformat has the value `'beta'` (default), then `CovB` is the estimated variance-covariance matrix of the coefficient estimates in beta.
- If varformat has the value `'full'`, then `CovB` is the estimated variance-covariance matrix of the combined estimates in beta and Sigma.

`logL` — Loglikelihood objective function value

scalar value

Loglikelihood objective function value after the last iteration, returned as a scalar value.

More About

Multivariate Normal Regression

Multivariate normal regression is the regression of a d-dimensional response on a design matrix of predictor variables, with normally distributed errors. The errors can be heteroscedastic and correlated.

The model is

$$\mathbf{y}_i = \mathbf{X}_i\beta + \mathbf{e}_i, \quad i = 1,\ldots,n,$$

where

- $\mathbf{y}_i$ is a d-dimensional vector of responses.
- $\mathbf{X}_i$ is a design matrix of predictor variables.
- β is vector or matrix of regression coefficients.
- $\mathbf{e}_i$ is a d-dimensional vector of error terms, with multivariate normal distribution

  $$\mathbf{e}_i \sim MVN_d(\mathbf{0}, \Sigma).$$

Conditionally Imputed Values

The expectation/conditional maximization (`'ecm'`) and covariance-weighted least squares (`'cwls'`) estimation algorithms include imputation of missing response values.

Let $\tilde{\mathbf{y}}$ denote missing observations. The conditionally imputed values are the expected value of the missing observation given the observed data, $\mathrm{E}(\tilde{\mathbf{y}} \mid \mathbf{y})$.

The joint distribution of the missing and observed responses is a multivariate normal distribution,

$$\begin{pmatrix} \tilde{\mathbf{y}} \\ \mathbf{y} \end{pmatrix} \sim MVN\left\{ \begin{pmatrix} \tilde{\mathbf{X}}\beta \\ \mathbf{X}\beta \end{pmatrix}, \begin{pmatrix} \Sigma_{\tilde{y}} & \Sigma_{\tilde{y}y} \\ \Sigma_{y\tilde{y}} & \Sigma_{y} \end{pmatrix} \right\}.$$

Using properties of the multivariate normal distribution, the imputed conditional expectation is given by

$$\mathrm{E}(\tilde{\mathbf{y}} \mid \mathbf{y}) = \tilde{\mathbf{X}}\beta + \Sigma_{\tilde{y}y}\Sigma_{y}^{-1}(\mathbf{y} - \mathbf{X}\beta).$$

Note: `mvregress` only imputes missing response values. Observations with missing values in the design matrix are removed.

- "Multivariate Linear Regression" on page 13-3
- "Estimation of Multivariate Regression Models" on page 13-6

References

[1] Little, Roderick J. A., and Donald B. Rubin. *Statistical Analysis with Missing Data*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 2002.

[2] Meng, Xiao-Li, and Donald B. Rubin. "Maximum Likelihood Estimation via the ECM Algorithm." *Biometrika*. Vol. 80, No. 2, 1993, pp. 267–278.

[3] Sexton, Joe, and A. R. Swensen. "ECM Algorithms that Converge at the Rate of EM." *Biometrika*. Vol. 87, No. 3, 2000, pp. 651–662.

[4] Dempster, A. P., N. M. Laird, and D. B. Rubin. "Maximum Likelihood from Incomplete Data via the EM Algorithm." *Journal of the Royal Statistical Society*. Series B, Vol. 39, No. 1, 1977, pp. 1–37.

See Also

`manova1` | `mvregresslike`

mvregresslike

Negative log-likelihood for multivariate regression

Syntax

```
nlogL = mvregresslike(X,Y,b,SIGMA,alg)
[nlogL,COVB] = mvregresslike(...)
[nlogL,COVB] = mvregresslike(...,type,format)
```

Description

`nlogL = mvregresslike(X,Y,b,SIGMA,alg)` computes the negative log-likelihood `nlogL` for a multivariate regression of the d-dimensional multivariate observations in the n-by-d matrix `Y` on the predictor variables in the matrix or cell array `X`, evaluated for the p-by-1 column vector `b` of coefficient estimates and the d-by-d matrix `SIGMA` specifying the covariance of a row of `Y`. If $d = 1$, `X` can be an n-by-p design matrix of predictor variables. For any value of d, `X` can also be a cell array of length n, with each cell containing a d-by-p design matrix for one multivariate observation. If all observations have the same d-by-p design matrix, `X` can be a single cell.

`NaN` values in `X` or `Y` are taken as missing. Observations with missing values in `X` are ignored. Treatment of missing values in `Y` depends on the algorithm specified by *`alg`*.

`alg` should match the algorithm used by `mvregress` to obtain the coefficient estimates `b`, and must be one of the following:

- `'ecm'` — ECM algorithm
- `'cwls'` — Least squares conditionally weighted by `SIGMA`
- `'mvn'` — Multivariate normal estimates computed after omitting rows with any missing values in `Y`

`[nlogL,COVB] = mvregresslike(...)` also returns an estimated covariance matrix `COVB` of the parameter estimates `b`.

`[nlogL,COVB] = mvregresslike(...,type,format)` specifies the type and format of `COVB`.

type is either:

- `'hessian'` — To use the Hessian or observed information. This method takes into account the increased uncertainties due to missing data. This is the default.
- `'fisher'` — To use the Fisher or expected information. This method uses the complete data expected information, and does not include uncertainty due to missing data.

format is either:

- `'beta'` — To compute `COVB` for `b` only. This is the default.
- `'full'` — To compute `COVB` for both `b` and `SIGMA`.

More About

- "Multivariate Normal Distribution" on page B-101

See Also

`mvregress` | `manova1`

mvnrnd

Multivariate normal random numbers

Syntax

```
R = mvnrnd(MU,SIGMA)
r = mvnrnd(MU,SIGMA,cases)
```

Description

`R = mvnrnd(MU,SIGMA)` returns an n-by-d matrix `R` of random vectors chosen from the multivariate normal distribution with mean `MU`, and covariance `SIGMA`. `MU` is a vector or n-by-d matrix, and `mvnrnd` generates each row of `R` using the corresponding row of `mu`. `SIGMA` is a d-by-d symmetric positive semi-definite matrix, or a d-by-d-by-n array. If `SIGMA` is an array, `mvnrnd` generates each row of `R` using the corresponding page of `SIGMA`, i.e., `mvnrnd` computes `R(i,:)` using `MU(i,:)` and `SIGMA(:,:,i)`. If the covariance matrix is diagonal, containing variances along the diagonal and zero covariances off the diagonal, `SIGMA` may also be specified as a `1`-by-d vector or a 1-by-d-by-n array, containing just the diagonal. If `MU` is a `1`-by-d vector, `mvnrnd` replicates it to match the trailing dimension of `SIGMA`.

`r = mvnrnd(MU,SIGMA,cases)` returns a `cases`-by-d matrix `R` of random vectors chosen from the multivariate normal distribution with a common `1`-by-`d` mean vector `MU`, and a common `d`-by-`d` covariance matrix `SIGMA`.

Examples

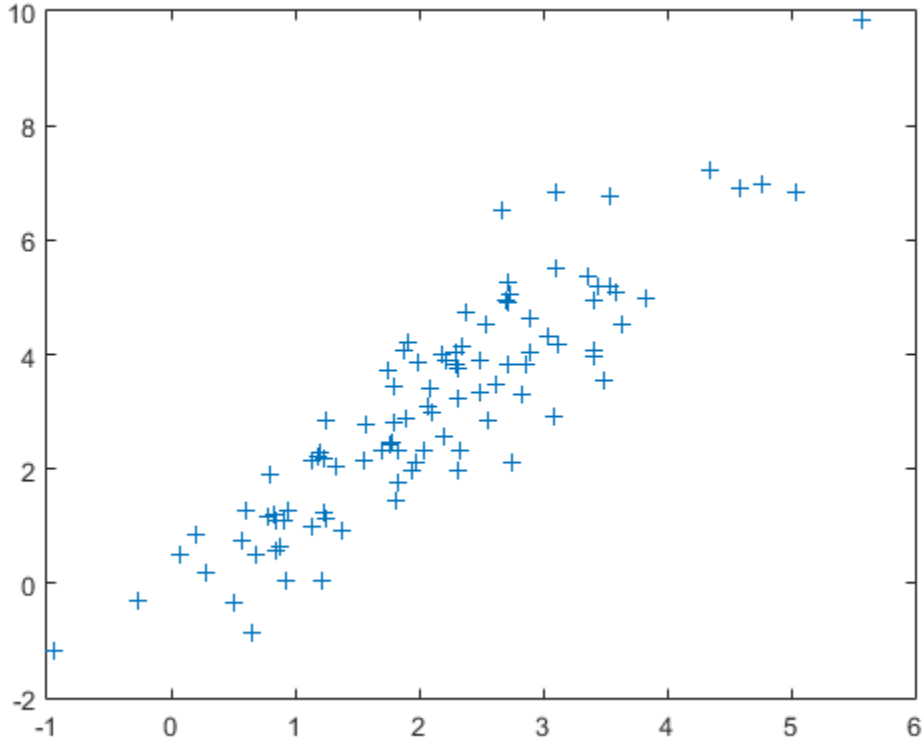
Generate Multivariate Normal Random Numbers

Generate random numbers from a multivariate normal distribution with parameters `mu = [2,3]` and `sigma = [1,1.5;1.5,3]`.

```
mu = [2,3];
sigma = [1,1.5;1.5,3];
rng default  % For reproducibility
r = mvnrnd(mu,sigma,100);
```

Plot the random numbers.

```
figure
plot(r(:,1),r(:,2),'+')
```



More About

- "Multivariate Normal Distribution" on page B-101

See Also

`mvnpdf` | `mvncdf` | `normrnd`

mvtcdf

Multivariate *t* cumulative distribution function

Syntax

```
y = mvtcdf(X,C,DF)
y = mvtcdf(xl,xu,C,DF)
[y,err] = mvtcdf(...)
[...] = mvntdf(...,options)
```

Description

`y = mvtcdf(X,C,DF)` returns the cumulative probability of the multivariate *t* distribution with correlation parameters `C` and degrees of freedom `DF`, evaluated at each row of `X`. Rows of the *n*-by-*d* matrix `X` correspond to observations or points, and columns correspond to variables or coordinates. `y` is an `n`-by-`1` vector.

`C` is a symmetric, positive definite, *d*-by-*d* matrix, typically a correlation matrix. If its diagonal elements are not 1, `mvtcdf` scales `C` to correlation form. `mvtcdf` does not rescale `X`. `DF` is a scalar, or a vector with *n* elements.

The multivariate *t* cumulative probability at `X` is defined as the probability that a random vector `T`, distributed as multivariate *t*, will fall within the semi-infinite rectangle with upper limits defined by `X`, i.e., $\Pr\{T(1) \le X(1), T(2) \le X(2), \ldots T(d) \le X(d)\}$.

`y = mvtcdf(xl,xu,C,DF)` returns the multivariate *t* cumulative probability evaluated over the rectangle with lower and upper limits defined by `xl` and `xu`, respectively.

`[y,err] = mvtcdf(...)` returns an estimate of the error in `y`. For bivariate and trivariate distributions, `mvtcdf` uses adaptive quadrature on a transformation of the *t* density, based on methods developed by Genz, as described in the references. The default absolute error tolerance for these cases is `1e-8`. For four or more dimensions, `mvtcdf` uses a quasi-Monte Carlo integration algorithm based on methods developed by Genz and Bretz, as described in the references. The default absolute error tolerance for these cases is `1e-4`.

`[...] = mvntdf(...,options)` specifies control parameters for the numerical integration used to compute `y`. This argument can be created by a call to `statset`. Choices of `statset` parameters are:

- `'TolFun'` — Maximum absolute error tolerance. Default is `1e-8` when $d < 4$, or `1e-4` when $d \geq 4$.
- `'MaxFunEvals'` — Maximum number of integrand evaluations allowed when $d \geq 4$. Default is `1e7`. `'MaxFunEvals'` is ignored when $d < 4$.
- `'Display'` — Level of display output. Choices are `'off'` (the default), `'iter'`, and `'final'`. `'Display'` is ignored when $d < 4$.

Examples

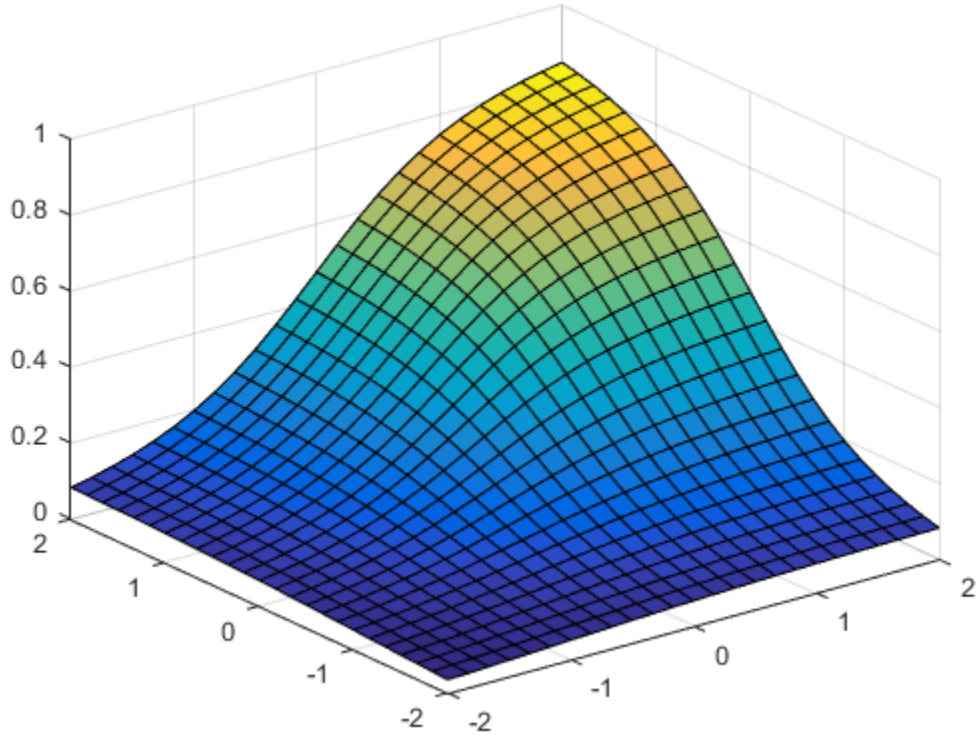
Compute the Multivariate *t* Distribution cdf

Compute the cdf of a multivariate t distribution with correlation parameters `C = [1 .4; .4 1]` and 2 degrees of freedom.

```
C = [1 .4; .4 1];
df = 2;
[X1,X2] = meshgrid(linspace(-2,2,25)',linspace(-2,2,25)');
X = [X1(:) X2(:)];
p = mvtcdf(X,C,df);
```

Plot the cdf.

```
figure;
surf(X1,X2,reshape(p,25,25));
```



More About

- "Multivariate *t* Distribution" on page B-107

References

[1] Genz, A. "Numerical Computation of Rectangular Bivariate and Trivariate Normal and t Probabilities." *Statistics and Computing*. Vol. 14, No. 3, 2004, pp. 251–260.

[2] Genz, A., and F. Bretz. "Numerical Computation of Multivariate t Probabilities with Application to Power Calculation of Multiple Contrasts." *Journal of Statistical Computation and Simulation*. Vol. 63, 1999, pp. 361–378.

[3] Genz, A., and F. Bretz. "Comparison of Methods for the Computation of Multivariate t Probabilities." *Journal of Computational and Graphical Statistics*. Vol. 11, No. 4, 2002, pp. 950–971.

See Also

`mvtpdf` | `mvtrnd`

mvtpdf

Multivariate *t* probability density function

Syntax

```
y = mvtpdf(X,C,df)
```

Description

`y = mvtpdf(X,C,df)` returns the probability density of the multivariate *t* distribution with correlation parameters `C` and degrees of freedom `df`, evaluated at each row of `X`. Rows of the *n*-by-*d* matrix `X` correspond to observations or points, and columns correspond to variables or coordinates. `C` is a symmetric, positive definite, *d*-by-*d* matrix, typically a correlation matrix. If its diagonal elements are not 1, `mvtpdf` scales `C` to correlation form. `mvtcdf` does not rescale `X`. `df` is a scalar, or a vector with *n* elements. `y` is an *n*-by-1 vector.

Examples

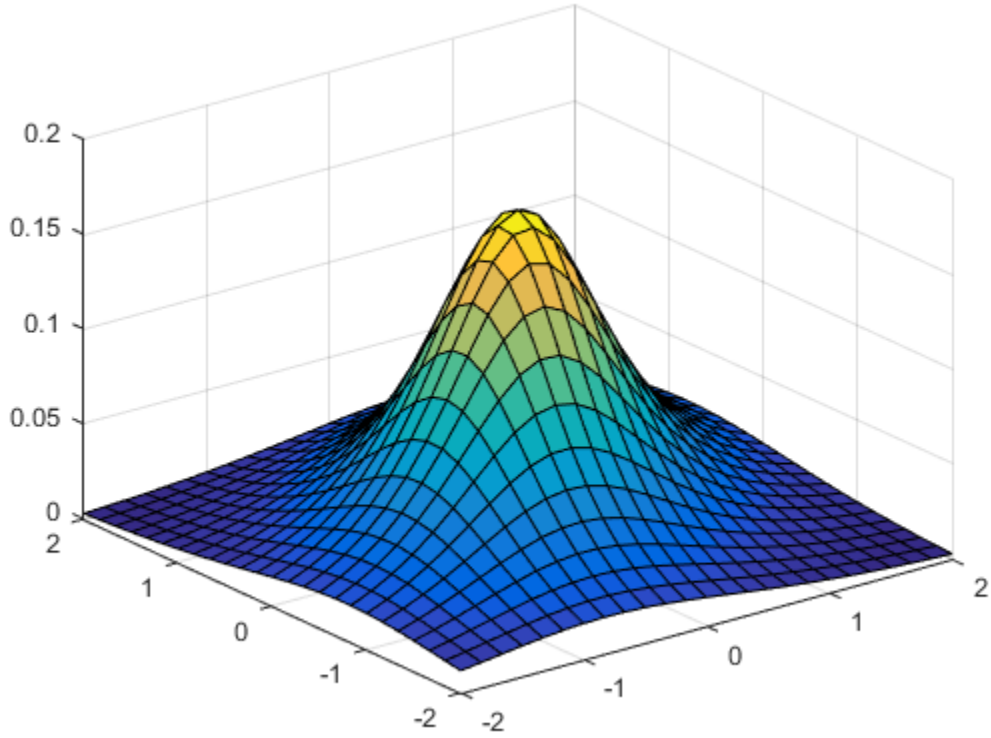
Compute the Multivariate *t* Distribution pdf

Compute the pdf of a multivariate *t* distribution with correlation parameters `C = [1 .4; .4 1]` and 2 degrees of freedom.

```
[X1,X2] = meshgrid(linspace(-2,2,25)',linspace(-2,2,25)');
X = [X1(:) X2(:)];
C = [1 .4; .4 1];
df = 2;
p = mvtpdf(X,C,df);
```

Plot the pdf.

```
figure;
surf(X1,X2,reshape(p,25,25))
```



More About

- "Multivariate *t* Distribution" on page B-107

See Also

`mvtcdf` | `mvtrnd`

mvtrnd

Multivariate *t* random numbers

Syntax

```
R = mvtrnd(C,df,cases)
R = mvtrnd(C,df)
```

Description

`R = mvtrnd(C,df,cases)` returns a matrix of random numbers chosen from the multivariate *t* distribution, where `C` is a correlation matrix. `df` is the degrees of freedom and is either a scalar or is a vector with `cases` elements. If `p` is the number of columns in `C`, then the output `R` has `cases` rows and `p` columns.

Let `t` represent a row of `R`. Then the distribution of `t` is that of a vector having a multivariate normal distribution with mean 0, variance 1, and covariance matrix `C`, divided by an independent chi-square random value having `df` degrees of freedom. The rows of `R` are independent.

`C` must be a square, symmetric and positive definite matrix. If its diagonal elements are not all 1 (that is, if `C` is a covariance matrix rather than a correlation matrix), `mvtrnd` rescales `C` to transform it to a correlation matrix before generating the random numbers.

`R = mvtrnd(C,df)` returns a single random number from the multivariate *t* distribution.

Examples

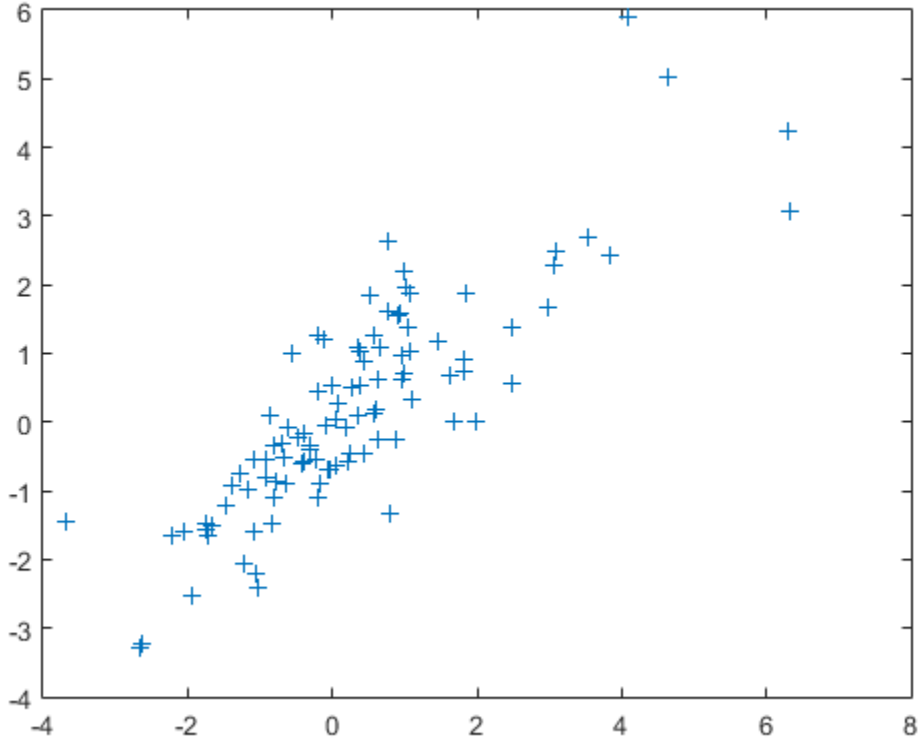
Generate Multivariate *t* Distribution Random Numbers

Generate random numbers from a multivariate *t* distribution with correlation parameters `SIGMA = [1 0.8;0.8 1]` and 3 degrees of freedom.

```
rng default;  % For reproducibility
SIGMA = [1 0.8;0.8 1];
R = mvtrnd(SIGMA,3,100);
```

Plot the random numbers.

```
figure;
plot(R(:,1),R(:,2),'+')
```



More About

- "Multivariate *t* Distribution" on page B-107

See Also

`mvtpdf` | `mvtcdf`

NumObservations property

Class: cvpartition

Number of observations (including observations with missing `group` values)

Description

Number of observations (including observations with missing `group` values).

NaiveBayes class

Naive Bayes classifier

Description

A `NaiveBayes` object defines a Naive Bayes classifier. A Naive Bayes classifier assigns a new observation to the most probable class, assuming the features are conditionally independent given the class value.

Construction

.NaiveBayes	Create NaiveBayes object

Methods

disp	Display `NaiveBayes` classifier object
display	Display `NaiveBayes` classifier object
fit	Create Naive Bayes classifier object by fitting training data
posterior	Compute posterior probability of each class for test data
predict	Predict class label for test data
subsasgn	Subscripted reference for `NaiveBayes` object

subsref	Subscripted reference for `NaiveBayes` object

Properties

CIsNonEmpty	Flag for non-empty classes
ClassLevels	Class levels
Prior	Class priors
Dist	Distribution names
NClasses	Number of classes
NDims	Number of dimensions
Params	Parameter estimates

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

Examples

Predict the class label using the Naive Bayes classifier:

```
load fisheriris
```

Use the default Gaussian distribution and a confusion matrix:

```
O1 = fitNaiveBayes(meas,species);
```

```
C1 = O1.predict(meas);
cMat1 = confusionmat(species,C1)
```
This returns:

```
cMat1 =

    50     0     0
     0    47     3
     0     3    47
```
Use the Gaussian distribution for features 1 and 3 and use the kernel density estimation for features 2 and 4:

```
O2 = fitNaiveBayes(meas,species,'dist',...
{'normal','kernel','normal','kernel'});
C2 = O2.predict(meas);
cMat2 = confusionmat(species,C2)
```
This returns:

```
cMat2 =

    50     0     0
     0    47     3
     0     3    47
```

References

[1] Mitchell, T. (1997) Machine Learning, McGraw Hill.

[2] Vangelis M., Ion A., and Geogios P. Spam Filtering with Naive Bayes - Which Naive Bayes? (2006) Third Conference on Email and Anti-Spam.

[3] George H. John and Pat Langley. Estimating continuous distributions in bayesian classifiers (1995) the Eleventh Conference on Uncertainty in Artificial Intelligence.

How To

- “Naive Bayes Classification” on page 15-31
- “Grouping Variables” on page 2-52

NaiveBayes

Class: NaiveBayes

Create NaiveBayes object

Description

You cannot create a `NaiveBayes` classifier by calling the constructor. Use `fitNaiveBayes` to create a `NaiveBayes` classifier by fitting the object to training data.

See Also

`fitNaiveBayes`

prob.NakagamiDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Nakagami probability distribution object

Description

`prob.NakagamiDistribution` is an object consisting of parameters, a model description, and sample data for a Nakagami probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Nakagami')` creates a Nakagami probability distribution object using the default parameter values.

`pd = makedist('Nakagami','mu',mu,'omega',omega)` creates a Nakagami probability distribution object using the specified parameter values.

Input Arguments

`mu` — Shape parameter

1 (default) | positive scalar value

Shape parameter for the Nakagami distribution, specified as a positive scalar value.

Data Types: `single` | `double`

`omega` — Scale parameter

1 (default) | positive scalar value

Scale parameter for the Nakagami distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

`mu` — Shape parameter

positive scalar value

Shape parameter for the Nakagami distribution, stored as a positive scalar value.

Data Types: `single | double`

`omega` — Scale parameter

positive scalar value

Scale parameter for the Nakagami distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Nakagami Distribution

The Nakagami distribution is commonly used in communication theory to model scattered signals that reach a receiver using multiple paths.

The Nakagami distribution uses the following parameters.

Parameter	Description	Support
`mu`	Shape parameter	$\mu > 0$
`omega`	Scale parameter	$\omega > 0$

The probability density function (pdf) is

$$f(x \mid \mu,\omega) = 2\left(\frac{\mu^{\mu}}{\omega}\right)\frac{1}{\Gamma(\mu)}x^{(2\mu-1)}\exp\left\{\frac{-\mu}{\omega}x^{2}\right\} \quad ; \quad x > 0\,,$$

where $\Gamma(\cdot)$ is the Gamma function.

Examples

Create a Nakagami Distribution Object Using Default Parameters

Create a Nakagami distribution object using the default parameter values.

```
pd = makedist('Nakagami')
```

```
pd =

  NakagamiDistribution

  Nakagami distribution
       mu = 1
    omega = 1
```

Create a Nakagami Distribution Object Using Specified Parameters

Create a Nakagami distribution object by specifying parameter values.

```
pd = makedist('Nakagami','mu',5,'omega',2)
```

```
pd =

  NakagamiDistribution

  Nakagami distribution
       mu = 5
    omega = 2
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =
```

```
1.3794
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Nakagami Distribution"
- Class Attributes
- Property Attributes

nancov

Covariance ignoring NaN values

Syntax

```
Y = nancov(X)
Y = nancov(X1,X2)
Y = nancov(...,1)
Y = nancov(...,'pairwise')
```

Description

`Y = nancov(X)` is the covariance `cov` of `X`, computed after removing observations with `NaN` values.

For vectors `x`, `nancov(x)` is the sample variance of the remaining elements, once `NaN` values are removed. For matrices `X`, `nancov(X)` is the sample covariance of the remaining observations, once observations (rows) containing any `NaN` values are removed.

`Y = nancov(X1,X2)`, where `X1` and `X2` are matrices with the same number of elements, is equivalent to `nancov(X)`, where `X = [X1(:) X2(:)]`.

`nancov` removes the mean from each variable (column for matrix `X`) before calculating `Y`. If n is the number of remaining observations after removing observations with `NaN` values, `nancov` normalizes `Y` by either $n - 1$ or n , depending on whether $n > 1$ or $n = 1$, respectively. To specify normalization by n, use `Y = nancov(...,1)`.

`Y = nancov(...,'pairwise')` computes `Y(i,j)` using rows with no `NaN` values in columns `i` or `j`. The result `Y` may not be a positive definite matrix.

Examples

Generate random data for two variables (columns) with random missing values:

```
X = rand(10,2);
```

```
p = randperm(numel(X));
X(p(1:5)) = NaN
X =
    0.8147    0.1576
       NaN       NaN
    0.1270    0.9572
    0.9134       NaN
    0.6324       NaN
    0.0975    0.1419
    0.2785    0.4218
    0.5469    0.9157
    0.9575    0.7922
    0.9649       NaN
```

Establish a correlation between a third variable and the other two variables:

```
X(:,3) = sum(X,2)
X =
    0.8147    0.1576    0.9723
       NaN       NaN       NaN
    0.1270    0.9572    1.0842
    0.9134       NaN       NaN
    0.6324       NaN       NaN
    0.0975    0.1419    0.2394
    0.2785    0.4218    0.7003
    0.5469    0.9157    1.4626
    0.9575    0.7922    1.7497
    0.9649       NaN       NaN
```

Compute the covariance matrix for the three variables after removing observations (rows) with `NaN` values:

```
Y = nancov(X)
Y =
    0.1311    0.0096    0.1407
    0.0096    0.1388    0.1483
    0.1407    0.1483    0.2890
```

See Also

`NaN` | `cov` | `var` | `nanvar`

nanmax

Maximum ignoring NaN values

Syntax

```
y = nanmax(X)
Y = nanmax(X1,X2)
y = nanmax(X,[],dim)
[y,indices] = nanmax(...)
```

Description

`y = nanmax(X)` is the maximum `max` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmax(x)` is the maximum of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmax(X)` is a row vector of column maxima, once `NaN` values are removed. For multidimensional arrays `X`, `nanmax` operates along the first nonsingleton dimension.

`Y = nanmax(X1,X2)` returns an array `Y` the same size as `X1` and `X2` with `Y(i,j) = nanmax(X1(i,j),X2(i,j))`. Scalar inputs are expanded to an array of the same size as the other input.

`y = nanmax(X,[],dim)` operates along the dimension `dim` of `X`.

`[y,indices] = nanmax(...)` also returns the row indices of the maximum values for each column in the vector `indices`.

Examples

Find column maxima and their indices for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
```

```
     3     5   NaN
     4   NaN   NaN
[y,indices] = nanmax(X)
y =
     4     5   NaN
indices =
     3     2     1
```

See Also

NaN | max | nanmin

nanmean

Mean ignoring NaN values

Syntax

```
y = nanmean(X)
y = nanmean(X,dim)
```

Description

`y = nanmean(X)` is the `mean` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmean(x)` is the mean of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmean(X)` is a row vector of column means, once `NaN` values are removed. For multidimensional arrays `X`, `nanmean` operates along the first nonsingleton dimension.

`y = nanmean(X,dim)` takes the mean along dimension `dim` of `X`.

Note: If `X` contains a vector of all `NaN` values along some dimension, the vector is empty once the `NaN` values are removed, so the sum of the remaining elements is `0`. Since the mean involves division by `0`, its value is `NaN`. The output `NaN` is not a mean of `NaN` values.

Examples

Find column means for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nanmean(X)
y =
```

```
   3.5000   3.0000   NaN
```

See Also

NaN | mean | nanmedian

nanmedian

Median ignoring NaN values

Syntax

```
y = nanmedian(X)
y = nanmedian(X,dim)
```

Description

`y = nanmedian(X)` is the `median` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmedian(x)` is the median of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmedian(X)` is a row vector of column medians, once `NaN` values are removed. For multidimensional arrays `X`, `nanmedian` operates along the first nonsingleton dimension.

`y = nanmedian(X,dim)` takes the mean along dimension `dim` of `X`.

Examples

Find column medians for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nanmedian(X)
y =
   3.5000  3.0000  NaN
```

See Also

`NaN` | `median` | `nanmean`

nanmin

Minimum ignoring NaN values

Syntax

```
y = nanmin(X)
Y = nanmin(X1,X2)
y = nanmin(X,[],dim)
[y,indices] = nanmin(...)
```

Description

`y = nanmin(X)` is the minimum `min` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanmin(x)` is the minimum of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanmin(X)` is a row vector of column minima, once `NaN` values are removed. For multidimensional arrays `X`, `nanmin` operates along the first nonsingleton dimension.

`Y = nanmin(X1,X2)` returns an array `Y` the same size as `X1` and `X2` with `Y(i,j) = nanmin(X1(i,j),X2(i,j))`. Scalar inputs are expanded to an array of the same size as the other input.

`y = nanmin(X,[],dim)` operates along the dimension `dim` of `X`.

`[y,indices] = nanmin(...)` also returns the row indices of the minimum values for each column in the vector `indices`.

Examples

Find column minima and their indices for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
```

```
     3     5   NaN
     4   NaN   NaN
[y,indices] = nanmin(X)
y =
     3     1   NaN
indices =
     2     1     1
```

See Also

NaN | min | nanmax

nanstd

Standard deviation ignoring NaN values

Syntax

```
y = nanstd(X)
y = nanstd(X,1)
y = nanstd(X,flag,dim)
```

Description

`y = nanstd(X)` is the standard deviation `std` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanstd(x)` is the sample standard deviation of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanstd(X)` is a row vector of column sample standard deviations, once `NaN` values are removed. For multidimensional arrays `X`, `nanstd` operates along the first nonsingleton dimension.

If n is the number of remaining observations after removing observations with `NaN` values, `nanstd` normalizes `y` by $n–1$. To specify normalization by n, use `y = nanstd(X,1)`.

`y = nanstd(X,flag,dim)` takes the standard deviation along the dimension `dim` of `X`. The `flag` is `0` or `1` to specify normalization by $n - 1$ or n, respectively, where n is the number of remaining observations after removing observations with `NaN` values.

Examples

Find column standard deviations for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
```

```
     4   NaN   NaN
y = nanstd(X)
y =
   0.7071  2.8284  NaN
```

See Also

NaN | std | nanvar | nanmean

nansum

Sum ignoring NaN values

Syntax

```
y = nansum(X)
y = nansum(X,dim)
```

Description

`y = nansum(X)` is the `sum` of `X`, computed after removing `NaN` values.

For vectors `x`, `nansum(x)` is the sum of the remaining elements, once `NaN` values are removed. For matrices `X`, `nansum(X)` is a row vector of column sums, once `NaN` values are removed. For multidimensional arrays `X`, `nansum` operates along the first nonsingleton dimension.

`y = nansum(X,dim)` takes the sum along dimension `dim` of `X`.

Note: If `X` contains a vector of all `NaN` values along some dimension, the vector is empty once the `NaN` values are removed, so the sum of the remaining elements is `0`. The output `0` is not a sum of `NaN` values.

Examples

Find column sums for data with missing values:

```
X = magic(3);
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nansum(X)
y =
```

```
     7     6     0
```

See Also

`NaN` | `sum`

nanvar

Variance, ignoring NaN values

Syntax

```
y = nanvar(X)
y = nanvar(X,1)
y = nanvar(X,w)
y = nanvar(X,w,dim)
```

Description

`y = nanvar(X)` is the variance `var` of `X`, computed after removing `NaN` values.

For vectors `x`, `nanvar(x)` is the sample variance of the remaining elements, once `NaN` values are removed. For matrices `X`, `nanvar(X)` is a row vector of column sample variances, once `NaN` values are removed. For multidimensional arrays `X`, `nanvar` operates along the first nonsingleton dimension.

`nancov` removes the mean from each variable (column for matrix `X`) before calculating `Y`. If n is the number of remaining observations after removing observations with `NaN` values, `nanvar` normalizes `y` by either $n - 1$ or n , depending on whether $n > 1$ or $n = 1$, respectively. To specify normalization by n, use `y = nanvar(X,1)`.

`y = nanvar(X,w)` computes the variance using the weight vector `w`. The length of `w` must equal the length of the dimension over which `nanvar` operates, and its elements must be nonnegative. Elements of `X` corresponding to `NaN` values of `w` are ignored.

`y = nanvar(X,w,dim)` takes the variance along the dimension `dim` of `X`. Set `w` to `[]` to use the default normalization by $n - 1$.

Examples

Find column standard deviations for data with missing values:

```
X = magic(3);
```

```
X([1 6:9]) = repmat(NaN,1,5)
X =
   NaN     1   NaN
     3     5   NaN
     4   NaN   NaN
y = nanvar(X)
y =
   0.5000  8.0000  NaN
```

See Also

NaN | var | nanstd | nanmean

nbincdf

Negative binomial cumulative distribution function

Syntax

```
y = nbincdf(x,R,p)
y = nbincdf(x,R,p,'upper')
```

Description

`y = nbincdf(x,R,p)` computes the negative binomial cdf at each of the values in `x` using the corresponding number of successes, `R` and probability of success in a single trial, `p`. `x`, `R`, and `p` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `y`. A scalar input for `x`, `R`, or `p` is expanded to a constant array with the same dimensions as the other inputs.

`y = nbincdf(x,R,p,'upper')` returns the complement of the negative binomial cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The negative binomial cdf is

$$y = F(x \mid r, p) = \sum_{i=0}^{x} \binom{r+i-1}{i} p^r q^i I_{(0,1,\ldots)}(i)$$

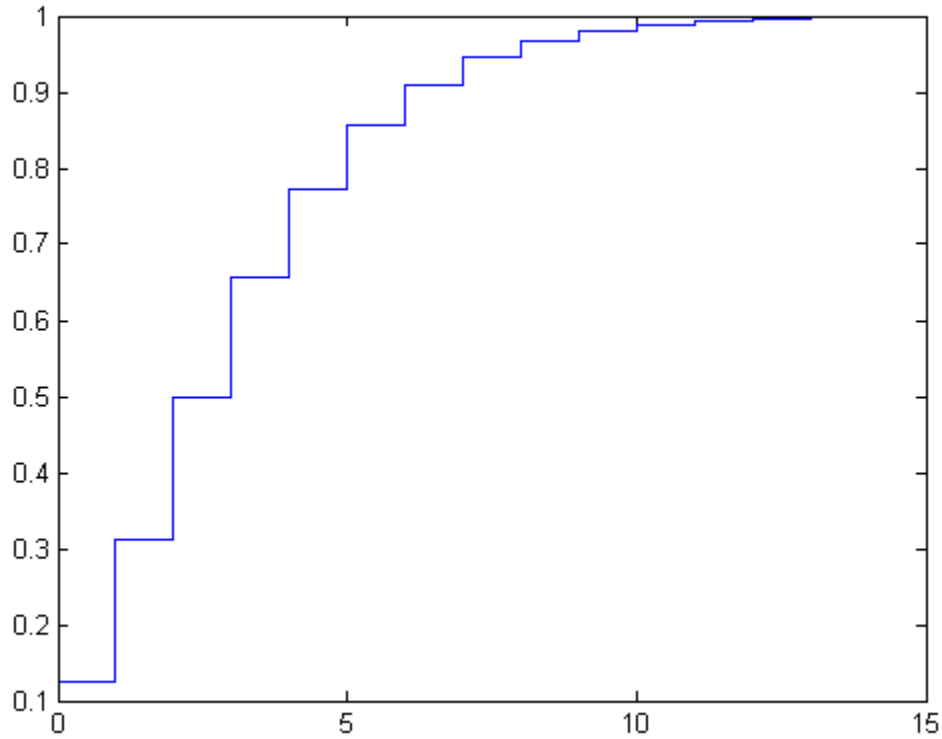
The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `p` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbincdf` allows `R` to be any positive value, including nonintegers. When `R` is noninteger, the binomial coefficient in the definition of the cdf is replaced by the equivalent expression

$$\frac{\Gamma(r+i)}{\Gamma(r)\Gamma(i+1)}$$

Examples

Compute Negative Binomial Distribution CDF

```
x = (0:15);
p = nbincdf(x,3,0.5);
stairs(x,p)
```



More About

- “Negative Binomial Distribution” on page B-115

See Also

cdf | nbinpdf | nbininv | nbinstat | nbinfit | nbinrnd

nbinfit

Negative binomial parameter estimates

Syntax

```
parmhat = nbinfit(data)
[parmhat,parmci] = nbinfit(data,alpha)
[...] = nbinfit(data,alpha,options)
```

Description

`parmhat = nbinfit(data)` returns the maximum likelihood estimates (MLEs) of the parameters of the negative binomial distribution given the data in the vector `data`.

`[parmhat,parmci] = nbinfit(data,alpha)` returns MLEs and `100(1-alpha)` percent confidence intervals. By default, `alpha = 0.05`, which corresponds to 95% confidence intervals.

`[...] = nbinfit(data,alpha,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. The negative binomial fit function accepts an `options` structure which you can create using the function `statset`. Enter `statset('nbinfit')` to see the names and default values of the parameters that `nbinfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Note The variance of a negative binomial distribution is greater than its mean. If the sample variance of the data in `data` is less than its sample mean, `nbinfit` cannot compute MLEs. You should use the `poissfit` function instead.

More About

- “Negative Binomial Distribution” on page B-115

See Also

nbincdf | nbininv | nbinpdf | nbinrnd | nbinstat | mle | statset

nbininv

Negative binomial inverse cumulative distribution function

Syntax

```
X = nbininv(Y,R,P)
```

Description

`X = nbininv(Y,R,P)` returns the inverse of the negative binomial cdf with corresponding number of successes, `R` and probability of success in a single trial, `P`. Since the binomial distribution is discrete, `nbininv` returns the least integer `X` such that the negative binomial cdf evaluated at `X` equals or exceeds `Y`. `Y`, `R`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `Y`, `R`, or `P` is expanded to a constant array with the same dimensions as the other inputs.

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbininv` allows `R` to be any positive value, including nonintegers.

Examples

How many times would you need to flip a fair coin to have a 99% probability of having observed 10 heads?

```
flips = nbininv(0.99,10,0.5) + 10
flips =
  33
```

Note that you have to flip at least 10 times to get 10 heads. That is why the second term on the right side of the equals sign is a 10.

More About

- "Negative Binomial Distribution" on page B-115

See Also

`icdf` | `nbincdf` | `nbinpdf` | `nbinstat` | `nbinfit` | `nbinrnd`

nbinpdf

Negative binomial probability density function

Syntax

```
Y = nbinpdf(X,R,P)
```

Description

`Y = nbinpdf(X,R,P)` returns the negative binomial pdf at each of the values in `X` using the corresponding number of successes, `R` and probability of success in a single trial, `P`. `X`, `R`, and `P` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `X`, `R`, or `P` is expanded to a constant array with the same dimensions as the other inputs. Note that the density function is zero unless the values in `X` are integers.

The negative binomial pdf is

$$y = f(x \mid r, p) = \binom{r + x - 1}{x} p^r q^x I_{(0,1,\ldots)}(x)$$

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbinpdf` allows `R` to be any positive value, including nonintegers. When `R` is noninteger, the binomial coefficient in the definition of the pdf is replaced by the equivalent expression

$$\frac{\Gamma(r + x)}{\Gamma(r)\Gamma(x + 1)}$$

Examples

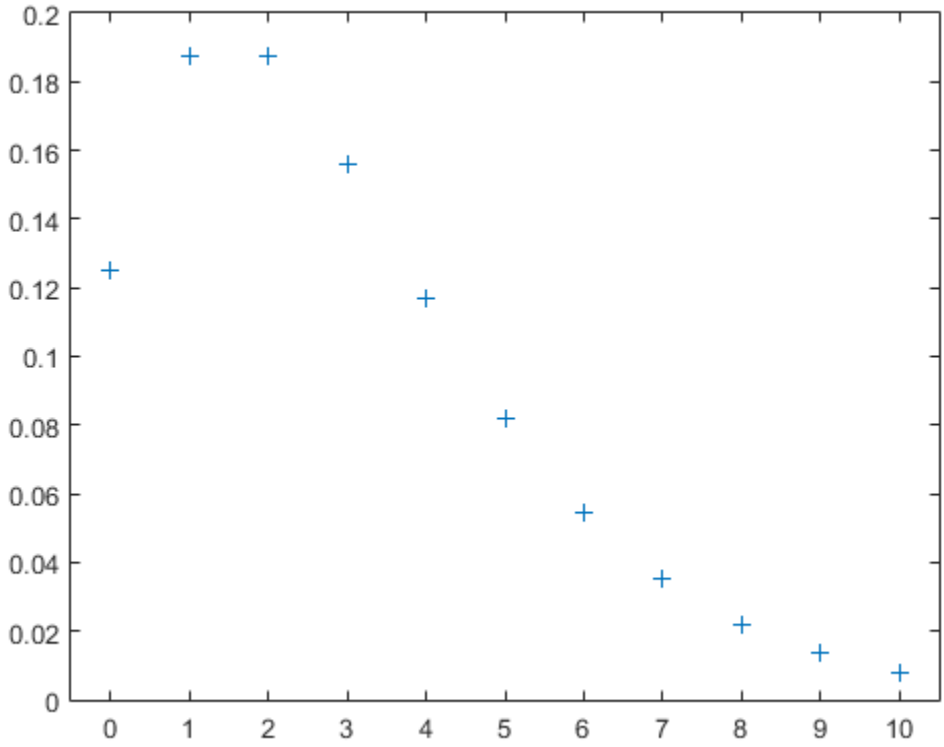
Compute the Negative Binomial Distribution pdf

Compute the pdf of a negative binomial distribution with parameters `R = 3` and `p = 0.5`.

```
x = (0:10);
y = nbinpdf(x,3,0.5);
```

Plot the pdf.

```
figure;
plot(x,y,'+')
xlim([-0.5,10.5])
```



More About

- "Negative Binomial Distribution" on page B-115

See Also

`pdf` | `nbincdf` | `nbininv` | `nbinstat` | `nbinfit` | `nbinrnd`

nbinrnd

Negative binomial random numbers

Syntax

```
RND = nbinrnd(R,P)
RND = nbinrnd(R,P,m,n,...)
RND = nbinrnd(R,P,[m,n,...])
```

Description

`RND = nbinrnd(R,P)` is a matrix of random numbers chosen from a negative binomial distribution with corresponding number of successes, `R` and probability of success in a single trial, `P`. `R` and `P` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `RND`. A scalar input for `R` or `P` is expanded to a constant array with the same dimensions as the other input.

`RND = nbinrnd(R,P,m,n,...)` or `RND = nbinrnd(R,P,[m,n,...])` generates an `m`-by-`n`-by-... array. The `R`, `P` parameters can each be scalars or arrays of the same size as `R`.

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbinrnd` allows `R` to be any positive value, including nonintegers.

Examples

Suppose you want to simulate a process that has a defect probability of 0.01. How many units might Quality Assurance inspect before finding three defective items?

```
r = nbinrnd(3,0.01,1,6)+3
r =
  496  142  420  396  851  178
```

More About

- "Negative Binomial Distribution" on page B-115

See Also

`random` | `nbinpdf` | `nbincdf` | `nbininv` | `nbinstat` | `nbinfit`

nbinstat

Negative binomial mean and variance

Syntax

```
[M,V] = nbinstat(R,P)
```

Description

`[M,V] = nbinstat(R,P)` returns the mean of and variance for the negative binomial distribution with corresponding number of successes, `R` and probability of success in a single trial, `P`. `R` and `P` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `R` or `P` is expanded to a constant array with the same dimensions as the other input.

The mean of the negative binomial distribution with parameters r and p is rq / p, where $q = 1 - p$. The variance is rq / p^2.

The simplest motivation for the negative binomial is the case of successive random trials, each having a constant probability `P` of success. The number of *extra* trials you must perform in order to observe a given number `R` of successes has a negative binomial distribution. However, consistent with a more general interpretation of the negative binomial, `nbinstat` allows `R` to be any positive value, including nonintegers.

Examples

```
p = 0.1:0.2:0.9;
r = 1:5;
[R,P] = meshgrid(r,p);
[M,V] = nbinstat(R,P)
M =
  9.0000  18.0000  27.0000  36.0000  45.0000
  2.3333  4.6667  7.0000  9.3333  11.6667
  1.0000  2.0000  3.0000  4.0000  5.0000
  0.4286  0.8571  1.2857  1.7143  2.1429
  0.1111  0.2222  0.3333  0.4444  0.5556
```

```
V =
  90.0000 180.0000 270.0000 360.0000 450.0000
  7.7778  15.5556  23.3333  31.1111  38.8889
  2.0000  4.0000  6.0000  8.0000  10.0000
  0.6122  1.2245  1.8367  2.4490  3.0612
  0.1235  0.2469  0.3704  0.4938  0.6173
```

More About

- "Negative Binomial Distribution" on page B-115

See Also

`nbinpdf` | `nbincdf` | `nbininv` | `nbinfit` | `nbinrnd`

ncfcdf

Noncentral F cumulative distribution function

Syntax

```
p = ncfcdf(x,nu1,nu2,delta)
p = ncfcdf(x,nu1,nu2,delta,'upper')
```

Description

`p = ncfcdf(x,nu1,nu2,delta)` computes the noncentral F cdf at each value in `x` using the corresponding numerator degrees of freedom in `nu1`, denominator degrees of freedom in `nu2`, and positive noncentrality parameters in `delta`. `nu1`, `nu2`, and `delta` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `p`. A scalar input for `x`, `nu1`, `nu2`, or `delta` is expanded to a constant array with the same dimensions as the other inputs.

`p = ncfcdf(x,nu1,nu2,delta,'upper')` returns the complement of the noncentral F cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The noncentral F cdf is

$$F(x \mid \nu_1,\nu_2,\delta) = \sum_{j=0}^{\infty}\left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!}e^{\frac{-\delta}{2}}\right) I\left(\frac{\nu_1 \cdot x}{\nu_2+\nu_1 \cdot x}\middle|\frac{\nu_1}{2}+j,\frac{\nu_2}{2}\right)$$

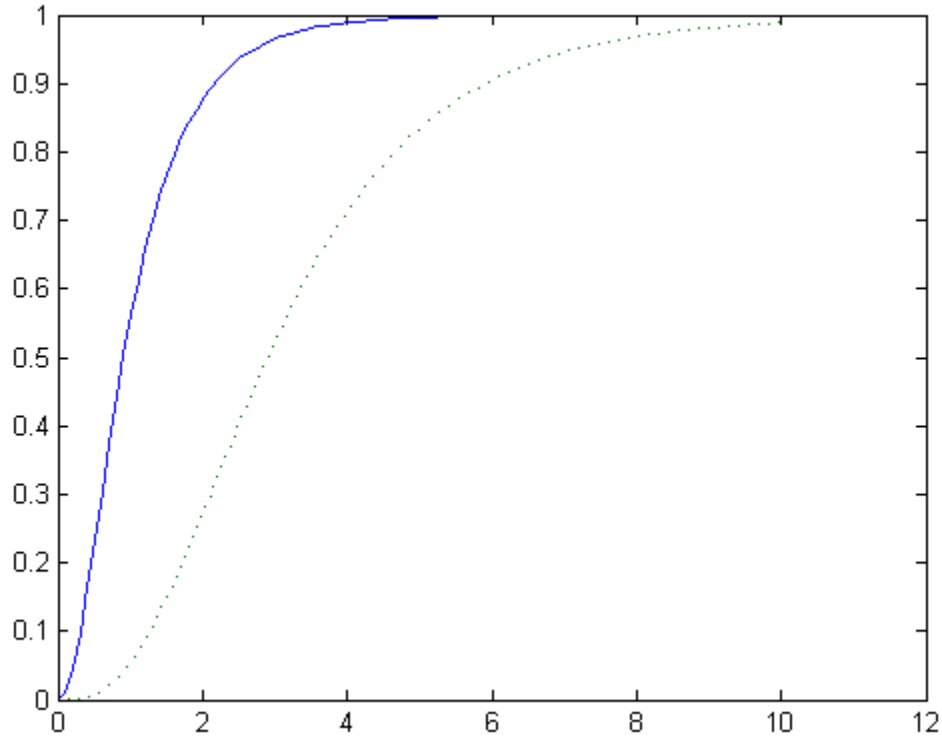
where $I(x \mid a,b)$ is the incomplete beta function with parameters a and b.

Examples

Compute Noncentral F Distribution cdf

Compare the noncentral F cdf with $\delta = 10$ to the F cdf with the same number of numerator and denominator degrees of freedom (5 and 20 respectively).

```
x = (0.01:0.1:10.01)';
p1 = ncfcdf(x,5,20,10);
p = fcdf(x,5,20);
plot(x,p,'-',x,p1,'-')
```



More About

- “Noncentral F Distribution” on page B-123

References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`cdf` | `ncfpdf` | `ncfinv` | `ncfstat` | `ncfrnd`

ncfinv

Noncentral F inverse cumulative distribution function

Syntax

```
X = ncfinv(P,NU1,NU2,DELTA)
```

Description

`X = ncfinv(P,NU1,NU2,DELTA)` returns the inverse of the noncentral F cdf with numerator degrees of freedom `NU1`, denominator degrees of freedom `NU2`, and positive noncentrality parameter `DELTA` for the corresponding probabilities in `P`. `P`, `NU1`, `NU2`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `NU1`, `NU2`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Examples

One hypothesis test for comparing two sample variances is to take their ratio and compare it to an F distribution. If the numerator and denominator degrees of freedom are 5 and 20 respectively, then you reject the hypothesis that the first variance is equal to the second variance if their ratio is less than that computed below.

```
critical = finv(0.95,5,20)
critical =
  2.7109
```

Suppose the truth is that the first variance is twice as big as the second variance. How likely is it that you would detect this difference?

```
prob = 1 - ncfcdf(critical,5,20,2)
prob =
  0.1297
```

If the true ratio of variances is 2, what is the typical (median) value you would expect for the F statistic?

```
ncfinv(0.5,5,20,2)
ans =
    1.2786
```

More About

- "Noncentral F Distribution" on page B-123

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. Hoboken, NJ: Wiley-Interscience, 2000.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`icdf` | `ncfcdf` | `ncfpdf` | `ncfstat` | `ncfrnd`

ncfpdf

Noncentral *F* probability density function

Syntax

```
Y = ncfpdf(X,NU1,NU2,DELTA)
```

Description

`Y = ncfpdf(X,NU1,NU2,DELTA)` computes the noncentral *F* pdf at each of the values in `X` using the corresponding numerator degrees of freedom in `NU1`, denominator degrees of freedom in `NU2`, and positive noncentrality parameters in `DELTA`. `X`, `NU1`, `N2`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `P`, `NU1`, `NU2`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

The *F* distribution is a special case of the noncentral *F* where $\delta = 0$. As δ increases, the distribution flattens like the plot in the example.

Examples

Compute Noncentral *F* Distribution pdf

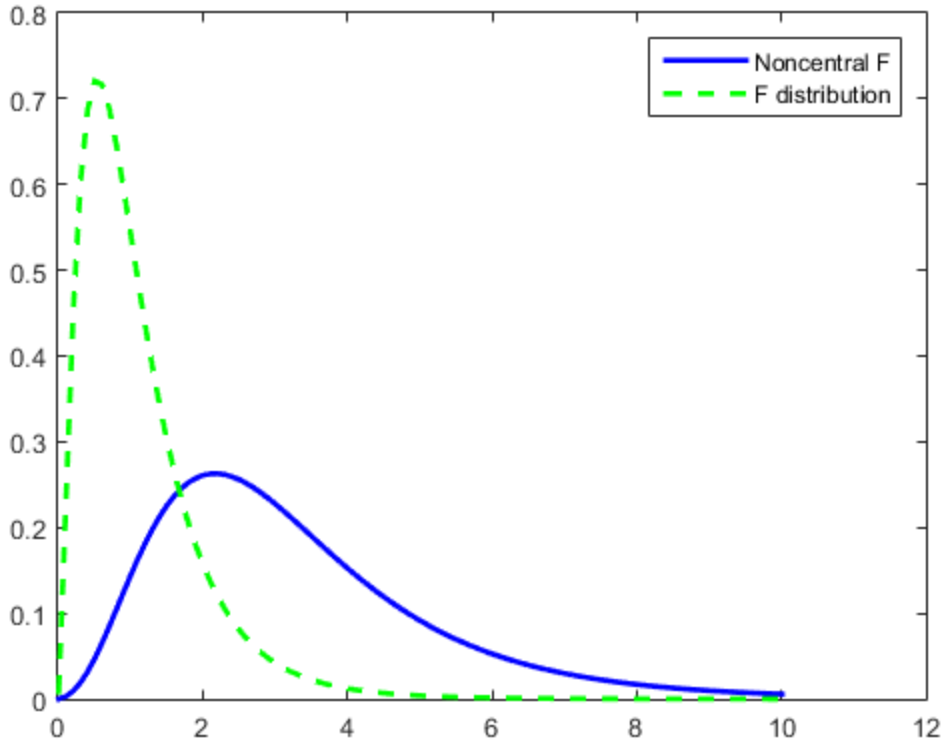
Compute the pdf of a noncentral *F* distribution with degrees of freedom `NU1 = 5` and `NU2 = 20`, and noncentrality parameter `DELTA = 10`. For comparison, also compute the pdf of an *F* distribution with the same degrees of freedom.

```
x = (0.01:0.1:10.01)';
p1 = ncfpdf(x,5,20,10);
p = fpdf(x,5,20);
```

Plot the pdf of the noncentral *F* distribution and the pdf of the *F* distribution on the same figure.

```
figure;
plot(x,p1,'b-','LineWidth',2)
hold on
```

```
plot(x,p,'g--','LineWidth',2)
legend('Noncentral F','F distribution')
```



More About

- "Noncentral F Distribution" on page B-123

References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`pdf` | `ncfcdf` | `ncfinv` | `ncfstat` | `ncfrnd`

ncfrnd

Noncentral F random numbers

Syntax

```
R = ncfrnd(NU1,NU2,DELTA)
R = ncfrnd(NU1,NU2,DELTA,m,n,...)
R = ncfrnd(NU1,NU2,DELTA,[m,n,...])
```

Description

`R = ncfrnd(NU1,NU2,DELTA)` returns a matrix of random numbers chosen from the noncentral F distribution with corresponding numerator degrees of freedom in `NU1`, denominator degrees of freedom in `NU2`, and positive noncentrality parameters in `DELTA`. `NU1`, `NU2`, and `DELTA` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `NU1`, `NU2`, or `DELTA` is expanded to a constant matrix with the same dimensions as the other inputs.

`R = ncfrnd(NU1,NU2,DELTA,m,n,...)` or `R = ncfrnd(NU1,NU2,DELTA,[m,n,...])` generates an `m`-by-`n`-by-... array. The `NU1`, `NU2`, `DELTA` parameters can each be scalars or arrays of the same size as `R`.

Examples

Compute six random numbers from a noncentral F distribution with 10 numerator degrees of freedom, 100 denominator degrees of freedom and a noncentrality parameter, δ, of 4.0. Compare this to the F distribution with the same degrees of freedom.

```
r = ncfrnd(10,100,4,1,6)
r =
  2.5995  0.8824  0.8220  1.4485  1.4415  1.4864

r1 = frnd(10,100,1,6)
r1 =
  0.9826  0.5911  1.0967  0.9681  2.0096  0.6598
```

More About

- "Noncentral F Distribution" on page B-123

References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`random` | `ncfpdf` | `ncfcdf` | `ncfinv` | `ncfstat`

ncfstat

Noncentral F mean and variance

Syntax

```
[M,V] = ncfstat(NU1,NU2,DELTA)
```

Description

`[M,V] = ncfstat(NU1,NU2,DELTA)` returns the mean of and variance for the noncentral F pdf with corresponding numerator degrees of freedom in `NU1`, denominator degrees of freedom in `NU2`, and positive noncentrality parameters in `DELTA`. `NU1`, `NU2`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `NU1`, `NU2`, or `DELTA` is expanded to a constant array with the same dimensions as the other input.

The mean of the noncentral F distribution with parameters ν_1, ν_2, and δ is

$$\frac{\nu_2(\delta+\nu_1)}{\nu_1(\nu_2-2)}$$

where $\nu_2 > 2$.

The variance is

$$2\left(\frac{\nu_2}{\nu_1}\right)^2\left[\frac{(\delta+\nu_1)^2+(2\delta+\nu_1)(\nu_2-2)}{(\nu_2-2)^2(\nu_2-4)}\right]$$

where $\nu_2 > 4$.

Examples

```
[m,v]= ncfstat(10,100,4)
```

```
m =
  1.4286
v =
  0.4252
```

More About

- "Noncentral F Distribution" on page B-123

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 73–74.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 189–200.

See Also

`ncfpdf` | `ncfcdf` | `ncfinv` | `ncfrnd`

NClasses property

Class: NaiveBayes

Number of classes

Description

The `NClasses` property specifies the number of classes in the grouping variable used to create the Naive Bayes classifier.

NumComponents property

Class: gmdistribution

Number k of mixture components

Description

The number k of mixture components.

nctcdf

Noncentral *t* cumulative distribution function

Syntax

```
p = nctcdf(x,nu,delta)
p = nctcdf(x,nu,delta,'upper')
```

Description

`p = nctcdf(x,nu,delta)` computes the noncentral *t* cdf at each value in `x` using the corresponding degrees of freedom in `nu` and noncentrality parameters in `delta`. `x`, `nu`, and `delta` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `p`. A scalar input for `x`, `nu`, or `delta` is expanded to a constant array with the same dimensions as the other inputs.

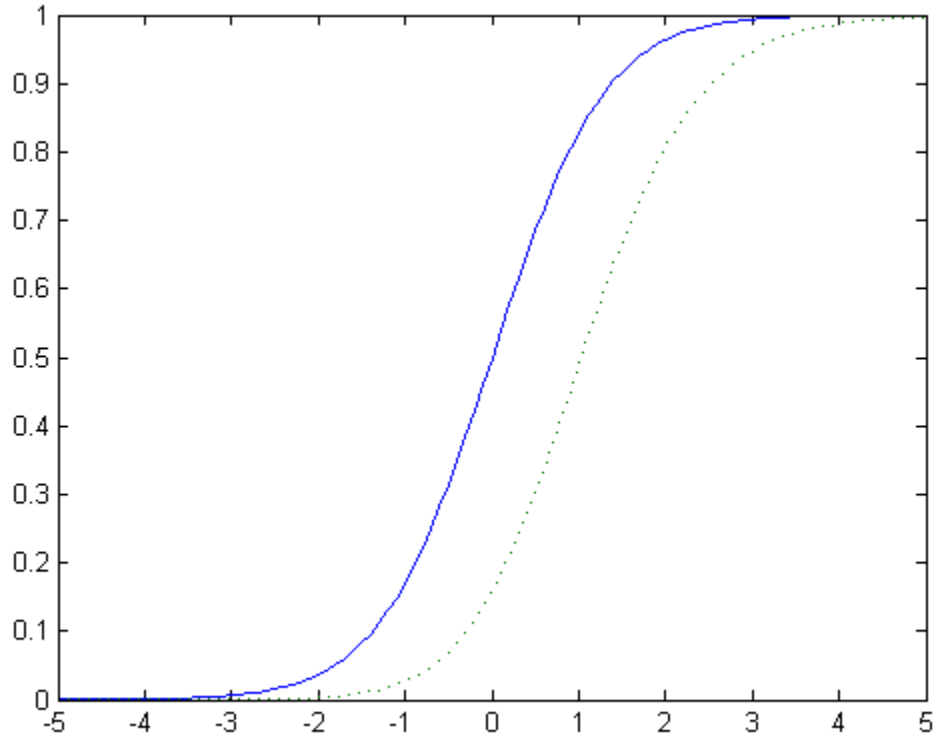
`p = nctcdf(x,nu,delta,'upper')` returns the complement of the noncentral *t* cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

Examples

Compute Noncentral *t* Distribution cdf

Compare the noncentral *t* cdf with `DELTA = 1` to the *t* cdf with the same number of degrees of freedom (10).

```
x = (-5:0.1:5)';
p1 = nctcdf(x,10,1);
p = tcdf(x,10);
plot(x,p,'-',x,p1,':')
```



More About

- "Noncentral t Distribution" on page B-126

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`cdf` | `nctpdf` | `nctinv` | `nctstat` | `nctrnd`

nctinv

Noncentral *t* inverse cumulative distribution function

Syntax

```
X = nctinv(P,NU,DELTA)
```

Description

`X = nctinv(P,NU,DELTA)` returns the inverse of the noncentral *t* cdf with `NU` degrees of freedom and noncentrality parameter `DELTA` for the corresponding probabilities in `P`. `P`, `NU`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `NU`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Examples

```
x = nctinv([0.1 0.2],10,1)
x =
  -0.2914  0.1618
```

More About

- "Noncentral t Distribution" on page B-126

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`icdf` | `nctcdf` | `nctpdf` | `nctstat` | `nctrnd`

nctpdf

Noncentral *t* probability density function

Syntax

```
Y = nctpdf(X,V,DELTA)
```

Description

`Y = nctpdf(X,V,DELTA)` computes the noncentral *t* pdf at each of the values in `X` using the corresponding degrees of freedom in `V` and noncentrality parameters in `DELTA`. Vector or matrix inputs for `X`, `V`, and `DELTA` must have the same size, which is also the size of `Y`. A scalar input for `X`, `V`, or `DELTA` is expanded to a constant matrix with the same dimensions as the other inputs.

Examples

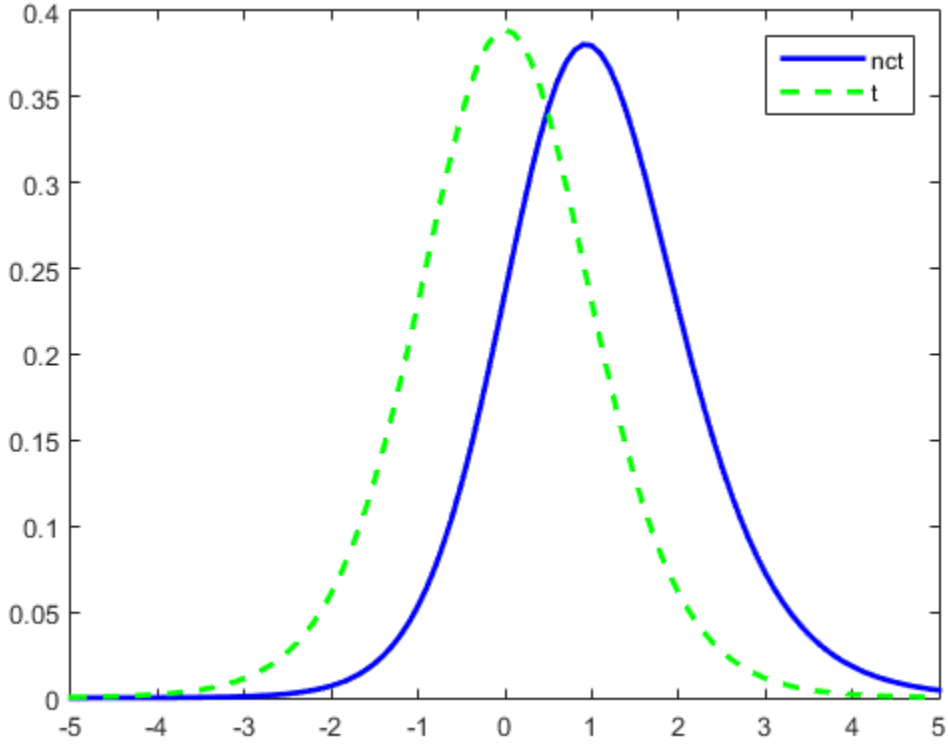
Compute Noncentral *t* Distribution pdf

Compute the pdf of a noncentral *t* distribution with degrees of freedom `V = 10` and noncentrality parameter `DELTA = 1`. For comparison, also compute the pdf of a *t* distribution with the same degrees of freedom.

```
x = (-5:0.1:5)';
nct = nctpdf(x,10,1);
t = tpdf(x,10);
```

Plot the pdf of the noncentral *t* distribution and the pdf of the *t* distribution on the same figure.

```
plot(x,nct,'b-','LineWidth',2)
hold on
plot(x,t,'g--','LineWidth',2)
legend('nct','t')
```



More About

- "Noncentral t Distribution" on page B-126

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`pdf` | `nctcdf` | `nctinv` | `nctstat` | `nctrnd`

nctrnd

Noncentral *t* random numbers

Syntax

```
R = nctrnd(V,DELTA)
R = nctrnd(V,DELTA,m,n,...)
R = nctrnd(V,DELTA,[m,n,...])
```

Description

`R = nctrnd(V,DELTA)` returns a matrix of random numbers chosen from the noncentral T distribution using the corresponding degrees of freedom in `V` and noncentrality parameters in `DELTA`. `V` and `DELTA` can be vectors, matrices, or multidimensional arrays. A scalar input for `V` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

`R = nctrnd(V,DELTA,m,n,...)` or `R = nctrnd(V,DELTA,[m,n,...])` generates an `m`-by-`n`-by-... array. The `V`, `DELTA` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
nctrnd(10,1,5,1)
ans =
  1.6576
  1.0617
  1.4491
  0.2930
  3.6297
```

More About

- “Noncentral t Distribution” on page B-126

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`random` | `nctpdf` | `nctcdf` | `nctinv` | `nctstat`

nctstat

Noncentral *t* mean and variance

Syntax

```
[M,V] = nctstat(NU,DELTA)
```

Description

`[M,V] = nctstat(NU,DELTA)` returns the mean of and variance for the noncentral t pdf with `NU` degrees of freedom and noncentrality parameter `DELTA`. `NU` and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `NU` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

The mean of the noncentral t distribution with parameters ν and δ is

$$\frac{\delta(\nu/2)^{1/2}\Gamma((\nu-1)/2)}{\Gamma(\nu/2)}$$

where $\nu > 1$.

The variance is

$$\frac{\nu}{(\nu-2)}(1+\delta^2)-\frac{\nu}{2}\delta^2\left[\frac{\Gamma((\nu-1)/2)}{\Gamma(\nu/2)}\right]^2$$

where $\nu > 2$.

Examples

```
[m,v] = nctstat(10,1)

m =
```

```
    1.0837

v =
    1.3255
```

More About

- "Noncentral t Distribution" on page B-126

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 147–148.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 201–219.

See Also

`nctpdf` | `nctcdf` | `nctinv` | `nctrnd`

ncx2cdf

Noncentral chi-square cumulative distribution function

Syntax

```
p = ncx2cdf(x,v,delta)
p = ncx2cdf(x,v,delta,'upper')
```

Description

`p = ncx2cdf(x,v,delta)` computes the noncentral chi-square cdf at each value in `x` using the corresponding degrees of freedom in `v` and positive noncentrality parameters in `delta`. `x`, `v`, and `delta` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `p`. A scalar input for `x`, `v`, or `delta` is expanded to a constant array with the same dimensions as the other inputs.

`p = ncx2cdf(x,v,delta,'upper')` returns the complement of the noncentral chi-square cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

Some texts refer to this distribution as the generalized Rayleigh, Rayleigh-Rice, or Rice distribution.

The noncentral chi-square cdf is

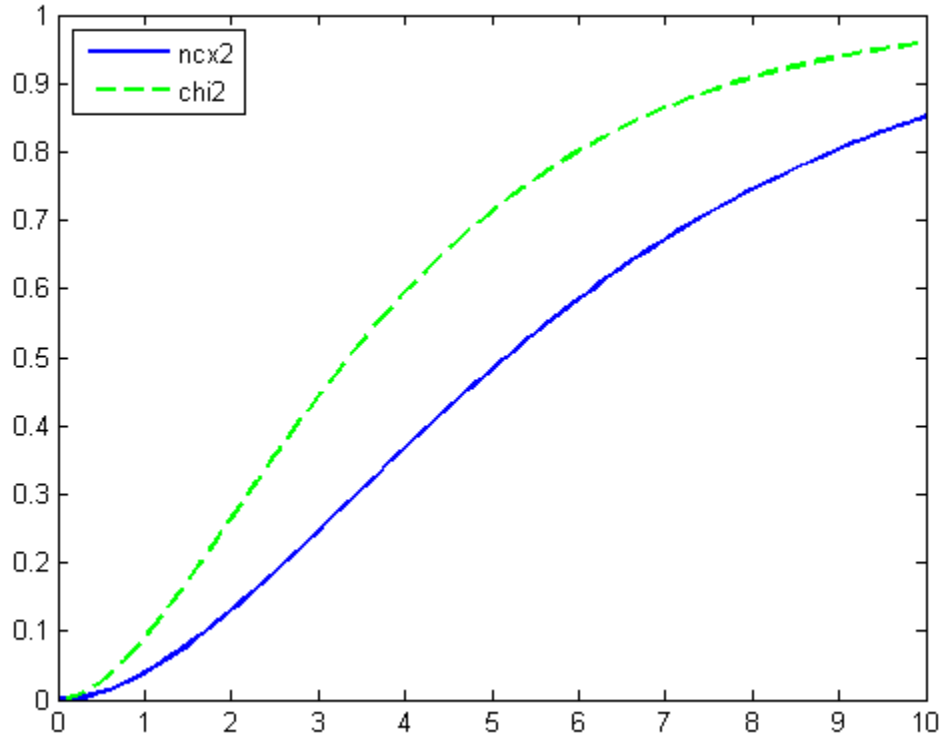
$$F(x \mid \nu,\delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!} e^{\frac{-\delta}{2}} \right) \Pr\left[\chi^2_{\nu+2j} \le x\right]$$

Examples

Compute Noncentral Chi-Square cdf

Compare the noncentral chi-square cdf with `DELTA = 2` to the chi-square cdf with the same number of degrees of freedom (4):

```
x = (0:0.1:10)';
ncx2 = ncx2cdf(x,4,2);
chi2 = chi2cdf(x,4);

plot(x,ncx2,'b-','LineWidth',2)
hold on
plot(x,chi2,'g--','LineWidth',2)
legend('ncx2','chi2','Location','NW')
```



More About

- “Noncentral Chi-Square Distribution” on page B-120

References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`cdf` | `ncx2pdf` | `ncx2inv` | `ncx2stat` | `ncx2rnd`

ncx2inv

Noncentral chi-square inverse cumulative distribution function

Syntax

```
X = ncx2inv(P,V,DELTA)
```

Description

`X = ncx2inv(P,V,DELTA)` returns the inverse of the noncentral chi-square cdf using the corresponding degrees of freedom in `V` and positive noncentrality parameters in `DELTA`, at the corresponding probabilities in `P`. `P`, `V`, and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `X`. A scalar input for `P`, `V`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Examples

```
ncx2inv([0.01 0.05 0.1],4,2)
ans =
  0.4858  1.1498  1.7066
```

More About

Algorithms

`ncx2inv` uses Newton's method to converge to the solution.

- “Noncentral Chi-Square Distribution” on page B-120

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 50–52.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`icdf` | `ncx2cdf` | `ncx2pdf` | `ncx2stat` | `ncx2rnd`

ncx2pdf

Noncentral chi-square probability density function

Syntax

```
Y = ncx2pdf(X,V,DELTA)
```

Description

`Y = ncx2pdf(X,V,DELTA)` computes the noncentral chi-square pdf at each of the values in `X` using the corresponding degrees of freedom in `V` and positive noncentrality parameters in `DELTA`. Vector or matrix inputs for `X`, `V`, and `DELTA` must have the same size, which is also the size of `Y`. A scalar input for `X`, `V`, or `DELTA` is expanded to a constant array with the same dimensions as the other inputs.

Some texts refer to this distribution as the generalized Rayleigh, Rayleigh-Rice, or Rice distribution.

Examples

Compute Noncentral Chi-Square Distribution pdf

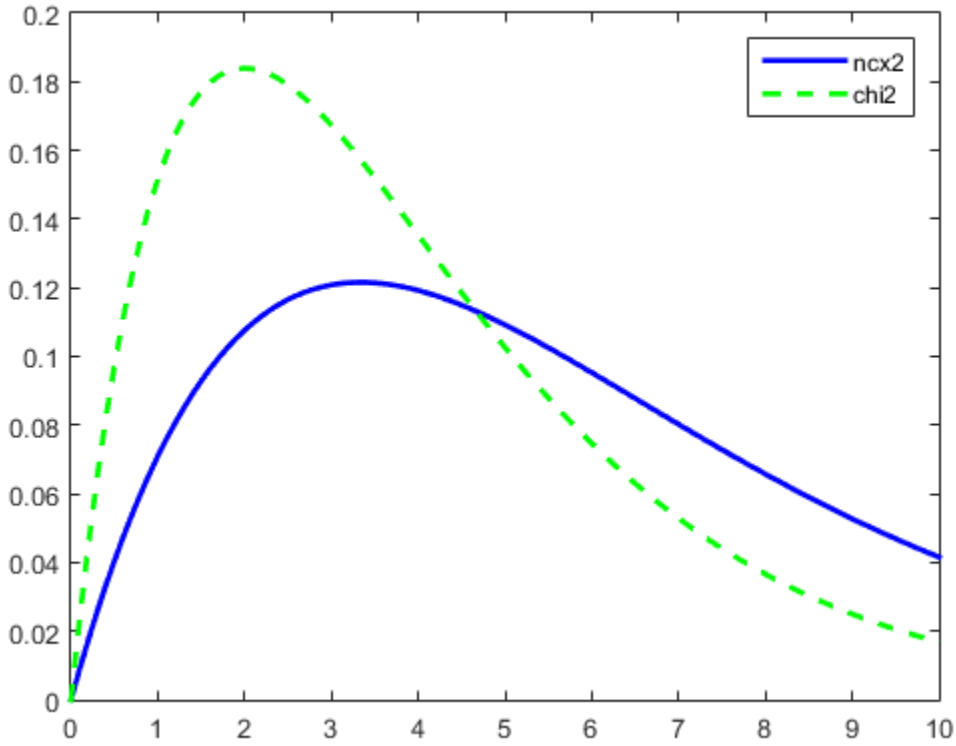
Compute the pdf of a noncentral chi-square distribution with degrees of freedom `V = 4` and noncentrality parameter `DELTA = 2`. For comparison, also compute the pdf of a chi-square distribution with the same degrees of freedom.

```
x = (0:0.1:10)';
ncx2 = ncx2pdf(x,4,2);
chi2 = chi2pdf(x,4);
```

Plot the pdf of the noncentral chi-square distribution on the same figure as the pdf of the chi-square distribution.

```
figure;
plot(x,ncx2,'b-','LineWidth',2)
hold on
plot(x,chi2,'g--','LineWidth',2)
```

```
legend('ncx2','chi2')
```



More About

- "Noncentral Chi-Square Distribution" on page B-120

References

[1] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`pdf` | `ncx2cdf` | `ncx2inv` | `ncx2stat` | `ncx2rnd`

ncx2rnd

Noncentral chi-square random numbers

Syntax

```
R = ncx2rnd(V,DELTA)
R = ncx2rnd(V,DELTA,m,n,...)
R = ncx2rnd(V,DELTA,[m,n,...])
```

Description

`R = ncx2rnd(V,DELTA)` returns a matrix of random numbers chosen from the noncentral chi-square distribution using the corresponding degrees of freedom in `V` and positive noncentrality parameters in `DELTA`. `V` and `DELTA` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `V` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

`R = ncx2rnd(V,DELTA,m,n,...)` or `R = ncx2rnd(V,DELTA,[m,n,...])` generates an `m`-by-`n`-by-... array. The `V`, `DELTA` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
ncx2rnd(4,2,6,3)
ans =
  6.8552  5.9650  11.2961
  5.2631  4.2640  5.9495
  9.1939  6.7162  3.8315
 10.3100  4.4828  7.1653
  2.1142  1.9826  4.6400
  3.8852  5.3999  0.9282
```

More About

- “Noncentral Chi-Square Distribution” on page B-120

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 50–52.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`random` | `ncx2pdf` | `ncx2cdf` | `ncx2inv` | `ncx2stat`

ncx2stat

Noncentral chi-square mean and variance

Syntax

```
[M,V] = ncx2stat(NU,DELTA)
```

Description

`[M,V] = ncx2stat(NU,DELTA)` returns the mean of and variance for the noncentral chi-square pdf with `NU` degrees of freedom and noncentrality parameter `DELTA`. `NU` and `DELTA` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `NU` or `DELTA` is expanded to a constant array with the same dimensions as the other input.

The mean of the noncentral chi-square distribution with parameters v and δ is v+δ, and the variance is 2(v+2δ).

Examples

```
[m,v] = ncx2stat(4,2)
m =
   6
v =
  16
```

More About

- “Noncentral Chi-Square Distribution” on page B-120

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. 2nd ed., Hoboken, NJ: John Wiley & Sons, Inc., 1993, pp. 50–52.

[2] Johnson, N., and S. Kotz. *Distributions in Statistics: Continuous Univariate Distributions-2*. Hoboken, NJ: John Wiley & Sons, Inc., 1970, pp. 130–148.

See Also

`ncx2pdf` | `ncx2cdf` | `ncx2inv` | `ncx2rnd`

NumVariables property

Class: gmdistribution

Dimension d of multivariate Gaussian distributions

Description

The dimension d of the multivariate Gaussian distributions.

ndims

Class: dataset

Number of dimensions of dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
n = ndims(A)
```

Description

`n = ndims(A)` returns the number of dimensions in the dataset `A`. The number of dimensions in an array is always 2.

See Also

`size`

ndims

Class: qrandset

Number of dimensions in matrix

Syntax

```
n = ndims(p)
```

Description

`n = ndims(p)` returns the number of dimensions in the matrix that is created by the syntax `p(:,:)`. Since this is always a 2-D matrix, `n` is always equal to 2.

See Also

`qrandset` | `size`

NDims property

Class: NaiveBayes

Number of dimensions

Description

The `NDims` property specifies the number of dimensions, which is equal to the number of features in the training data used to create the Naive Bayes classifier.

ne

Class: qrandstream

Not equal relation for handles

Syntax

```
h1 ~= h2
```

Description

Handles are equal if they are handles for the same object and are unequal otherwise.

`h1 ~= h2` performs element-wise comparisons between handle arrays `h1` and `h2`. `h1` and `h2` must be of the same dimensions unless one is a scalar. The result is a logical array of the same dimensions, where each element is an element-wise `~=` result.

If one of `h1` or `h2` is scalar, scalar expansion is performed and the result will match the dimensions of the array that is not scalar.

`tf = ne(h1, h2)` stores the result in a logical array of the same dimensions.

See Also

`qrandstream` | `ge` | `gt` | `lt` | `eq` | `le`

prob.NegativeBinomialDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Negative binomial distribution object

Description

`prob.NegativeBinomialDistribution` is an object consisting of parameters, a model description, and sample data for a negative binomial probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('NegativeBinomial')` creates a negative binomial probability distribution object using the default parameter values.

`pd = makedist('NegativeBinomial','R',R,'p',p)` creates a negative binomial probability distribution object using the specified parameter values.

Input Arguments

`R` — Number of successes

1 (default) | positive scalar value

Number of successes for the negative binomial distribution, specified as a positive scalar value.

Data Types: `single` | `double`

`p` — Probability of success

0.5 (default) | positive scalar value in the range (0,1]

Probability of success of any individual trial for the negative binomial distribution, specified as a positive scalar value in the range (0,1].

Data Types: `single` | `double`

Properties

`R` — Number of successes
positive scalar value

Number of successes for the negative binomial distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`p` — Probability of success
positive scalar value in the range (0,1]

Probability of success of any individual trial for the negative binomial distribution, specified as a positive scalar value in the range (0,1].

Data Types: `single` | `double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution
`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object

pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Negative Binomial Distribution

The negative binomial distribution models the number of failures x before a specified number of successes is reached in a series of independent, identical trials. This distribution can also model count data, in which case r does not need to be an integer value.

The negative binomial distribution uses the following parameters.

Parameter	Description	Support
R	Number of successes	$r > 0$
p	Probability of success	$0 < p \le 1$

The probability density function (pdf) when R is an integer is

$$f(x \mid R,p) = \binom{R+x+1}{x} p^R q^x \quad ; \quad x = 1,2,\ldots,\infty ,$$

where $q = 1 - p$ and $\binom{R+x+1}{x}$ is the binomial coefficient.

When R is not an integer, the binomial coefficient in the definition of the pdf is replaced by the equivalent expression

$$\frac{\Gamma(r+x)}{\Gamma(r)\Gamma(x+1)},$$

where $\Gamma(\cdot)$ is the Gamma function.

Examples

Create a Negative Binomial Distribution Object Using Default Parameters

Create a negative binomial distribution object using the default parameter values.

```
pd = makedist('NegativeBinomial')
```

```
pd =

  NegativeBinomialDistribution

  Negative Binomial distribution
    R =   1
```

```
    P = 0.5
```

Create a Negative Binomial Distribution Object Using Specified Parameters

Create a negative binomial distribution object by specifying the parameter values.

```
pd = makedist('NegativeBinomial','r',5,'p',.1)
```

```
pd =

  NegativeBinomialDistribution

  Negative Binomial distribution
    R =   5
    P = 0.1
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    45
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- “Negative Binomial Distribution”
- Class Attributes
- Property Attributes

negloglik

Negative log likelihood of probability distribution

Syntax

```
nll = negloglik(pd)
```

Description

`nll = negloglik(pd)` returns the value of the negative loglikelihood function for the data used to fit the probability distribution pd.

Examples

Negative Log Likelihood for a Fitted Distribution

Load the sample data.

```
load carsmall;
```

Create a Weibull distribution object by fitting it to the mile per gallon (MPG) data.

```
pd = fitdist(MPG,'Weibull')
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 26.5079   [24.8333, 28.2954]
    B = 3.27193   [2.79441, 3.83104]
```

Compute the negative log likelihood for the fitted Weibull distribution.

```
wnll = negloglik(pd)
```

```
wnll =
```

```
327.4942
```

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`nll` — Negative log likelihood

scalar value

Negative log likelihood value for the data used to fit the distribution, returned as a scalar value.

See Also

`dfittool` | `fitdist` | `makedist`

negloglik

Class: prob.KernelDistribution
Package: prob

Negative loglikelihood

Syntax

```
nll = negloglik(pd)
```

Description

`nll = negloglik(pd)` returns the value of the negative log likelihood function for the data used to fit the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Fit a probability distribution object to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`nll` — Negative log likelihood

scalar value

Negative log likelihood value for the data used to fit the distribution, returned as a scalar value.

Examples

Negative Loglikelihood for a Kernel Distribution

Load the sample data. Fit a kernel distribution to the miles per gallon (MPG) data.

```
load carsmall;
pd = fitdist(MPG,'Kernel')
```

```
pd =

  KernelDistribution

    Kernel = normal
    Bandwidth = 4.11428
    Support = unbounded
```

Compute the negative loglikelihood.

```
nll = negloglik(pd)
```

```
nll =

  327.3139
```

See Also

`dfittool` | `fitdist`

negloglik

Class: prob.ToolboxFittableParametricDistribution
Package: prob

Negative log likelihood of probability distribution object

Syntax

```
nll = negloglik(pd)
```

Description

`nll = negloglik(pd)` returns the value of the negative log likelihood function for the data used to fit the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`nll` — Negative log likelihood

scalar value

Negative log likelihood value for the data used to fit the distribution, returned as a scalar value.

Examples

Negative Log Likelihood for a Fitted Distribution

Load the sample data.

```
load carsmall;
```

Create a Weibull distribution object by fitting it to the mile per gallon (MPG) data.

```
pd = fitdist(MPG,'Weibull')
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 26.5079   [24.8333, 28.2954]
    B = 3.27193   [2.79441, 3.83104]
```

Compute the negative log likelihood for the fitted Weibull distribution.

```
wnll = negloglik(pd)
```

```
wnll =

  327.4942
```

See Also

dfittool | fitdist | makedist

net

Class: qrandset

Generate quasi-random point set

Syntax

```
X = net(p,n)
```

Description

`X = net(p,n)` returns the first `n` points `X` from the point set `p` of the `qrandset` class. `X` is `n`-by-*d*, where *d* is the dimension of the point set.

Objects `p` of the `@qrandset` class encapsulate properties of a specified quasi-random sequence. Values of the point set are not generated and stored in memory until `p` is accessed using `net` or parenthesis indexing.

Examples

Use `haltonset` to generate a 3-D Halton point set, skip the first 1000 values, and then retain every 101st point:

```
p = haltonset(3,'Skip',1e3,'Leap',1e2)
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

Use `scramble` to apply reverse-radix scrambling:

```
p = scramble(p,'RR2')
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
```

```
              Skip : 1000
              Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.0928    0.6950    0.0029
    0.6958    0.2958    0.8269
    0.3013    0.6497    0.4141
    0.9087    0.7883    0.2166
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.0928    0.6950    0.0029
    0.9087    0.7883    0.2166
    0.3843    0.9840    0.9878
    0.6831    0.7357    0.7923
```

See Also

`haltonset` | `sobolset` | `qrandstream`

nLinearCoeffs

Class: CompactClassificationDiscriminant

Number of nonzero linear coefficients

Syntax

```
ncoeffs = nLinearCoeffs(obj)
ncoeffs = nLinearCoeffs(obj,delta)
```

Description

`ncoeffs = nLinearCoeffs(obj)` returns the number of nonzero linear coefficients in the linear discriminant model `obj`.

`ncoeffs = nLinearCoeffs(obj,delta)` returns the number of nonzero linear coefficients for threshold parameter `delta`.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

`delta`

Scalar or vector value of the `Delta` parameter. See “Gamma and Delta” on page 22-3152.

Output Arguments

`ncoeffs`

Nonnegative integer, the number of nonzero coefficients in the discriminant analysis model `obj`.

If you call `nLinearCoeffs` with a `delta` argument, `ncoeffs` is the number of nonzero linear coefficients for threshold parameter `delta`. If `delta` is a vector, `ncoeffs` is a vector with the same number of elements.

If `obj` is a quadratic discriminant model, `ncoeffs` is the number of predictors in `obj`.

Definitions

Gamma and Delta

Regularization is the process of finding a small set of predictors that yield an effective predictive model. For linear discriminant analysis, there are two parameters, γ and δ, that control regularization as follows. `cvshrink` helps you select appropriate values of the parameters.

Let Σ represent the covariance matrix of the data X, and let $\hat{X}$ be the centered data (the data X minus the mean by class). Define

$$D = \mathrm{diag}\left(\hat{X}^T * \hat{X}\right).$$

The regularized covariance matrix $\tilde{\Sigma}$ is

$$\tilde{\Sigma} = (1-\gamma)\Sigma + \gamma D.$$

Whenever $\gamma \geq$ `MinGamma`, $\tilde{\Sigma}$ is nonsingular.

Let μ_k be the mean vector for those elements of X in class k, and let μ_0 be the global mean vector (the mean of the rows of X). Let C be the correlation matrix of the data X, and let $\tilde{C}$ be the regularized correlation matrix:

$$\tilde{C} = (1-\gamma)C + \gamma I,$$

where I is the identity matrix.

The linear term in the regularized discriminant analysis classifier for a data point x is

$$(x-\mu_0)^T\tilde{\Sigma}^{-1}(\mu_k-\mu_0)=\left[(x-\mu_0)^T D^{-1/2}\right]\left[\tilde{C}^{-1}D^{-1/2}(\mu_k-\mu_0)\right].$$

The parameter δ enters into this equation as a threshold on the final term in square brackets. Each component of the vector $\left[\tilde{C}^{-1}D^{-1/2}(\mu_k-\mu_0)\right]$ is set to zero if it is smaller in magnitude than the threshold δ. Therefore, for class k, if component j is thresholded to zero, component j of x does not enter into the evaluation of the posterior probability.

The `DeltaPredictor` property is a vector related to this threshold. When $\delta \geq$ `DeltaPredictor(i)`, all classes k have

$$\left|\tilde{C}^{-1}D^{-1/2}(\mu_k-\mu_0)\right|\leq\delta.$$

Therefore, when $\delta \geq$ `DeltaPredictor(i)`, the regularized classifier does not use predictor `i`.

Examples

Find the Number of Nonzero Coefficients in a Discriminant Analysis Classifier

Find the number of nonzero coefficients in a discriminant analysis classifier for various `Delta` values.

Create a discriminant analysis classifier from the `fishseriris` data.

```
load fisheriris
obj = fitcdiscr(meas,species);
```

Find the number of nonzero coefficients in `obj`.

```
ncoeffs = nLinearCoeffs(obj)
```

```
ncoeffs =

     4
```

Find the number of nonzero coefficients for `delta` = 1, 2, 4, and 8.

```
delta = [1 2 4 8];
ncoeffs = nLinearCoeffs(obj,delta)
```

```
ncoeffs =

     4
     4
     3
     0
```

The `DeltaPredictor` property gives the values of `delta` where the number of nonzero coefficients changes.

```
ncoeffs2 = nLinearCoeffs(obj,obj.DeltaPredictor)
```

```
ncoeffs2 =

     4
     3
     1
     2
```

See Also

`CompactClassificationDiscriminant` | `cvshrink` | `fitcdiscr`

More About

- “Discriminant Analysis” on page 15-3

nlinfit

Nonlinear regression

Syntax

```
beta = nlinfit(X,Y,modelfun,beta0)
beta = nlinfit(X,Y,modelfun,beta0,options)
beta = nlinfit(___,Name,Value)
[beta,R,J,CovB,MSE,ErrorModelInfo] = nlinfit(___)
```

Description

`beta = nlinfit(X,Y,modelfun,beta0)` returns a vector of estimated coefficients for the nonlinear regression of the responses in Y on the predictors in X using the model specified by modelfun. The coefficients are estimated using iterative least squares estimation, with initial values specified by beta0.

`beta = nlinfit(X,Y,modelfun,beta0,options)` fits the nonlinear regression using the algorithm control parameters in the structure options. You can return any of the output arguments in the previous syntaxes.

`beta = nlinfit(___,Name,Value)` uses additional options specified by one or more name-value pair arguments. For example, you can specify observation weights or a nonconstant error model. You can use any of the input arguments in the previous syntaxes.

`[beta,R,J,CovB,MSE,ErrorModelInfo] = nlinfit(___)` additionally returns the residuals, R, the Jacobian of `modelfun`, J, the estimated variance-covariance matrix for the estimated coefficients, CovB, an estimate of the variance of the error term, MSE, and a structure containing details about the error model, ErrorModelInfo.

Examples

Nonlinear Regression Model Using Default Options

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Fit the Hougen-Watson model to the rate data using the initial values in `beta0`.

```
beta = nlinfit(X,y,@hougen,beta0)
```

```
beta =

    1.2526
    0.0628
    0.0400
    0.1124
    1.1914
```

Nonlinear Regression Using Robust Options

Generate sample data from the nonlinear regression model

$$y = b_1 + b_2 \exp\{-b_3 x\} + \varepsilon,$$

where b_1, b_2, and b_3 are coefficients, and the error term is normally distributed with mean 0 and standard deviation 0.1.

```
modelfun = @(b,x)(b(1)+b(2)*exp(-b(3)*x));

rng('default') % for reproducibility
b = [1;3;2];
x = exprnd(2,100,1);
y = modelfun(b,x) + normrnd(0,0.1,100,1);
```

Set robust fitting options.

```
opts = statset('nlinfit');
opts.RobustWgtFun = 'bisquare';
```

Fit the nonlinear model using the robust fitting options.

```
beta0 = [2;2;2];
beta = nlinfit(x,y,modelfun,beta0,opts)
```

```
beta =
```

```
    1.0041
    3.0997
    2.1483
```

Nonlinear Regression Using Observation Weights

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Specify a vector of known observation weights.

```
W = [8 2 1 6 12 9 12 10 10 12 2 10 8]';
```

Fit the Hougen-Watson model to the rate data using the specified observation weights.

```
[beta,R,J,CovB] = nlinfit(X,y,@hougen,beta0,'Weights',W);
beta
```

```
beta =

    2.2068
    0.1077
    0.0766
    0.1818
    0.6516
```

Display the coefficient standard errors.

```
sqrt(diag(CovB))
```

```
ans =

    2.5721
    0.1251
    0.0950
    0.2043
    0.7735
```

Nonlinear Regression Using Weights Function Handle

Load sample data.

```
S = load('reaction');
```

```
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Specify a function handle for observation weights. The function accepts the model fitted values as input, and returns a vector of weights.

```
a = 1; b = 1;
weights = @(yhat) 1./((a + b*abs(yhat)).^2);
```

Fit the Hougen-Watson model to the rate data using the specified observation weights function.

```
[beta,R,J,CovB] = nlinfit(X,y,@hougen,beta0,'Weights',weights);
beta
```

```
beta =

    0.8308
    0.0409
    0.0251
    0.0801
    1.8261
```

Display the coefficient standard errors.

```
sqrt(diag(CovB))
```

```
ans =

    0.5822
    0.0297
    0.0197
    0.0578
    1.2810
```

Nonlinear Regression Using Nonconstant Error Model

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Fit the Hougen-Watson model to the rate data using the combined error model.

```
[beta,R,J,CovB,MSE,ErrorModelInfo] = nlinfit(X,y,@hougen,beta0,'ErrorModel','combined')
beta
```

```
beta =

    1.2526
    0.0628
    0.0400
    0.1124
    1.1914
```

Display the error model information.

```
ErrorModelInfo
```

```
ErrorModelInfo =

              ErrorModel: 'combined'
         ErrorParameters: [0.1517 5.6783e-08]
           ErrorVariance: @(x)mse*(errorparam(1)+errorparam(2)*abs(model(beta,x))).^2
                     MSE: 1.6245
          ScheffeSimPred: 6
          WeightFunction: 0
            FixedWeights: 0
    RobustWeightFunction: 0
```

Input Arguments

X — Predictor variables

matrix

Predictor variables for the nonlinear regression function, specified as a matrix. Typically, `X` is a design matrix of predictor (independent variable) values, with one row for each value in Y, and one column for each coefficient. However, `X` can be any array that modelfun can accept.

Data Types: `single` | `double`

Y — Response values

vector

Response values (dependent variable) for fitting the nonlinear regression function, specified as a vector with the same number of rows as X.

Data Types: `single` | `double`

`modelfun` — Nonlinear regression model function

function handle

Nonlinear regression model function, specified as a function handle. `modelfun` must accept two input arguments, a coefficient vector and an array `X`—in that order—and return a vector of fitted response values.

For example, to specify the `hougen` nonlinear regression function, use the function handle `@hougen`.

Data Types: `function_handle`

`beta0` — Initial coefficient values

vector

Initial coefficient values for the least squares estimation algorithm, specified as a vector.

Note: Poor starting values can lead to a solution with large residual error.

Data Types: `single` | `double`

`options` — Estimation algorithm options

structure created using `statset`

Estimation algorithm options, specified as a structure you create using `statset`. The following `statset` parameters are applicable to `nlinfit`.

`DerivStep` — Relative difference for finite difference gradient

`eps^(1/3)` (default) | positive scalar value | vector

Relative difference for the finite difference gradient calculation, specified as a positive scalar value, or a vector the same size as beta. Use a vector to specify a different relative difference for each coefficient.

`Display` — Level of output display

`'off'` (default) | `'iter'` | `'final'`

Level of output display during estimation, specified as one of `'off'`, `'iter'`, or `'final'`. If you specify `'iter'`, output is displayed at each iteration. If you specify `'final'`, output is displayed after the final iteration.

`FunValCheck` — Indicator for whether to check for invalid values

`'on'` (default) | `'off'`

Indicator for whether to check for invalid values such as `NaN` or `Inf` from the objective function, specified as `'on'` or `'off'`.

`MaxIter` — Maximum number of iterations

100 (default) | positive integer

Maximum number of iterations for the estimation algorithm, specified as a positive integer. Iterations continue until estimates are within the convergence tolerance, or the maximum number of iterations specified by `MaxIter` is reached.

`RobustWgtFun` — Weight function

string | function handle | `[ ]`

Weight function for robust fitting, specified as a valid string or function handle.

Note: `RobustWgtFun` must have value `[ ]` when you use observation weights, `W`.

The following table describes the possible string values. Let r denote normalized residuals and w denote robust weights. The indicator function I[x] is equal to 1 if the expression x is true, and 0 otherwise.

Weight Function	Equation	Default Tuning Constant
`''` (default)	No robust fitting	—
`'andrews'`	$w = I\left[\lvert r\rvert < \pi\right] \times \sin(r) / r$	1.339
`'bisquare'`	$w = I\left[\lvert r\rvert < 1\right] \times \left(1 - r^2\right)^2$	4.685
`'cauchy'`	$w = 1 \Big/ \left(1 + r^2\right)$	2.385
`'fair'`	$w = 1 \Big/ \left(1 + \lvert r\rvert\right)$	1.400

Weight Function	Equation	Default Tuning Constant
`'huber'`	$w = 1 / \max(1, \lvert r \rvert)$	1.345
`'logistic'`	$w = \tanh(r) / r$	1.205
`'talwar'`	$w = I[\lvert r \rvert < 1]$	2.795
`'welsch'`	$w = \exp\{-r^2\}$	2.985

You can alternatively specify a function handle that accepts a vector of normalized residuals as input, and returns a vector of robust weights as output. If you use a function handle, you must provide a Tune constant.

`Tune` — Tuning constant

positive scalar value

Tuning constant for robust fitting, specified as a positive scalar value. The tuning constant is used to normalize residuals before applying a robust weight function. The default tuning constant depends on the function specified by RobustWgtFun.

If you use a function handle to specify RobustWgtFun, then you must specify a value for `Tune`.

`TolFun` — Termination tolerance on residual sum of squares

`1e-8` (default) | positive scalar value

Termination tolerance for the residual sum of squares, specified as a positive scalar value. Iterations continue until estimates are within the convergence tolerance, or the maximum number of iterations specified by `MaxIter` is reached.

`TolX` — Termination tolerance on estimated coefficients

`1e-8` (default) | positive scalar value

Termination tolerance on the estimated coefficients, beta, specified as a positive scalar value. Iterations continue until estimates are within the convergence tolerance, or the maximum number of iterations specified by `MaxIter` is reached.

`Robust` — Indicator for robust fitting

`'off'` (default) | `'on'`

Indicator for robust fitting, specified as `'off'` or `'on'`.

Note: `Robust` will be removed in a future software release. Use `RobustWgtFun` for robust fitting.

`WgtFun` — Weight function for robust fitting

string | function handle

Weight function for robust fitting, specified as a string indicating a weight function, or a function handle. `WgtFun` is valid only when `Robust` has value `'on'`.

Note: `WgtFun` will be removed in a future software release. Use `RobustWgtFun` instead.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'ErrorModel','proportional','ErrorParameters',0.5` specifies a proportional error model, with initial value 0.5 for the error parameter estimation

`'ErrorModel'` — Form of error term

`'constant'` (default) | `'proportional'` | `'combined'`

Form of the error term, specified as the comma-separated pair consisting of `'ErrorModel'` and one of the following strings indicating the error model. Each model defines the error using a standard mean-zero and unit-variance variable e in combination with independent components: the function value f, and one or two parameters a and b.

`'constant'` (default)	$y = f + ae$
`'proportional'`	$y = f + bfe$
`'combined'`	$y = f + \left(a + b\left\|f\right\|\right)e$

The only allowed error model when using Weights is `'constant'`.

Note: `options.RobustWgtFun` must have value `[]` when using an error model other than `'constant'`.

`'ErrorParameters'` — Initial estimates for error model parameters

1 or `[1,1]` (default) | scalar value | two-element vector

Initial estimates for the error model parameters in the chosen ErrorModel, specified as the comma-separated pair consisting of `'ErrorParameters'` and a scalar value or two-element vector.

Error Model	Parameters	Default Values
`'constant'`	a	1
`'proportional'`	b	1
`'combined'`	a, b	`[1,1]`

For example, if `'ErrorModel'` has the value `'combined'`, you can specify the starting value 1 for a and the starting value 2 for b as follows.

Example: `'ErrorParameters',[1,2]`

You can only use the `'constant'` error model when using Weights.

Note: `options.RobustWgtFun` must have value `[]` when using an error model other than `'constant'`.

Data Types: `double` | `single`

`'Weights'` — Observation weights

vector | function handle

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of real positive weights or a function handle. You can use observation weights to down-weight the observations that you want to have less influence on the fitted model.

- If `W` is a vector, then it must be the same size as Y.
- If `W` is a function handle, then it must accept a vector of predicted response values as input, and return a vector of real positive weights as output.

Note: `options.RobustWgtFun` must have value `[]` when you use observation weights.

Data Types: `double` | `single` | `function_handle`

Output Arguments

`beta` — Estimated regression coefficients

vector

Estimated regression coefficients, returned as a vector. The number of elements in `beta` equals the number of elements in beta0.

Let $f(X_i,\mathbf{b})$ denote the nonlinear function specified by modelfun, where $\mathbf{x}_i$ are the predictors for observation i, $i = 1,...,N$, and $\mathbf{b}$ are the regression coefficients. The vector of coefficients returned in `beta` minimizes the weighted least squares equation,

$$\sum_{i=1}^{N} w_i \left[y_i - f(\mathbf{x}_i,\mathbf{b})\right]^2.$$

For unweighted nonlinear regression, all of the weight terms are equal to 1.

`R` — Residuals

vector

Residuals for the fitted model, returned as a vector.

- If you specify observation weights using the name-value pair argument Weights, then `R` contains weighted residuals.
- If you specify an error model other than `'constant'` using the name-value pair argument ErrorModel, then you can no longer interpret R as model fit residuals.

`J` — Jacobian

matrix

Jacobian of the nonlinear regression model, modelfun, returned as an N-by-p matrix, where N is the number of observations and p is the number of estimated coefficients.

- If you specify observation weights using the name-value pair argument Weights, then `J` is the weighted model function Jacobian.

- If you specify an error model other than `'constant'` using the name-value pair argument ErrorModel, then you can no longer interpret J as the model function Jacobian.

`CovB` — Estimated variance-covariance matrix

matrix

Estimated variance-covariance matrix for the fitted coefficients, beta, returned as a *p*-by-*p* matrix, where *p* is the number of estimated coefficients. If the model Jacobian, J, has full column rank, then `CovB = inv(J'*J)*MSE`, where MSE is the mean squared error.

`MSE` — Mean squared error

scalar value

Mean squared error (MSE) of the fitted model, returned as a scalar value. MSE is an estimate of the variance of the error term. If the model Jacobian, J, has full column rank, then `MSE = (R'*R)/(N-p)`, where `N` is the number of observations, and `p` is the number of estimated coefficients.

`ErrorModelInfo` — Information about error model fit

structure

Information about the error model fit, returned as a structure with the following fields:

`ErrorModel`	Chosen error model
`ErrorParameters`	Estimated error parameters
`ErrorVariance`	Function handle that accepts an *N*-by-*p* matrix, `X`, and returns an *N*-by-1 vector of error variances using the estimated error model
`MSE`	Mean squared error
`ScheffeSimPred`	Scheffé parameter for simultaneous prediction intervals when using the estimated error model
`WeightFunction`	Logical with value `true` if you used a custom weight function previously in `nlinfit`
`FixedWeights`	Logical with value `true` if you used fixed weights previously in `nlinfit`
`RobustWeightFunction`	Logical with value `true` if you used robust fitting previously in

More About

Weighted Residuals

A *weighted residual* is a residual multiplied by the square root of the corresponding observation weight.

Given estimated regression coefficients, $\mathbf{b}$, the residual for observation i is

$$r_i = y_i - f(\mathbf{x}_i, \mathbf{b}),$$

where y_i is the observed response and $f(\mathbf{x}_i, \mathbf{b})$ is the fitted response at predictors $\mathbf{x}_i$.

When you fit a weighted nonlinear regression with weights w_i, $i = 1,...,N$, `nlinfit` returns the weighted residuals,

$$r_i^* = \sqrt{w_i}\left(y_i - f(\mathbf{x}_i, \mathbf{b})\right).$$

Weighted Model Function Jacobian

The *weighted model function Jacobian* is the nonlinear model Jacobian multiplied by the square root of the observation weight matrix.

Given estimated regression coefficients, $\mathbf{b}$, the estimated model Jacobian, $\mathbf{J}$, for the nonlinear function $f(\mathbf{x}_i, \mathbf{b})$ has elements

$$\mathbf{J}_{ij} = \frac{\partial f(\mathbf{x}_i, \mathbf{b})}{\partial b_j},$$

where b_j is the jth element of $\mathbf{b}$.

When you fit a weighted nonlinear regression with diagonal weights matrix $\mathbf{W}$, `nlinfit` returns the weighted Jacobian matrix,

$$\mathbf{J}^* = \mathbf{W}^{1/2}\mathbf{J}.$$

Tips

- To produce error estimates on predictions, use the optional output arguments `R`, `J`, `CovB`, or `MSE` as inputs to `nlpredci`.
- To produce error estimates on the estimated coefficients, `beta`, use the optional output arguments `R`, `J`, `CovB`, or `MSE` as inputs to `nlparci`.
- If you use the robust fitting option, RobustWgtFun, you must use `CovB`—and might need `MSE`—as inputs to `nlpredci` or `nlparci` to ensure that the confidence intervals take the robust fit properly into account.

Algorithms

- `nlinfit` treats `NaN` values in Y or `modelfun(beta0,X)` as missing data, and ignores the corresponding observations.
- For nonrobust estimation, `nlinfit` uses the Levenberg-Marquardt nonlinear least squares algorithm [1].
- For robust estimation, `nlinfit` uses an iterative reweighted least squares algorithm ([2], [3]). At each iteration, the robust weights are recalculated based on each observation's residual from the previous iteration. These weights downweight outliers, so that their influence on the fit is decreased. Iterations continue until the weights converge.
- When you specify a function handle for observation weights, the weights depend on the fitted model. In this case, `nlinfit` uses an iterative generalized least squares algorithm to fit the nonlinear regression model.

- "Nonlinear Regression" on page 11-2

References

[1] Seber, G. A. F., and C. J. Wild. *Nonlinear Regression*. Hoboken, NJ: Wiley-Interscience, 2003.

[2] DuMouchel, W. H., and F. L. O'Brien. "Integrating a Robust Option into a Multiple Regression Computing Environment." *Computer Science and Statistics: Proceedings of the 21st Symposium on the Interface*. Alexandria, VA: American Statistical Association, 1989.

[3] Holland, P. W., and R. E. Welsch. "Robust Regression Using Iteratively Reweighted Least-Squares." *Communications in Statistics: Theory and Methods*, *A6*, 1977, pp. 813–827.

See Also

`fitnlm` | `nlintool` | `nlparci` | `nlpredci`

nlintool

Interactive nonlinear regression

Syntax

```
nlintool(X,y,fun,beta0)
nlintool(X,y,fun,beta0,alpha)
nlintool(X,y,fun,beta0,alpha,'xname','yname')
```

Description

`nlintool(X,y,fun,beta0)` is a graphical user interface to the `nlinfit` function, and uses the same input arguments. The interface displays plots of the fitted response against each predictor, with the other predictors held fixed. The fixed values are in the text boxes below each predictor axis. Change the fixed values by typing in a new value or by dragging the vertical lines in the plots to new positions. When you change the value of a predictor, all plots update to display the model at the new point in predictor space. Dashed red curves show 95% simultaneous confidence bands for the function.

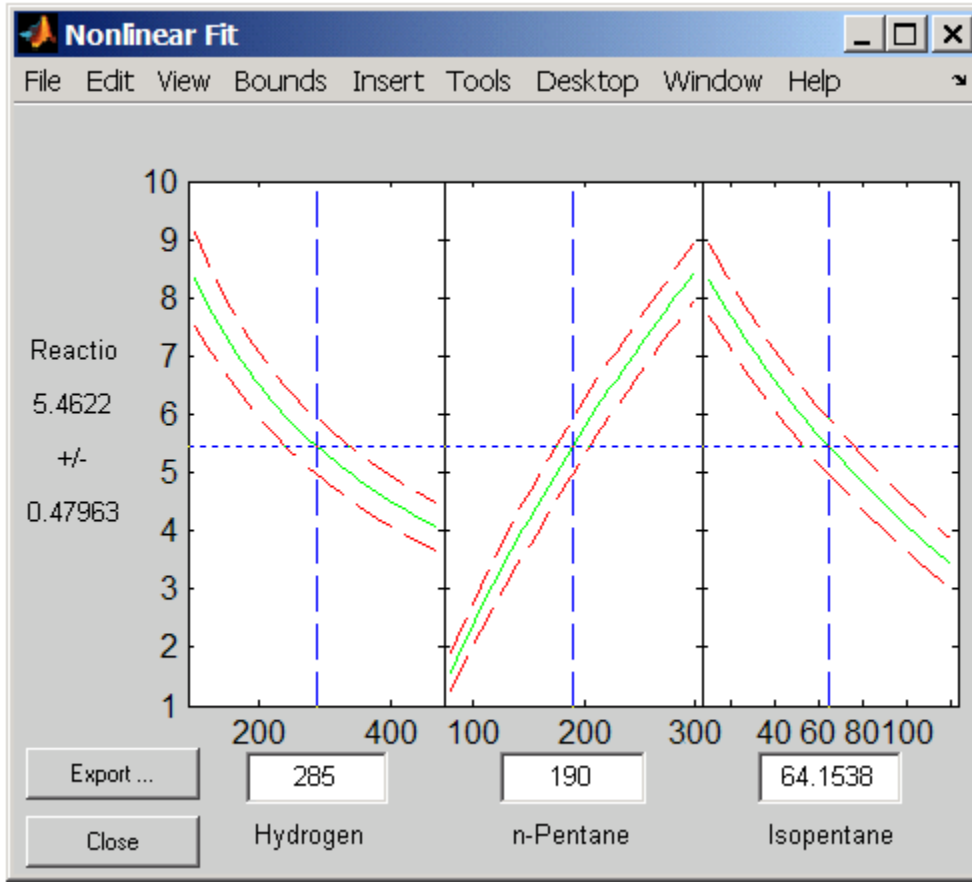
`nlintool(X,y,fun,beta0,alpha)` shows `100(1-alpha)`% confidence bands. These are simultaneous confidence bounds for the function value. Using the **Bounds** menu you can switch between simultaneous and non-simultaneous bounds, and between bounds on the function and bounds for predicting a new observation.

`nlintool(X,y,fun,beta0,alpha,'xname','yname')` labels the plots using the string matrix `'xname'` for the predictors and the string `'yname'` for the response.

Examples

The data in `reaction.mat` are partial pressures of three chemical reactants and the corresponding reaction rates. The function `hougen` implements the nonlinear Hougen-Watson model for reaction rates. The following fits the model to the data:

```
load reaction
nlintool(reactants,rate,@hougen,beta,0.01,xn,yn)
```



See Also

`nlinfit` | `polytool` | `rstool`

nlmefit

Nonlinear mixed-effects estimation

Syntax

```
beta = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI] = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI,stats] = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0)
[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0,'Name',value)
```

Description

`beta = nlmefit(X,y,group,V,fun,beta0)` fits a nonlinear mixed-effects regression model and returns estimates of the fixed effects in `beta`. By default, `nlmefit` fits a model in which each parameter is the sum of a fixed and a random effect, and the random effects are uncorrelated (their covariance matrix is diagonal).

`X` is an n-by-h matrix of n observations on h predictors.

`y` is an n-by-1 vector of responses.

`group` is a grouping variable indicating m groups in the observations. `group` is a categorical variable, a numeric vector, a character matrix with rows for group names, or a cell array of strings. For more information on grouping variables, see “Grouping Variables” on page 2-52.

`V` is an m-by-g matrix or cell array of g group-specific predictors. These are predictors that take the same value for all observations in a group. The rows of `V` are assigned to groups using `grp2idx`, according to the order specified by `grp2idx(group)`. Use a cell array for `V` if group predictors vary in size across groups. Use `[]` for `V` if there are no group-specific predictors.

`fun` is a handle to a function that accepts predictor values and model parameters and returns fitted values. `fun` has the form

```
yfit = modelfun(PHI,XFUN,VFUN)
```

The arguments are:

- `PHI` — A 1-by-p vector of model parameters.
- `XFUN` — A k-by-h array of predictors, where:
  - $k = 1$ if `XFUN` is a single row of `X`.
  - $k = n_i$ if `XFUN` contains the rows of `X` for a single group of size n_i.
  - $k = n$ if `XFUN` contains all rows of `X`.
- `VFUN` — Group-specific predictors given by one of:
  - A 1-by-g vector corresponding to a single group and a single row of `V`.
  - An n-by-g array, where the jth row is V(`I`,:) if the jth observation is in group `I`.

  If `V` is empty, `nlmefit` calls `modelfun` with only two inputs.
- `yfit` — A k-by-1 vector of fitted values

When either `PHI` or `VFUN` contains a single row, it corresponds to all rows in the other two input arguments.

Note: If `modelfun` can compute `yfit` for more than one vector of model parameters per call, use the `'Vectorization'` parameter (described later) for improved performance.

`beta0` is a q-by-1 vector with initial estimates for q fixed effects. By default, q is the number of model parameters p.

`nlmefit` fits the model by maximizing an approximation to the marginal likelihood with random effects integrated out, assuming that:

- Random effects are multivariate normally distributed and independent between groups.
- Observation errors are independent, identically normally distributed, and independent of the random effects.

`[beta,PSI] = nlmefit(X,y,group,V,fun,beta0)` also returns `PSI`, an r-by-r estimated covariance matrix for the random effects. By default, r is equal to the number of model parameters p.

`[beta,PSI,stats] = nlmefit(X,y,group,V,fun,beta0)` also returns `stats`, a structure with fields:

- `dfe` — The error degrees of freedom for the model

- `logl` — The maximized loglikelihood for the fitted model
- `rmse` — The square root of the estimated error variance (computed on the log scale for the `exponential` error model)
- `errorparam` — The estimated parameters of the error variance model
- `aic` — The Akaike information criterion, calculated as `aic` = -2 * `logl` + 2 * `numParam`, where `numParam` is the number of fitting parameters, including the degree of freedom for covariance matrix of the random effects, the number of fixed effects and the number of parameters of the error model, and `logl` is a field in the `stats` structure
- `bic` — The Bayesian information criterion, calculated as `bic` = –2*`logl` + log(`M`) * `numParam`

  - `M` is the number of groups.
  - `numParam` and `logl` are defined as in `aic`.

  Note that some literature suggests that the computation of `bic` should be , `bic` = –2*`logl` + log(`N`) * `numParam`, where `N` is the number of observations.
- `covb` — The estimated covariance matrix of the parameter estimates
- `sebeta` — The standard errors for `beta`
- `ires` — The population residuals `(y-y_population)`, where `y_population` is the individual predicted values
- `pres` — The population residuals `(y-y_population)`, where `y_population` is the population predicted values
- `iwres` — The individual weighted residuals
- `pwres` — The population weighted residuals
- `cwres` — The conditional weighted residuals

`[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0)` also returns `B`, an *r*-by-*m* matrix of estimated random effects for the *m* groups. By default, *r* is equal to the number of model parameters *p*.

`[beta,PSI,stats,B] = nlmefit(X,y,group,V,fun,beta0,'`*`Name`*`,`*`value`*`)` specifies one or more optional parameter name/value pairs. Specify *`Name`* inside single quotes.

Use the following parameters to fit a model different from the default. (The default model is obtained by setting both `FEConstDesign` and `REConstDesign` to `eye(p)`, or by setting both `FEParamsSelect` and `REParamsSelect` to `1:p`.) Use at most one

parameter with an 'FE' prefix and one parameter with an 'RE' prefix. The nlmefit function requires you to specify at least one fixed effect and one random effect.

Parameter	Value
FEParamsSelect	A vector specifying which elements of the parameter vector PHI include a fixed effect, given as a numeric vector of indices from 1 to p or as a 1-by-*p* logical vector. If *q* is the specified number of elements, then the model includes *q* fixed effects.
FEConstDesign	A *p*-by-*q* design matrix ADESIGN, where ADESIGN*beta are the fixed components of the *p* elements of PHI.
FEGroupDesign	A *p*-by-*q*-by-*m* array specifying a different *p*-by-*q* fixed-effects design matrix for each of the *m* groups.
FEObsDesign	A *p*-by-*q*-by-*n* array specifying a different *p*-by-*q* fixed-effects design matrix for each of the *n* observations.
REParamsSelect	A vector specifying which elements of the parameter vector PHI include a random effect, given as a numeric vector of indices from 1 to p or as a 1-by-*p* logical vector. The model includes *r* random effects, where *r* is the specified number of elements.
REConstDesign	A *p*-by-*r* design matrix BDESIGN, where BDESIGN*B are the random components of the *p* elements of PHI.
REGroupDesign	A *p*-by-*r*-by-*m* array specifying a different *p*-by-*r* random-effects design matrix for each of *m* groups.
REObsDesign	A *p*-by-*r*-by-*n* array specifying a different *p*-by-*r* random-effects design matrix for each of *n* observations.

Use the following parameters to control the iterative algorithm for maximizing the likelihood:

Parameter	Value
RefineBeta0	Determines whether nlmefit makes an initial refinement of beta0 by first fitting modelfun without random effects and replacing beta0 with beta.

Parameter	Value
	Choices are 'on' and 'off'. The default value is 'on'.
ErrorModel	A string specifying the form of the error term. Default is 'constant'. Each model defines the error using a standard normal (Gaussian) variable e, the function value f, and one or two parameters a and b. Choices are: • 'constant': $y = f + a*e$ • 'proportional': $y = f + b*f*e$ • 'combined': $y = f + (a+b*f)*e$ • 'exponential': $y = f*\exp(a*e)$, or equivalently $\log(y) = \log(f) + a*e$ If this parameter is given, the output stats.errorparam field has the value • a for 'constant' and 'exponential' • b for 'proportional' • $[a\ b]$ for 'combined'
ApproximationType	The method used to approximate the likelihood of the model. Choices are: • 'LME' — Use the likelihood for the linear mixed-effects model at the current conditional estimates of beta and B. This is the default. • 'RELME' — Use the restricted likelihood for the linear mixed-effects model at the current conditional estimates of beta and B. • 'FO' — First-order Laplacian approximation without random effects. • 'FOCE' — First-order Laplacian approximation at the conditional estimates of B.

Parameter	Value
`Vectorization`	Indicates acceptable sizes for the `PHI`, `XFUN`, and `VFUN` input arguments to `modelfun`. Choices are: • `'SinglePhi'` — `modelfun` can only accept a single set of model parameters at a time, so `PHI` must be a single row vector in each call. `nlmefit` calls `modelfun` in a loop, if necessary, with a single `PHI` vector and with `XFUN` containing rows for a single observation or group at a time. `VFUN` may be a single row that applies to all rows of `XFUN`, or a matrix with rows corresponding to rows in `XFUN`. This is the default. • `'SingleGroup'` — `modelfun` can only accept inputs corresponding to a single group in the data, so `XFUN` must contain rows of `X` from a single group in each call. Depending on the model, `PHI` is a single row that applies to the entire group or a matrix with one row for each observation. `VFUN` is a single row. • `'Full'` — `modelfun` can accept inputs for multiple parameter vectors and multiple groups in the data. Either `PHI` or `VFUN` may be a single row that applies to all rows of `XFUN` or a matrix with rows corresponding to rows in `XFUN`. This option can improve performance by reducing the number of calls to `modelfun`, but may require `modelfun` to perform singleton expansion on `PHI` or `V`.
`CovParameterization`	Specifies the parameterization used internally for the scaled covariance matrix. Choices are `'chol'` for the Cholesky factorization or `'logm'` the matrix logarithm. The default is `'logm'`.

Parameter	Value
CovPattern	Specifies an *r*-by-*r* logical or numeric matrix P that defines the pattern of the random-effects covariance matrix PSI. nlmefit estimates the variances along the diagonal of PSI and the covariances specified by nonzeros in the off-diagonal elements of P. Covariances corresponding to zero off-diagonal elements in P are constrained to be zero. If P does not specify a row-column permutation of a block diagonal matrix, nlmefit adds nonzero elements to P as needed. The default value of P is eye(r), corresponding to uncorrelated random effects. Alternatively, P may be a 1-by-*r* vector containing values in 1:r, with equal values specifying groups of random effects. In this case, nlmefit estimates covariances only within groups, and constrains covariances across groups to be zero.
ParamTransform	A vector of *p*-values specifying a transformation function *f*() for each of the P parameters: XB = ADESIGN*BETA + BDESIGN*B PHI = *f*(XB). Each element of the vector must be one of the following integer codes specifying the transformation for the corresponding value of PHI: • 0: PHI = XB (default for all parameters) • 1: log(PHI) = XB • 2: probit(PHI) = XB • 3: logit(PHI) = XB

Parameter	Value

`Options`	A structure of the form returned by `statset`. `nlmefit` uses the following `statset` parameters:
	• `'DerivStep'` — Relative difference used in finite difference gradient calculation. May be a scalar, or a vector whose length is the number of model parameters p. The default is `eps^(1/3)`.
	• `'Display'` — Level of iterative display during estimation. Choices are:
	  • `'off'` (default) — Displays no information
	  • `'final'` — Displays information after the final iteration
	  • `'iter'` — Displays information at each iteration
	• `'FunValCheck'` — Check for invalid values, such as `NaN` or `Inf`, from `modelfun`. Choices are `'on'` and `'off'`. The default is `'on'`.
	• `'MaxIter'` — Maximum number of iterations allowed. The default is `200`.
	• `'OutputFcn'` — Function handle specified using `@`, a cell array with function handles or an empty array (default). The solver calls all output functions after each iteration.
	• `'TolFun'` — Termination tolerance on the loglikelihood function. The default is `1e-4`.
	• `'TolX'` — Termination tolerance on the estimated fixed and random effects. The default is `1e-4`.

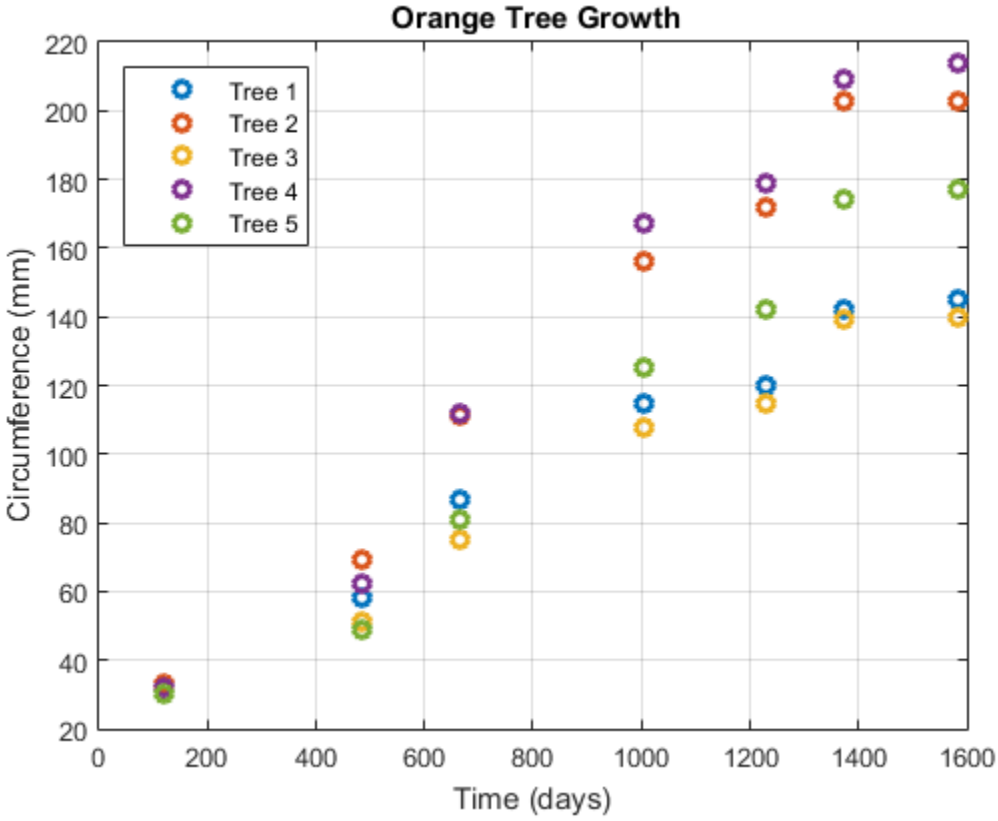
`OptimFun`	Specifies the optimization function used in maximizing the likelihood. Choices are `'fminsearch'` to use `fminsearch` or `'fminunc'` to use `fminunc`. The default is `'fminsearch'`. You can specify `'fminunc'` only if Optimization Toolbox software is installed.

Examples

Nonlinear Mixed-Effects Model

Enter and display data on the growth of five orange trees.

```
CIRC = [30 58 87 115 120 142 145;
        33 69 111 156 172 203 203;
        30 51 75 108 115 139 140;
        32 62 112 167 179 209 214;
        30 49 81 125 142 174 177];
time = [118 484 664 1004 1231 1372 1582];

h = plot(time,CIRC','o','LineWidth',2);
xlabel('Time (days)')
ylabel('Circumference (mm)')
title('{\bf Orange Tree Growth}')
legend([repmat('Tree ',5,1),num2str((1:5)')],...
       'Location','NW')
grid on
hold on
```



Use an anonymous function to specify a logistic growth model.

```
model = @(PHI,t)(PHI(:,1))./(1+exp(-(t-PHI(:,2))./PHI(:,3)));
```

Fit the model using `nlmefit` with default settings (that is, assuming each parameter is the sum of a fixed and a random effect, with no correlation among the random effects):

```
TIME = repmat(time,5,1);
NUMS = repmat((1:5)',size(time));

beta0 = [100 100 100];
[beta1,PSI1,stats1] = nlmefit(TIME(:),CIRC(:),NUMS(:),...
                              [],model,beta0)
```

```
beta1 =

  191.3189
  723.7608
  346.2517


PSI1 =

  962.1533         0         0
         0    0.0000         0
         0         0  297.9880


stats1 =

           dfe: 28
          logl: -131.5457
           mse: 59.7882
          rmse: 7.9016
    errorparam: 7.7323
           aic: 277.0913
           bic: 274.3574
          covb: [3x3 double]
        sebeta: [15.2249 33.1579 26.8235]
          ires: [35x1 double]
          pres: [35x1 double]
         iwres: [35x1 double]
         pwres: [35x1 double]
         cwres: [35x1 double]
```

The negligible variance of the second random effect, `PSI1(2,2)`, suggests that it can be removed to simplify the model.

```
[beta2,PSI2,stats2,b2] = nlmefit(TIME(:),CIRC(:),...
    NUMS(:),[],model,beta0,'REParamsSelect',[1 3])


beta2 =

  191.3189
  723.7613
  346.2502
```

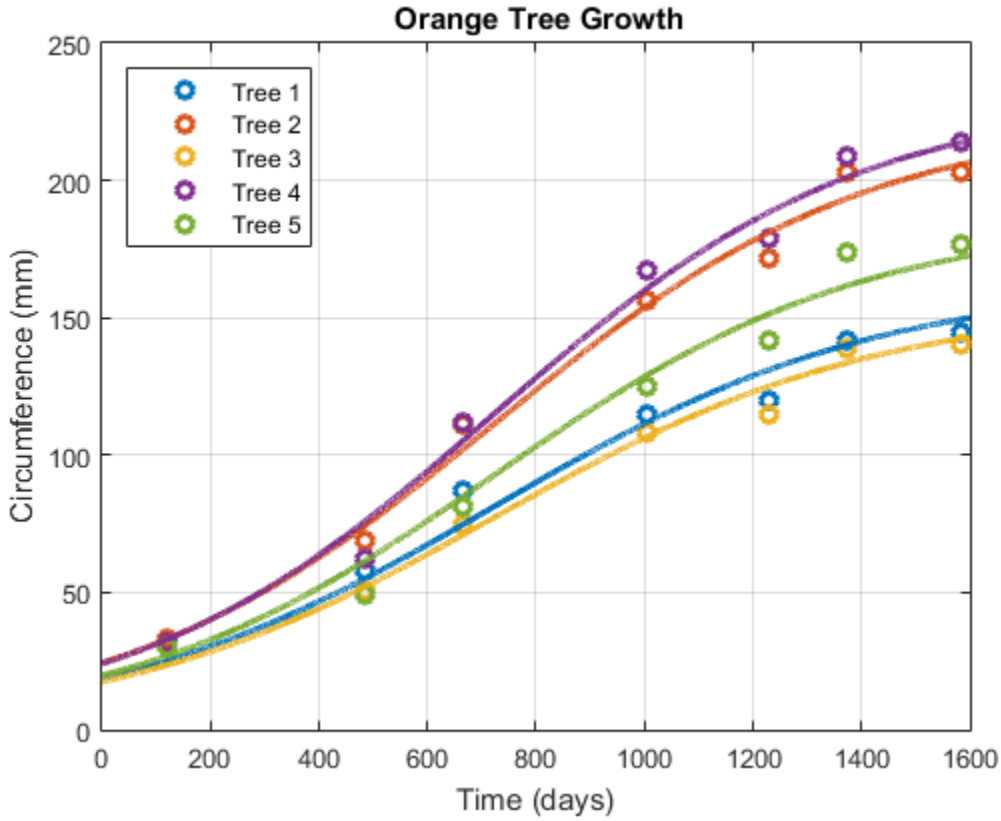
```
PSI2 =

  962.5602         0
         0  297.4975


stats2 =

           dfe: 29
          logl: -131.5457
           mse: 59.7869
          rmse: 7.7645
    errorparam: 7.7322
           aic: 275.0913
           bic: 272.7479
          covb: [3x3 double]
        sebeta: [15.2275 33.1579 26.8214]
          ires: [35x1 double]
          pres: [35x1 double]
         iwres: [35x1 double]
         pwres: [35x1 double]
         cwres: [35x1 double]


b2 =

  -28.5275   31.6066  -36.5086   39.0762   -5.6467
    9.9837   -0.7608    5.9959   -9.4449   -5.7738
```

The loglikelihood `logl` is unaffected, and both the Akaike and Bayesian information criteria (`aic` and `bic`) are reduced, supporting the decision to drop the second random effect from the model.

Use the estimated fixed effects in `beta2` and the estimated random effects for each tree in `b2` to plot the model through the data.

```
PHI = repmat(beta2,1,5) + ...          % Fixed effects
      [b2(1,:);zeros(1,5);b2(2,:)];    % Random effects

tplot = 0:0.1:1600;
for I = 1:5
  fitted_model=@(t)(PHI(1,I))./(1+exp(-(t-PHI(2,I))./ ...
```

```
        PHI(3,I)));
    plot(tplot,fitted_model(tplot),'Color',h(I).Color, ...
      'LineWidth',2)
end
```



More About

- “Mixed-Effects Models” on page 11-20
- “Grouping Variables” on page 2-52

References

[1] Lindstrom, M. J., and D. M. Bates. "Nonlinear mixed-effects models for repeated measures data." *Biometrics*. Vol. 46, 1990, pp. 673–687.

[2] Davidian, M., and D. M. Giltinan. *Nonlinear Models for Repeated Measurements Data*. New York: Chapman & Hall, 1995.

[3] Pinheiro, J. C., and D. M. Bates. "Approximations to the log-likelihood function in the nonlinear mixed-effects model." *Journal of Computational and Graphical Statistics*. Vol. 4, 1995, pp. 12–35.

[4] Demidenko, E. *Mixed Models: Theory and Applications*. Hoboken, NJ: John Wiley & Sons, Inc., 2004.

See Also

`nlinfit` | `nlpredci` | `nlmefitsa`

nlmefitsa

Fit nonlinear mixed-effects model with stochastic EM algorithm

Syntax

```
[BETA,PSI,STATS,B] = nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0)
[BETA,PSI,STATS,B] =
nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0,'Name',Value)
```

Description

`[BETA,PSI,STATS,B] = nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0)` fits a nonlinear mixed-effects regression model and returns estimates of the fixed effects in `BETA`. By default, `nlmefitsa` fits a model where each model parameter is the sum of a corresponding fixed and random effect, and the covariance matrix of the random effects is diagonal, i.e., uncorrelated random effects.

The `BETA`, `PSI`, and other values this function returns are the result of a random (Monte Carlo) simulation designed to converge to the maximum likelihood estimates of the parameters. Because the results are random, it is advisable to examine the plot of simulation to results to be sure that the simulation has converged. It may also be helpful to run the function multiple times, using multiple starting values, or use the `'Replicates'` parameter to perform multiple simulations.

`[BETA,PSI,STATS,B] = nlmefitsa(X,Y,GROUP,V,MODELFUN,BETA0,'Name',Value)` accepts one or more comma-separated parameter name/value pairs. Specify *`Name`* inside single quotes.

Input Arguments

Definitions:

In the following list of arguments, the following variable definitions apply:

- n — number of observations

- h — number of predictor variables
- m — number of groups
- g — number of group-specific predictor variables
- p — number of parameters
- f — number of fixed effects

`X`

An n-by-h matrix of n observations on h predictor variables.

`Y`

An n-by-1 vector of responses.

`GROUP`

A grouping variable indicating to which of m groups each observation belongs. `GROUP` can be a categorical variable, a numeric vector, a character matrix with rows for group names, or a cell array of strings.

`V`

An m-by-g matrix of g group-specific predictor variables for each of the m groups in the data. These are predictor values that take on the same value for all observations in a group. Rows of `V` are ordered according to `GRP2IDX(GROUP)`. Use an m-by-g cell array for `V` if any of the group-specific predictor values vary in size across groups. Specify `[]` for `V` if there are no group predictors.

`MODELFUN`

A handle to a function that accepts predictor values and model parameters, and returns fitted values. `MODELFUN` has the form `YFIT = MODELFUN(PHI,XFUN,VFUN)` with input arguments

- `PHI` — A 1-by-p vector of model parameters.
- `XFUN` — An l-by-h array of predictor variables where
  - l is 1 if `XFUN` is a single row of `X`
  - l is n_i if `XFUN` contains the rows of `X` for a single group of size n_i
  - l is n if `XFUN` contains all rows of `X`.

- VFUN — Either
  - A 1-by-*g* vector of group-specific predictors for a single group, corresponding to a single row of V
  - An *n*-by-*g* matrix, where the *k*-th row of VFUN is V(*i*,:) if the *k*-th observation is in group *i*.

  If V is empty, nlmefitsa calls MODELFUN with only two inputs.

MODELFUN returns an *l*-by-1 vector of fitted values YFIT. When either PHI or VFUN contains a single row, that one row corresponds to all rows in the other two input arguments. For improved performance, use the 'Vectorization' parameter name/value pair (described below) if MODELFUN can compute YFIT for more than one vector of model parameters in one call.

BETA0

An *f*-by-1 vector with initial estimates for the *f* fixed effects. By default, *f* is equal to the number of model parameters *p*. BETA0 can also be an *f*-by-REPS matrix, and the estimation is repeated REPS times using each column of BETA0 as a set of starting values.

Name-Value Pair Arguments

By default, nlmefitsa fits a model where each model parameter is the sum of a corresponding fixed and random effect. Use the following parameter name/value pairs to fit a model with a different number of or dependence on fixed or random effects. Use at most one parameter name with an 'FE' prefix and one parameter name with an 'RE' prefix. Note that some choices change the way nlmefitsa calls MODELFUN, as described further below.

'FEParamsSelect'

A vector specifying which elements of the model parameter vector PHI include a fixed effect, as a numeric vector with elements in 1:*p*, or as a 1-by-*p* logical vector. The model will include *f* fixed effects, where *f* is the specified number of elements.

'FEConstDesign'

A *p*-by-*f* design matrix ADESIGN, where ADESIGN*BETA are the fixed components of the *p* elements of PHI.

'FEGroupDesign'

A *p*-by-*f*-by-*m* array specifying a different *p*-by-*f* fixed effects design matrix for each of the *m* groups.

'REParamsSelect'

A vector specifying which elements of the model parameter vector PHI include a random effect, as a numeric vector with elements in 1:*p*, or as a 1-by-*p* logical vector. The model will include *r* random effects, where *r* is the specified number of elements.

'REConstDesign'

A *p*-by-*r* design matrix BDESIGN, where BDESIGN*B are the random components of the *p* elements of PHI. This matrix must consist of 0s and 1s, with at most one 1 per row.

The default model is equivalent to setting both FEConstDesign and REConstDesign to eye(p), or to setting both FEParamsSelect and REParamsSelect to 1:*p*.

Additional optional parameter name/value pairs control the iterative algorithm used to maximize the likelihood:

'CovPattern'

Specifies an *r*-by-*r* logical or numeric matrix PAT that defines the pattern of the random effects covariance matrix PSI. nlmefitsa computes estimates for the variances along the diagonal of PSI as well as covariances that correspond to non-zeroes in the off-diagonal of PAT. nlmefitsa constrains the remaining covariances, i.e., those corresponding to off-diagonal zeroes in PAT, to be zero. PAT must be a row-column permutation of a block diagonal matrix, and nlmefitsa adds non-zero elements to PAT as needed to produce such a pattern. The default value of PAT is eye(r), corresponding to uncorrelated random effects.

Alternatively, specify PAT as a 1-by-*r* vector containing values in 1:*r*. In this case, elements of PAT with equal values define groups of random effects, nlmefitsa estimates covariances only within groups, and constrains covariances across groups to be zero.

'CovO'

Initial value for the covariance matrix PSI. Must be an *r*-by-*r* positive definite matrix. If empty, the default value depends on the values of BETA0.

'ComputeStdErrors'

`true` to compute standard errors for the coefficient estimates and store them in the output `STATS` structure, or `false` (default) to omit this computation.

'ErrorModel'

A string specifying the form of the error term. Default is `'constant'`. Each model defines the error using a standard normal (Gaussian) variable e, the function value f, and one or two parameters a and b. Choices are

- `'constant'` — $y = f + a*e$
- `'proportional'` — $y = f + b*f*e$
- `'combined'` — $y = f + (a+b*f)*e$
- `'exponential'` — $y = f*\exp(a*e)$, or equivalently $\log(y) = \log(f) + a*e$

If this parameter is given, the output `STATS.errorparam` field has the value

- a for `'constant'` and `'exponential'`
- b for `'proportional'`
- [a b] for `'combined'`

'ErrorParameters'

A scalar or two-element vector specifying starting values for parameters of the error model. This specifies the a, b, or [a b] values depending on the `ErrorModel` parameter.

'LogLikMethod'

Specifies the method for approximating the loglikelihood. Choices are:

- `'is'` — Importance sampling
- `'gq'` — Gaussian quadrature
- `'lin'` — Linearization
- `'none'` — Omit the loglikelihood approximation (default)

'NBurnIn'

Number of initial burn-in iterations during which the parameter estimates are not recomputed. Default is 5.

`'NChains'`

Number *c* of "chains" simulated. Default is 1. Setting *c*>1 causes *c* simulated coefficient vectors to be computed for each group during each iteration. Default depends on the data, and is chosen to provide about 100 groups across all chains.

`'NIterations'`

Number of iterations. This can be a scalar or a three-element vector. Controls how many iterations are performed for each of three phases of the algorithm:

1 simulated annealing

2 full step size

3 reduced step size

Default is `[150 150 100]`. A scalar is distributed across the three phases in the same proportions as the default.

`'NMCMCIterations'`

Number of Markov Chain Monte Carlo (MCMC) iterations. This can be a scalar or a three-element vector. Controls how many of three different types of MCMC updates are performed during each phase of the main iteration:

1 full multivariate update

2 single coordinate update

3 multiple coordinate update

Default is `[2 2 2]`. A scalar value is treated as a three-element vector with all elements equal to the scalar.

`'OptimFun'`

Either `'fminsearch'` or `'fminunc'`, specifying the optimization function to be used during the estimation process. Default is `'fminsearch'`. Use of `'fminunc'` requires Optimization Toolbox.

`'Options'`

A structure created by a call to `statset`. `nlmefitsa` uses the following `statset` parameters:

- `'DerivStep'` — Relative difference used in finite difference gradient calculation. May be a scalar, or a vector whose length is the number of model parameters p. The default is `eps^(1/3)`.
- `Display` — Level of display during estimation.
  - `'off'` (default) — Displays no information
  - `'final'` — Displays information after the final iteration of the estimation algorithm
  - `'iter'` — Displays information at each iteration
- `FunValCheck`
  - `'on'` (sdefault) — Check for invalid values (such as `NaN` or `Inf`) from `MODELFUN`
  - `'off'` — Skip this check
- `OutputFcn` — Function handle specified using `@`, a cell array with function handles or an empty array. `nlmefitsa` calls all output functions after each iteration. See `nlmefitoutputfcn.m` (the default output function for `nlmefitsa`) for an example of an output function.

`'ParamTransform'`

A vector of p-values specifying a transformation function `f()` for each of the p parameters:

```
XB = ADESIGN*BETA + BDESIGN*B
PHI = f(XB)
```

Each element of the vector must be one of the following integer codes specifying the transformation for the corresponding value of `PHI`:

- 0: `PHI = XB` (default for all parameters)
- 1: `log(PHI) = XB`
- 2: `probit(PHI) = XB`
- 3: `logit(PHI) = XB`

`'Replicates'`

Number `REPS` of estimations to perform starting from the starting values in the vector `BETA0`. If `BETA0` is a matrix, `REPS` must match the number of columns in `BETA0`. Default is the number of columns in `BETA0`.

'Vectorization'

Determines the possible sizes of the PHI, XFUN, and VFUN input arguments to MODELFUN. Possible values are:

- 'SinglePhi' — MODELFUN is a function (such as an ODE solver) that can only compute YFIT for a single set of model parameters at a time, i.e., PHI must be a single row vector in each call. nlmefitsa calls MODELFUN in a loop if necessary using a single PHI vector and with XFUN containing rows for a single observation or group at a time. VFUN may be a single row that applies to all rows of XFUN, or a matrix with rows corresponding to rows in XFUN.
- 'SingleGroup' — MODELFUN can only accept inputs corresponding to a single group in the data, i.e., XFUN must contain rows of X from a single group in each call. Depending on the model, PHI is a single row that applies to the entire group, or a matrix with one row for each observation. VFUN is a single row.
- 'Full' — MODELFUN can accept inputs for multiple parameter vectors and multiple groups in the data. Either PHI or VFUN may be a single row that applies to all rows of XFUN, or a matrix with rows corresponding to rows in XFUN. Using this option can improve performance by reducing the number of calls to MODELFUN, but may require MODELFUN to perform singleton expansion on PHI or V.

The default for 'Vectorization' is 'SinglePhi'. In all cases, if V is empty, nlmefitsa calls MODELFUN with only two inputs.

Output Arguments

BETA

Estimates of the fixed effects

PSI

An *r*-by-*r* estimated covariance matrix for the random effects. By default, *r* is equal to the number of model parameters *p*.

STATS

A structure with the following fields:

- `logl` — The maximized loglikelihood for the fitted model; empty if the `LogLikMethod` parameter has its default value of `'none'`
- `rmse` — The square root of the estimated error variance (computed on the log scale for the `exponential` error model)
- `errorparam` — The estimated parameters of the error variance model
- `aic` — The Akaike information criterion (empty if `logl` is empty), calculated as `aic` = –2 * `logl` + 2 * `numParam`, where
  - `logl` is the maximized loglikelihood.
  - `numParam` is the number of fitting parameters, including the degree of freedom for covariance matrix of the random effects, the number of fixed effects and the number of parameters of the error model.
- `bic` — The Bayesian information criterion (empty if `logl` is empty), calculated as `bic` = -2*`logl` + log(`M`) * `numParam`
  - `M` is the number of groups.
  - `logl` and `numParam` are defined as in `aic`.

  Note that some literature suggests that the computation of `bic` should be , `bic` = -2*`logl` + log(`N`) * `numParam`, where `N` is the number of observations. To adjust the value of the output you can redefine `bic` as follows: `bic` = `bic` - `numel`(`unique`(`group`)) + `numel`(`Y`)
- `sebeta` — The standard errors for BETA (empty if the `ComputeStdErrors` parameter has its default value of false)
- `covb` — The estimated covariance of the parameter estimates (empty if `ComputeStdErrors` is false)
- `dfe` — The error degrees of freedom
- `pres` — The population residuals `(y-y_population)`, where `y_population` is the population predicted values
- `ires` — The population residuals `(y-y_population)`, where `y_population` is the individual predicted values
- `pwres` — The population weighted residuals
- `cwres` — The conditional weighted residuals
- `iwres` — The individual weighted residuals

Examples

Nonlinear Mixed-Effects Model with Stochastic EM Algorithm

Load the sample data.

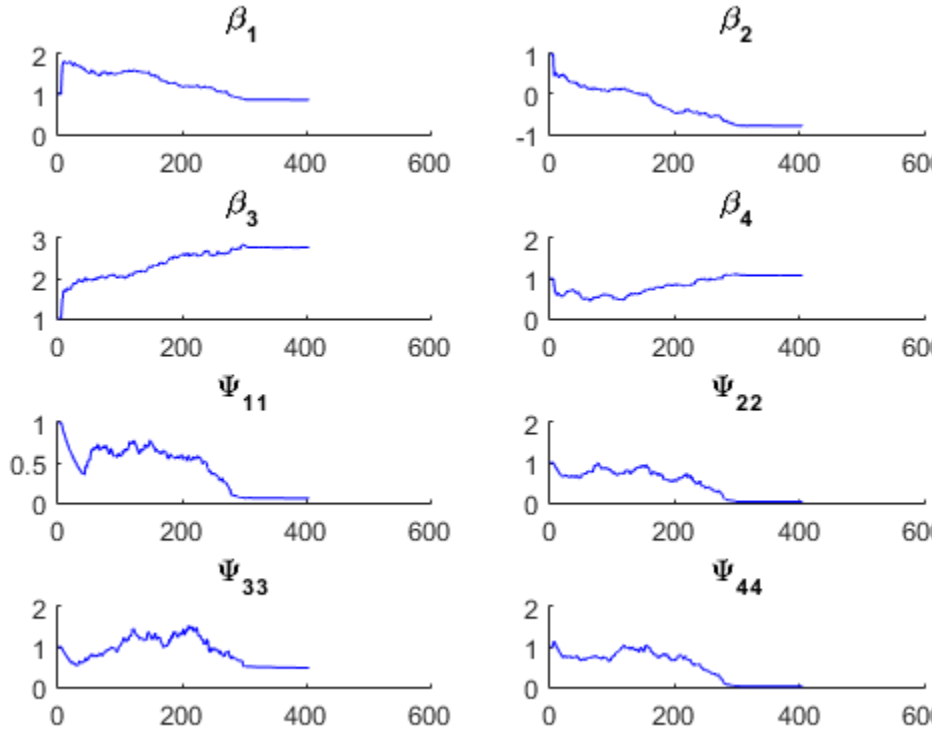
```
load indomethacin
```

Fit a model to data on concentrations of the drug indomethacin in the bloodstream of six subjects over eight hours.

```
model = @(phi,t)(phi(:,1).*exp(-phi(:,2).*t)+phi(:,3).*exp(-phi(:,4).*t));
phi0 = [1 1 1 1];
xform = [0 1 0 1]; % log transform for 2nd and 4th parameters
[beta,PSI,stats,br] = nlmefitsa(time,concentration,...
   subject,[],model,phi0,'ParamTransform',xform)
```

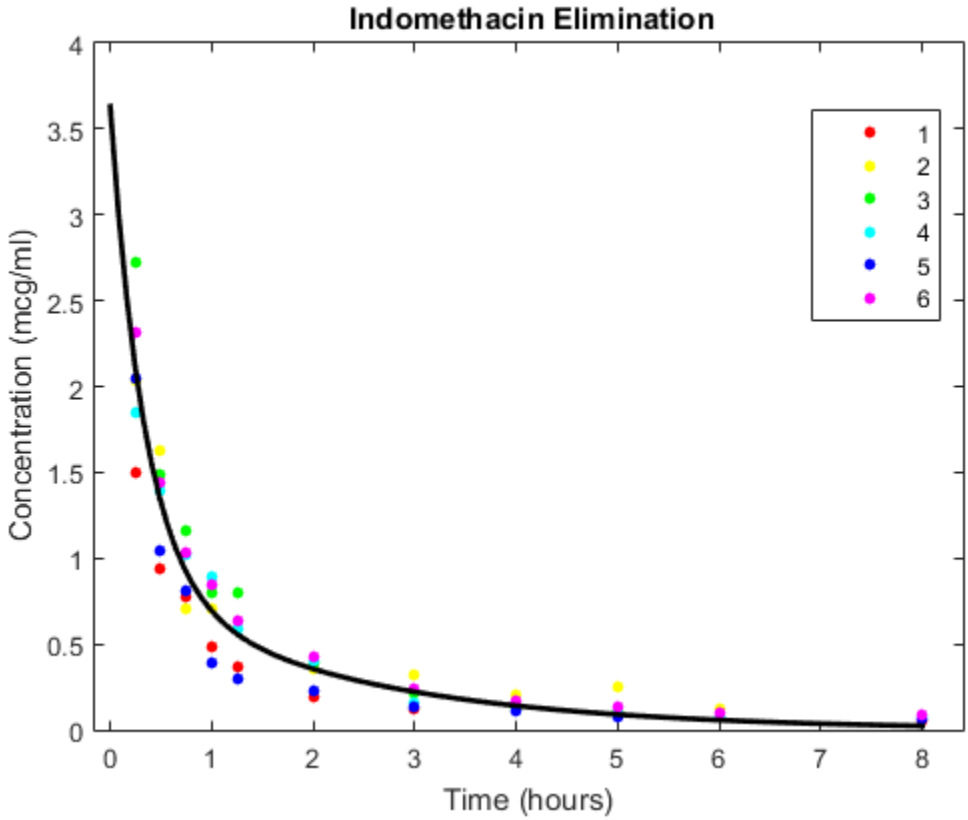
```
beta =

    0.8563
   -0.7950
    2.7744
    1.0772


PSI =

    0.0529         0         0         0
         0    0.0220         0         0
         0         0    0.4762         0
         0         0         0    0.0120


stats =

          logl: []
           aic: []
           bic: []
        sebeta: []
           dfe: 57
          covb: []
    errorparam: 0.0809
          rmse: 0.0775
```

```
          ires: [66x1 double]
          pres: [66x1 double]
         iwres: [66x1 double]
         pwres: [66x1 double]
         cwres: [66x1 double]

br =

   -0.2255    0.0063    0.1600    0.1773   -0.3269    0.1157
    0.0350   -0.1384    0.0058    0.0431    0.0093   -0.0453
   -0.7557   -0.0550    0.8736   -0.7875    0.5304    0.1727
   -0.0010   -0.0198    0.0137   -0.0757    0.0478   -0.0076
```



Plot the data along with an overall population fit

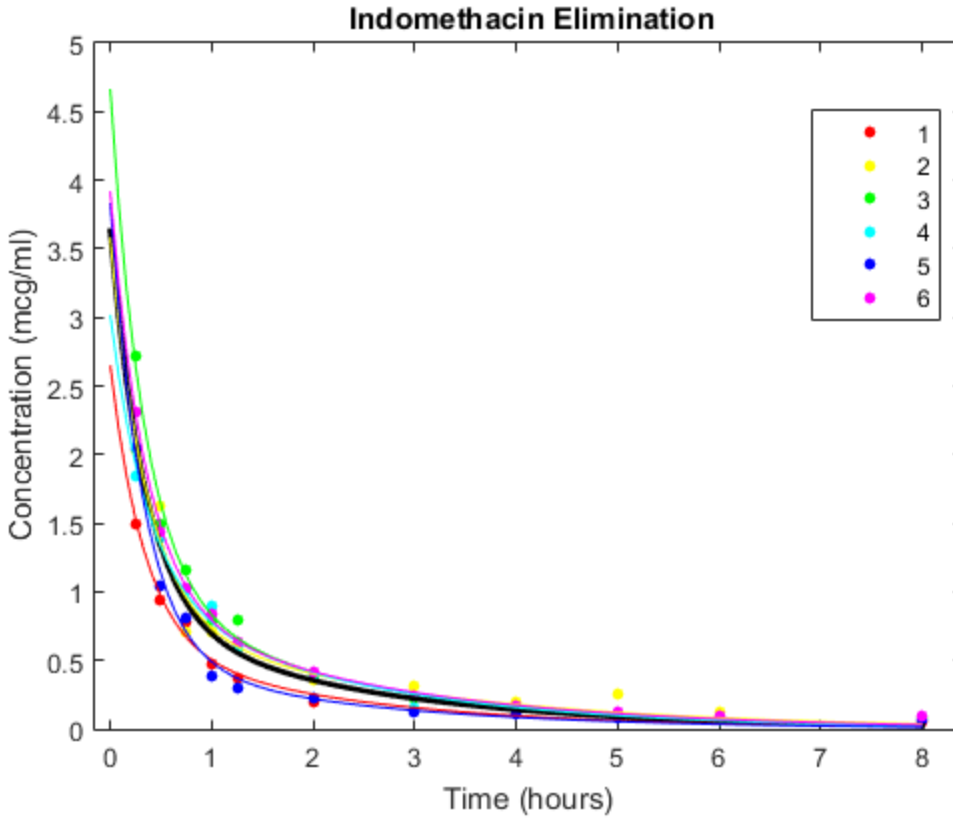
```
clf
phi = [beta(1), exp(beta(2)), beta(3), exp(beta(4))];
h = gscatter(time,concentration,subject);
xlabel('Time (hours)')
ylabel('Concentration (mcg/ml)')
title('{\bf Indomethacin Elimination}')
xx = linspace(0,8);
line(xx,model(phi,xx),'linewidth',2,'color','k')
```



Plot individual curves based on random-effect estimates.

```
for j=1:6
```

```
    phir = [beta(1)+br(1,j), exp(beta(2)+br(2,j)), ...
            beta(3)+br(3,j), exp(beta(4)+br(4,j))];
    line(xx,model(phir,xx),'color',get(h(j),'color'))
end
```



More About

Algorithms

In order to estimate the parameters of a nonlinear mixed effects model, we would like to choose the parameter values that maximize a likelihood function. These values are called the maximum likelihood estimates. The likelihood function can be written in the form

$$p\left(y \mid \beta, \sigma^2, \Sigma\right) = \int p\left(y \mid \beta, b, \sigma^2\right) p\left(b \mid \Sigma\right) db$$

where

- y is the response data
- ß is the vector of population coefficients
- σ^2 is the residual variance
- $\sum$ is the covariance matrix for the random effects
- b is the set of unobserved random effects

Each $p()$ function on the right-hand-side is a normal (Gaussian) likelihood function that may depend on covariates.

Since the integral does not have a closed form, it is difficult to find parameters that maximize it. Delyon, Lavielle, and Moulines [1] proposed to find the maximum likelihood estimates using an Expectation-Maximization (EM) algorithm in which the E step is replaced by a stochastic procedure. They called their algorithm SAEM, for Stochastic Approximation EM. They demonstrated that this algorithm has desirable theoretical properties, including convergence under practical conditions and convergence to a local maximum of the likelihood function. Their proposal involves three steps:

1. Simulation: Generate simulated values of the random effects b from the posterior density $p(b \mid \Sigma)$ given the current parameter estimates.
2. Stochastic approximation: Update the expected value of the loglikelihood function by taking its value from the previous step, and moving part way toward the average value of the loglikelihood calculated from the simulated random effects.
3. Maximization step: Choose new parameter estimates to maximize the loglikelihood function given the simulated values of the random effects.

- "Mixed-Effects Models" on page 11-20
- "Grouping Variables" on page 2-52

References

[1] Delyon, B., M. Lavielle, and E. Moulines, *Convergence of a stochastic approximation version of the EM algorithm*, Annals of Statistics, 27, 94-128, 1999.

[2] Mentré, France, and Marc Lavielle, *Stochastic EM algorithms in population PKPD analyses*, 2008.

See Also

`nlinfit` | `nlpredci` | `nlmefit`

NegativeLogLikelihood property

Class: gmdistribution

Negative of log-likelihood

Description

The negative of the log-likelihood of the data.

Note: This property applies only to `gmdistribution` objects constructed with `fitgmdist`.

NLogL property

Class: ProbDistParametric

Read-only value specifying negative log likelihood for input data to ProbDistParametric object

Description

`NLogL` is a read-only property of the `ProbDistParametric` class. `NLogL` is a value specifying the negative log likelihood for input data used to fit a distribution represented by a ProbDistParametric object.

Values

The value is a numeric scalar for a distribution fit to input data, that is, a distribution created using the `fitdist` function. This property is empty for distributions created without fitting to data, that is, by using the `ProbDistUnivParam` constructor. Use this information to view and compare the negative log likelihood for input data supplied to create distributions.

NLogL property

Class: ProbDistUnivKernel

Read-only value specifying negative log likelihood for input data to ProbDistUnivKernel object

Description

`NLogL` is a read-only property of the `ProbDistUnivKernel` class. `NLogL` is a value specifying the negative log likelihood for input data used to fit a distribution represented by a ProbDistUnivKernel object.

Values

The value is a numeric scalar for a distribution fit to input data, that is, a distribution created using the `fitdist` function. Use this information to view and compare the negative log likelihood for input data used to create distributions.

nlparci

Nonlinear regression parameter confidence intervals

Syntax

```
ci = nlparci(beta,resid,'covar',sigma)
ci = nlparci(beta,resid,'jacobian',J)
ci = nlparci(...,'alpha',alpha)
```

Description

`ci = nlparci(beta,resid,'covar',sigma)` returns the 95% confidence intervals `ci` for the nonlinear least squares parameter estimates `beta`. Before calling `nlparci`, use `nlinfit` to fit a nonlinear regression model and get the coefficient estimates `beta`, residuals `resid`, and estimated coefficient covariance matrix `sigma`.

`ci = nlparci(beta,resid,'jacobian',J)` is an alternative syntax that also computes 95% confidence intervals. `J` is the Jacobian computed by `nlinfit`. If the `'robust'` option is used with `nlinfit`, use the `'covar'` input rather than the `'jacobian'` input so that the required `sigma` parameter takes the robust fitting into account.

`ci = nlparci(...,'alpha',alpha)` returns `100(1-alpha)`% confidence intervals.

`nlparci` treats `NaN`s in `resid` or `J` as missing values, and ignores the corresponding observations.

The confidence interval calculation is valid for systems where the length of `resid` exceeds the length of `beta` and `J` has full column rank. When `J` is ill-conditioned, confidence intervals may be inaccurate.

Examples

Fit to exponential decay

Suppose you have data, and want to fit a model of the form

$y_i = a_1 + a_2\exp(-a_3 x_i) + \varepsilon_i$.

Here the a_i are the parameters you want to estimate, x_i are the data points, the y_i are the responses, and the ε_i are noise terms.

1. Write a function handle that represents the model:

```
mdl = @(a,x)(a(1) + a(2)*exp(-a(3)*x));
```

2. Generate synthetic data with parameters `a = [1;3;2]`, with the `x` data points distributed exponentially with parameter `2`, and normally distributed noise with standard deviation `0.1`:

```
rng(9845,'twister') % for reproducibility
a = [1;3;2];
x = exprnd(2,100,1);
epsn = normrnd(0,0.1,100,1);
y = mdl(a,x) + epsn;
```

3. Fit the model to data starting from the arbitrary guess `a0 = [2;2;2]`:

```
a0 = [2;2;2];
[ahat,r,J,cov,mse] = nlinfit(x,y,mdl,a0);
ahat

ahat =
    1.0153
    3.0229
    2.1070
```

4. Check whether `[1;3;2]` is in a 95% confidence interval using the Jacobian argument in `nlparci`:

```
ci = nlparci(ahat,r,'Jacobian',J)

ci =
    0.9869    1.0438
    2.9401    3.1058
    1.9963    2.2177
```

5. You can obtain the same result using the covariance argument:

```
ci = nlparci(ahat,r,'covar',cov)

ci =
    0.9869    1.0438
    2.9401    3.1058
```

```
    1.9963    2.2177
```

See Also

`nlinfit` | `nlpredci`

nlpredci

Nonlinear regression prediction confidence intervals

Syntax

```
[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Covar',CovB)
[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Covar',CovB,Name,Value)

[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Jacobian',J)
[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Jacobian',J,Name,Value)
```

Description

`[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Covar',CovB)` returns predictions, Ypred, and 95% confidence interval half-widths, delta, for the nonlinear regression model `modelfun` at input values `X`. Before calling `nlpredci`, use `nlinfit` to fit `modelfun` and get the estimated coefficients, `beta`, residuals, `R`, and variance-covariance matrix, `CovB`.

`[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Covar',CovB,Name,Value)` uses additional options specified by one or more name-value pair arguments.

`[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Jacobian',J)` returns predictions, Ypred, and 95% confidence interval half-widths, delta, for the nonlinear regression model `modelfun` at input values `X`. Before calling `nlpredci`, use `nlinfit` to fit `modelfun` and get the estimated coefficients, `beta`, residuals, `R`, and Jacobian, `J`.

If you use a robust option with `nlinfit`, then you should use the `Covar` syntax rather than the `Jacobian` syntax. The variance-covariance matrix, CovB, is required to properly take the robust fitting into account.

`[Ypred,delta] = nlpredci(modelfun,X,beta,R,'Jacobian',J,Name,Value)` uses additional options specified by one or more name-value pair arguments.

Examples

Confidence Interval for Nonlinear Regression Curve

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Fit the Hougen-Watson model to the rate data using the initial values in `beta0`.

```
[beta,R,J] = nlinfit(X,y,@hougen,beta0);
```

Obtain the predicted response and 95% confidence interval half-width for the value of the curve at average reactant levels.

```
[ypred,delta] = nlpredci(@hougen,mean(X),beta,R,'Jacobian',J)
```

```
ypred =

    5.4622


delta =

    0.1921
```

Compute the 95% confidence interval for the value of the curve.

```
[ypred-delta,ypred+delta]
```

```
ans =

    5.2702    5.6543
```

Prediction Interval for New Observation

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Fit the Hougen-Watson model to the rate data using the initial values in `beta0`.

```
[beta,R,J] = nlinfit(X,y,@hougen,beta0);
```

Obtain the predicted response and 95% prediction interval half-width for a new observation with reactant levels `[100,100,100]`.

```
[ypred,delta] = nlpredci(@hougen,[100,100,100],beta,R,'Jacobian',J,...
                         'PredOpt','observation')
```

```
ypred =

    1.8346


delta =

    0.5101
```

Compute the 95% prediction interval for the new observation.

```
[ypred-delta,ypred+delta]
```

```
ans =

    1.3245    2.3447
```

Simultaneous Confidence Intervals for Robust Fit Curve

Generate sample data from the nonlinear regression model

$$y = b_1 + b_2 \exp\{-b_3 x\} + \varepsilon,$$

where b_1, b_2, and b_3 are coefficients, and the error term is normally distributed with mean 0 and standard deviation 0.5.

```
modelfun = @(b,x)(b(1)+b(2)*exp(-b(3)*x));

rng('default') % for reproducibility
b = [1;3;2];
x = exprnd(2,100,1);
y = modelfun(b,x) + normrnd(0,0.5,100,1);
```

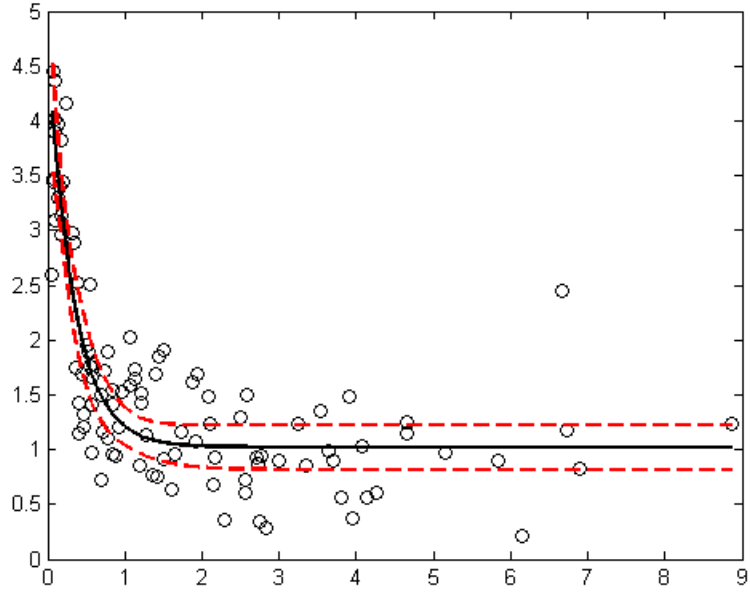
Fit the nonlinear model using robust fitting options.

```
opts = statset('nlinfit');
```

```
opts.RobustWgtFun = 'bisquare';
beta0 = [2;2;2];
[beta,R,J,CovB,MSE] = nlinfit(x,y,modelfun,beta0,opts);
```

Plot the fitted regression model and simultaneous 95% confidence bounds.

```
xrange = min(x):.01:max(x);
[ypred,delta] = nlpredci(modelfun,xrange,beta,R,'Covar',CovB,...
                         'MSE',MSE,'SimOpt','on');
lower = ypred - delta;
upper = ypred + delta;

figure()
plot(x,y,'ko') % observed data
hold on
plot(xrange,ypred,'k','LineWidth',2)
plot(xrange,[lower;upper],'r--','LineWidth',1.5)
```



Confidence Interval Using Observation Weights

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Specify a function handle for observation weights, then fit the Hougen-Watson model to the rate data using the specified observation weights function.

```
a = 1; b = 1;
weights = @(yhat) 1./((a + b*abs(yhat)).^2);
[beta,R,J,CovB] = nlinfit(X,y,@hougen,beta0,'Weights',weights);
```

Compute the 95% prediction interval for a new observation with reactant levels `[100,100,100]` using the observation weight function.

```
[ypred,delta] = nlpredci(@hougen,[100,100,100],beta,R,'Jacobian',J,...
                         'PredOpt','observation','Weights',weights);
[ypred-delta,ypred+delta]
```

```
ans =

    1.5264    2.1033
```

Confidence Interval Using Nonconstant Error Model

Load sample data.

```
S = load('reaction');
X = S.reactants;
y = S.rate;
beta0 = S.beta;
```

Fit the Hougen-Watson model to the rate data using the combined error variance model.

```
[beta,R,J,CovB,MSE,S] = nlinfit(X,y,@hougen,beta0,'ErrorModel','combined');
```

Compute the 95% prediction interval for a new observation with reactant levels `[100,100,100]` using the fitted error variance model.

```
[ypred,delta] = nlpredci(@hougen,[100,100,100],beta,R,'Jacobian',J,...
                         'PredOpt','observation','ErrorModelInfo',S);
[ypred-delta,ypred+delta]
```

```
ans =
```

```
    1.3245    2.3447
```

Input Arguments

`modelfun` — Nonlinear regression model function

function handle

Nonlinear regression model function, specified as a function handle. `modelfun` must accept two input arguments, a coefficient vector and an array `X`—in that order—and return a vector of fitted response values.

For example, to specify the `hougen` nonlinear regression function, use the function handle `@hougen`.

Data Types: `function_handle`

`X` — Input values for predictions

matrix

Input values for predictions, specified as a matrix. `nlpredci` makes a prediction for the covariates in each row of `X`. There should be a column in `X` for each coefficient in the model.

Data Types: `single | double`

`beta` — Estimated regression coefficients

vector returned by `nlinfit`

Estimated regression coefficients, specified as the vector of fitted coefficients returned by a previous call to `nlinfit`.

Data Types: `single | double`

`R` — Residuals

vector returned by `nlinfit`

Residuals for the fitted modelfun, specified as the vector of residuals returned by a previous call to `nlinfit`.

`CovB` — Estimated variance-covariance matrix

matrix returned by `nlinfit`

Estimated variance-covariance matrix for the fitted coefficients, beta, specified as the variance-covariance matrix returned by a previous call to `nlinfit`.

`J` — Estimated Jacobian

matrix returned by `nlinfit`

Estimated Jacobian of the nonlinear regression model, modelfun, specified as the Jacobian matrix returned by a previous call to `nlinfit`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alpha',0.1,'PredOpt','observation'` specifies 90% prediction intervals for new observations.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level for the confidence interval, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1). If `Alpha` has value α, then `nlpredci` returns intervals with $100\times(1-\alpha)\%$ confidence level.

The default confidence level is 95% ($\alpha = 0.05$).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

`'ErrorModelInfo'` — Information about error model fit

structure returned by `nlinfit`

Information about the error model fit, specified as the comma-separated pair consisting of `'ErrorModelInfo'` and a structure returned by a previous call to `nlinfit`.

ErrorModelInfo only has an effect on the returned prediction interval when PredOpt has the value `'observation'`. If you do not use ErrorModelInfo, then `nlpredci` assumes the error variance model is `'constant'`.

The error model structure returned by `nlinfit` has the following fields:

`ErrorModel`	Chosen error model
`ErrorParameters`	Estimated error parameters
`ErrorVariance`	Function handle that accepts an *N*-by-*p* matrix, `X`, and returns an *N*-by-1 vector of error variances using the estimated error model
`MSE`	Mean squared error
`ScheffeSimPred`	Scheffé parameter for simultaneous prediction intervals when using the estimated error model
`WeightFunction`	Logical with value `true` if you used a custom weight function previously in `nlinfit`
`FixedWeights`	Logical with value `true` if you used fixed weights previously in `nlinfit`
`RobustWeightFunction`	Logical with value `true` if you used robust fitting previously in

`'MSE'` — Mean squared error

MSE returned by `nlinfit`

Mean squared error (MSE) for the fitted nonlinear regression model, specified as the comma-separated pair consisting of `'MSE'` and the MSE value returned by a previous call to `nlinfit`.

If you use a robust option with `nlinfit`, then you must specify the MSE when predicting new observations to properly take the robust fitting into account. If you do not specify the MSE, then `nlpredci` computes the MSE from the residuals, R, and does not take the robust fitting into account.

For example, if `mse` is the MSE value returned by `nlinfit`, then you can specify `'MSE',mse`.

Data Types: `single` | `double`

`'PredOpt'` — Prediction interval to compute

`'curve'` (default) | `'observation'`

Prediction interval to compute, specified as the comma-separated pair consisting of `'PredOpt'` and either `'curve'` or `'observation'`.

- If you specify the value `'curve'`, then `nlpredci` returns confidence intervals for the estimated curve (function value) at the observations X.
- If you specify the value `'observation'`, then `nlpredci` returns prediction intervals for new observations at X.

If you specify `'observation'` after using a robust option with `nlinfit`, then you must also specify a value for MSE to provide the robust estimate of the mean squared error.

Example: `'PredOpt','observation'`

Data Types: `char`

`'SimOpt'` — Indicator for specifying simultaneous bounds

`'off'` (default) | `'on'`

Indicator for specifying simultaneous bounds, specified as the comma-separated pair consisting of `'SimOpt'` and either `'off'` or `'on'`. Use the value `'off'` to compute nonsimultaneous bounds, and `'on'` for simultaneous bounds.

`'Weights'` — Observation weights

vector | function handle

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of positive scalar values or a function handle. The default is no weights.

- If you specify a vector of weights, then it must have the same number of elements as the number of observations (rows) in X.
- If you specify a function handle for the weights, then it must accept a vector of predicted response values as input, and return a vector of real positive weights as output.

Given weights, `W`, `nlpredci` estimates the error variance at observation `i` by `mse*(1/W(i))`, where `mse` is the mean squared error value specified using MSE.

Example: `'Weights',@WFun`

Data Types: `double | single | function_handle`

Output Arguments

`Ypred` — Predicted responses

vector

Predicted responses, returned as a vector with the same number of rows as X.

`delta` — Confidence interval half-widths

vector

Confidence interval half-widths, returned as a vector with the same number of rows as X. By default, `delta` contains the half-widths for nonsimultaneous 95% confidence intervals for modelfun at the observations in X. You can compute the lower and upper bounds of the confidence intervals as `Ypred-delta` and `Ypred+delta`, respectively.

If `'PredOpt'` has value `'observation'`, then `delta` contains the half-widths for prediction intervals of new observations at the values in X.

More About

Confidence Intervals for Estimable Predictions

When the estimated model Jacobian is not of full rank, then it might not be possible to construct sensible confidence intervals at all prediction points. In this case, `nlpredci` still tries to construct confidence intervals for any *estimable* prediction points.

For example, suppose you fit the linear function $f(\mathbf{x}_i, \beta) = \beta_1 x_{i1} + \beta_2 x_{i2} + \beta_3 x_{i3}$ at the points in the design matrix

$$\mathbf{X} = \begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 1 & 0 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \\ 1 & 0 & 1 \end{pmatrix}.$$

The estimated Jacobian at the values in $\mathbf{X}$ is the design matrix itself, $\mathbf{J} = \mathbf{X}$. Thus, the Jacobian is not of full rank:

```
rng('default') % For reproducibility
y = randn(6,1);

linfun = @(b,x) x*b;
```

```
beta0 = [1;1;1];
X = [repmat([1 1 0],3,1); repmat([1 0 1],3,1)];

[beta,R,J]  = nlinfit(X,y,linfun,beta0);

Warning: The Jacobian at the solution is ill-conditioned, and
some model parameters may not be estimated well (they are not
identifiable).  Use caution in making predictions.
> In nlinfit at 283
```

In this example, `nlpredci` can only compute prediction intervals at points that satisfy the linear relationship

$$x_{i1} = x_{i2} + x_{i3}.$$

If you try to compute confidence intervals for predictions at nonidentifiable points, `nlpredci` returns `NaN` for the corresponding interval half-widths:

```
xpred = [1 1 1;0 1 -1;2 1 1];
[ypred,delta] = nlpredci(linfun,xpred,beta,R,'Jacobian',J)

ypred =

   -0.0035
    0.0798
   -0.0047


delta =

       NaN
    3.8102
    3.8102
```

Here, the first element of `delta` is `NaN` because the first row in `xpred` does not satisfy the required linear dependence, and is therefore not an estimable contrast.

Tips

- To compute confidence intervals for complex parameters or data, you need to split the problem into its real and imaginary parts. When calling `nlinfit`:

  1. Define your parameter vector beta as the concatenation of the real and imaginary parts of the original parameter vector.

2 Concatenate the real and imaginary parts of the response vector `Y` as a single vector.

3 Modify your model function modelfun to accept X and the purely real parameter vector, and return a concatenation of the real and imaginary parts of the fitted values.

With the problem formulated this way, `nlinfit` computes real estimates, and confidence intervals are feasible.

Algorithms

- `nlpredci` treats `NaN` values in the residuals, R, or the Jacobian, J, as missing values, and ignores the corresponding observations.
- If the Jacobian, J, does not have full column rank, then some of the model parameters might be nonidentifiable. In this case, `nlpredci` tries to construct confidence intervals for estimable predictions, and returns `NaN` for those that are not.

References

[1] Lane, T. P. and W. H. DuMouchel. "Simultaneous Confidence Intervals in Multiple Regression." *The American Statistician*. Vol. 48, No. 4, 1994, pp. 315–321.

[2] Seber, G. A. F., and C. J. Wild. *Nonlinear Regression*. Hoboken, NJ: Wiley-Interscience, 2003.

See Also

`nlinfit` | `nlparci` | `NonLinearModel`

nnmf

Nonnegative matrix factorization

Syntax

```
[W,H] = nnmf(A,k)
[W,H] = nnmf(A,k,param1,val1,param2,val2,...)
[W,H,D] = nnmf(...)
```

Description

`[W,H] = nnmf(A,k)` factors the nonnegative n-by-m matrix `A` into nonnegative factors `W` (n-by-`k`) and `H` (`k`-by-m). The factorization is not exact; `W*H` is a lower-rank approximation to `A`. The factors `W` and `H` are chosen to minimize the root-mean-squared residual `D` between `A` and `W*H`:

```
D = norm(A-W*H,'fro')/sqrt(N*M)
```

The factorization uses an iterative method starting with random initial values for `W` and `H`. Because the root-mean-squared residual `D` may have local minima, repeated factorizations may yield different `W` and `H`. Sometimes the algorithm converges to a solution of lower rank than k, which may indicate that the result is not optimal.

`W` and `H` are normalized so that the rows of `H` have unit length. The columns of `W` are ordered by decreasing length.

`[W,H] = nnmf(A,k,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs from the following table.

Parameter	Value
`'algorithm'`	Either `'als'` (the default) to use an alternating least-squares algorithm, or `'mult'` to use a multiplicative update algorithm. In general, the `'als'` algorithm converges faster and more consistently. The `'mult'` algorithm is more sensitive to initial values, which makes it a good choice when using `'replicates'` to find `W` and `H` from multiple random starting values.

Parameter	Value
`'w0'`	An *n*-by-`k` matrix to be used as the initial value for `W`.
`'h0'`	A `k`-by-*m* matrix to be used as the initial value for `H`.

`'options'`	An options structure as created by the `statset` function. `nnmf` uses the following fields of the options structure:
	• `Display` — Level of display. Choices:
	  • `'off'` (default) — No display
	  • `'final'` — Display final result
	  • `'iter'` — Iterative display of intermediate results
	• `MaxIter` — Maximum number of iterations. Default is `100`. Unlike in optimization settings, reaching `MaxIter` iterations is treated as convergence.
	• `TolFun` — Termination tolerance on change in size of the residual. Default is `1e-4`.
	• `TolX` — Termination tolerance on relative change in the elements of `W` and `H`. Default is `1e-4`.
	• `UseParallel` — Set to `true` to compute in parallel. Default is `false`.
	• `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
	• `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `nnmf` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
	  • You have an open Parallel pool
	  • `UseParallel` is `true`
	  • `UseSubstreams` is `false`
	  In that case, use a cell array the same size as the Parallel pool.

Parameter	Value
`'replicates'`	The number of times to repeat the factorization, using new random starting values for `W` and `H`, except at the first replication if `'w0'` and `'h0'` are given. This is most beneficial with the `'mult'` algorithm. The default is `1`.

`[W,H,D] = nnmf(...)` also returns `D`, the root mean square residual.

Examples

Nonnegative Rank-Two Approximation and Biplot

Load the sample data.

```
load fisheriris
```

Compute a nonnegative rank-two approximation of the measurements of the four variables in Fisher's iris data.

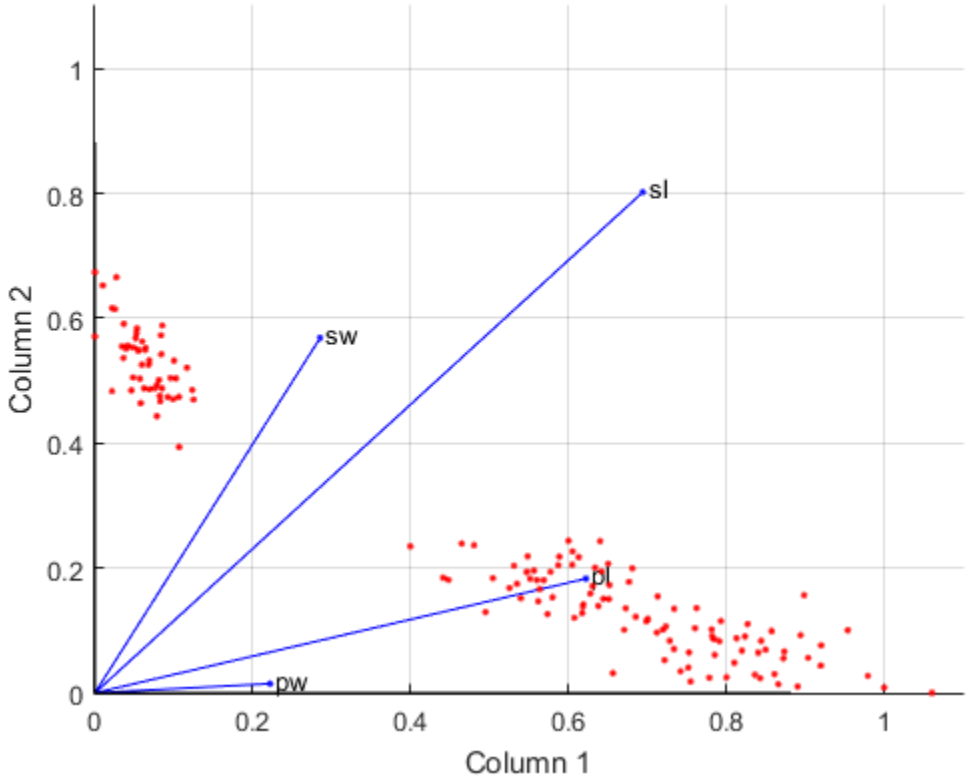
```
[W,H] = nnmf(meas,2);
H
```

```
H =

    0.6943    0.2853    0.6223    0.2220
    0.8020    0.5685    0.1830    0.0147
```

The first and third variables in `meas` (sepal length and petal length, with coefficients 0.6852 and 0.6357, respectively) provide relatively strong weights to the first column of `W`. The first and second variables in `meas` (sepal length and sepal width, with coefficients 0.8011 and 0.5740) provide relatively strong weights to the second column of `W`.

Create a `biplot` of the data and the variables in `meas` in the column space of `W`.

```
biplot(H','scores',W,'varlabels',{'sl','sw','pl','pw'});
axis([0 1.1 0 1.1])
xlabel('Column 1')
ylabel('Column 2')
```



Change Algorithm

Starting from a random array `X` with rank 20, try a few iterations at several replicates using the multiplicative algorithm:

```
X = rand(100,20)*rand(20,50);
opt = statset('MaxIter',5,'Display','final');
[W0,H0] = nnmf(X,5,'replicates',10,...
                   'options',opt,...
                   'algorithm','mult');

   rep iteration     rms resid     |delta x|
     1         5      0.560887     0.0245182
     2         5       0.66418     0.0364471
```

```
      3         5     0.609125    0.0358355
      4         5     0.608894    0.0415491
      5         5     0.619291    0.0455135
      6         5     0.621549    0.0299965
      7         5     0.640549    0.0438758
      8         5     0.673015    0.0366856
      9         5     0.606835    0.0318931
     10         5     0.633526    0.0319591
Final root mean square residual = 0.560887
```

Continue with more iterations from the best of these results using alternating least squares:

```
opt = statset('Maxiter',1000,'Display','final');
[W,H] = nnmf(X,5,'w0',W0,'h0',H0,...
                 'options',opt,...
                 'algorithm','als');
```

```
  rep    iteration    rms resid   |delta x|
      1        24     0.257336   0.00271859
Final root mean square residual = 0.257336
```

References

[1] Berry, M. W., et al. “Algorithms and Applications for Approximate Nonnegative Matrix Factorization.” *Computational Statistics and Data Analysis*. Vol. 52, No. 1, 2007, pp. 155–173.

See Also

`pca` | `factoran` | `statset`

nodeclass

Class: classregtree

Class values of nodes of classification tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
NAME=nodeclass(T)
NAME=nodeclass(T,J)
[NAME,ID]=nodeclass(...)
```

Description

`NAME=nodeclass(T)` returns an *n*-element cell array with the names of the most probable classes in each node of the tree `T`, where *n* is the number of nodes in the tree. Every element of this array is a string equal to one of the class names returned by `classname(T)`. For regression trees, `nodeclass` returns an empty cell array.

`NAME=nodeclass(T,J)` takes an array `J` of node numbers and returns the class names for the specified nodes.

`[NAME,ID]=nodeclass(...)` also returns a numeric array with the class index for each node. The class index is determined by the order of classes `classname` returns.

See Also

`classregtree` | `numnodes` | `classname`

nodeerr

Class: classregtree

Return vector of node errors

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
e = nodeerr(t)
e = nodeerr(t,nodes)
```

Description

`e = nodeerr(t)` returns an *n*-element vector `e` of the errors of the nodes in the tree `t`, where *n* is the number of nodes. For a regression tree, the error `e(i)` for node `i` is the variance of the observations assigned to node `i`. For a classification tree, `e(i)` is the misclassification probability for node `i`.

`e = nodeerr(t,nodes)` takes a vector `nodes` of node numbers and returns the errors for the specified nodes.

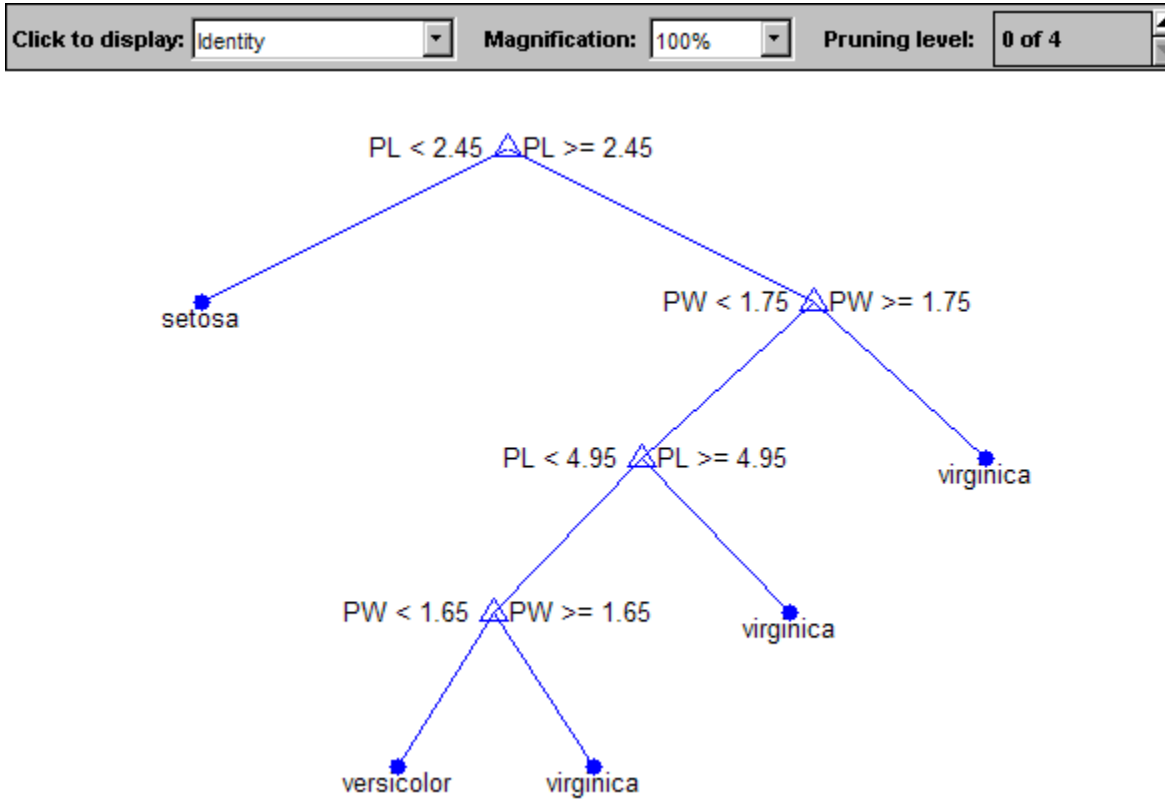
The error `e` is the so-called *resubstitution error* computed by applying the tree to the same data used to create the tree. This error is likely to under estimate the error you would find if you applied the tree to new data. The `test` function provides options to compute the error (or cost) using cross-validation or a test sample.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;
```

```
t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
e = nodeerr(t)
```

```
e =
    0.6667
         0
    0.5000
    0.0926
    0.0217
    0.0208
    0.3333
         0
         0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `test` | `numnodes`

nodemean

Class: classregtree

Mean values of nodes of regression tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
NM = nodemean(T)
NM = nodemean(T,J)
```

Description

`NM = nodemean(T)` returns an n-element numeric array with mean values in each node of the tree `T`, where n is the number of nodes in the tree. Every element of this array is computed by averaging true `Y` values over all observations in the node. For classification trees, `nodemean` returns an empty numeric array.

`NM = nodemean(T,J)` takes an array `J` of node numbers and returns the mean values for the specified nodes.

See Also

`classregtree` | `numnodes`

nodeprob

Class: classregtree

Node probabilities

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
p = nodeprob(t)
p = nodeprob(t,nodes)
```

Description

`p = nodeprob(t)` returns an n-element vector `p` of the probabilities of the nodes in the tree `t`, where n is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. For a classification tree, this proportion is adjusted for any prior probabilities assigned to each class.

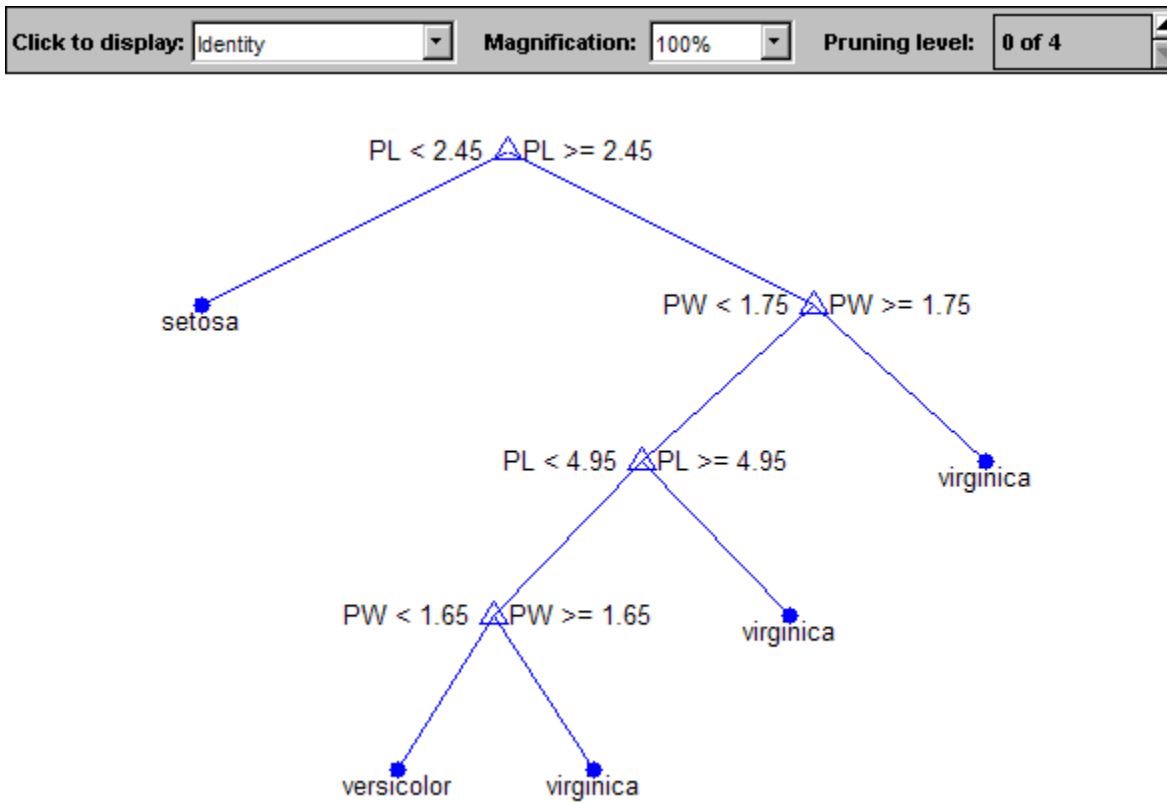
`p = nodeprob(t,nodes)` takes a vector `nodes` of node numbers and returns the probabilities for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
```

```
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
p = nodeprob(t)
p =
    1.0000
    0.3333
```

```
0.6667
0.3600
0.3067
0.3200
0.0400
0.3133
0.0067
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes` | `nodesize`

nodesize

Class: classregtree

Return node size

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
sizes = nodesize(t)
sizes = nodesize(t,nodes)
```

Description

`sizes = nodesize(t)` returns an n-element vector `sizes` of the sizes of the nodes in the tree `t`, where n is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

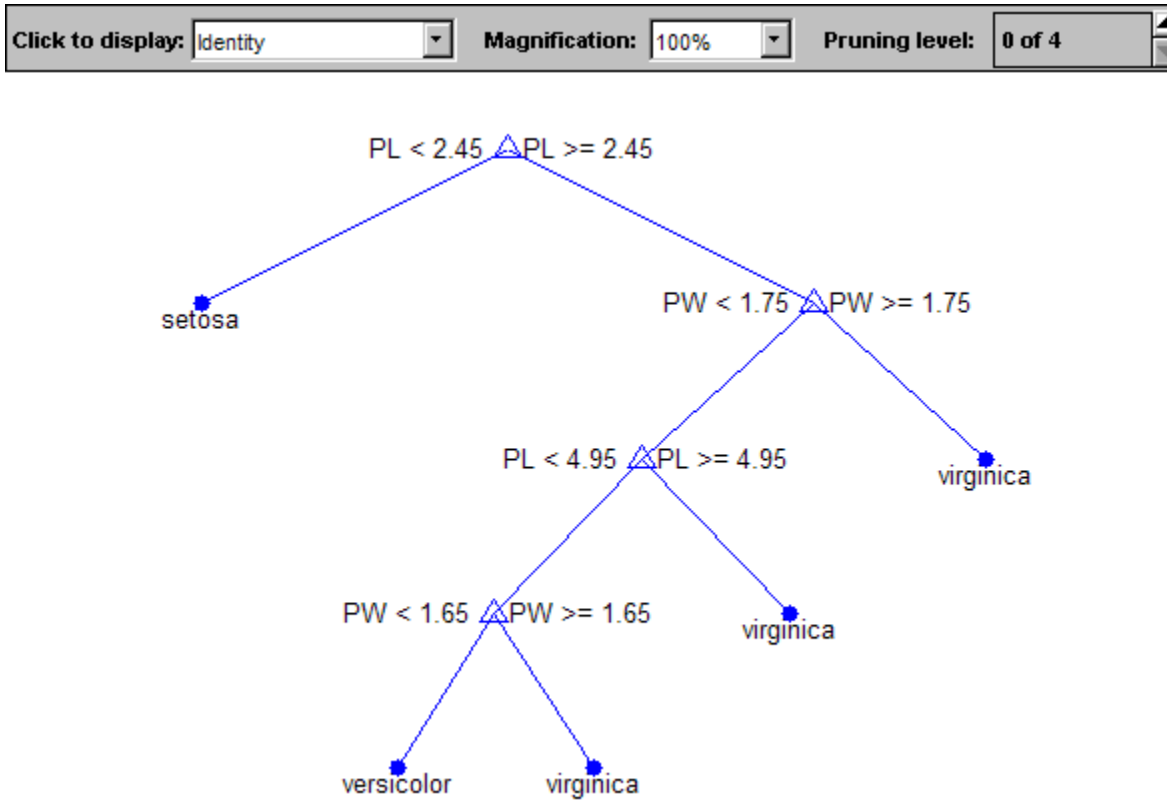
`sizes = nodesize(t,nodes)` takes a vector `nodes` of node numbers and returns the sizes for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
```

```
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
sizes = nodesize(t)
sizes =
   150
    50
   100
    54
```

```
    46
    48
     6
    47
     1
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes`

nominal

Create nominal array

After creating a `nominal` array, you can use related functions to add, drop, or merge categories, and more.

For more information, see Using nominal Objects.

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
B = nominal(X)
B = nominal(X,labels)
B = nominal(X,labels,levels)

B = nominal(X,labels,[],edges)
```

Description

`B = nominal(X)` creates a nominal array B from the array X. `nominal` creates the levels of B from the sorted unique values in X, and creates default labels for them.

`B = nominal(X,labels)` labels the levels in B according to labels.

`B = nominal(X,labels,levels)` creates a nominal array with possible levels defined by levels.

`B = nominal(X,labels,[],edges)` creates a nominal array by binning a numeric array X with bin edges given by the numeric vector edges.

Examples

Create and Label Nominal Arrays

Create nominal arrays from a cell array of strings and from integer data, and provide explicit labels.

Create a nominal array from a cell array of strings with values `'r'`, `'g'`, and `'b'`. Label these levels `'red'`, `'green'`, and `'blue'`, respectively. Note that the labels are specified according to the sorted (alphabetical) order of the elements in `X`.

```
X = {'r' 'b' 'g';'g' 'r' 'b';'b' 'r' 'g'}
B = nominal(X,{'blue','green','red'})
```

```
X =

    'r'    'b'    'g'
    'g'    'r'    'b'
    'b'    'r'    'g'


B =

     red        blue      green
     green      red       blue
     blue       red       green
```

Create a nominal array from integer data with values 1 to 4, merging odd and even values into two nominal levels with labels `'odd'` and `'even'`. Achieve the merging by duplicating the labels.

```
X = randi([1 4],5,2)
B = nominal(X,{'odd','even','odd','even'})
```

```
X =

     4     1
     4     2
     1     3
     4     4
     3     4
```

```
B =

    even    odd
    even    even
    odd     odd
    even    even
    odd     even
```

- "Create Nominal and Ordinal Arrays" on page 2-4
- "Plot Data Grouped by Category" on page 2-25

Input Arguments

X — Input array

numeric | logical | character | categorical | cell array of strings

Input array to convert to `nominal`, specified as a numeric, logical, character, or categorical array, or a cell array of strings. The levels of the resulting `nominal` array correspond to the sorted unique values in X.

`labels` — Labels for the discrete levels

character array | cell array of strings

Labels for the discrete levels, specified as a character array or cell array of strings. By default, `nominal` assigns the labels to the levels in B in order according to the sorted unique values in X.

You can include duplicate labels in labels in order to merge multiple values in X into a single level in B.

Data Types: `char` | `cell`

`levels` — Possible nominal levels

vector

Possible nominal levels for the output `nominal` array, specified as a vector whose values can be compared to those in X using the equality operator. `nominal` assigns labels to each level from the corresponding elements of labels. If X contains any values not present in levels, the levels of the corresponding elements of B are undefined.

`edges` — Bin edges

numeric vector

Bin edges to create a nominal array by binning a numeric array, specified as a numeric vector. The uppermost bin includes values equal to the right-most edge. `nominal` assigns labels to each level in the resulting nominal array from the corresponding elements of labels. When you specify edges, it must have one more element than labels.

Output Arguments

`B` — Nominal array

`nominal` array object

Nominal array, returned as a `nominal` array object.

By default, an element of B is undefined if the corresponding element of X is `NaN` (when X is numeric), an empty string (when X is a character), or undefined (when X is categorical). `nominal` treats such elements as "undefined" or "missing" and does not include entries for them among the possible levels. To create an explicit level for such elements instead of treating them as undefined, you must use the levels input argument, and include `NaN`, the empty string, or an undefined element.

More About

- Using nominal Objects

See Also

`ordinal`

Using nominal Objects

Arrays for nominal data

Nominal data are discrete, nonnumeric values that do not have a natural ordering. `nominal` array objects provide efficient storage and convenient manipulation of such data, while also maintaining meaningful labels for the values.

You can manipulate `nominal` arrays much like ordinary numeric arrays, including subscripting, concatenating, and reshaping. It can be useful to use `nominal` arrays as grouping variables when the elements indicate the group an observation belongs to.

Note: The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Examples

Create and Manipulate Nominal Arrays

Create a nominal array from string data in a cell array.

```
colors = nominal({'r','b','g';'g','r','b';'b','r','g'},...
                 {'blue','green','red'})
```

```
colors =

     red        blue       green
     green      red        blue
     blue       red        green
```

Identify the elements in `colors` that are members of the level `'red'`. A value of `1` in the resulting array indicates that the corresponding element of `colors` is a member of `'red'`.

```
colors == 'red'
```

```
ans =

     1     0     0
     0     1     0
     0     1     0
```

Identify the elements of `colors` that are members of either `'red'` or `'blue'`.

```
ismember(colors,{'red' 'blue'})
```

```
ans =

     1     1     0
     0     1     1
     1     1     0
```

Merge the elements of the `'red'` and `'blue'` levels into a new level labeled `'purple'`.

```
colors = mergelevels(colors,{'red','blue'},'purple')
```

```
colors =

     purple      purple      green
     green       purple      purple
     purple      purple      green
```

Display the levels of `colors`.

```
getlevels(colors)
```

```
ans =

     purple      green
```

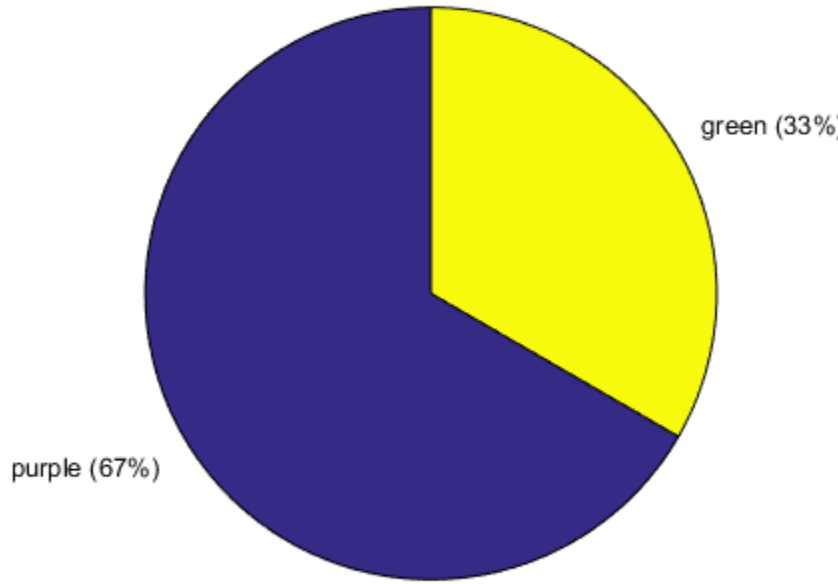
Summarize the number of elements in each level. By default, `summary` returns counts for each column of the input array.

```
summary(colors)
```

```
purple      2       3       1
green       1       0       2
```

Create a pie chart for the data in `colors`.

```
pie(colors)
```



- "Create Nominal and Ordinal Arrays" on page 2-4
- "Add and Drop Category Levels" on page 2-21
- "Plot Data Grouped by Category" on page 2-25
- "Summary Statistics Grouped by Category" on page 2-38

Properties

`labels` — Level labels
cell array of strings

Level labels, specified as a cell array of string. Access labels using `getlabels`.

Data Types: `cell`

`undeflabel` — Label for undefined levels
`'<undefined>'` (default)

Label for undefined levels, specified as `'<undefined>'`. You can find undefined elements in categorical arrays using `isundefined`.

Object Functions

`addlevels` `droplevels` `getlabels` `getlevels` `islevel` `levelcounts` `mergelevels` `reorderlevels` `setlabels`

You can also use many other MATLAB array functions with categorical arrays. The following is a partial list. For a complete list, see "Other MATLAB Functions Supporting Nominal and Ordinal Arrays" on page 2-3.
`double` `histogram` `isequal` `isundefined` `piesummary` `times`

Create Object

Create `nominal` arrays using the `nominal` function.

See Also

`ordinal`

More About

- "Advantages of Using Categorical Arrays" on page 2-44
- "Index and Search Using Categorical Arrays" on page 2-47
- "Grouping Variables" on page 2-52

notify

Class: qrandstream

Notify listeners of event

Syntax

```
notify(h,'eventname')
notify(h,'eventname',data)
```

Description

`notify(h,'eventname')` notifies listeners added to the event named `eventname` on handle object array `h` that the event is taking place. `h` is the array of handles to objects triggering the event, and `eventname` must be a string.

`notify(h,'eventname',data)` provides a way of encapsulating information about an event which can then be accessed by each registered listener. `data` must belong to the `event.eventdata` class.

See Also

`addlistener` | `event.EventData` | `events` | `qrandstream`

NonLinearModel class

Nonlinear regression model class

Description

An object comprising training data, model description, diagnostic information, and fitted coefficients for a nonlinear regression. Predict model responses with the `predict` or `feval` methods.

Construction

`nlm = fitnlm(tbl,modelfun,beta0)` or `nlm = fitnlm(X,y,modelfun,beta0)` create a nonlinear model of a table or dataset array `tbl`, or of the responses `y` to a data matrix `X`. For details, see `fitnlm`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see “Grouping Variables” on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelfun` — Functional form of the model

function handle | string of the form `'y ~ f(b1,b2,...,bj,x1,x2,...,xk)'`

Functional form of the model, specified as either of the following.

- Function handle `@modelfun` or `@(b,x)modelfun`, where

  - `b` is a coefficient vector with the same number of elements as `beta0`.
  - `x` is a matrix with the same number of columns as `X` or the number of predictor variable columns of `tbl`.

  `modelfun(b,x)` returns a column vector that contains the same number of rows as `x`. Each row of the vector is the result of evaluating `modelfun` on the corresponding row of `x`. In other words, `modelfun` is a vectorized function, one that operates on all data rows and returns all evaluations in one function call. `modelfun` should return real numbers to obtain meaningful coefficients.
- String of the form `'y ~ f(b1,b2,...,bj,x1,x2,...,xk)'`, where `f` represents a scalar function of the scalar coefficient variables `b1`,...,`bj` and the scalar data variables `x1`,...,`xk`.

`beta0` — Coefficients

numeric vector

Coefficients for the nonlinear model, specified as a numeric vector. `NonLinearModel` starts its search for optimal coefficients from `beta0`.

Data Types: `single` | `double`

Properties

`CoefficientCovariance`

Covariance matrix of coefficient estimates.

`CoefficientNames`

Cell array of strings containing a label for each coefficient.

`Coefficients`

Coefficient values stored as a table. `Coefficients` has one row for each coefficient and these columns:

- `Estimate` — Estimated coefficient value
- `SE` — Standard error of the estimate
- `tStat` — t statistic for a test that the coefficient is zero
- `pValue` — p-value for the t statistic

To obtain any of these columns as a vector, index into the property using dot notation. For example, in `mdl` the estimated coefficient vector is

```
beta = mdl.Coefficients.Estimate
```

Use `coefTest` to perform other tests on the coefficients.

`Diagnostics`

Table with diagnostics helpful in finding outliers and influential observations. The table contains the following fields.

Field	Meaning	Utility
`Leverage`	Diagonal elements of `HatMatrix`	Leverage indicates to what extent the predicted value for an observation is determined by the observed value for that observation. A value close to `1` indicates that the prediction is largely determined by that observation, with little contribution from the

Field	Meaning	Utility
		other observations. A value close to `0` indicates the fit is largely determined by the other observations. For a model with `P` coefficients and `N` observations, the average value of `Leverage` is `P/N`. An observation with `Leverage` larger than `2*P/N` can be regarded as having high leverage.
`CooksDistance`	Cook's measure of scaled change in fitted values	`CooksDistance` is a measure of scaled change in fitted values. An observation with `CooksDistance` larger than three times the mean Cook's distance can be an outlier.
`HatMatrix`	Projection matrix to compute fitted from observed responses	`HatMatrix` is an `N`-by-`N` matrix such that `Fitted = HatMatrix*Y`, where `Y` is the response vector and `Fitted` is the vector of fitted response values.

`DFE`

Degrees of freedom for error (residuals), equal to the number of observations minus the number of estimated coefficients.

`Fitted`

Vector of predicted values based on the training data. `fitnlm` attempts to make `Fitted` as close as possible to the response data.

`Formula`

Object that represents the mathematical form of the model.

`Iterative`

Structure with information about the fitting process. Fields:

- `InitialCoefs` — Initial coefficient values (the `beta0` vector)
- `IterOpts` — Options included in the `Options` name-value pair argument for `fitnlm`.

`LogLikelihood`

Log likelihood of the model distribution at the response values, with mean fitted from the model, and other parameters estimated as part of the model fit.

ModelCriterion

`AIC` and other information criteria for comparing models. A structure with fields:

- `AIC` — Akaike information criterion
- `AICc` — Akaike information criterion corrected for sample size
- `BIC` — Bayesian information criterion
- `CAIC` — Consistent Akaike information criterion

To obtain any of these values as a scalar, index into the property using dot notation. For example, in a model `mdl`, the AIC value `aic` is:

```
aic = mdl.ModelCriterion.AIC
```

MSE

Mean squared error, a scalar that is an estimate of the variance of the error term in the model.

NumCoefficients

Number of coefficients in the fitted model, a scalar. `NumCoefficients` is the same as `NumEstimatedCoefficients` for `NonLinearModel` objects. `NumEstimatedCoefficients` is equal to the degrees of freedom for regression.

NumEstimatedCoefficients

Number of estimated coefficients in the fitted model, a scalar. `NumEstimatedCoefficients` is the same as `NumCoefficients` for `NonLinearModel` objects. `NumEstimatedCoefficients` is equal to the degrees of freedom for regression.

NumPredictors

Number of variables `fitnlm` used as predictors for fitting.

NumVariables

Number of variables in the data. `NumVariables` is the number of variables in the original table or dataset, or the total number of columns in the predictor matrix and response vector when the fit is based on those arrays. It includes variables, if any, that are not used as predictors or as the response.

`ObservationInfo`

Table with the same number of rows as the input data (`tbl` or `X`).

Field	Description
`Weights`	Observation weights. Default is all `1`.
`Excluded`	Logical value, `1` indicates an observation that you excluded from the fit with the `Exclude` name-value pair.
`Missing`	Logical value, `1` indicates a missing value in the input. Missing values are not used in the fit.
`Subset`	Logical value, `1` indicates the observation is not excluded or missing, so is used in the fit.

`ObservationNames`

Cell array of strings containing the names of the observations used in the fit.

- If the fit is based on a table or dataset containing observation names, `ObservationNames` uses those names.
- Otherwise, `ObservationNames` is an empty cell array

`PredictorNames`

Cell array of strings, the names of the predictors used in fitting the model.

`Residuals`

Table of residuals, with one row for each observation and these variables.

Field	Description
`Raw`	Observed minus fitted values.
`Pearson`	Raw residuals divided by RMSE.
`Standardized`	Raw residuals divided by their estimated standard deviation.
`Studentized`	Residual divided by an independent estimate of the residual standard deviation. The residual for observation i is divided by an estimate of the error standard deviation based on all observations except for observation i.

To obtain any of these columns as a vector, index into the property using dot notation. For example, in a model `mdl`, the ordinary raw residual vector `r` is:

```
r = mdl.Residuals.Raw
```

Rows not used in the fit because of missing values (in `ObservationInfo.Missing`) contain `NaN` values.

Rows not used in the fit because of excluded values (in `ObservationInfo.Excluded`) contain `NaN` values, with the following exceptions:

- `raw` contains the difference between the observed and predicted values.
- `standardized` is the residual, standardized in the usual way.
- `studentized` matches the standardized values because this residual is not used in the estimate of the residual standard deviation.

`ResponseName`

String giving naming the response variable.

`RMSE`

Root mean squared error, a scalar that is an estimate of the standard deviation of the error term in the model.

`Robust`

Structure that is empty unless `fitnlm` constructed the model using robust regression.

Field	Description
`WgtFun`	Robust weighting function, such as `'bisquare'` (see `robustfit`)
`Tune`	Value specified for tuning parameter (can be `[]`)
`Weights`	Vector of weights used in final iteration of robust fit

`Rsquared`

Proportion of total sum of squares explained by the model. The ordinary R-squared value relates to the `SSR` and `SST` properties:

`Rsquared = SSR/SST = 1 - SSE/SST`.

For a linear or nonlinear model, `Rsquared` is a structure with two fields:

- `Ordinary` — Ordinary (unadjusted) R-squared
- `Adjusted` — R-squared adjusted for the number of coefficients

For a generalized linear model, `Rsquared` is a structure with five fields:

- `Ordinary` — Ordinary (unadjusted) R-squared
- `Adjusted` — R-squared adjusted for the number of coefficients
- `LLR` — Log-likelihood ratio
- `Deviance` — Deviance
- `AdjGeneralized` — Adjusted generalized R-squared

To obtain any of these values as a scalar, index into the property using dot notation. For example, the adjusted R-squared value in `mdl` is

```
r2 = mdl.Rsquared.Adjusted
```

SSE

Sum of squared errors (residuals).

The Pythagorean theorem implies
`SST = SSE + SSR`.

SSR

Regression sum of squares, the sum of squared deviations of the fitted values from their mean.

The Pythagorean theorem implies
`SST = SSE + SSR`.

SST

Total sum of squares, the sum of squared deviations of `y` from `mean(y)`.

The Pythagorean theorem implies
`SST = SSE + SSR`.

VariableInfo

Table containing metadata about `Variables`. There is one row for each term in the model, and the following columns.

Field	Description
`Class`	String giving variable class, such as `'double'`
`Range`	Cell array giving variable range: • Continuous variable — Two-element vector `[min,max]`, the minimum and maximum values • Categorical variable — Cell array of distinct variable values
`InModel`	Logical vector, where `true` indicates the variable is in the model
`IsCategorical`	Logical vector, where `true` indicates a categorical variable

VariableNames

Cell array of strings containing names of the variables in the fit.

- If the fit is based on a table or dataset, this property provides the names of the variables in that table or dataset.
- If the fit is based on a predictor matrix and response vector, `VariableNames` is the values in the `VarNames` name-value pair of the fitting method.
- Otherwise the variables have the default fitting names.

Variables

Table containing the data, both observations and responses, that the fitting function used to construct the fit. If the fit is based on a table or dataset array, `Variables` contains all of the data from that table or dataset array. Otherwise, `Variables` is a table created from the input data matrix `X` and response vector `y`.

Methods

coefCI	Confidence intervals of coefficient estimates of nonlinear regression model

coefTest	Linear hypothesis test on nonlinear regression model coefficients
disp	Display nonlinear regression model
feval	Evaluate nonlinear regression model prediction
fit	Fit nonlinear regression model
plotDiagnostics	Plot diagnostics of nonlinear regression model
plotResiduals	Plot residuals of nonlinear regression model
plotSlice	Plot of slices through fitted nonlinear regression surface
predict	Predict response of nonlinear regression model
random	Simulate responses for nonlinear regression model

Definitions

Hat Matrix

The *hat matrix H* is defined in terms of the data matrix *X* and the Jacobian matrix *J*:

$$J_{i,j} = \left.\frac{\partial f}{\partial \beta_j}\right|_{x_i,\beta}$$

Here f is the nonlinear model function, and β is the vector of model coefficients.

The Hat Matrix H is
$H = J(J^TJ)^{-1}J^T$.

The diagonal elements H_{ii} satisfy

$$0 \le h_{ii} \le 1$$

$$\sum_{i=1}^{n} h_{ii} = p,$$

where n is the number of observations (rows of X), and p is the number of coefficients in the regression model.

Leverage

The *leverage* of observation i is the value of the ith diagonal term, h_{ii}, of the hat matrix H. Because the sum of the leverage values is p (the number of coefficients in the regression model), an observation i can be considered to be an outlier if its leverage substantially exceeds p/n, where n is the number of observations.

Cook's Distance

The Cook's distance D_i of observation i is

$$D_i = \frac{\sum_{j=1}^{n} \left(\hat{y}_j - \hat{y}_{j(i)}\right)^2}{p\,MSE},$$

where

- $\hat{y}_j$ is the jth fitted response value.
- $\hat{y}_{j(i)}$ is the jth fitted response value, where the fit does not include observation i.
- MSE is the mean squared error.
- p is the number of coefficients in the regression model.

Cook's distance is algebraically equivalent to the following expression:

$$D_i = \frac{r_i^2}{p\,MSE}\left(\frac{h_{ii}}{(1-h_{ii})^2}\right),$$

where e_i is the ith residual.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Nonlinear Model

Create a nonlinear model for auto mileage based on the `carbig` data. Predict the mileage of an average car.

Load the data and create a nonlinear model.

```
load carbig
X = [Horsepower,Weight];
y = MPG;
modelfun = @(b,x)b(1) + b(2)*x(:,1).^b(3) + ...
    b(4)*x(:,2).^b(5);
beta0 = [-50 500 -1 500 -1];
mdl = fitnlm(X,y,modelfun,beta0)
```

```
mdl =


Nonlinear regression model:
    y ~ b1 + b2*x1^b3 + b4*x2^b5

Estimated Coefficients:
          Estimate      SE        tStat       pValue
          ________    _______    ________    ________
```

```
    b1      -49.383      119.97    -0.41164      0.68083
    b2       376.43      567.05     0.66384      0.50719
    b3    -0.78193     0.47168     -1.6578     0.098177
    b4       422.37      776.02     0.54428      0.58656
    b5    -0.24127     0.48325    -0.49926      0.61788


Number of observations: 392, Error degrees of freedom: 387
Root Mean Squared Error: 3.96
R-Squared: 0.745,  Adjusted R-Squared 0.743
F-statistic vs. constant model: 283, p-value = 1.79e-113
```

Find the predicted mileage of an average auto. The data contain some observations with `NaN`, so compute the mean using `nanmean`.

```
Xnew = nanmean(X)

Xnew =
   1.0e+03 *
    0.1051    2.9794

MPGnew = predict(mdl,Xnew)

MPGnew =

   21.8073
```

- "Nonlinear Regression Workflow" on page 11-14

See Also

`fitnlm` | `GeneralizedLinearModel` | `LinearModel` | `nlinfit` | `NonLinearModel.predict`

More About

- "Nonlinear Regression" on page 11-2

prob.NormalDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Normal probability distribution object

Description

`prob.NormalDistribution` is an object consisting of parameters, a model description, and sample data for a normal probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Normal')` creates a normal probability distribution object using the default parameter values.

`pd = makedist('Normal','mu',mu,'sigma',sigma)` creates a normal distribution object using the specified parameter values.

Input Arguments

`mu` — Mean

0 (default) | scalar value

Mean of the normal distribution, specified as a scalar value.

Data Types: `single` | `double`

`sigma` — Standard deviation

1 (default) | nonnegative scalar value

Standard deviation of the normal distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

Properties

`mu` — Mean

scalar value

Mean of the normal distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Standard deviation

nonnegative scalar value

Standard deviation of the normal distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Normal Distribution

The normal distribution, sometimes called the Gaussian distribution, is a two-parameter family of curves. The usual justification for using the normal distribution for modeling is the Central Limit theorem, which states (roughly) that the sum of independent samples from any distribution with finite mean and variance converges to the normal distribution as the sample size goes to infinity.

The normal distribution uses the following parameters.

Parameter	Description	Support
`mu`	Mean	$-\infty < \mu < \infty$
`sigma`	Standard deviation	$\sigma \geq 0$

The probability density function (pdf) is

$$f(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}} \quad , \quad -\infty < x < \infty.$$

Examples

Create a Normal Distribution Object Using Default Parameters

Create a normal distribution object using the default parameter values.

```
pd = makedist('Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Create a Normal Distribution Object Using Specified Parameters

Create a normal distribution object by specifying the parameter values.

```
pd = makedist('Normal','mu',75,'sigma',10)
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75
    sigma = 10
```

Compute the interquartile range of the distribution.

```
r = iqr(pd)
```

```
r =
```

```
   13.4898
```

Fit a Normal Distribution Object

Load the sample data. Create a vector containing the first column of students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Create a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Normal Distribution"
- Class Attributes
- Property Attributes

normcdf

Normal cumulative distribution function

Syntax

```
p = normcdf(x)
p = normcdf(x,mu,sigma)
[p,plo,pup] = normcdf(x,mu,sigma,pcov,alpha)
[p,plo,pup] = normcdf( ___ ,'upper')
```

Description

`p = normcdf(x)` returns the standard normal cdf at each value in `x`. The standard normal distribution has parameters `mu = 0` and `sigma = 1`. `x` can be a vector, matrix, or multidimensional array.

`p = normcdf(x,mu,sigma)` returns the normal cdf at each value in `x` using the specified values for the mean `mu` and standard deviation `sigma`. `x`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `sigma` must be positive.

`[p,plo,pup] = normcdf(x,mu,sigma,pcov,alpha)` returns confidence bounds for `p` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is 0.05. `plo` and `pup` are arrays of the same size as `p` containing the lower and upper confidence bounds.

`[p,plo,pup] = normcdf( ___ ,'upper')` returns the complement of the normal cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities. You can use `'upper'` with any of the previous syntaxes.

The function `normcdf` computes confidence bounds for `p` using a normal approximation to the distribution of the estimate

$$\frac{X - \hat{\mu}}{\hat{\sigma}}$$

and then transforming those bounds to the scale of the output `p`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The normal cdf is

$$p = F(x \mid \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_{-\infty}^{x} e^{\frac{-(t-\mu)^2}{2\sigma^2}} dt$$

The result, p, is the probability that a single observation from a normal distribution with parameters μ and σ will fall in the interval $(-\infty\ x]$.

The *standard normal* distribution has $\mu = 0$ and $\sigma = 1$.

Examples

Compute Normal Distribution cdf

What is the probability that an observation from a standard normal distribution will fall on the interval [-1 1]?

```
p = normcdf([-1 1]);
p(2)-p(1)
```

```
ans =
  0.6827
```

More generally, about 68% of the observations from a normal distribution fall within one standard deviation, σ, of the mean, μ.

More About

- “Normal Distribution” on page B-130

See Also

`cdf` | `normpdf` | `norminv` | `normstat` | `normfit` | `normlike` | `normrnd`

normfit

Normal parameter estimates

Syntax

```
[muhat,sigmahat] = normfit(data)
[muhat,sigmahat,muci,sigmaci] = normfit(data)
[muhat,sigmahat,muci,sigmaci] = normfit(data,alpha)
[...] = normfit(data,alpha,censoring)
[...] = normfit(data,alpha,censoring,freq)
[...] = normfit(data,alpha,censoring,freq,options)
```

Description

`[muhat,sigmahat] = normfit(data)` returns an estimate of the mean μ in `muhat`, and an estimate of the standard deviation σ in `sigmahat`, of the normal distribution given the data in `data`.

`[muhat,sigmahat,muci,sigmaci] = normfit(data)` returns 95% confidence intervals for the parameter estimates on the mean and standard deviation in the arrays `muci` and `sigmaci`, respectively. The first row of `muci` contains the lower bounds of the confidence intervals for μ the second row contains the upper bounds. The first row of `sigmaci` contains the lower bounds of the confidence intervals for σ, and the second row contains the upper bounds.

`[muhat,sigmahat,muci,sigmaci] = normfit(data,alpha)` returns 100(1 - `alpha`) % confidence intervals for the parameter estimates, where `alpha` is a value in the range `[0 1]` specifying the width of the confidence intervals. By default, `alpha` is `0.05`, which corresponds to 95% confidence intervals.

`[...] = normfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly. `data` must be a vector in order to pass in the argument `censoring`.

`[...] = normfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. Typically, `freq` contains integer frequencies for the

corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = normfit(data,alpha,censoring,freq,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates when there is censoring. The normal fit function accepts an `options` structure which you can create using the function `statset`. Enter `statset('normfit')` to see the names and default values of the parameters that `normfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Note: With no censoring, `normfit` computes `muhat` using the sample mean and `sigmahat` using the square root of the unbiased estimator of the variance. With censoring, both `muhat` and `sigmahat` are the maximum likelihood estimates.

Examples

In this example the data is a two-column random normal matrix. Both columns have $\mu = 10$ and $\sigma = 2$. Note that the confidence intervals below contain the "true values."

```
data = normrnd(10,2,100,2);
[mu,sigma,muci,sigmaci] = normfit(data)
mu =
  10.1455  10.0527
sigma =
  1.9072  2.1256
muci =
  9.7652  9.6288
  10.5258  10.4766
sigmaci =
  1.6745  1.8663
  2.2155  2.4693
```

More About

- “Normal Distribution” on page B-130

See Also

`mle` | `normlike` | `normpdf` | `normcdf` | `norminv` | `normstat` | `normrnd`

norminv

Normal inverse cumulative distribution function

Syntax

```
X = norminv(P,mu,sigma)
[X,XLO,XUP] = norminv(P,mu,sigma,pcov,alpha)
```

Description

`X = norminv(P,mu,sigma)` computes the inverse of the normal cdf using the corresponding mean `mu` and standard deviation `sigma` at the corresponding probabilities in `P`. `P`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `sigma` must be positive, and the values in `P` must lie in the interval [0 1].

`[X,XLO,XUP] = norminv(P,mu,sigma,pcov,alpha)` produces confidence bounds for `X` when the input parameters `mu` and `sigma` are estimates. `pcov` is the covariance matrix of the estimated parameters. `alpha` specifies 100(1 - `alpha`)% confidence bounds. The default value of `alpha` is `0.05`. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

The function `norminv` computes confidence bounds for `P` using a normal approximation to the distribution of the estimate

$$\hat{\mu} + \hat{\sigma} q$$

where q is the `P`th quantile from a normal distribution with mean 0 and standard deviation 1. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds may be more accurate.

The normal inverse function is defined in terms of the normal cdf as

$$x = F^{-1}(p \mid \mu,\sigma) = \{x : F(x \mid \mu,\sigma) = p\}$$

where

$$p = F(x \mid \mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_{-\infty}^{x} e^{\frac{-(t-\mu)^2}{2\sigma^2}} dt$$

The result, x, is the solution of the integral equation above where you supply the desired probability, p.

Examples

Find an interval that contains 95% of the values from a standard normal distribution.

```
x = norminv([0.025 0.975],0,1)
x =
  -1.9600  1.9600
```

Note that the interval `x` is not the only such interval, but it is the shortest.

```
xl = norminv([0.01 0.96],0,1)
xl =
  -2.3263  1.7507
```

The interval `xl` also contains 95% of the probability, but it is longer than `x`.

More About

- "Normal Distribution" on page B-130

See Also

`icdf` | `normcdf` | `normpdf` | `normstat` | `normfit` | `normlike` | `normrnd`

normlike

Normal negative log-likelihood

Syntax

```
nlogL = normlike(params,data)
[nlogL,AVAR] = normlike(params,data)
[...] = normlike(param,data,censoring)
[...] = normlike(param,data,censoring,freq)
```

Description

`nlogL = normlike(params,data)` returns the negative of the normal log-likelihood function. `params(1)` is the mean, `mu`, and `params(2)` is the standard deviation, `sigma`.

`[nlogL,AVAR] = normlike(params,data)` also returns the inverse of Fisher's information matrix, `AVAR`. If the input parameter values in `params` are the maximum likelihood estimates, the diagonal elements of `AVAR` are their asymptotic variances. `AVAR` is based on the observed Fisher's information, not the expected information.

`[...] = normlike(param,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = normlike(param,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

`normlike` is a utility function for maximum likelihood estimation.

More About

- “Normal Distribution” on page B-130

See Also

normfit | normpdf | normcdf | norminv | normstat | normrnd

normpdf

Normal probability density function

Syntax

```
Y = normpdf(X,mu,sigma)
Y = normpdf(X)
Y = normpdf(X,mu)
```

Description

`Y = normpdf(X,mu,sigma)` computes the pdf at each of the values in `X` using the normal distribution with mean `mu` and standard deviation `sigma`. `X`, `mu`, and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `sigma` must be positive.

The normal pdf is

$$y = f(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

The *likelihood function* is the pdf viewed as a function of the parameters. Maximum likelihood estimators (MLEs) are the values of the parameters that maximize the likelihood function for a fixed value of `x`.

The *standard normal* distribution has $\mu = 0$ and $\sigma = 1$.

If x is standard normal, then $x\sigma + \mu$ is also normal with mean μ and standard deviation σ. Conversely, if y is normal with mean μ and standard deviation σ, then $x = (y - \mu) / \sigma$ is standard normal.

`Y = normpdf(X)` uses the standard normal distribution (`mu = 0`, `sigma = 1`).

`Y = normpdf(X,mu)` uses the normal distribution with unit standard deviation (`sigma = 1`).

Examples

```
mu = [0:0.1:2];
[y i] = max(normpdf(1.5,mu,1));
MLE = mu(i)
MLE =
  1.5000
```

More About

- "Normal Distribution" on page B-130

See Also

pdf | normcdf | norminv | normstat | normfit | normlike | normrnd | mvnpdf

normplot

Normal probability plot

Syntax

```
h = normplot(X)
```

Description

`h = normplot(X)` displays a normal probability plot of the data in `X`. For matrix `X`, normplot displays a line for each column of `X`. `h` is a handle to the plotted lines.

The plot has the sample data displayed with the plot symbol `'+'`. Superimposed on the plot is a line joining the first and third quartiles of each column of `X` (a robust linear fit of the sample order statistics.) This line is extrapolated out to the ends of the sample to help evaluate the linearity of the data.

The purpose of a normal probability plot is to graphically assess whether the data in `X` could come from a normal distribution. If the data are normal the plot will be linear. Other distribution types will introduce curvature in the plot. `normplot` uses midpoint probability plotting positions. Use `probplot` when the data included censored observations.

Examples

Generate a Normal Probability Plot

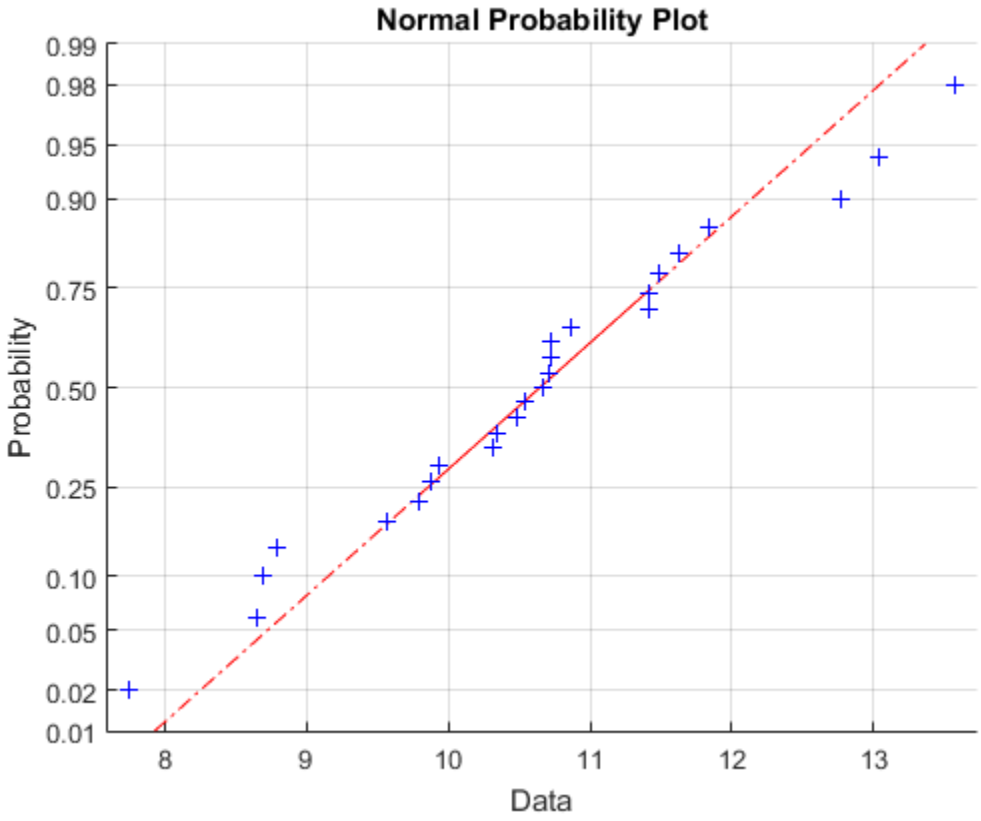
Generate random sample data from a normal distribution with `mu = 10` and `sigma = 1`.

```
rng default;  % For reproducibility
x = normrnd(10,1,25,1);
```

Create a normal probability plot of the sample data.

```
figure;
```

```
normplot(x)
```



The plot indicates that the data follows a normal distribution.

More About

- "Normal Distribution" on page B-130

See Also

`cdfplot` | `wblplot` | `probplot` | `histogram` | `normfit` | `norminv` | `normpdf` | `normspec` | `normstat` | `normcdf` | `normrnd` | `normlike`

normrnd

Normal random numbers

Syntax

```
R = normrnd(mu,sigma)
R = normrnd(mu,sigma,m,n,...)
R = normrnd(mu,sigma,[m,n,...])
```

Description

`R = normrnd(mu,sigma)` generates random numbers from the normal distribution with mean parameter `mu` and standard deviation parameter `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `R`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

`R = normrnd(mu,sigma,m,n,...)` or `R = normrnd(mu,sigma,[m,n,...])` generates an `m`-by-`n`-by-... array. The `mu`, `sigma` parameters can each be scalars or arrays of the same size as `R`.

Examples

```
n1 = normrnd(1:6,1./(1:6))
n1 =
  2.1650  2.3134  3.0250  4.0879  4.8607  6.2827

n2 = normrnd(0,1,[1 5])
n2 =
  0.0591  1.7971  0.2641  0.8717  -1.4462

n3 = normrnd([1 2 3;4 5 6],0.1,2,3)
n3 =
  0.9299  1.9361  2.9640
  4.1246  5.0577  5.9864
```

More About

- "Normal Distribution" on page B-130

See Also

`random` | `normpdf` | `normcdf` | `norminv` | `normstat` | `normfit` | `normlike` | `mvnrnd` | `lognrnd`

normspec

Normal density plot between specifications

Syntax

```
normspec(specs)
normspec(specs,mu,sigma)
normspec(specs,mu,sigma,region)
p = normspec(...)
[p,h] = normspec(...)
```

Description

`normspec(specs)` plots the standard normal density, shading the portion inside the specification limits given by the two-element vector `specs`. Set `specs(1)` to `-Inf` if there is no lower limit; set `specs(2)` to `Inf` if there is no upper limit.

`normspec(specs,mu,sigma)` shades the portion inside the specification limits of a normal density with parameters `mu` and `sigma`. The defaults are `mu = 0` and `sigma = 1`.

`normspec(specs,mu,sigma,region)` shades the *`region`* either `'inside'` or `'outside'` the specification limits. The default is `'inside'`.

`p = normspec(...)` also returns the probability, `p`, of the shaded area.

`[p,h] = normspec(...)` also returns a handle `h` to the line objects.

Examples

Create a Normal Density Plot

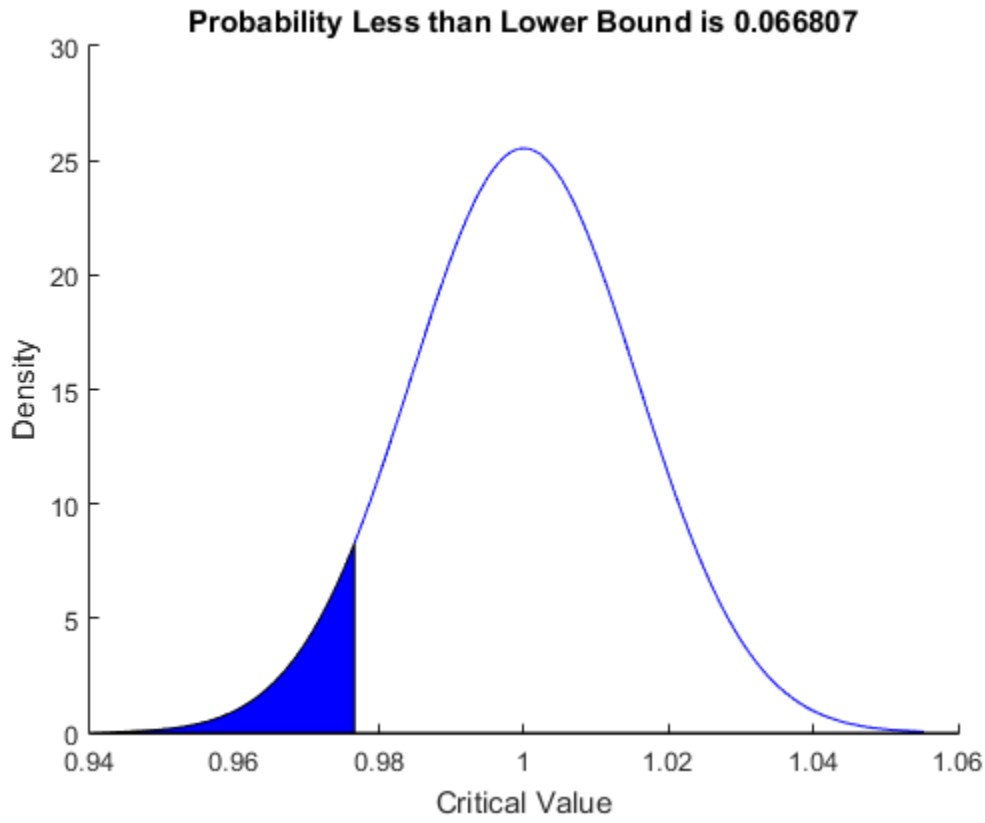
This example shows how to create a normal density plot.

A production process fills cans of paint. The average amount of paint in any can is 1 gallon, but variability in the process produces a standard deviation of 2 ounces (2/128

gallons). What is the probability that the cans will be filled under specification by 3 or more ounces?

```
p = normspec([1-3/128,Inf],1,2/128,'outside')
```

```
p =

    0.0668
```



More About

- "Normal Distribution" on page B-130

See Also

`capaplot` | `histfit`

normstat

Normal mean and variance

Syntax

```
[M,V] = normstat(mu,sigma)
```

Description

`[M,V] = normstat(mu,sigma)` returns the mean of and variance for the normal distribution using the corresponding mean `mu` and standard deviation `sigma`. `mu` and `sigma` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `M` and `V`. A scalar input for `mu` or `sigma` is expanded to a constant array with the same dimensions as the other input.

The mean of the normal distribution with parameters μ and σ is μ, and the variance is σ^2.

Examples

```
n = 1:5;
[m,v] = normstat(n'*n,n'*n)
m =
   1   2   3   4   5
   2   4   6   8  10
   3   6   9  12  15
   4   8  12  16  20
   5  10  15  20  25

v =
   1   4   9  16  25
   4  16  36  64 100
   9  36  81 144 225
  16  64 144 256 400
  25 100 225 400 625
```

More About

- "Normal Distribution" on page B-130

See Also

`normpdf` | `normcdf` | `norminv` | `normfit` | `normlike` | `normrnd`

nsegments

Class: piecewisedistribution

Number of segments

Syntax

```
n = nsegments(obj)
```

Description

`n = nsegments(obj)` returns the number of segments `n` in the piecewise distribution object `obj`.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

n = nsegments(obj)
n =
     3
```

See Also

`paretotails` | `boundary` | `segment`

NTrees property

Class: TreeBagger

Number of decision trees in ensemble

Description

The `NTrees` property is a scalar equal to the number of decision trees in the ensemble.

See Also

`Trees`

NumParams property

Class: ProbDistParametric

Read-only value specifying number of parameters of ProbDistParametric object

Description

`NumParams` is a read-only property of the `ProbDistParametric` class. `NumParams` is a value specifying the number of parameters of a distribution represented by a ProbDistParametric object.

Values

This value is an integer that counts both the specified parameters and parameters that are fit to the data. Use this information to view and compare the number of parameters supplied to create distributions.

numel

Class: dataset

Number of elements in dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
n = numel(A)
n = numel(A, varargin)
```

Description

`n = numel(A)` returns 1. To find the number of elements, `n`, in the dataset array `A`, use `prod(size(A))` or `numel(A,':',':')`.

`n = numel(A, varargin)` returns the number of subscripted elements, `n`, in `A(index1, index2, ..., indexn)`, where `varargin` is a cell array whose elements are `index1, index2, ... indexn`.

See Also

`length` | `size`

numnodes

Class: classregtree

Number of nodes

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
n = numnodes(t)
```

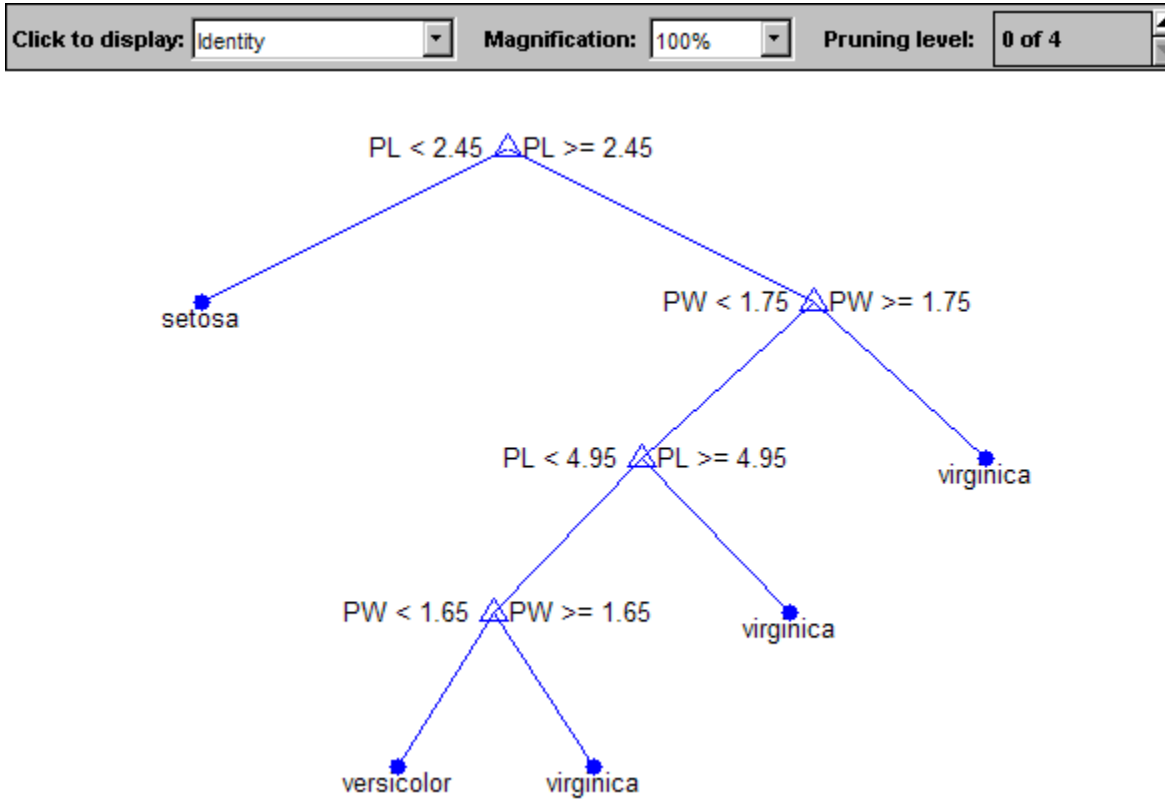
Description

`n = numnodes(t)` returns the number of nodes `n` in the tree `t`.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t=
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica
view(t)
```




```
n = numnodes(t)
n =
     9
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree`

NumTestSets property

Class: cvpartition

Number of test sets

Description

Value is the number of folds in partitions of type `'kfold'` and `'leaveout'`.

Value is `1` in partitions of type `'holdout'` and `'resubstitution'`.

NVarToSample property

Class: TreeBagger

Number of variables for random feature selection

Description

The `NVarToSample` property specifies the number of predictor or feature variables to select at random for each decision split. By default, it is set to the square root of the total number of variables for classification and one third of the total number of variables for regression. Setting this argument to any valid value except `'all'` invokes Breiman's "random forest" algorithm.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

ObsNames property

Class: dataset

Cell array of nonempty, distinct strings giving names of observations in data set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

A cell array of nonempty, distinct strings giving the names of the observations in the data set. This property may be empty, but if not empty, the number of strings must equal the number of observations.

optimalleaforder

Optimal leaf ordering for hierarchical clustering

Syntax

```
leafOrder = optimalleaforder(tree,D)
leafOrder = optimalleaforder(tree,D,Name,Value)
```

Description

`leafOrder = optimalleaforder(tree,D)` returns an optimal leaf ordering for the hierarchical binary cluster tree, `tree`, using the distances, D. An optimal leaf ordering of a binary tree maximizes the sum of the similarities between adjacent leaves by flipping tree branches without dividing the clusters.

`leafOrder = optimalleaforder(tree,D,Name,Value)` returns the optimal leaf ordering using one or more name-value pair arguments.

Examples

Plot Dendrogram With Optimal Leaf Order

Create a hierarchical binary cluster tree using `linkage`. Then, compare the dendrogram plot with the default ordering to a dendrogram with an optimal leaf ordering.

Generate sample data.

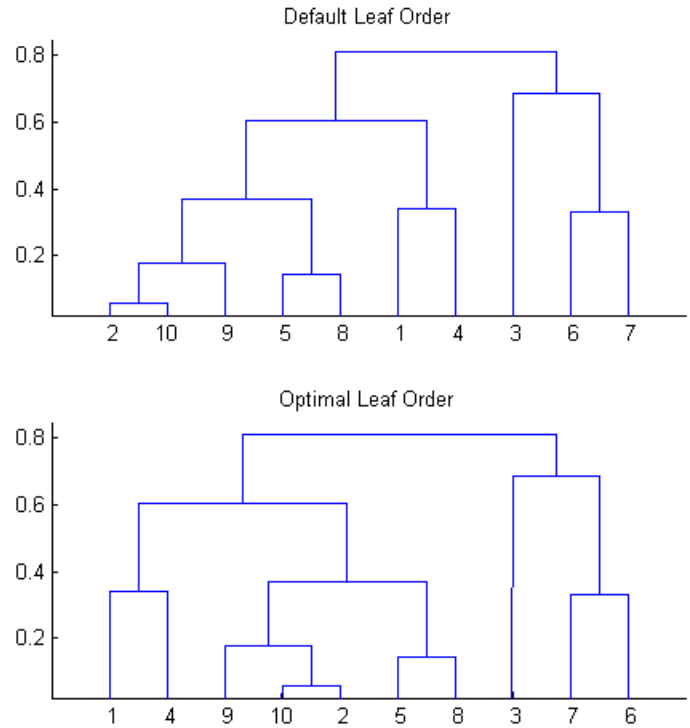
```
rng('default') % For reproducibility
X = rand(10,2);
```

Create a distance vector and a hierarchical binary clustering tree. Use the distances and clustering tree to determine an optimal leaf order.

```
D = pdist(X);
tree = linkage(D,'average');
leafOrder = optimalleaforder(tree,D);
```

Plot the dendrogram with the default ordering and the dendrogram with the optimal leaf ordering.

```
figure()
subplot(2,1,1)
dendrogram(tree)
title('Default Leaf Order')

subplot(2,1,2)
dendrogram(tree,'reorder',leafOrder)
title('Optimal Leaf Order')
```



The order of the leaves in the bottom figure corresponds to the elements in `leafOrder`.

```
leafOrder
```

```
leafOrder =

     1     4     9    10     2     5     8     3     7     6
```

Optimal Leaf Order Using Inverse Distance Similarity

Generate sample data.

```
rng('default') % For reproducibility
X = rand(10,2);
```

Create a distance vector and a hierarchical binary clustering tree.

```
D = pdist(X);
tree = linkage(D,'average');
```

Use the inverse distance similarity transformation to determine an optimal leaf order.

```
leafOrder = optimalleaforder(tree,D,'Transformation','inverse')
```

```
leafOrder =

     1     4     9    10     2     5     8     3     7     6
```

Input Arguments

`tree` — Hierarchical binary cluster tree

matrix returned by `linkage`

Hierarchical binary cluster tree, specified as an $(M-1)$-by-3 matrix that you generate using `linkage`, where M is the number of leaves.

`D` — Distances

matrix | vector

Distances for determining similarities between leaves, specified as a matrix or vector of distances. For example, you can generate distances using `pdist`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Criteria','group','Transformation','inverse'` specifies that the sum of similarities be maximized between every leaf and all other leaves in adjacent clusters, using an inverse similarity transformation.

`'Criteria'` — Optimization criterion

`'adjacent'` (default) | `'group'`

Optimization criterion for determining an optimal leaf ordering, specified as the comma-separated pair consisting of `'criteria'` and one of these strings:

`'adjacent'`	Maximize the sum of similarities between adjacent leaves.
`'group'`	Maximize the sum of similarities between every leaf and all other leaves in the adjacent clusters at the same level of the dendrogram.

Example: `'Criteria','group'`

Data Types: `char`

`'Transformation'` — Method for transforming distances to similarities

`'linear'` (default) | `'inverse'` | function handle

Method for transforming distances to similarities, specified as the comma-separated pair consisting of `'Transformation'` and one of `'linear'`, `'inverse'`, or a function handle.

Let $d_{i,j}$ and $Sim_{i,j}$ denote the distance and similarity between leaves i and j, respectively. The included similarity transformations are:

`'linear'`	$Sim_{i,j} = \max_{i,j}(d_{i,j}) - d_{i,j}$
`'inverse'`	$Sim_{i,j} = 1/d_{i,j}$

To use a custom transformation function, specify a handle to a function that accepts a matrix of distances, `D`, and returns a matrix of similarities, `S`. The function should be monotonic decreasing in the range of distance values. `S` must have the same size as `D`, with `S(i,j)` being the similarity computed based on `D(i,j)`.

Example: `'Transformation',@myTransform`

Data Types: `char | function_handle`

Output Arguments

`leafOrder` — Optimal leaf order

vector

Optimal leaf order, returned as a length-*M* vector, where *M* is the number of leaves. `leafOrder` is a permutation of the vector `1:M`, giving an optimal leaf ordering based on the specified distances and similarity transformation.

References

[1] Bar-Joseph, Z., Gifford, D.K., and Jaakkola, T.S. (2001). Fast optimal leaf ordering for hierarchical clustering. Bioinformatics *17*, Suppl 1:S22–9. PMID: 11472989.

See Also

`dendrogram` | `linkage` | `pdist`

oobEdge

Class: ClassificationBaggedEnsemble

Out-of-bag classification edge

Syntax

```
edge = oobEdge(ens)
edge = oobEdge(ens,Name,Value)
```

Description

`edge = oobEdge(ens)` returns out-of-bag classification edge for `ens`.

`edge = oobEdge(ens,Name,Value)` computes classification edge with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `ens.NumTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`edge`

Classification edge, a weighted average of the classification margin.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in `ens.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `ens.X`.

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates

many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Examples

Find the out-of-bag edge for a bagged ensemble from the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
edge = oobEdge(ens)

edge =
    0.8730
```

See Also

`oobMargin` | `oobPredict` | `oobLoss`

oobError

Class: TreeBagger

Out-of-bag error

Syntax

```
err = oobError(B)
err = oobError(B,'param1',val1,'param2',val2,...)
```

Description

`err = oobError(B)` computes the misclassification probability (for classification trees) or mean squared error (for regression trees) for out-of-bag observations in the training data, using the trained bagger `B`. `err` is a vector of length `NTrees`, where `NTrees` is the number of trees in the ensemble.

`err = oobError(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `oobError` computes errors. If set to `'cumulative'` (default), the method computes cumulative errors and `err` is a vector of length `NTrees`, where the first element gives error from `trees(1)`, second element gives error from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `err` is a vector of length `NTrees`, where each element is an error from each tree in the ensemble. If set to `'ensemble'`, `err` is a scalar showing the cumulative error for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element

	gives error from `trees(1)`, the second element gives error from `trees(1:2)` etc.
`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. `oobError` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.error`

OOBIndices property

Class: TreeBagger

Indicator matrix for out-of-bag observations

Description

The `OOBIndices` property is a logical array of size `Nobs`-by-`NTrees` where `Nobs` is the number of observations in the training data and `NTrees` is the number of trees in the ensemble. The `(I,J)` element is true if observation `I` is out-of-bag for tree `J` and false otherwise. In other words, a true value means observation `I` was not selected for the training data used to grow tree `J`.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

OOBInstanceWeight property

Class: TreeBagger

Count of out-of-bag trees for each observation

Description

The `OOBInstanceWeight` property is a numeric array of size `Nobs`-by-1 containing the number of trees used for computing out-of-bag response for each observation. `Nobs` is the number of observations in the training data used to create the ensemble.

oobLoss

Class: ClassificationBaggedEnsemble

Out-of-bag classification error

Syntax

```
L = oobloss(ens)
L = oobloss(ens,Name,Value)
```

Description

`L = oobloss(ens)` returns the classification error for `ens` computed for out-of-bag data.

`L = oobloss(ens,Name,Value)` computes error with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'lossfun'`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-3306
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 22-3306
- `'hinge'` — See "Loss Functions" on page 22-3306.
- `'mincost'` — Smallest misclassification cost as given by the obj`.Cost` matrix. See "Loss Functions" on page 22-3306.

You can write your own loss function in the syntax described in "Loss Functions" on page 22-3306.

Default: `'classiferror'`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Classification error of the out-of-bag observations, a scalar. `L` can be a vector, or can represent a different quantity, depending on the name-value settings.

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

  $$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

  $$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'hinge'` — Classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in tree, represented in `tree.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` cost function uses a cost of `0` for correct classification, and `1` for misclassification. In other words, `'classiferror'` uses `COST=ones(K)-eye(K)`.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Find the out-of-bag error for a bagged ensemble from the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
L = oobLoss(ens)

L =
    0.0467
```

See Also

`loss` | `oobMargin` | `oobPredict` | `oobEdge`

oobLoss

Class: RegressionBaggedEnsemble

Out-of-bag regression error

Syntax

```
L = oobLoss(ens)
L = oobLoss(ens,Name,Value)
```

Description

`L = oobLoss(ens)` returns the mean squared error for `ens` computed for out-of-bag data.

`L = oobLoss(ens,Name,Value)` computes error with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A regression bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'lossfun'`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `oobLoss` calls it as

```
FUN(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length. `Y` is the observed response, `Yfit` is the predicted response, and `W` is the observation weights.

Default: `'mse'`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Mean squared error of the out-of-bag observations, a scalar. `L` can be a vector, or can represent a different quantity, depending on the name-value settings.

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates

many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Examples

Compute the out-of-bag error for the `carsmall` data:

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression');
L = oobLoss(ens)

L =
   17.0665
```

See Also

`oobPredict` | `loss`

oobMargin

Class: ClassificationBaggedEnsemble

Out-of-bag classification margins

Syntax

```
margin = oobMargin(ens)
margin = oobMargin(ens,Name,Value)
```

Description

`margin = oobMargin(ens)` returns out-of-bag classification margins.

`margin = oobMargin(ens,Name,Value)` calculates margins with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to ens`.NumTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NumTrained`

Output Arguments

`margin`

A numeric column vector of length `size(ens.X,1)`.

Definitions

Out of Bag

Bagging, which stands for “bootstrap aggregation”, is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `ens.X`.

Examples

Find the out-of-bag margin for a bagged ensemble from the Fisher iris data: Find how many elements of margin are equal to `1`.

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
margin = oobMargin(ens);
sum(margin == 1)

ans =
   108
```

See Also

oobPredict | oobLoss | oobEdge | margin

oobMargin

Class: TreeBagger

Out-of-bag margins

Syntax

```
mar = oobMargin(B)
mar = oobMargin(B,'param1',val1,'param2',val2,...)
```

Description

`mar = oobMargin(B)` computes an `Nobs`-by-`NTrees` matrix of classification margins for out-of-bag observations in the training data, using the trained bagger `B`.

`mar = oobMargin(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `oobMargin` computes errors. If set to `'cumulative'` (default), the method computes cumulative margins and `mar` is an `Nobs`-by-`NTrees` matrix, where the first column gives margins from `trees(1)`, second column gives margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is an `Nobs`-by-`NTrees` matrix, where each column gives margins from each tree in the ensemble. If set to `'ensemble'`, `mar` is a single column of length `Nobs` showing the cumulative margins for the entire ensemble.
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If 'trees' is a numeric vector, the method returns an `Nobs`-by-`NTrees` matrix for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a single column for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first column gives margins from `trees(1)`, the second column gives margins from `trees(1:2)` etc.

`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. `oobMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.margin`

oobMeanMargin

Class: TreeBagger

Out-of-bag mean margins

Syntax

```
mar = oobMeanMargin(B)
mar = oobMeanMargin(B,'param1',val1,'param2',val2,...)
```

Description

`mar = oobMeanMargin(B)` computes average classification margins for out-of-bag observations in the training data, using the trained bagger `B`. `oobMeanMargin` averages the margins over all out-of-bag observations. `mar` is a row-vector of length `NTrees`, where `NTrees` is the number of trees in the ensemble.

`mar = oobMeanMargin(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'mode'`	String indicating how `oobMargin` computes errors. If set to `'cumulative'` (default), is a vector of length NTrees where the first element gives mean margin from `trees(1)`, second column gives mean margins from `trees(1:2)` etc, up to `trees(1:NTrees)`. If set to `'individual'`, `mar` is a vector of length `NTrees`, where each element is a mean margin from each tree in the ensemble . If set to `'ensemble'`, `mar` is a scalar showing the cumulative mean margin for the entire ensemble .
`'trees'`	Vector of indices indicating what trees to include in this calculation. By default, this argument is set to `'all'` and the method uses all trees. If `'trees'` is a numeric vector, the method returns a vector of length `NTrees` for `'cumulative'` and `'individual'` modes, where `NTrees` is the number of elements in the input vector, and a scalar for `'ensemble'` mode. For example, in the `'cumulative'` mode, the first element gives mean margin from `trees(1)`, the second element gives mean margin from `trees(1:2)` etc.

`'treeweights'`	Vector of tree weights. This vector must have the same length as the `'trees'` vector. `oobMeanMargin` uses these weights to combine output from the specified trees by taking a weighted average instead of the simple nonweighted majority vote. You cannot use this argument in the `'individual'` mode.

See Also

`CompactTreeBagger.meanMargin`

OOBPermutedVarCountRaiseMargin property

Class: TreeBagger

Variable importance for raising margin

Description

The `OOBPermutedVarCountRaiseMargin` property is a numeric array of size 1-by-`Nvars` containing a measure of variable importance for each predictor. For any variable, the measure is the difference between the number of raised margins and the number of lowered margins if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble. This property is empty for regression trees.

OOBPermutedVarDeltaError property

Class: TreeBagger

Variable importance for prediction error

Description

The `OOBPermutedVarDeltaError` property is a numeric array of size 1-by-*Nvars* containing a measure of importance for each predictor variable (feature). For any variable, the measure is the increase in prediction error if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble.

OOBPermutedVarDeltaMeanMargin property

Class: TreeBagger

Variable importance for classification margin

Description

The `OOBPermutedVarDeltaMeanMargin` property is a numeric array of size 1-by-`Nvars` containing a measure of importance for each predictor variable (feature). For any variable, the measure is the decrease in the classification margin if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble. This property is empty for regression trees.

oobPredict

Class: ClassificationBaggedEnsemble

Predict out-of-bag response of ensemble

Syntax

```
[label,score] = oobPredict(ens)
[label,score] = oobPredict(ens,Name,Value)
```

Description

`[label,score] = oobPredict(ens)` returns class labels and scores for `ens` for out-of-bag data.

`[label,score] = oobPredict(ens,Name,Value)` computes labels and scores with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A classification bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to ens`.NumTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NumTrained`

Output Arguments

`label`

Classification labels of the same data type as the training data `Y`. There are `N` elements or rows, where `N` is the number of training observations. The label is the class with the highest score. In case of a tie, the label is earliest in ens`.ClassNames`.

`score`

An `N`-by-`K` numeric matrix for `N` observations and `K` classes. A high score indicates that an observation is likely to come from this class. Scores are in the range `0` to `1`.

Definitions

Out of Bag

Bagging, which stands for "bootstrap aggregation", is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the out-of-bag predictions and scores for the Fisher iris data. Find the scores in the range `(0.2,0.8)`; these are the scores where there is notable uncertainty in the resulting classifications.

```
load fisheriris
ens = fitensemble(meas,species,'Bag',100,...
    'Tree','type','classification');
[label score] = oobPredict(ens);
unsure = ( (score > .2) & (score < .8));
sum(sum(unsure)) % How many uncertain predictions?

ans =
    16
```

See Also

`oobMargin` | `oobPredict` | `oobLoss` | `oobEdge` | `predict`

oobPredict

Class: RegressionBaggedEnsemble

Predict out-of-bag response of ensemble

Syntax

```
Yfit = oobPredict(ens)
Yfit = oobPredict(ens,Name,Value)
```

Description

`Yfit = oobPredict(ens)` returns the predicted responses for the out-of-bag data in `ens`.

`Yfit = oobPredict(ens,Name,Value)` predicts responses with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A regression bagged ensemble, constructed with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NumTrained`

Output Arguments

`Yfit`

A vector of predicted responses for out-of-bag data. `Yfit` has `size(ens.X,1)` elements.

You can find the indices of out-of-bag observations for weak learner `L` with the command

```
~ens.UseObsForLearner(:,L)
```

Definitions

Out of Bag

Bagging, which stands for “bootstrap aggregation”, is a type of ensemble learning. To bag a weak learner such as a decision tree on a dataset, `fitensemble` generates many bootstrap replicas of the dataset and grows decision trees on these replicas. `fitensemble` obtains each bootstrap replica by randomly selecting `N` observations out of `N` with replacement, where `N` is the dataset size. To find the predicted response of a trained ensemble, `predict` take an average over predictions from individual trees.

Drawing `N` out of `N` observations with replacement omits on average 37% (1/*e*) of observations for each decision tree. These are "out-of-bag" observations. For each observation, `oobLoss` estimates the out-of-bag prediction by averaging over predictions from all trees in the ensemble for which this observation is out of bag. It then compares the computed prediction against the true response for this observation. It calculates the out-of-bag error by comparing the out-of-bag predicted responses against the true responses for all observations used for training. This out-of-bag average is an unbiased estimator of the true ensemble error.

Examples

Compute out-of-bag predictions for the `carsmall` data. Look at the first three terms of the fit:

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression');
Yfit = oobPredict(ens);
Yfit(1:3) % first three terms

ans =
   15.7964
   14.7162
   14.8062
```

See Also

oobLoss | predict

oobPredict

Class: TreeBagger

Ensemble predictions for out-of-bag observations

Syntax

```
Y = oobPredict(B)
Y = oobPredict(B,'param1',val1,'param2',val2,...)
```

Description

`Y = oobPredict(B)` computes predicted responses using the trained bagger `B` for out-of-bag observations in the training data. The output has one prediction for each observation in the training data. The returned Y is a cell array of strings for classification and a numeric array for regression.

`Y = oobPredict(B,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Array of tree indices to use for computation of responses. Default is `'all'`.
`'treeweights'`	Array of `NTrees` weights for weighting votes from the specified trees.

See Also

`CompactTreeBagger.predict` | `OOBIndices`

ordinal

Create ordinal array

After creating an `ordinal` array, you can use related functions to add, drop, or merge categories, and more.

For more information, see Using ordinal Objects.

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
B = ordinal(X)
B = ordinal(X,labels)
B = ordinal(X,labels,levels)

B = ordinal(X,labels,[],edges)
```

Description

`B = ordinal(X)` creates an `ordinal` array object B from the array X. `ordinal` creates the levels of B from the sorted unique values in X, and creates default labels for them.

`B = ordinal(X,labels)` labels the levels in B according to labels.

`B = ordinal(X,labels,levels)` creates an ordinal array with possible levels defined by levels.

`B = ordinal(X,labels,[],edges)` creates an ordinal array by binning a numeric array X with bin edges given by the numeric vector edges.

Examples

Create and Label Ordinal Arrays

Create an ordinal array from integer data, providing explicit labels.

```
quality = ordinal([1 2 3 3 2 1 2 1 3],...
   {'low' 'medium' 'high'})
```

```
quality =

  Columns 1 through 7

     low      medium      high      high      medium      low      medium

  Columns 8 through 9

     low      high
```

Show that the first element is less than the second element (low is less than medium).

```
quality(1) < quality(2)
```

```
ans =

     1
```

Create an ordinal array by binning values between 0 and 1 into thirds with labels `'small'`, `'medium'`, and `'large'`.

```
X = rand(5,2)
A = ordinal(X,{'small' 'medium' 'large'},[],[0 1/3 2/3 1])
```

```
X =

    0.8147    0.0975
    0.9058    0.2785
    0.1270    0.5469
    0.9134    0.9575
```

```
    0.6324    0.9649

A =

     large       small
     large       small
     small       medium
     large       large
     medium      large
```

- “Create Nominal and Ordinal Arrays” on page 2-4

Input Arguments

X — Input array

numeric | logical | character | categorical | cell array of strings

Input array to convert to `ordinal`, specified as a numeric, logical, character, or categorical array, or a cell array of strings. The levels of the resulting `ordinal` array correspond to the sorted unique values in X.

`labels` — Labels for the discrete levels

character array | cell array of strings

Labels for the discrete levels, specified as a character array or cell array of strings. By default, `ordinal` assigns the labels to the levels in B in order according to the sorted unique values in X.

You can include duplicate labels in labels in order to merge multiple values in X into a single level in B.

Data Types: `char` | `cell`

`levels` — Possible ordinal levels

vector

Possible ordinal levels for the output `ordinal` array, specified as a vector whose values can be compared to those in X using the equality operator. `ordinal` assigns labels to each level from the corresponding elements of labels. If X contains any values not present in levels, the levels of the corresponding elements of B are undefined.

`edges` — Bin edges

numeric vector

Bin edges to create a ordinal array by binning a numeric array, specified as a numeric vector. The uppermost bin includes values equal to the right-most edge. `ordinal` assigns labels to each level in the resulting nominal array from the corresponding elements of labels. When you specify edges, it must have one more element than labels.

Output Arguments

`B` — Ordinal array

`ordinal` array object

Nominal array, returned as an `ordinal` array object.

By default, an element of B is undefined if the corresponding element of X is `NaN` (when X is numeric), an empty string (when X is a character), or undefined (when X is categorical). `nominal` treats such elements as "undefined" or "missing" and does not include entries for them among the possible levels. To create an explicit level for such elements instead of treating them as undefined, you must use the levels input argument, and include `NaN`, the empty string, or an undefined element.

More About

- Using ordinal Objects

See Also

`nominal`

Using ordinal Objects

Arrays for ordinal data

Ordinal data are discrete, nonnumeric values that have a natural ordering. `ordinal` array objects provide efficient storage and convenient manipulation of such data, while also maintaining meaningful labels for the values.

You can manipulate `ordinal` arrays much like ordinary numeric arrays, including subscripting, concatenating, and reshaping. It can be useful to use `ordinal` arrays as grouping variables when the elements indicate the group an observation belongs to.

Note: The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Examples

Create and Manipulate Ordinal Arrays

Create an ordinal array from integer data.

```
quality = ordinal([1 2 3; 3 2 1; 2 1 3],{'low' 'medium' 'high'})
```

```
quality =

     low         medium      high
     high        medium      low
     medium      low         high
```

Identify the elements in `quality` that are members of a level that is greater than or equal to `'medium'`. A value of `1` in the resulting array indicates that the corresponding element of `quality` is in this category.

```
quality >= 'medium'
```

```
ans =
```

```
     0     1     1
     1     1     0
     1     0     1
```

Identify the elements of `quality` that are members of either `'low'` or `'high'`.

```
ismember(quality,{'low' 'high'})
```

```
ans =

     1     0     1
     1     0     1
     0     1     1
```

Merge the elements of the `'medium'` and `'high'` levels into a new level labeled `'ok'`.

```
quality = mergelevels(quality,{'medium','high'},'ok')
```

```
quality =

     low       ok        ok
     ok        ok        low
     ok        low       ok
```

Display the levels of `quality`.

```
getlevels(quality)
```

```
ans =

     low       ok
```

Summarize the number of elements in each level. By default, `summary` returns counts for each column of the input array.

```
summary(quality)
```

```
     low       1       1       1
```

```
ok       2       2       2
```


- "Create Nominal and Ordinal Arrays" on page 2-4
- "Reorder Category Levels" on page 2-11
- "Categorize Numeric Data" on page 2-16
- "Merge Category Levels" on page 2-19
- "Sort Ordinal Arrays" on page 2-40

Properties

`labels` — Level labels

cell array of strings

Level labels, specified as a cell array of string. Access labels using `getlabels`.

Data Types: `cell`

`undeflabel` — Label for undefined levels

`'<undefined>'` (default)

Label for undefined levels, specified as `'<undefined>'`. You can find undefined elements in categorical arrays using `isundefined`.

Object Functions

`addlevels` `droplevels` `getlabels` `getlevels` `islevel` `levelcounts` `mergelevels` `reorderlevels` `setlabels`

You can also use many other MATLAB array functions with categorical arrays. The following is a partial list. For a complete list, see "Other MATLAB Functions Supporting Nominal and Ordinal Arrays" on page 2-3.

`double` `histogram` `isequal` `isundefined` `pie` `summary` `times`

Create Object

Create `ordinal` arrays using the `ordinal` function.

See Also

`nominal`

More About

- “Advantages of Using Categorical Arrays” on page 2-44
- “Index and Search Using Categorical Arrays” on page 2-47
- “Grouping Variables” on page 2-52

outlierMeasure

Class: CompactTreeBagger

Outlier measure for data

Syntax

```
out = outlierMeasure(B,X)
out = outlierMeasure(B,X,'param1',val1,'param2',val2,...)
```

Description

`out = outlierMeasure(B,X)` computes outlier measures for predictors `X` using trees in the ensemble `B`. The method computes the outlier measure for a given observation by taking an inverse of the average squared proximity between this observation and other observations. `outlierMeasure` then normalizes these outlier measures by subtracting the median of their distribution, taking the absolute value of this difference, and dividing by the median absolute deviation. A high value of the outlier measure indicates that this observation is an outlier.

You can supply the proximity matrix directly by using the `'data'` parameter.

`out = outlierMeasure(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'data'`	Flag indicating how to treat the `X` input argument. If set to `'predictors'` (default), the method assumes `X` is a matrix of predictors and uses it for computation of the proximity matrix. If set to `'proximity'`, the method treats `X` as a proximity matrix returned by the `proximity` method. If you do not supply the proximity matrix, `outlierMeasure` computes it internally. If you use the `proximity` method to compute a proximity matrix, supplying it as input to `outlierMeasure` reduces computing time.
`'labels'`	Vector of true class labels. True class labels can be either a numeric vector, character matrix, or cell array of strings. When you supply this parameter, the method performs the outlier calculation for any

observations using only other observations from the same class. This parameter must specify one label for each observation (row) in `X`.

See Also

`proximity`

OutlierMeasure property

Class: TreeBagger

Measure for determining outliers

Description

The `OutlierMeasure` property is a numeric array of size `Nobs`-by-1, where `Nobs` is the number of observations in the training data, containing outlier measures for each observation.

See Also

`CompactTreeBagger.outlierMeasure`

parallelcoords

Parallel coordinates plot

Syntax

```
parallelcoords(X)
parallelcoords(X,...,'Standardize','on')
parallelcoords(X,...,'Standardize','PCA')
parallelcoords(X,...,'Standardize','PCAStd')
parallelcoords(X,...,'Quantile',alpha)
parallelcoords(X,...,'Group',group)
parallelcoords(X,...,'Labels',labels)
parallelcoords(X,...,PropertyName,PropertyValue,...)
h = parallelcoords(X,...)
parallelcoords(axes,...)
```

Description

`parallelcoords(X)` creates a parallel coordinates plot of the multivariate data in the *n*-by-*p* matrix `X`. Rows of `X` correspond to observations, columns to variables. A parallel coordinates plot is a tool for visualizing high dimensional data, where each observation is represented by the sequence of its coordinate values plotted against their coordinate indices. `parallelcoords` treats `NaN`s in `X` as missing values and does not plot those coordinate values.

`parallelcoords(X,...,'Standardize','on')` scales each column of `X` to have mean 0 and standard deviation 1 before making the plot.

`parallelcoords(X,...,'Standardize','PCA')` creates a parallel coordinates plot from the principal component scores of `X`, in order of decreasing eigenvalues. `parallelcoords` removes rows of `X` containing missing values (`NaN`s) for principal components analysis (PCA) standardization.

`parallelcoords(X,...,'Standardize','PCAStd')` creates a parallel coordinates plot using the standardized principal component scores.

`parallelcoords(X,...,'Quantile',alpha)` plots only the median and the `alpha` and `1-alpha` quantiles of $f(t)$ at each value of t. This is useful if `X` contains many observations.

`parallelcoords(X,...,'Group',group)` plots the data in different groups with different colors. Groups are defined by `group`, a numeric array containing a group index for each observation. `group` can also be a categorical variable, character matrix, or cell array of strings, containing a group name for each observation.

`parallelcoords(X,...,'Labels',labels)` labels the coordinate tick marks along the horizontal axis using `labels`, a character array or cell array of strings.

`parallelcoords(X,...,`*`PropertyName`*`,`*`PropertyValue`*`,...)` sets properties to the specified property values for all line graphics objects created by `parallelcoords`.

`h = parallelcoords(X,...)` returns a column vector of handles to the line objects created by parallelcoords, one handle per row of `X`. If you use the `'Quantile'` input argument, `h` contains one handle for each of the three lines objects created. If you use both the `'Quantile'` and the `'Group'` input arguments, `h` contains three handles for each group.

`parallelcoords(axes,...)` plots into the axes with handle `axes`.

Examples

```
% Make a grouped plot of the raw data
load fisheriris
labels = {'Sepal Length','Sepal Width',...
          'Petal Length','Petal Width'};
parallelcoords(meas,'group',species,'labels',labels);

% Plot only the median and quartiles of each group
parallelcoords(meas,'group',species,'labels',labels,...
               'quantile',.25);
```

More About

- “Grouping Variables” on page 2-52

See Also

`andrewsplot` | `glyphplot`

paramci

Confidence intervals for probability distribution parameters

Syntax

```
ci = paramci(pd)
ci = paramci(pd,Name,Value)
```

Description

`ci = paramci(pd)` returns the array ci containing the lower and upper boundaries of the 95% confidence interval for each parameter in probability distribution pd.

`ci = paramci(pd,Name,Value)` returns confidence intervals with additional options specified by one or more name-value pair arguments. For example, you can specify a different percentage for the confidence interval, or compute confidence intervals only for selected parameters.

Examples

Parameter Confidence Intervals

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution
```

```
  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the 95% confidence interval for the distribution parameters.

```
ci = paramci(pd)

ci =

   73.4321    7.7391
   76.5846    9.9884
```

Column 1 of `ci` contains the lower and upper 95% confidence interval boundaries for the mu parameter, and column 2 contains the boundaries for the sigma parameter.

Change Parameter Confidence Intervals

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')

pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the 99% confidence interval for the distribution parameters.

```
ci = paramci(pd,'Alpha',.01)

ci =

   72.9245    7.4627
   77.0922   10.4403
```

Column 1 of `ci` contains the lower and upper 99% confidence interval boundaries for the mu parameter, and column 2 contains the boundaries for the sigma parameter.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alpha',0.01` specifies a 99% confidence interval.

`'Alpha'` — Alpha level

`0.05` (default) | scalar value in the range (0,1)

Alpha level for the confidence interval, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1). The default value `0.05` corresponds to a 95% confidence interval.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Parameter'` — Parameter list

vector | cell array of strings

Parameter list for which to compute confidence intervals, specified as the comma-separated pair consisting of `'Parameter'` and a vector or a cell array of strings containing the parameter names. By default, `paramci` computes confidence intervals for all distribution parameters.

Example: `'Parameter','mu'`

Data Types: `char`

`'Type'` — Computation method

`'exact' | 'Wald' | 'lr'`

Computation method for the confidence intervals, specified as the comma-separated pair consisting of `'Type'` and `'exact'`, `'Wald'`, or `'lr'`.

`'exact'` computes the confidence intervals using an exact method, and is available for the following distributions.

Binomial	Compute using the Clopper-Pearson method based on exact probability calculations. This method does not provide exact coverage probabilities.
Exponential	Compute using a method based on a chi-square distribution. This method provides exact coverage for complete and Type 2 censored samples.
Normal	Computation method based on *t* and chi-square distributions for uncensored samples provides exact coverage for uncensored samples. For censored samples, `paramci` uses the Wald method if `Type` is `exact`.
Lognormal	Computation method based on *t* and chi-square distributions for uncensored samples provides exact coverage. For censored samples, `paramci` uses the Wald method if `Type` is `exact`.
Poisson	Computation method based on a chi-square distribution provides exact coverage. For large degrees of freedom, the chi-square is approximated by a normal distribution for numerical efficiency.
Rayleigh	Computation method based on a chi-square distribution provides exact coverage probabilities.

`'exact'` is the default when it is available. Alternatively, you can specify `'Wald'` to compute the confidence intervals using the Wald method, or `'lr'` to compute the confidence intervals using the likelihood radio method.

Example: `'Type','Wald'`

`'LogFlag'` — Boolean flag for log scale

vector

Boolean flag for the log scale, specified as the comma-separated pair consisting of `'LogFlag'` and a vector containing Boolean values corresponding to each distribution parameter. The flag specifies which Wald intervals to compute on a log scale. The default values depend on the distribution.

Example: `'LogFlag',[0,1]`

Data Types: `logical`

Output Arguments

`ci` — Confidence interval

array

Confidence interval, returned as a *p*-by-2 array containing the lower and upper bounds of the (1 - `Alpha`)% confidence interval for each distribution parameter. *p* is the number of distribution parameters.

See Also

`dfittool` | `fitdist` | `makedist`

paramci

Class: ProbDistUnivParam

Return parameter confidence intervals of ProbDistUnivParam object

Syntax

```
CI = paramci(PD)
CI = paramci(PD, Alpha)
```

Description

`CI = paramci(PD)` returns `CI`, a 2-by-`N` array containing 95% confidence intervals for the parameters of the `ProbDistUnivParam` object `PD`. `N` is the number of parameters in the distribution. When you create `PD` by specifying parameters (such as using the `ProbDistUnivParam` constructor or using the `fitdist` function and specifying a `'binomial'` or `'generalized pareto'` distribution) rather than by fitting to data, the confidence intervals have a width of `0` because the parameters are viewed as estimates of an unknown parameter.

`CI = paramci(PD, Alpha)` returns `100*(1 - Alpha)`% confidence intervals. Default `Alpha` is `0.05`, which specifies 95% confidence intervals.

Note: If you create `PD` with a distribution that does not support confidence intervals, then `CI` contains `NaN` values.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam`.
`Alpha`	A value between `0` and `1` that specifies a confidence interval. Default is `0.05`, which specifies 95% confidence intervals.

Output Arguments

`CI`	A 2-by-`N` array containing `100*(1 - Alpha)`% confidence intervals for the parameters of the `ProbDistUnivParam` object `PD`. `N` is the number of parameters in the distribution.

See Also

`fitdist`

paramci

Class: prob.ToolboxFittableParametricDistribution
Package: prob

Confidence intervals for probability distribution parameters

Syntax

```
ci = paramci(pd)
ci = paramci(pd,Name,Value)
```

Description

`ci = paramci(pd)` returns the array ci containing the lower and upper boundaries of the 95% confidence interval for each parameter in probability distribution pd.

`ci = paramci(pd,Name,Value)` returns confidence intervals with additional options specified by one or more name-value pair arguments. For example, you can specify a different percentage for the confidence interval, or compute confidence intervals only for selected parameters.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alpha',0.01` specifies a 99% confidence interval.

`'Alpha'` — Alpha level

`0.05` (default) | scalar value in the range (0,1)

Alpha level for the confidence interval, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1). The default value `0.05` corresponds to a 95% confidence interval.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Parameter'` — Parameter list

vector | cell array of strings

Parameter list for which to compute confidence intervals, specified as the comma-separated pair consisting of `'Parameter'` and a vector or a cell array of strings containing the parameter names. By default, `paramci` computes confidence intervals for all distribution parameters.

Example: `'Parameter','mu'`

Data Types: `char`

`'Type'` — Computation method

`'exact'` | `'Wald'` | `'lr'`

Computation method for the confidence intervals, specified as the comma-separated pair consisting of `'Type'` and `'exact'`, `'Wald'`, or `'lr'`.

`'exact'` computes the confidence intervals using an exact method, and is available for the following distributions.

Binomial	Compute using the Clopper-Pearson method based on exact probability calculations. This method does not provide exact coverage probabilities.
Exponential	Compute using a method based on a chi-square distribution. This method provides exact coverage for complete and Type 2 censored samples.

Normal	Computation method based on *t* and chi-square distributions for uncensored samples provides exact coverage for uncensored samples. For censored samples, `paramci` uses the Wald method if `Type` is `exact`.
Lognormal	Computation method based on *t* and chi-square distributions for uncensored samples provides exact coverage. For censored samples, `paramci` uses the Wald method if `Type` is `exact`.
Poisson	Computation method based on a chi-square distribution provides exact coverage. For large degrees of freedom, the chi-square is approximated by a normal distribution for numerical efficiency.
Rayleigh	Computation method based on a chi-square distribution provides exact coverage probabilities.

`'exact'` is the default when it is available. Alternatively, you can specify `'Wald'` to compute the confidence intervals using the Wald method, or `'lr'` to compute the confidence intervals using the likelihood radio method.

Example: `'Type','Wald'`

`'LogFlag'` — Boolean flag for log scale

vector

Boolean flag for the log scale, specified as the comma-separated pair consisting of `'LogFlag'` and a vector containing Boolean values corresponding to each distribution parameter. The flag specifies which Wald intervals to compute on a log scale. The default values depend on the distribution.

Example: `'LogFlag',[0,1]`

Data Types: `logical`

Output Arguments

`ci` — Confidence interval

array

Confidence interval, returned as a *p*-by-2 array containing the lower and upper bounds of the (1 - `Alpha`)% confidence interval for each distribution parameter. *p* is the number of distribution parameters.

Examples

Parameter Confidence Intervals

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the 95% confidence interval for the distribution parameters.

```
ci = paramci(pd)
```

```
ci =

   73.4321    7.7391
   76.5846    9.9884
```

Column 1 of `ci` contains the lower and upper 95% confidence interval boundaries for the mu parameter, and column 2 contains the boundaries for the sigma parameter.

Change Parameter Confidence Intervals

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the 99% confidence interval for the distribution parameters.

```
ci = paramci(pd,'Alpha',.01)
```

```
ci =

   72.9245    7.4627
   77.0922   10.4403
```

Column 1 of `ci` contains the lower and upper 99% confidence interval boundaries for the mu parameter, and column 2 contains the boundaries for the sigma parameter.

See Also

`dfittool` | `fitdist` | `makedist`

ParamCov property

Class: ProbDistParametric

Read-only covariance matrix of parameter estimates of ProbDistParametric object

Description

`ParamCov` is a read-only property of the `ProbDistParametric` class. `ParamCov` is a covariance matrix containing the parameter estimates of a distribution represented by a ProbDistParametric object. `ParamCov` has a size of `NumParams`-by-`NumParams`.

Values

This covariance matrix includes estimates for both the specified parameters and parameters that are fit to the data. For specified parameters, the covariance is `0`, indicating the parameter is known exactly. Use this information to view and compare the descriptions of parameters supplied to create distributions.

ParamDescription property

Class: ProbDistParametric

Read-only cell array specifying descriptions of parameters of ProbDistParametric object

Description

`ParamDescription` is a read-only property of the `ProbDistParametric` class. `ParamDescription` is a cell array of strings specifying the descriptions or meanings of the parameters of a distribution represented by a ProbDistParametric object. `ParamDescription` has a length of `NumParams`.

Values

This cell array includes a brief description of the meaning of both the specified parameters and parameters that are fit to the data. The description is the same as the parameter name when no further description information is available. Use this information to view and compare the descriptions of parameters used to create distributions.

ParamIsFixed property

Class: ProbDistParametric

Read-only logical array specifying fixed parameters of ProbDistParametric object

Description

`ParamIsFixed` is a read-only property of the `ProbDistParametric` class. `ParamIsFixed` is a logical array specifying the fixed parameters of a distribution represented by a ProbDistParametric object. `ParamIsFixed` has a length of `NumParams`.

Values

This array specifies a `1` (`true`) for fixed parameters, and a `0` (`false`) for parameters that are estimated from the input data. Use this information to view and compare the fixed parameters used to create distributions.

ParamNames property

Class: ProbDistParametric

Read-only cell array specifying names of parameters of ProbDistParametric object

Description

`ParamNames` is a read-only property of the `ProbDistParametric` class. `ParamNames` is a cell array of strings specifying the names of the parameters of a distribution represented by a ProbDistParametric object. `ParamNames` has a length of `NumParams`.

Values

This cell array includes the names of both the specified parameters and parameters that are fit to the data. Use this information to view and compare the names of parameters used to create distributions.

Params property

Class: NaiveBayes

Parameter estimates

Description

The `Params` property is an `NClasses`-by-`NDims` cell array containing the parameter estimates, excluding the class priors. `Params(i,j)` contains the parameter estimates for the `j`th feature in the `i`th class. `Params(i,j)` is an empty cell if the `i`th class is empty.

The entry in `Params(i,j)` depends on the distribution type used for the `jth` feature, as follows:

`'normal'`	A vector of length two. The first element is the mean, and the second element is standard deviation.
`'kernel'`	A `ProbDistUnivKernel` object
`'mvmn'`	A vector containing the probability for each possible value of the `j`th feature in the `i`th class. The order of the probabilities is decided by the sorted order of all the unique values of the `j`th feature.
`'mn'`	A scalar representing the probability the `j`th token appearing in the `i`th class, `Prob(token j | class i)`. It is estimated as `(1 + the number of occurrence of token J in class I)/ (NDims + the total number of token occurrence in class I)`.

Params property

Class: ProbDistParametric

Read-only array specifying values of parameters of ProbDistParametric object

Description

`Params` is a read-only property of the `ProbDistParametric` class. `Params` is an array of values specifying the values of the parameters of a distribution represented by a ProbDistParametric object. `Params` has a length of `NumParams`.

Values

This array includes the values of both the specified parameters and parameters that are fit to the data. Use this information to view and compare the values of parameters used to create distributions.

prob.ParametricTruncatableDistribution class

Package: prob
Superclasses: prob.TruncatableDistribution

Parametric truncatable probability distribution object

Description

Create a probability distribution object with specified parameter values using `makedist`.

Methods

mean	Mean of probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object

pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object

See Also

`makedist`

More About

- Class Attributes
- Property Attributes

parent

Class: classregtree

Parent node

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
p = parent(t)
p = parent(t,nodes)
```

Description

`p = parent(t)` returns an n-element vector `p` containing the number of the parent node for each node in the tree `t`, where n is the number of nodes. The parent of the root node is `0`.

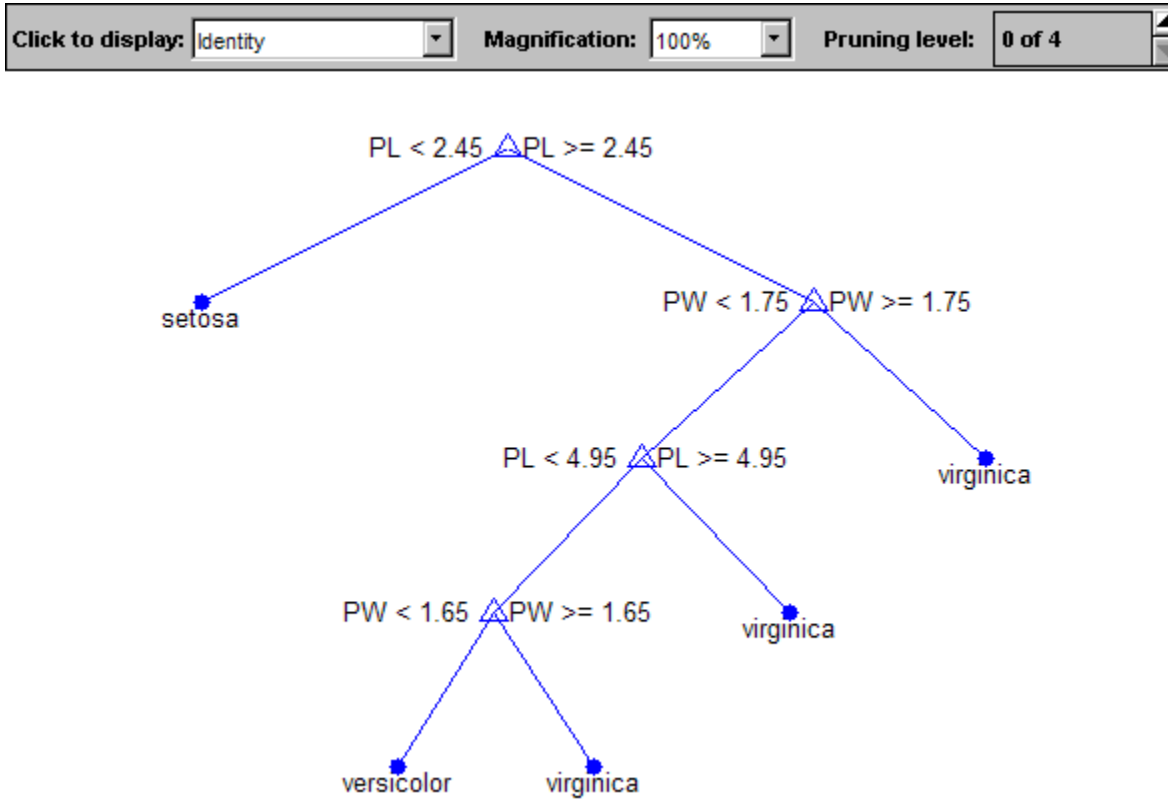
`p = parent(t,nodes)` takes a vector `nodes` of node numbers and returns the parent nodes for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
```

```
1  if PL<2.45 then node 2 else node 3
2  class = setosa
3  if PW<1.75 then node 4 else node 5
4  if PL<4.95 then node 6 else node 7
5  class = virginica
6  if PW<1.65 then node 8 else node 9
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
p = parent(t)
p =
```

```
     0
     1
     1
     3
     3
     4
     4
     6
     6
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `numnodes` | `children`

paretotails class

Superclasses: piecewisedistribution

Empirical distributions with Pareto tails

Construction

.paretotails	Construct Pareto tails object

Methods

lowerparams	Lower Pareto tails parameters
upperparams	Upper Pareto tails parameters

Inherited Methods

Methods in the following table are inherited from `piecewisedistribution`.

boundary	Piecewise distribution boundaries
cdf	Cumulative distribution function for piecewise distribution
disp	Display piecewisedistribution object
display	Display piecewisedistribution object
icdf	Inverse cumulative distribution function for piecewise distribution

nsegments	Number of segments
pdf	Probability density function for piecewise distribution
random	Random numbers from piecewise distribution
segment	Segments containing values

Properties

Objects of the `paretotails` class have no properties accessible by dot indexing, `get` methods, or `set` methods. To obtain information about a `paretotails` object, use the appropriate method.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

How To

- “Generalized Pareto Distribution”

paretotails

Class: paretotails

Construct Pareto tails object

Syntax

```
obj = paretotails(x,pl,pu)
obj = paretotails(x,pl,pu,cdffun)
```

Description

`obj = paretotails(x,pl,pu)` creates an object `obj` defining a distribution consisting of the empirical distribution of `x` in the center and Pareto distributions in the tails. `x` is a real-valued vector of data values whose extreme observations are fit to generalized Pareto distributions (GPDs). `pl` and `pu` identify the lower- and upper-tail cumulative probabilities such that `100*pl` and `100*(1-pu)` percent of the observations in `x` are, respectively, fit to a GPD by maximum likelihood. If `pl` is `0`, or if there are not at least two distinct observations in the lower tail, then no lower Pareto tail is fit. If `pu` is `1`, or if there are not at least two distinct observations in the upper tail, then no upper Pareto tail is fit.

`obj = paretotails(x,pl,pu,cdffun)` uses *`cdffun`* to estimate the cdf of `x` between the lower and upper tail probabilities. *`cdffun`* may be any of the following:

- `'ecdf'` — Uses an interpolated empirical cdf, with data values as the midpoints in the vertical steps in the empirical cdf, and computed by linear interpolation between data values. This is the default.
- `'kernel'` — Uses a kernel-smoothing estimate of the cdf.
- `@fun` — Uses a handle to a function of the form `[p,xi] = fun(x)` that accepts the input data vector `x` and returns a vector `p` of cdf values and a vector `xi` of evaluation points. Values in `xi` must be sorted and distinct but need not equal the values in `x`.

`cdffun` is used to compute the quantiles corresponding to `pl` and `pu` by inverse interpolation, and to define the fitted distribution between these quantiles.

The output object `obj` is a Pareto tails object with methods to evaluate the cdf, inverse cdf, and other functions of the fitted distribution. These methods are well-suited to copula and other Monte Carlo simulations. The pdf method in the tails is the GPD density, but in the center it is computed as the slope of the interpolated cdf.

The `paretotails` class is a subclass of the `piecewisedistribution` class, and many of its methods are derived from that class.

Examples

Fit Pareto Tails to a Probability Distribution

Generate sample data containing 100 random numbers from a *t* distribution with 3 degrees of freedom.

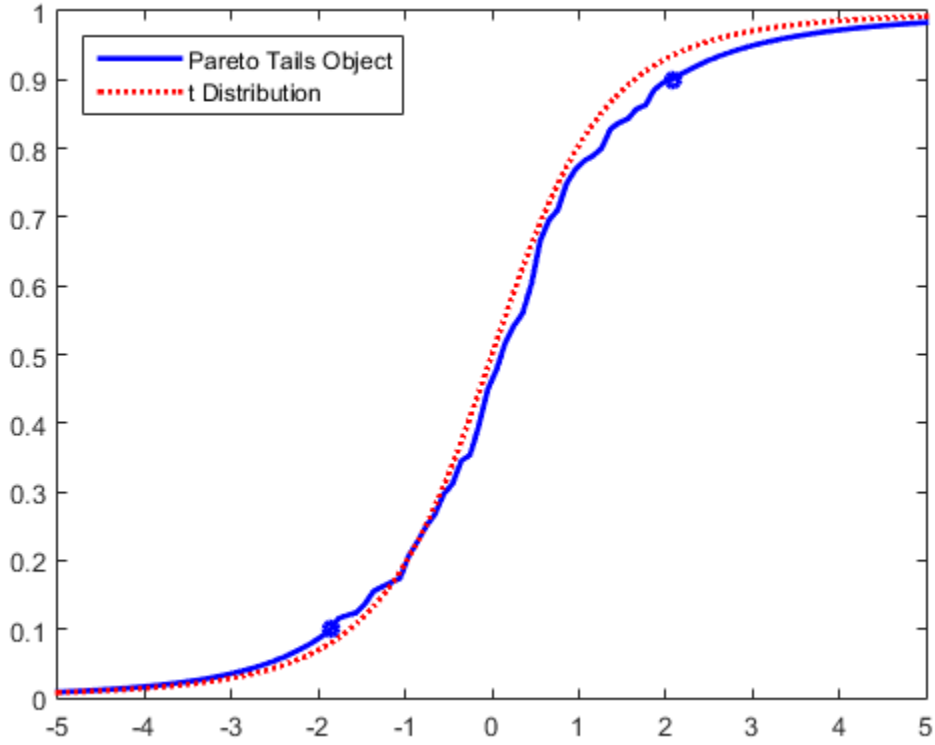
```
rng default;  % For reproducibility
t = trnd(3,100,1);
```

Fit pareto tails to the distribution at cumulative probabilities 0.1 and 0.9.

```
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj);
```

Plot the cdf of the Pareto tails and the cdf of the fitted *t* distribution on the same figure.

```
x = linspace(-5,5);
plot(x,cdf(obj,x),'b-','LineWidth',2)
hold on;
plot(x,tcdf(x,3),'r:','LineWidth',2)
plot(q,p,'bo','LineWidth',2,'MarkerSize',5)
legend('Pareto Tails Object','t Distribution',...
       'Location','NW')
hold off;
```



See Also

`icdf` | `ksdensity` | `cdf` | `ecdf` | `gpfit`

partialcorr

Linear or rank partial correlation coefficients

Syntax

```
rho = partialcorr(x)
rho = partialcorr(x,z)
rho = partialcorr(x,y,z)
rho = partialcorr( ___ ,Name,Value)
[rho,pval] = partialcorr( ___ )
```

Description

`rho = partialcorr(x)` returns the sample linear partial correlation coefficients between pairs of variables in x, controlling for the remaining variables in x.

`rho = partialcorr(x,z)` returns the sample linear partial correlation coefficients between pairs of variables in x, controlling for the variables in z.

`rho = partialcorr(x,y,z)` returns the sample linear partial correlation coefficients between pairs of variables in x and y, controlling for the variables in z.

`rho = partialcorr( ___ ,Name,Value)` returns the sample linear partial correlation coefficients with additional options specified by one or more name-value pair arguments, using input arguments from any of the previous syntaxes. For example, you can specify whether to use Pearson or Spearman partial correlations, or specify how to treat missing values.

`[rho,pval] = partialcorr( ___ )` also returns a matrix pval of *p*-values for testing the hypothesis of no partial correlation against the one- or two-sided alternative that there is a nonzero partial correlation.

Examples

Compute Partial Correlation Coefficients

Compute partial correlation coefficients between pairs of variables in the input matrix.

Load the sample data. Convert the strings in `hospital.Sex` to numeric group identifiers.

```
load hospital;
hospital.SexID = grp2idx(hospital.Sex);
```

Create an input matrix containing the sample data.

```
x = [hospital.SexID hospital.Age hospital.Smoker hospital.Weight];
```

Each row in `x` contains a patient's gender, age, smoking status, and weight.

Compute partial correlation coefficients between pairs of variables in `x`, while controlling for the effects of the remaining variables in `x`.

```
rho = partialcorr(x)
```

```
rho =

    1.0000   -0.0105    0.0273    0.9421
   -0.0105    1.0000    0.0419    0.0369
    0.0273    0.0419    1.0000    0.0451
    0.9421    0.0369    0.0451    1.0000
```

The matrix `rho` indicates, for example, a correlation of 0.9421 between gender and weight after controlling for all other variables in `x`. You can return the *p*-values as a second output, and examine them to confirm whether these correlations are statistically significant.

For a clearer display, create a table with appropriate variable and row labels.

```
rho = array2table(rho, ...
    'VariableNames',{'SexID','Age','Smoker','Weight'},...
    'RowNames',{'SexID','Age','Smoker','Weight'});

disp('Partial Correlation Coefficients')
disp(rho)
```

```
Partial Correlation Coefficients
               SexID        Age         Smoker      Weight
               --------    --------    --------    --------
    SexID           1    -0.01052    0.027324      0.9421
    Age       -0.01052           1    0.041945    0.036873
    Smoker    0.027324    0.041945           1    0.045106
```

```
    Weight      0.9421    0.036873    0.045106           1
```

Test for Partial Correlations with Controlled Variables

Test for partial correlation between pairs of variables in the input matrix, while controlling for the effects of a second set of variables.

Load the sample data. Convert the strings in `hospital.Sex` to numeric group identifiers.

```
load hospital;
hospital.SexID = grp2idx(hospital.Sex);
```

Create two matrices containing the sample data.

```
x = [hospital.Age hospital.BloodPressure];
z = [hospital.SexID hospital.Smoker hospital.Weight];
```

The `x` matrix contains the variables to test for partial correlation. The `z` matrix contains the variables to control for. The measurements for `BloodPressure` are contained in two columns: The first column contains the upper (systolic) number, and the second column contains the lower (diastolic) number. `partialcorr` treats each column as a separate variable.

Test for partial correlation between pairs of variables in `x`, while controlling for the effects of the variables in `z`. Compute the correlation coefficients.

```
[rho,pval] = partialcorr(x,z)
```

```
rho =

    1.0000    0.1300    0.0462
    0.1300    1.0000    0.0012
    0.0462    0.0012    1.0000


pval =

         0    0.2044    0.6532
    0.2044         0    0.9903
    0.6532    0.9903         0
```

The large values in `pval` indicate that there is no significant correlation between age and either blood pressure measurement after controlling for gender, smoking status, and weight.

For a clearer display, create tables with appropriate variable and row labels.

```
rho = array2table(rho, ...
    'VariableNames',{'Age','BPTop','BPBottom'},...
    'RowNames',{'SexID','Smoker','Weight'});

pval = array2table(pval, ...
    'VariableNames',{'Age','BPTop','BPBottom'},...
    'RowNames',{'SexID','Smoker','Weight'});

disp('Partial Correlation Coefficients')
disp(rho)
disp('p-values')
disp(pval)
```

```
Partial Correlation Coefficients
                Age          BPTop       BPBottom
              --------    ---------    ---------
    SexID            1         0.13     0.046202
    Smoker        0.13            1    0.0012475
    Weight    0.046202    0.0012475            1

p-values
                Age        BPTop     BPBottom
              -------    -------    --------
    SexID           0    0.20438     0.65316
    Smoker    0.20438          0     0.99032
    Weight    0.65316    0.99032           0
```

Test for Paired Partial Correlation Coefficients

Test for partial correlation between pairs of variables in the `x` and `y` input matrices, while controlling for the effects of a third set of variables.

Load the sample data. Convert the strings in `hospital.Sex` to numeric group identifiers.

```
load hospital;
hospital.SexID = grp2idx(hospital.Sex);
```

Create three matrices containing the sample data.

```
x = [hospital.BloodPressure];
y = [hospital.Weight hospital.Age];
z = [hospital.SexID hospital.Smoker];
```

`partialcorr` can test for partial correlation between the pairs of variables in `x` (the systolic and diastolic blood pressure measurements) and `y` (weight and age), while controlling for the variables in `z` (gender and smoking status). The measurements for `BloodPressure` are contained in two columns: The first column contains the upper (systolic) number, and the second column contains the lower (diastolic) number. `partialcorr` treats each column as a separate variable.

Test for partial correlation between pairs of variables in `x` and `y`, while controlling for the effects of the variables in `z`. Compute the correlation coefficients.

```
[rho,pval] = partialcorr(x,y,z)
```

```
rho =

   -0.0257    0.1289
    0.0292    0.0472


pval =

    0.8018    0.2058
    0.7756    0.6442
```

The results in `pval` indicate that, after controlling for gender and smoking status, there is no significant correlation between either of a patient's blood pressure measurements and that patient's weight or age.

For a clearer display, create tables with appropriate variable and row labels.

```
rho = array2table(rho, ...
    'VariableNames',{'BPTop','BPBottom'},...
    'RowNames',{'Weight','Age'});

pval = array2table(pval, ...
    'VariableNames',{'BPTop','BPBottom'},...
    'RowNames',{'Weight','Age'});

disp('Partial Correlation Coefficients')
disp(rho)
disp('p-values')
disp(pval)
```

```
Partial Correlation Coefficients
               BPTop      BPBottom
```

```
                 --------    --------
    Weight      -0.02568     0.12893
    Age         0.029168    0.047226

p-values
                  BPTop     BPBottom
                 -------    --------
    Weight      0.80182     0.2058
    Age         0.77556     0.64424
```

One-Tailed Partial Correlation Test

Test the hypothesis that pairs of variables have no correlation, against the alternative hypothesis that the correlation is greater than 0.

Load the sample data. Convert the strings in `hospital.Sex` to numeric group identifiers.

```
load hospital;
hospital.SexID = grp2idx(hospital.Sex);
```

Create three matrices containing the sample data.

```
x = [hospital.BloodPressure];
y = [hospital.Weight hospital.Age];
z = [hospital.SexID hospital.Smoker];
```

`partialcorr` can test for partial correlation between the pairs of variables in `x` (the systolic and diastolic blood pressure measurements) and `y` (weight and age), while controlling for the variables in `z` (gender and smoking status). The measurements for `BloodPressure` are contained in two columns: The first column contains the upper (systolic) number, and the second column contains the lower (diastolic) number. `partialcorr` treats each column as a separate variable.

Compute the correlation coefficients using a right-tailed test.

```
[rho,pval] = partialcorr(x,y,z,'Tail','right')

rho =

   -0.0257    0.1289
    0.0292    0.0472
```

```
pval =

    0.5991    0.1029
    0.3878    0.3221
```

The results in `pval` indicate that `partialcorr` does not reject the null hypothesis of nonzero correlations between the variables in `x` and `y`, after controlling for the variables in `z`, when the alternative hypothesis is that the correlations are greater than 0.

For a clearer display, create tables with appropriate variable and row labels.

```
rho = array2table(rho, ...
    'VariableNames',{'BPTop','BPBottom'},...
    'RowNames',{'Weight','Age'});

pval = array2table(pval, ...
    'VariableNames',{'BPTop','BPBottom'},...
    'RowNames',{'Weight','Age'});

disp('Partial Correlation Coefficients')
disp(rho)
disp('p-values')
disp(pval)
```

```
Partial Correlation Coefficients
              BPSys       BPDia
    Weight    -0.02568     0.12893
    Age       0.029168    0.047226

p-values
              BPSys      BPDia
    Weight    0.59909     0.1029
    Age       0.38778    0.32212
```

Input Arguments

x — Data matrix

matrix

Data matrix, specified as an n-by-p_x matrix. The rows of `x` correspond to observations, and the columns correspond to variables.

Data Types: `single` | `double`

y — Data matrix
matrix

Data matrix, specified as an n-by-p_y matrix. The rows of `y` correspond to observations, and the columns correspond to variables.

Data Types: `single` | `double`

z — Data matrix
matrix

Data matrix, specified as an n-by-p_z matrix. The rows of `z` correspond to observations, and columns correspond to variables.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Type','Spearman','Rows','complete'` computes Spearman partial correlations using only the data in rows that contain no missing values.

`'Type'` — Type of partial correlations
`'Pearson'` (default) | `'Spearman'`

Type of partial correlations to compute, specified as the comma-separated pair consisting of `'Type'` and one of the following.

`'Pearson'`	Compute Pearson (linear) partial correlations.
`'Spearman'`	Compute Spearman (rank) partial correlations.

Example: `'Type','Spearman'`

`'Rows'` — Rows to use in computation
`'all'` (default) | `'complete'` | `'pairwise'`

Rows to use in computation, specified as the comma-separated pair consisting of `'Rows'` and one of the following.

`'all'`	Use all rows regardless of missing (`NaN`) values.
`'complete'`	Use only rows with no missing values.
`'pairwise'`	Compute `rho(i,j)` using rows with no missing values in column `i` or `j`.

Using `'pairwise'` can produce a rho that is not positive definite. `'complete'` always produces a positive definite rho, but when data is missing, the estimates are generally based on fewer observations.

Example: `'Rows','complete'`

`'Tail'` — Alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Alternative hypothesis to test against, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the correlation is not 0.
`'right'`	Test the alternative hypothesis that the correlation is greater than 0.
`'left'`	Test the alternative hypothesis that the correlation is less than 0.

Example: `'Tail','right'`

Output Arguments

`rho` — Sample linear partial correlation coefficients

matrix

Sample linear partial correlation coefficients, returned as a matrix.

- If you input only an x matrix, `rho` is a symmetric p_x-by-p_x matrix. The (i,j)th entry is the sample linear partial correlation between the i-th and j-th columns in x.

- If you input x and z matrices, `rho` is a symmetric p_x-by-p_x matrix. The (i,j)th entry is the sample linear partial correlation between the ith and jth columns in x, controlled for the variables in z.
- If you input x, y, and z matrices, `rho` is a p_x-by-p_y matrix, where the (i,j)th entry is the sample linear partial correlation between the ith column in x and the jth column in y, controlled for the variables in z.

If the covariance matrix of `[x,z]` is

$$S = \begin{pmatrix} S_{xx} & S_{xz} \\ S_{xz}^T & S_{zz} \end{pmatrix},$$

then the partial correlation matrix of `x`, controlling for `z`, can be defined formally as a normalized version of the covariance matrix $S_{xy} = S_{xx} - (S_{xz}S_{zz}^{-1}S_{xz}^T)$

`pval` — *p*-values

matrix

p-values, returned as a matrix. Each element of `pval` is the *p*-value for the corresponding element of rho.

If `pval(i,j)` is small, then the corresponding partial correlation `rho(i,j)` is statistically significantly different from 0.

`partialcorr` computes *p*-values for linear and rank partial correlations using a Student's *t* distribution for a transformation of the correlation. This is exact for linear partial correlation when x and z are normal, but is a large-sample approximation otherwise.

See Also

`corr` | `corrcoef` | `partialcorri` | `tiedrank`

partialcorri

Partial correlation coefficients adjusted for internal variables

Syntax

```
rho = partialcorri(y,x)
rho = partialcorri(y,x,z)
rho = partialcorri( ___ ,Name,Value)
[rho,pval] = partialcorri( ___ )
```

Description

`rho = partialcorri(y,x)` returns the sample linear partial correlation coefficients between pairs of variables in y and x, adjusting for the remaining variables in x.

`rho = partialcorri(y,x,z)` returns the sample linear partial correlation coefficients between pairs of variables in y and x, adjusting for the remaining variables in x, after first controlling both x and y for the variables in z.

`rho = partialcorri( ___ ,Name,Value)` returns the sample linear partial correlation coefficients with additional options specified by one or more name-value pair arguments, using input arguments from any of the previous syntaxes. For example, you can specify whether to use Pearson or Spearman partial correlations, or specify how to treat missing values.

`[rho,pval] = partialcorri( ___ )` also returns a matrix pval of *p*-values for testing the hypothesis of no partial correlation against the one- or two-sided alternative that there is a nonzero partial correlation.

Examples

Compute Partial Correlation Coefficients

Compute partial correlation coefficients for each pair of variables in the `x` and `y` input matrices, while controlling for the effects of the remaining variables in `x`.

Load the sample data.

```
load carsmall;
```

The data contains measurements from cars manufactured in 1970, 1976, and 1982. It includes `MPG` and `Acceleration` as performance measures, and `Displacement`, `Horsepower`, and `Weight` as design variables. `Acceleration` is the time required to accelerate from 0 to 60 miles per hour, so a high value for `Acceleration` corresponds to a vehicle with low acceleration.

Define the input matrices. The `y` matrix includes the performance measures, and the `x` matrix includes the design variables.

```
y = [MPG,Acceleration];
x = [Displacement,Horsepower,Weight];
```

Compute the correlation coefficients. Include only rows with no missing values in the computation.

```
rho = partialcorri(y,x,'Rows','complete')
```

```
rho =

   -0.0537   -0.1520   -0.4856
   -0.3994   -0.4008    0.4912
```

The results suggest, for example, a 0.4912 correlation between weight and acceleration after controlling for the effects of displacement and horsepower. You can return the *p*-values as a second output, and examine them to confirm whether these correlations are statistically significant.

For a clearer display, create a table with appropriate variable and row labels.

```
rho = array2table(rho, ...
   'VariableNames',{'Displacement','Horsepower','Weight'}, ...
   'RowNames',{'MPG','Acceleration'});

disp('Partial Correlation Coefficients')
disp(rho)
```

```
Partial Correlation Coefficients
                    Displacement    Horsepower     Weight
                    ------------    ----------    --------
    MPG             -0.053684       -0.15199      -0.48563
```

```
    Acceleration      -0.39941        -0.40075        0.49123
```

Test Partial Correlations While Controlling for Additional Variables

Test for partial correlation between pairs of variables in the `x` and `y` input matrices, while controlling for the effects of the remaining variables in `x` plus additional variables in matrix `z`.

Load the sample data.

```
load carsmall;
```

The data contains measurements from cars manufactured in 1970, 1976, and 1982. It includes `MPG` and `Acceleration` as performance measures, and `Displacement`, `Horsepower`, and `Weight` as design variables. `Acceleration` is the time required to accelerate from 0 to 60 miles per hour, so a high value for `Acceleration` corresponds to a vehicle with low acceleration.

Create a new variable `Headwind`, and randomly generate data to represent the notion of an average headwind along the performance measurement route.

```
rng('default');  % For reproducibility
Headwind = (10:-0.2:-9.8)' + 5*randn(100,1);
```

Since headwind can affect the performance measures, control for its effects when testing for partial correlation between the remaining variables.

Define the input matrices. The `y` matrix includes the performance measures, and the `x` matrix includes the design variables. The `z` matrix contains additional variables to control for when computing the partial correlations, such as headwind.

```
y = [MPG,Acceleration];
x = [Displacement,Horsepower,Weight];
z = Headwind;
```

Compute the partial correlation coefficients. Include only rows with no missing values in the computation.

```
[rho,pval] = partialcorri(y,x,z,'Rows','complete')
```

```
rho =

    0.0572   -0.1055   -0.5736
   -0.3845   -0.3966    0.4674
```

```
pval =

    0.5923    0.3221    0.0000
    0.0002    0.0001    0.0000
```

The small returned p-value of 0.001 in `pval` indicates, for example, a significant negative correlation between horsepower and acceleration, after controlling for displacement, weight, and headwind.

For a clearer display, create tables with appropriate variable and row labels.

```
rho = array2table(rho, ...
   'VariableNames',{'Displacement','Horsepower','Weight'}, ...
   'RowNames',{'MPG','Acceleration'});

pval = array2table(pval, ...
   'VariableNames',{'Displacement','Horsepower','Weight'}, ...
   'RowNames',{'MPG','Acceleration'});

disp('Partial Correlation Coefficients, Accounting for Headwind')
disp(rho)
disp('p-values, Accounting for Headwind')
disp(pval)
```

```
Partial Correlation Coefficients, Accounting for Headwind
                   Displacement    Horsepower     Weight
                   ------------    ----------    --------
    MPG            0.057197        -0.10555      -0.57358
    Acceleration   -0.38452        -0.39658        0.4674

P-values, Accounting for Headwind
                   Displacement    Horsepower      Weight
                   ------------    ----------    ----------
    MPG               0.59233         0.32212    3.4401e-09
    Acceleration   0.00018272      0.00010902    3.4091e-06
```

Input Arguments

x — Data matrix

matrix

Data matrix, specified as an n-by-p_x matrix. The rows of `x` correspond to observations, and the columns correspond to variables.

Data Types: `single` | `double`

y — Data matrix

matrix

Data matrix, specified as an n-by-p_y matrix. The rows of `y` correspond to observations, and the columns correspond to variables.

Data Types: `single` | `double`

z — Data matrix

matrix

Data matrix, specified as an n-by-p_z matrix. The rows of `z` correspond to observations, and the columns correspond to variables.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Type','Spearman','Rows','complete'` computes Spearman partial correlations using only the data in rows that contain no missing values.

'Type' — Type of partial correlations

`'Pearson'` (default) | `'Spearman'`

Type of partial correlations to compute, specified as the comma-separated pair consisting of `'Type'` and either `'Pearson'` or `'Spearman'`. `Pearson` computes the Pearson (linear) partial correlations. `Spearman` computes the Spearman (rank) partial correlations.

Example: `'Type','Spearman'`

'Rows' — Rows to use in computation

`'all'` (default) | `'complete'` | `'pairwise'`

Rows to use in computation, specified as the comma-separated pair consisting of `'Rows'` and one of the following.

`'all'`	Use all rows regardless of missing (`NaN`) values.
`'complete'`	Use only rows with no missing values.
`'pairwise'`	Use all available values in each column of y when computing the partial correlation coefficients and *p*-values corresponding to that column. For each column of y, rows will be dropped corresponding to missing values in x (and/or z, if supplied). However, remaining rows with valid values in that column of y are used, even if there are missing values in other columns of y.

Example: `'Rows','complete'`

`'Tail'` — Alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Alternative hypothesis to test against, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the correlation is not zero.
`'right'`	Test the alternative hypothesis that the correlation is greater than 0.
`'left'`	Test the alternative hypothesis that the correlation is less than 0.

Example: `'Tail','right'`

Output Arguments

`rho` — Sample linear partial correlation coefficients

matrix

Sample linear partial correlation coefficients, returned as a p_y-by-p_x matrix.

- If you input x and y matrices, the (i,j)th entry is the sample linear partial correlation between the ith column in y and the jth column in x, controlled for all the columns of x except column j.

- If you input x, y, and z matrices, the (*i*,*j*)th entry is the sample linear partial correlation between the *i*th column in y and the *j*th column in x, adjusted for all the columns of x except column *j*, after first controlling both x and y for the variables in z.

`pval` — *p*-values

matrix

p-values, returned as a matrix. Each element of `pval` is the *p*-value for the corresponding element of rho. If `pval(i,j)` is small, then the corresponding partial correlation `rho(i,j)` is statistically significantly different from zero.

`partialcorri` computes *p*-values for linear and rank partial correlations using a Student's *t* distribution for a transformation of the correlation. This is exact for linear partial correlation when x and z are normal, but is a large-sample approximation otherwise.

See Also

`corr` | `partialcorr`

pca

Principal component analysis of raw data

Syntax

```
coeff = pca(X)
coeff = pca(X,Name,Value)
[coeff,score,latent] = pca(___)
[coeff,score,latent,tsquared] = pca(___)
[coeff,score,latent,tsquared,explained,mu] = pca(___)
```

Description

`coeff = pca(X)` returns the principal component coefficients, also known as loadings, for the *n*-by-*p* data matrix `X`. Rows of `X` correspond to observations and columns correspond to variables. The coefficient matrix is *p*-by-*p*. Each column of `coeff` contains coefficients for one principal component, and the columns are in descending order of component variance. By default, `pca` centers the data and uses the singular value decomposition (SVD) algorithm.

`coeff = pca(X,Name,Value)` returns any of the output arguments in the previous syntaxes using additional options for computation and handling of special data types, specified by one or more `Name,Value` pair arguments.

For example, you can specify the number of principal components `pca` returns or an algorithm other than SVD to use.

`[coeff,score,latent] = pca(___)` also returns the principal component scores in `score` and the principal component variances in `latent`. You can use any of the input arguments in the previous syntaxes.

Principal component scores are the representations of `X` in the principal component space. Rows of `score` correspond to observations, and columns correspond to components.

The principal component variances are the eigenvalues of the covariance matrix of `X`.

`[coeff,score,latent,tsquared] = pca( ___ )` also returns the Hotelling's T-squared statistic for each observation in `X`.

`[coeff,score,latent,tsquared,explained,mu] = pca( ___ )` also returns `explained`, the percentage of the total variance explained by each principal component and `mu`, the estimated mean of each variable in `X`.

Examples

Principal Components of a Data Set

Load the sample data set.

```
load hald
```

The ingredients data has 13 observations for 4 variables.

Find the principal components for the ingredients data.

```
coeff = pca(ingredients)
```

```
coeff =

   -0.0678   -0.6460    0.5673    0.5062
   -0.6785   -0.0200   -0.5440    0.4933
    0.0290    0.7553    0.4036    0.5156
    0.7309   -0.1085   -0.4684    0.4844
```

The rows of `coeff` contain the coefficients for the four ingredient variables, and its columns correspond to four principal components.

PCA in the Presence of Missing Data

Find the principal component coefficients when there are missing values in a data set.

Load the sample data set.

```
load imports-85
```

Data matrix `X` has 13 continuous variables in columns 3 to 15: wheel-base, length, width, height, curb-weight, engine-size, bore, stroke, compression-ratio, horsepower, peak-rpm, city-mpg, and highway-mpg. The variables bore and stroke are missing four values in

rows 56 to 59, and the variables horsepower and peak-rpm are missing two values in rows 131 and 132.

Perform principal component analysis.

```
coeff = pca(X(:,3:15));
```

By default, `pca` performs the action specified by the `'Rows','complete'` name-value pair argument. This option removes the observations with `NaN` values before calculation. Rows of `NaN`s are reinserted into `score` and `tsquared` at the corresponding locations, namely rows 56 to 59, 131, and 132.

Use `'pairwise'` to perform the principal component analysis.

```
coeff = pca(X(:,3:15),'Rows','pairwise');
```

In this case, `pca` computes the (i,j) element of the covariance matrix using the rows with no `NaN` values in the columns i or j of `X`. Note that the resulting covariance matrix might not be positive definite. This option applies when the algorithm `pca` uses is eigenvalue decomposition. When you don't specify the algorithm, as in this example, `pca` sets it to `'eig'`. If you require `'svd'` as the algorithm, with the `'pairwise'` option, then `pca` returns a warning message, sets the algorithm to `'eig'` and continues.

If you use the `'Rows','all'` name-value pair argument, `pca` terminates because this option assumes there are no missing values in the data set.

```
coeff = pca(X(:,3:15),'Rows','all');
```

```
Error using pca (line 180)
Raw data contains NaN missing value while 'Rows' option is set to 'all'. Consider using
```

Weighted PCA

Use the inverse variable variances as weights while performing the principal components analysis.

Load the sample data set.

```
load hald
```

Perform the principal component analysis using the inverse of variances of the ingredients as variable weights.

```
[wcoeff,~,latent,~,explained] = pca(ingredients,...
```

```
'VariableWeights','variance')

wcoeff =

   -2.7998    2.9940   -3.9736    1.4180
   -8.7743   -6.4411    4.8927    9.9863
    2.5240   -3.8749   -4.0845    1.7196
    9.1714    7.5529    3.2710   11.3273

latent =

    2.2357
    1.5761
    0.1866
    0.0016

explained =

   55.8926
   39.4017
    4.6652
    0.0406
```

Note that the coefficient matrix, `wcoeff`, is not orthonormal.

Calculate the orthonormal coefficient matrix.

```
coefforth = inv(diag(std(ingredients)))* wcoeff

coefforth =

   -0.4760    0.5090   -0.6755    0.2411
   -0.5639   -0.4139    0.3144    0.6418
    0.3941   -0.6050   -0.6377    0.2685
    0.5479    0.4512    0.1954    0.6767
```

Check orthonormality of the new coefficient matrix, `coefforth`.

```
 coefforth*coefforth'

ans =

    1.0000    0.0000   -0.0000   -0.0000
    0.0000    1.0000   -0.0000   -0.0000
   -0.0000   -0.0000    1.0000         0
```

```
   -0.0000   -0.0000         0    1.0000
```

PCA Using ALS for Missing Data

Find the principal components using the alternating least squares (ALS) algorithm when there are missing values in the data.

Load the sample data.

```
load hald
```

The ingredients data has 13 observations for 4 variables.

Perform principal component analysis using the ALS algorithm and display the component coefficients.

```
[coeff,score,latent,tsquared,explained] = pca(ingredients);
coeff
```

```
coeff =

   -0.0678   -0.6460    0.5673    0.5062
   -0.6785   -0.0200   -0.5440    0.4933
    0.0290    0.7553    0.4036    0.5156
    0.7309   -0.1085   -0.4684    0.4844
```

Introduce missing values randomly.

```
y = ingredients;
rng('default'); % for reproducibility
ix = random('unif',0,1,size(y))<0.30;
y(ix) = NaN
```

```
y =

     7    26     6   NaN
     1    29    15    52
   NaN   NaN     8    20
    11    31   NaN    47
     7    52     6    33
   NaN    55   NaN   NaN
   NaN    71   NaN     6
     1    31   NaN    44
     2   NaN   NaN    22
    21    47     4    26
```

```
   NaN    40    23    34
    11    66     9   NaN
    10    68     8    12
```

Approximately 30% of the data has missing values now, indicated by `NaN`.

Perform principal component analysis using the ALS algorithm and display the component coefficients.

```
[coeff1,score1,latent,tsquared,explained,mu1] = pca(y,...
'algorithm','als');
coeff1
```

```
coeff1 =

   -0.0362    0.8215   -0.5252    0.2190
   -0.6831   -0.0998    0.1828    0.6999
    0.0169    0.5575    0.8215   -0.1185
    0.7292   -0.0657    0.1261    0.6694
```

Display the estimated mean.

```
mu1
```

```
mu1 =

    8.9956   47.9088    9.0451   28.5515
```

Reconstruct the observed data.

```
t = score1*coeff1' + repmat(mu1,13,1)
```

```
t =

 7.0000   26.0000    6.0000   51.5250
 1.0000   29.0000   15.0000   52.0000
10.7819   53.0230    8.0000   20.0000
11.0000   31.0000   13.5500   47.0000
 7.0000   52.0000    6.0000   33.0000
10.4818   55.0000    7.8328   17.9362
 3.0982   71.0000   11.9491    6.0000
 1.0000   31.0000   -0.5161   44.0000
 2.0000   53.7914    5.7710   22.0000
21.0000   47.0000    4.0000   26.0000
21.5809   40.0000   23.0000   34.0000
11.0000   66.0000    9.0000    5.7078
```

```
10.0000   68.0000    8.0000   12.0000
```

The ALS algorithm estimates the missing values in the data.

Another way to compare the results is to find the angle between the two spaces spanned by the coefficient vectors. Find the angle between the coefficients found for complete data and data with missing values using ALS.

```
subspace(coeff,coeff1)
```

```
ans =

   2.2925e-16
```

This is a small value. It indicates that the results if you use `pca` with `'Rows','complete'` name-value pair argument when there is no missing data and if you use `pca` with `'algorithm','als'` name-value pair argument when there is missing data are close to each other.

Perform the principal component analysis using `'Rows','complete'` name-value pair argument and display the component coefficients.

```
[coeff2,score2,latent,tsquared,explained,mu2] = pca(y,...
'Rows','complete');
coeff2
```

```
coeff2 =

   -0.2054    0.8587    0.0492
   -0.6694   -0.3720    0.5510
    0.1474   -0.3513   -0.5187
    0.6986   -0.0298    0.6518
```

In this case, `pca` removes the rows with missing values, and `y` has only four rows with no missing values. `pca` returns only three principal components. You cannot use the `'Rows','pairwise'` option because the covariance matrix is not positive semidefinite and `pca` returns an error message.

Find the angle between the coefficients found for complete data and data with missing values using listwise deletion (when `'Rows','complete'`).

```
subspace(coeff(:,1:3),coeff2)
```

```
ans =
```

```
    0.3576
```

The angle between the two spaces is substantially larger. This indicates that these two results are different.

Display the estimated mean.

```
mu2
```

```
mu2 =

     7.8889   46.9091    9.8750   29.6000
```

In this case, the mean is just the sample mean of `y`.

Reconstruct the observed data.

```
score2*coeff2'
```

```
ans =

       NaN       NaN       NaN       NaN
   -7.5162  -18.3545    4.0968   22.0056
       NaN       NaN       NaN       NaN
       NaN       NaN       NaN       NaN
   -0.5644    5.3213   -3.3432    3.6040
       NaN       NaN       NaN       NaN
       NaN       NaN       NaN       NaN
       NaN       NaN       NaN       NaN
       NaN       NaN       NaN       NaN
   12.8315   -0.1076   -6.3333   -3.7758
       NaN       NaN       NaN       NaN
       NaN       NaN       NaN       NaN
    1.4680   20.6342   -2.9292  -18.0043
```

This shows that deleting rows containing `NaN` values does not work as well as the ALS algorithm. Using ALS is better when the data has too many missing values.

Principal Component Coefficients, Scores, and Variances

Find the coefficients, scores, and variances of the principal components.

Load the sample data set.

```
load hald
```

The ingredients data has 13 observations for 4 variables.

Find the principal component coefficients, scores, and variances of the components for the ingredients data.

```
[coeff,score,latent] = pca(ingredients)
```

```
coeff =

   -0.0678   -0.6460    0.5673    0.5062
   -0.6785   -0.0200   -0.5440    0.4933
    0.0290    0.7553    0.4036    0.5156
    0.7309   -0.1085   -0.4684    0.4844


score =

   36.8218   -6.8709   -4.5909    0.3967
   29.6073    4.6109   -2.2476   -0.3958
  -12.9818   -4.2049    0.9022   -1.1261
   23.7147   -6.6341    1.8547   -0.3786
   -0.5532   -4.4617   -6.0874    0.1424
  -10.8125   -3.6466    0.9130   -0.1350
  -32.5882    8.9798   -1.6063    0.0818
   22.6064   10.7259    3.2365    0.3243
   -9.2626    8.9854   -0.0169   -0.5437
   -3.2840  -14.1573    7.0465    0.3405
    9.2200   12.3861    3.4283    0.4352
  -25.5849   -2.7817   -0.3867    0.4468
  -26.9032   -2.9310   -2.4455    0.4116


latent =

  517.7969
   67.4964
   12.4054
    0.2372
```

Each column of `score` corresponds to one principal component. The vector, `latent`, stores the variances of the four principal components.

Reconstruct the centered ingredients data.

```
Xcentered = score*coeff'

Xcentered =

   -0.4615  -22.1538   -5.7692   30.0000
   -6.4615  -19.1538    3.2308   22.0000
    3.5385    7.8462   -3.7692  -10.0000
    3.5385  -17.1538   -3.7692   17.0000
   -0.4615    3.8462   -5.7692    3.0000
    3.5385    6.8462   -2.7692   -8.0000
   -4.4615   22.8462    5.2308  -24.0000
   -6.4615  -17.1538   10.2308   14.0000
   -5.4615    5.8462    6.2308   -8.0000
   13.5385   -1.1538   -7.7692   -4.0000
   -6.4615   -8.1538   11.2308    4.0000
    3.5385   17.8462   -2.7692  -18.0000
    2.5385   19.8462   -3.7692  -18.0000
```

The new data in `Xcentered` is the original ingredients data centered by subtracting the column means from corresponding columns.

T-Squared Statistic

Find the Hotelling's T-squared statistic values.

Load the sample data set.

```
load hald
```

The ingredients data has 13 observations for 4 variables.

Perform the principal component analysis and request the T-squared values.

```
[coeff,score,latent,tsquared] = pca(ingredients);
tsquared

tsquared =

    5.6803
    3.0758
    6.0002
    2.6198
    3.3681
    0.5668
    3.4818
```

```
    3.9794
    2.6086
    7.4818
    4.1830
    2.2327
    2.7216
```

Request only the first two principal components and compute the T-squared values in the reduced space of requested principal components.

```
[coeff,score,latent,tsquared] = pca(ingredients,'NumComponents',2);
tsquared
```

```
tsquared =

    5.6803
    3.0758
    6.0002
    2.6198
    3.3681
    0.5668
    3.4818
    3.9794
    2.6086
    7.4818
    4.1830
    2.2327
    2.7216
```

Note that even when you specify a reduced component space, `pca` computes the T-squared values in the full space, using all four components.

The T-squared value in the reduced space corresponds to the Mahalanobis distance in the reduced space.

```
tsqreduced = mahal(score,score)
```

```
tsqreduced =

    3.3179
    2.0079
    0.5874
    1.7382
    0.2955
    0.4228
```

```
    3.2457
    2.6914
    1.3619
    2.9903
    2.4371
    1.3788
    1.5251
```

Calculate the T-squared values in the discarded space by taking the difference of the T-squared values in the full space and Mahalanobis distance in the reduced space.

```
tsqdiscarded = tsquared - tsqreduced
```

```
tsqdiscarded =

    2.3624
    1.0679
    5.4128
    0.8816
    3.0726
    0.1440
    0.2362
    1.2880
    1.2467
    4.4915
    1.7459
    0.8539
    1.1965
```

Percent Variability Explained by Principal Components

Find the percent variability explained by the principal components.

Load the sample data set.

```
load imports-85
```

Data matrix `X` has 13 continuous variables in columns 3 to 15: wheel-base, length, width, height, curb-weight, engine-size, bore, stroke, compression-ratio, horsepower, peak-rpm, city-mpg, and highway-mpg.

Find the percent variability explained by principal components of these variables.

```
[coeff,score,latent,tsquared,explained] = pca(X(:,3:15));
```

```
explained
```

```
explained =

   64.3429
   35.4484
    0.1550
    0.0379
    0.0078
    0.0048
    0.0013
    0.0011
    0.0005
    0.0002
    0.0002
    0.0000
    0.0000
```

The first two components explain 99.79% of all variability.

To skip any of the outputs, you can use ~ instead in the corresponding element. For example, if you don't want to get the T-squared values, specify

```
[coeff,score,latent,~,explained] = pca(X(:,3:15));
```

- "Quality of Life in U.S. Cities" on page 13-76

Input Arguments

X — Input data

matrix

Input data for which to compute the principal components, specified as an n-by-p matrix. Rows of `X` correspond to observations and columns to variables.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Algorithm','eig','Centered',false,'Rows','all','NumComponents',3` specifies that `pca` uses eigenvalue decomposition algorithm, not center the data, use all of the observations, and return only the first three principal components.

`'Algorithm'` — Principal component algorithm

`'svd'` (default) | `'eig'` | `'als'`

Principal component algorithm that `pca` uses to perform the principal component analysis, specified as the comma-separated pair consisting of `'Algorithm'` and one of the following.

`'svd'`	Default. Singular value decomposition (SVD) of `X`.
`'eig'`	Eigenvalue decomposition (EIG) of the covariance matrix. The EIG algorithm is faster than SVD when the number of observations, *n*, exceeds the number of variables, *p*, but is less accurate because the condition number of the covariance is the square of the condition number of `X`.
`'als'`	Alternating least squares (ALS) algorithm. This algorithm finds the best rank-*k* approximation by factoring `X` into a *n*-by-*k* left factor matrix, L, and a *p*-by-*k* right factor matrix, R, where *k* is the number of principal components. The factorization uses an iterative method starting with random initial values. ALS is designed to better handle missing values. It is preferable to pairwise deletion (`'Rows','pairwise'`) and deals with missing values without listwise deletion (`'Rows','complete'`). It can work well for data sets with a small percentage of missing data at random, but might not perform well on sparse data sets.

Example: `'Algorithm','eig'`

Data Types: `char`

`'Centered'` — Indicator for centering columns

`true` (default) | `false`

Indicator for centering the columns, specified as the comma-separated pair consisting of `'Centered'` and one of these logical expressions.

`true`	Default. `pca` centers `X` by subtracting column means before computing singular value decomposition or eigenvalue decomposition. If `X` contains `NaN` missing values, `nanmean` is used to find the mean with any available data. You can reconstruct the centered data using `score*coeff'`.
`false`	In this case `pca` does not center the data. You can reconstruct the original data using `score*coeff'`.

Example: `'Centered',false`

Data Types: `logical`

`'Economy'` — Indicator for economy size output

`true` (default) | `false`

Indicator for the economy size output when the degrees of freedom, d, is smaller than the number of variables, p, specified as the comma-separated pair consisting of `'Economy'` and one of these logical expressions.

`true`	Default. `pca` returns only the first d elements of `latent` and the corresponding columns of `coeff` and `score`. This option can be significantly faster when the number of variables p is much larger than d.
`false`	`pca` returns all elements of `latent`. The columns of `coeff` and `score` corresponding to zero elements in `latent` are zeros.

Note that when $d < p$, `score(:,d+1:p)` and `latent(d+1:p)` are necessarily zero, and the columns of `coeff(:,d+1:p)` define directions that are orthogonal to `X`.

Example: `'Economy',false`

Data Types: `logical`

`'NumComponents'` — Number of components requested

number of variables (default) | scalar integer

Number of components requested, specified as the comma-separated pair consisting of `'NumComponents'` and a scalar integer k satisfying $0 < k \leq p$, where p is the number of original variables in `X`. When specified, `pca` returns the first k columns of `coeff` and `score`.

Example: `'NumComponents',3`

Data Types: `single` | `double`

`'Rows'` — Action to take for `NaN` values

`'complete'` (default) | `'pairwise'` | `'all'`

Action to take for `NaN` values in the data matrix `X`, specified as the comma-separated pair consisting of `'Rows'` and one of the following.

`'complete'`	Default. Observations with `NaN` values are removed before calculation. Rows of `NaN`s are reinserted into `score` and `tsquared` at the corresponding locations.
`'pairwise'`	This option only applies when the algorithm is `'eig'`. If you don't specify the algorithm along with `'pairwise'`, then `pca` sets it to `'eig'`. If you specify `'svd'` as the algorithm, along with the option `'Rows','pairwise'`, then `pca` returns a warning message, sets the algorithm to `'eig'` and continues. When you specify the `'Rows','pairwise'` option, `pca` computes the (i,j) element of the covariance matrix using the rows with no `NaN` values in the columns i or j of `X`. Note that the resulting covariance matrix might not be positive definite. In that case, `pca` terminates with an error message.
`'all'`	`X` is expected to have no missing values. `pca` uses all of the data and terminates if any `NaN` value is found.

Example: `'Rows','pairwise'`

Data Types: `char`

`'Weights'` — Observation weights

ones (default) | row vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of length n containing all positive elements.

Data Types: `single` | `double`

`'VariableWeights'` — Variable weights

row vector | `'variance'`

Variable weights, specified as the comma-separated pair consisting of `'VariableWeights'` and one of the following.

Vector of length p containing all positive elements.
The string `'variance'`. The variable weights are the inverse of sample variance. If you also assign weights to observations using `'Weights'`, then the variable weights become the inverse of weighted sample variance. If `'Centered'` is set to `true` at the same time, the data matrix `X` is centered and standardized. In this case, `pca` returns the principal components based on the correlation matrix.

Example: `'VariableWeights','variance'`

Data Types: `single` | `double` | `char`

`'Coeff0'` — Initial value for coefficients

matrix of random values (default) | p-by-k matrix

Initial value for the coefficient matrix coeff, specified as the comma-separated pair consisting of `'Coeff0'` and a p-by-k matrix, where p is the number of variables, and k is the number of principal components requested.

Note: You can use this name-value pair only when `'algorithm'` is `'als'`.

Data Types: `single` | `double`

`'Score0'` — Initial value for scores

matrix of random values (default) | k-by-m matrix

Initial value for scores matrix score, specified as a comma-separated pair consisting of `'Score0'` and an n-by-k matrix, where n is the number of observations and k is the number of principal components requested.

Note: You can use this name-value pair only when `'algorithm'` is `'als'`.

Data Types: `single` | `double`

'Options' — Options for iterations

structure

Options for the iterations, specified as a comma-separated pair consisting of 'Options' and a structure created by the statset function. pca uses the following fields in the options structure.

'Display'	Level of display output. Choices are 'off', 'final', and 'iter'.
'MaxIter'	Maximum number steps allowed. The default is 1000. Unlike in optimization settings, reaching the MaxIter value is regarded as convergence.
'TolFun'	Positive number giving the termination tolerance for the cost function. The default is 1e-6.
'TolX'	Positive number giving the convergence threshold for the relative change in the elements of the left and right factor matrices, L and R, in the ALS algorithm. The default is 1e-6.

Note: You can use this name-value pair only when 'algorithm' is 'als'.

You can change the values of these fields and specify the new structure in pca using the 'Options' name-value pair argument.

Example: `opt = statset('pca'); opt.MaxIter = 2000; coeff = pca(X,'Options',opt);`

Data Types: struct

Output Arguments

coeff — Principal component coefficients

matrix

Principal component coefficients, returned as a p-by-p matrix. Each column of coeff contains coefficients for one principal component. The columns are in the order of descending component variance, latent.

`score` — Principal component scores

matrix

Principal component scores, returned as a matrix. Rows of `score` correspond to observations, and columns to components.

`latent` — Principal component variances

column vector

Principal component variances, that is the eigenvalues of the covariance matrix of X, returned as a column vector.

`tsquared` — Hotelling's T-squared statistic

column vector

"Hotelling's T-Squared Statistic" on page 22-3406, which is the sum of squares of the standardized scores for each observation, returned as a column vector.

`explained` — Percentage of total variance explained

column vector

Percentage of the total variance explained by each principal component, returned as a column vector.

`mu` — Estimated means

row vector

Estimated means of the variables in X, returned as a row vector. When `'algorithm'` is `'als'`, this is estimated by ALS algorithm. When `'algorithm'` is not `'als'`, `mu` is equal to the sample mean of `X`.

More About

Hotelling's T-Squared Statistic

Hotelling's T-squared statistic is a statistical measure of the multivariate distance of each observation from the center of the data set.

Even when you request fewer components than the number of variables, `pca` uses all principal components to compute the T-squared statistic (computes it in the full space). If you want the T-squared statistic in the reduced or the discarded space, do one of the following:

- For the T-squared statistic in the reduced space, use `mahal(score,score)`.
- For the T-squared statistic in the discarded space, first compute the T-squared statistic using `[coeff,score,latent,tsquared] = pca(X,'NumComponents',k,...)`, compute the T-squared statistic in the reduced space using `tsqreduced = mahal(score,score)`, and then take the difference: `tsquared - tsqreduced`.

Degrees of Freedom

The degrees of freedom, d, is equal to $n - 1$, if data is centered and n otherwise, where:

- n is the number of rows without any `NaN`s if you use `'Rows','complete'`.
- n is the number of rows without any `NaN`s in the column pair that has the maximum number of rows without `NaN`s if you use `'Rows','pairwise'`.

Variable Weights

Note that when variable weights are used, the coefficient matrix is not orthonormal. Suppose the variable weights vector you used is called `varwei`, and the principal component coefficients vector `pca` returned is `wcoeff`. You can then calculate the orthonormal coefficients using the transformation `diag(sqrt(varwei))*wcoeff`.

- "Principal Component Analysis (PCA)" on page 13-75

References

[1] Jolliffe, I. T. *Principal Component Analysis*. 2nd ed., Springer, 2002.

[2] Krzanowski, W. J. *Principles of Multivariate Analysis*. Oxford University Press, 1988.

[3] Seber, G. A. F. *Multivariate Observations*. Wiley, 1984.

[4] Jackson, J. E. A. *User's Guide to Principal Components*. Wiley, 1988.

[5] Roweis, S. "EM Algorithms for PCA and SPCA." *In Proceedings of the 1997 Conference on Advances in Neural Information Processing Systems*. Vol.10 (NIPS 1997), Cambridge, MA, USA: MIT Press, 1998, pp. 626–632.

[6] Ilin, A., and T. Raiko. "Practical Approaches to Principal Component Analysis in the Presence of Missing Values." *J. Mach. Learn. Res.*. Vol. 11, August 2010, pp. 1957–2000.

See Also

barttest | biplot | canoncorr | factoran | pcacov | pcares | ppca | rotatefactors

pcacov

Principal component analysis on covariance matrix

Syntax

```
COEFF = pcacov(V)
[COEFF,latent] = pcacov(V)
[COEFF,latent,explained] = pcacov(V)
```

Description

`COEFF = pcacov(V)` performs principal components analysis on the p-by-p covariance matrix `V` and returns the principal component coefficients, also known as loadings. `COEFF` is a p-by-p matrix, with each column containing coefficients for one principal component. The columns are in order of decreasing component variance.

`pcacov` does not standardize `V` to have unit variances. To perform principal components analysis on standardized variables, use the correlation matrix `R = V./(SD*SD')`, where `SD = sqrt(diag(V))`, in place of `V`. To perform principal components analysis directly on the data matrix, use `pca`.

`[COEFF,latent] = pcacov(V)` returns `latent`, a vector containing the principal component variances, that is, the eigenvalues of `V`.

`[COEFF,latent,explained] = pcacov(V)` returns `explained`, a vector containing the percentage of the total variance explained by each principal component.

Examples

```
load hald
covx = cov(ingredients);
[COEFF,latent,explained] = pcacov(covx)
COEFF =
  0.0678 -0.6460  0.5673 -0.5062
  0.6785 -0.0200 -0.5440 -0.4933
 -0.0290  0.7553  0.4036 -0.5156
```

```
 -0.7309 -0.1085 -0.4684 -0.4844

latent =
  517.7969
  67.4964
  12.4054
  0.2372

explained =
  86.5974
  11.2882
  2.0747
  0.0397
```

References

[1] Jackson, J. E. *A User's Guide to Principal Components*. Hoboken, NJ: John Wiley and Sons, 1991.

[2] Jolliffe, I. T. *Principal Component Analysis*. 2nd ed., New York: Springer-Verlag, 2002.

[3] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[4] Seber, G. A. F., *Multivariate Observations*, Wiley, 1984.

See Also

`barttest` | `biplot` | `factoran` | `pcares` | `pca` | `rotatefactors`

pcares

Residuals from principal component analysis

Syntax

```
residuals = pcares(X,ndim)
[residuals,reconstructed] = pcares(X,ndim)
```

Description

`residuals = pcares(X,ndim)` returns the `residuals` obtained by retaining `ndim` principal components of the n-by-p matrix `X`. Rows of `X` correspond to observations, columns to variables. `ndim` is a scalar and must be less than or equal to p. `residuals` is a matrix of the same size as `X`. Use the data matrix, *not* the covariance matrix, with this function.

`pcares` does not normalize the columns of X. To perform the principal components analysis based on standardized variables, that is, based on correlations, use `pcares(zscore(X), ndim)`. You can perform principal components analysis directly on a covariance or correlation matrix, but without constructing residuals, by using `pcacov`.

`[residuals,reconstructed] = pcares(X,ndim)` returns the reconstructed observations; that is, the approximation to `X` obtained by retaining its first `ndim` principal components.

Examples

This example shows the drop in the residuals from the first row of the Hald data as the number of component dimensions increases from one to three.

```
load hald
r1 = pcares(ingredients,1);
r2 = pcares(ingredients,2);
r3 = pcares(ingredients,3);
```

```
r11 = r1(1,:)
r11 =
  2.0350  2.8304  -6.8378  3.0879

r21 = r2(1,:)
r21 =
  -2.4037  2.6930  -1.6482  2.3425

r31 = r3(1,:)
r31 =
  0.2008  0.1957  0.2045  0.1921
```

References

[1] Jackson, J. E., *A User's Guide to Principal Components*, John Wiley and Sons, 1991.

[2] Jolliffe, I. T., *Principal Component Analysis*, 2nd Edition, Springer, 2002.

[3] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[4] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`factoran` | `pcacov` | `pca`

ppca

Probabilistic principal component analysis

Syntax

```
[coeff,score,pcvar] = ppca(Y,K)
[coeff,score,pcvar] = ppca(Y,K,Name,Value)
[coeff,score,pcvar,mu] = ppca( ___ )
[coeff,score,pcvar,mu,v,S] = ppca( ___ )
```

Description

`[coeff,score,pcvar] = ppca(Y,K)` returns the principal component coefficients for the *n*-by-*p* data matrix `Y` based on a probabilistic principal component analysis (PPCA). It also returns the principal component scores, which are the representations of `Y` in the principal component space, and the principal component variances, which are the eigenvalues of the covariance matrix of `Y`, in `pcvar`.

Each column of `coeff` contains coefficients for one principal component, and the columns are in descending order of component variance. Rows of `score` correspond to observations, and columns correspond to components. Rows of `Y` correspond to observations and columns correspond to variables.

Probabilistic principal component analysis might be preferable to other algorithms that handle missing data, such as the alternating least squares algorithm when any data vector has one or more missing values. It assumes that the values are missing at random through the data set. An expectation-maximization algorithm is used for both complete and missing data.

`[coeff,score,pcvar] = ppca(Y,K,Name,Value)` returns the principal component coefficients, scores, and variances using additional options for computation and handling of special data types, specified by one or more `Name,Value` pair arguments.

For example, you can introduce initial values for the residual variance, `v`, or change the termination criteria.

`[coeff,score,pcvar,mu] = ppca( ___ )` also returns the estimated mean of each variable in `Y`. You can use any of the input arguments in the previous syntaxes.

`[coeff,score,pcvar,mu,v,S] = ppca( ___ )` also returns the isotropic residual variance in `v` and the final results at convergence in structure `S`.

Examples

Perform Probabilistic Principal Component Analysis

Load the sample data.

```
load fisheriris
```

The double matrix `meas` consists of four types of measurements on the flowers, which, respectively, are the length and width of sepals and petals.

Introduce missing values randomly.

```
y = meas;
rng('default'); % for reproducibility
ix = random('unif',0,1,size(y))<0.20;
y(ix) = NaN;
```

Now, approximately 20% of the data is missing, indicated by `NaN`.

Perform probabilistic principal component analysis and request the component coefficients and variances.

```
[coeff,score,pcvar,mu] = ppca(y,3);
coeff
```

```
coeff =

    0.3562    0.6709   -0.5518
   -0.0765    0.7121    0.6332
    0.8592   -0.1596    0.0596
    0.3592   -0.1318    0.5395
```

```
pcvar
```

```
pcvar =

   4.0912
   0.2126
   0.0617
```

Perform principal component analysis using the alternating least squares algorithm and request the component coefficients and variances.

```
[coeff2,score2,pcvar2,mu2] = pca(y,'algorithm','als',...
'NumComponents',3);
coeff2
```

```
coeff2 =

    0.3376    0.4955    0.7404
   -0.0731    0.8607   -0.4479
    0.8657   -0.1169   -0.1231
    0.3623   -0.0087   -0.4859
```

```
pcvar2
```

```
pcvar2 =

    4.0734
    0.2651
    0.1221
```

The coefficients and the variances of the first two principal components are similar.

Another way to compare the results is to find the angle between the two spaces spanned by the coefficient vectors.

```
subspace(coeff,coeff2)
```

```
ans =

     0.0881
```

The angle between the two spaces is pretty small. This indicates that these two results are close to each other.

Change the Termination Criteria for Probabilistic Principal Component Analysis

Load the sample data set.

```
load imports-85
```

Data matrix `X` has 13 continuous variables in columns 3 to 15: wheel-base, length, width, height, curb-weight, engine-size, bore, stroke, compression-ratio, horsepower, peak-rpm, city-mpg, and highway-mpg. The variables bore and stroke are missing four values in

rows 56 to 59, and the variables horsepower and peak-rpm are missing two values in rows 131 and 132.

Perform probabilistic principal component analysis and display the first three principal components.

```
[coeff,score,pcvar] = ppca(X(:,3:15),3);
```

```
Warning: Maximum number of iterations 1000 reached'.
> In ppca at 249
```

Change the termination tolerance for the cost function to 0.01.

```
opt = statset('ppca');
opt.TolFun = 0.01;
```

Perform probabilistic principal component analysis.

```
[coeff,score,pcvar] = ppca(X(:,3:15),3,'Options',opt);
```

`ppca` now terminates before the maximum number of iterations is reached because it meets the tolerance for the cost function.

Reconstruct Observations

Load the sample data.

```
load hald
y = ingredients;
```

The ingredients data has 13 observations for 4 variables.

Introduce missing values to the data.

```
y(2:16:end) = NaN;
```

Every 16th value is `NaN`. This corresponds to 7.69% of the data.

Find the first three principal components of data using PPCA and display the reconstructed observations.

```
[coeff,score,pcvar,mu,v,S] = ppca(y,3);
S.Recon
```

```
ans =
```

```
    6.8533   25.8675    5.8388   59.8755
    1.0431   28.9690   14.9652   51.9758
   11.5770   56.5080    8.6352   20.5062
   11.0833   31.0707    8.0920   47.0764
    7.0684   52.2539    6.0753   33.0597
   11.0486   55.0442    9.0534   22.0410
    2.8494   70.8719   16.8338    5.8624
    1.0331   31.0267   19.6906   44.0321
    2.0401   54.0364   18.0440   22.0337
   20.7823   46.8096    3.7603   25.8075
    0.9540   39.9590   22.9495   31.1540
   10.8251   65.8498    8.8072   11.8420
    9.9174   67.9309    7.9087   11.9230
```

You can also reconstruct the observations using the principal components and the estimated mean.

```
t = score*coeff' + repmat(mu,13,1);
```

Results at Convergence

Load the sample data.

```
load hald
```

Here, `ingredients` is a real-valued matrix of predictor variables.

Perform the probabilistic principal components analysis and display coefficients.

```
[coeff,score,pcvariance,mu,v,S] = ppca(ingredients,3);
coeff
```

```
coeff =

   -0.0693   -0.6459    0.5673
   -0.6786   -0.0184   -0.5440
    0.0308    0.7552    0.4036
    0.7306   -0.1102   -0.4684
```

Display the algorithm results at convergence of the PPCA.

```
S
```

```
S =

           W: [4x3 double]
```

```
        Xexp: [13x3 double]
       Recon: [13x4 double]
           v: 0.2372
     NumIter: 1000
    RMSResid: 0.2340
      nloglk: 149.3388
```

Display the matrix `W`.

```
S.W
```

```
ans =

    0.5624    2.0279    5.4075
    4.8320  -10.3894    5.9202
   -3.7521   -3.0555   -4.1552
   -1.5144   11.7122   -7.2564
```

Orthogonalizing `W` recovers the coefficients.

```
orth(S.W)
```

```
ans =

   -0.0693    0.6459    0.5673
   -0.6786    0.0184   -0.5440
    0.0308   -0.7552    0.4036
    0.7306    0.1102   -0.4684
```

Input Arguments

Y — Input data

n-by-*p* matrix

Input data for which to compute the principal components, specified as an *n*-by-*p* matrix. Rows of `Y` correspond to observations and columns correspond to variables.

Data Types: `single` | `double`

K — Number of principal components

positive integer value less than rank

Number of principal components to return, specified as an integer value less than the rank of data. The maximum possible rank is min(*n*,*p*), where *n* is the number of

observations and p is the number of variables. However, if the data is correlated, the rank might be smaller than min(n,p).

`ppca` orders the components based on their variance.

If `K` is min(n,p), `ppca` sets `K` equal to min(n,p) – 1, and `'W0'` is truncated to min(p,n) – 1 columns if you specify a p-by-p `W0` matrix.

For example, you can request only the first three components, based on the component variance as follows.

Example: `coeff = ppca(Y,3)`

Data Types: `single | double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'W0',init,'Options',opt` specifies that the initial values for `'W0'` are in matrix `init` and `ppca` uses the options defined by `opt`.

`'W0'` — Initial value of *W*

matrix of random values (default) | p-by-k matrix

Initial value of W in the probabilistic principal component analysis algorithm, specified as a comma-separated pair consisting of `'W0'` and a p-by-k matrix.

Data Types: `single | double`

`'v0'` — Initial value of residual variance

random number (default) | positive scalar value

Initial value of residual variance, specified as the comma-separated pair consisting of `'v0'` and a positive scalar value.

Data Types: `single | double`

`'Options'` — Options for iterations

structure

Options for the iterations, specified as a comma-separated pair `'Options'` and a structure created by the `statset` function. `ppca` uses the following fields in the options structure.

`'Display'`	Level of display output. Choices are `'off'`, `'final'`, and `'iter'`.
`'MaxIter'`	Maximum number of steps allowed. The default is 1000. Unlike in optimization settings, reaching the `MaxIter` value is regarded as convergence.
`'TolFun'`	Positive integer stating the termination tolerance for the cost function. The default is 1e-6.
`'TolX'`	Positive integer stating the convergence threshold for the relative change in the elements of *W*. The default is 1e-6.

You can change the values of these fields and specify the new structure in `ppca` using the `'Options'` name-value pair argument.

Example: `opt = statset('ppca'); opt.MaxIter = 2000; coeff = ppca(Y,3,'Options',opt);`

Data Types: `struct`

Output Arguments

`coeff` — Principal component coefficients

p-by-*k* matrix

Principal component coefficients, returned as a *p*-by-*k* matrix. Each column of `coeff` contains coefficients for one principal component. The columns are in the order of descending component variance, pcvar.

`score` — Principal component scores

n-by-*k* matrix

Principal component scores, returned as an *n*-by-*k* matrix. Rows of `score` correspond to observations, and columns correspond to components.

`pcvar` — Principal component variances

column vector

Principal component variances, which are the eigenvalues of the covariance matrix of Y, returned as a column vector.

`mu` — Estimated mean

row vector

Estimated mean of each variable in Y, returned as a row vector.

`v` — Isotropic residual variance

scalar value

Isotropic residual variance, returned as a scalar value.

`S` — Final results at convergence

structure

Final results at convergence, returned as a structure containing the following fields.

`W`	*W* at convergence.
`Xexp`	Conditional expectation of the estimated latent variable *x*.
`Recon`	Reconstructed observations using *k* principal components. This is a low dimension approximation of the input data `Y`, and is equal to `mu` + `score*coeff'`.
`v`	Residual variance.
`RMSResid`	Root mean square of residuals.
`NumIter`	Number of iteration counts.
`nloglk`	Negative loglikelihood function value.

More About

Probabilistic Principal Component Analysis

Probabilistic principal component analysis (PPCA) is a method to estimate the principal axes when any data vector has one or more missing values.

PPCA is based on an isotropic error model. It seeks to relate a *p*-dimensional observation vector *y* to a corresponding *k*-dimensional vector of latent (or unobserved) variable *x*, which is normal with mean zero and covariance I(*k*). The relationship is

$$y^T = W * x^T + \mu + \varepsilon,$$

where y is the row vector of observed variable, x is the row vector of latent variables, and ε is the isotropic error term. ε is Gaussian with mean zero and covariance of v*I(k), where v is the residual variance. Here, k needs to be smaller than the rank for the residual variance to be greater than 0 (v>0). Standard principal component analysis, where the residual variance is zero, is the limiting case of PPCA. The observed variables, y, are conditionally independent given the values of the latent variables, x. So, the latent variables explain the correlations between the observation variables and the error explains the variability unique to a particular y_i. The p-by-k matrix W relates the latent and observation variables, and the vector μ permits the model to have a nonzero mean. PPCA assumes that the values are missing at random through the data set. This means that whether a data value is missing or not does not depend on the latent variable given the observed data values.

Under this model,

$$y \sim N\left(\mu, W * W^T + v * I(k)\right).$$

There is no closed-form analytical solution for W and v, so their estimates are determined by iterative maximization of the corresponding loglikelihood using an expectation-maximization (EM) algorithm. This EM algorithm handles missing values by treating them as additional latent variables. At convergence, the columns of W spans the subspace, but they are not orthonormal. `ppca` obtains the orthonormal coefficients, `coeff`, for the components by orthogonalization of W.

References

[1] Tipping, M. E., and C. M. Bishop. Probabilistic Principal Component Analysis. Journal of the Royal Statistical Society. Series B (Statistical Methodology), Vol. 61, No.3, 1999, pp. 611–622.

[2] Roweis, S. "EM Algorithms for PCA and SPCA." *In Proceedings of the 1997 Conference on Advances in Neural Information Processing Systems*. Vol.10 (NIPS 1997), Cambridge, MA, USA: MIT Press, 1998, pp. 626–632.

[3] Ilin, A., and T. Raiko. "Practical Approaches to Principal Component Analysis in the Presence of Missing Values." *J. Mach. Learn. Res.*. Vol. 11, August, 2010, pp. 1957–2000.

See Also

barttest | biplot | canoncorr | factoran | pca | pcacov | pcares | rotatefactors

ComponentProportion property

Class: gmdistribution

Input vector of mixing proportions

Description

Optional input vector of mixing proportions p, or its default value.

pdf

Probability density functions

Syntax

```
y = pdf('name',x,A)
y = pdf('name',x,A,B)
y = pdf('name',x,A,B,C)

y = pdf(pd,x)
```

Description

`y = pdf('name',x,A)` returns the probability density function (pdf) for the one-parameter distribution family specified by 'name', evaluated at the values in x. A contains the parameter value for the distribution.

`y = pdf('name',x,A,B)` returns the pdf for the two-parameter distribution family specified by 'name', evaluated at the values in x. A and B contain the parameter values for the distribution.

`y = pdf('name',x,A,B,C)` returns the pdf for the three-parameter distribution family specified by 'name', evaluated at the values in x. A, B, and C contain the parameter values for the distribution.

`y = pdf(pd,x)` returns the probability density function of the probability distribution object, pd, evaluated at the values in x.

Examples

Compute the Normal Distribution pdf

Create a standard normal distribution object with the mean μ equal to 0 and the standard deviation σ equal to 1.

```
mu = 0;
sigma = 1;
```

```
pd = makedist('Normal',mu,sigma);
```

Define the input vector x to contain the values at which to calculate the pdf.

```
x = [-2 -1 0 1 2];
```

Compute the pdf values for the standard normal distribution at the values in x.

```
y = pdf(pd,x)
```

```
y =

    0.0540    0.2420    0.3989    0.2420    0.0540
```

Each value in y corresponds to a value in the input vector x. For example, at the value x equal to 1, the corresponding pdf value y is equal to 0.2420.

Alternatively, you can compute the same pdf values without creating a probability distribution object. Use the `pdf` function, and specify a standard normal distribution using the same parameter values for μ and σ.

```
y2 = pdf('Normal',x,mu,sigma)
```

```
y2 =

    0.0540    0.2420    0.3989    0.2420    0.0540
```

The pdf values are the same as those computed using the probability distribution object.

Compute the Poisson Distribution pdf

Create a Poisson distribution object with the rate parameter, λ, equal to 2.

```
lambda = 2;
pd = makedist('Poisson',lambda);
```

Define the input vector x to contain the values at which to calculate the pdf.

```
x = [0 1 2 3 4];
```

Compute the pdf values for the Poisson distribution at the values in x.

```
y = pdf(pd,x)
```

```
y =

    0.1353    0.2707    0.2707    0.1804    0.0902
```

Each value in y corresponds to a value in the input vector x. For example, at the value x equal to 3, the corresponding pdf value in y is equal to 0.1804.

Alternatively, you can compute the same pdf values without creating a probability distribution object. Use the `pdf` function, and specify a Poisson distribution using the same value for the rate parameter, λ.

```
y2 = pdf('Poisson',x,lambda)
```

```
y2 =

    0.1353    0.2707    0.2707    0.1804    0.0902
```

The pdf values are the same as those computed using the probability distribution object.

Input Arguments

`'name'` — Probability distribution name

probability distribution name string

Probability distribution name, specified as one of the following probability distribution name strings.

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
`'Beta'`	"Beta Distribution" on page B-4	a: first shape parameter	b: second shape parameter	—
`'Binomial'`	"Binomial Distribution" on page B-9	n: number of trials	p: probability of success for each trial	—
`'BirnbaumSaund`	"Birnbaum-Saunders Distribution" on page B-13	β: scale parameter	γ: shape parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'Burr'	"Burr Type XII Distribution" on page B-15	α: scale parameter	c: first shape parameter	k: second shape parameter
'Chisquare'	"Chi-Square Distribution" on page B-29	ν: degrees of freedom	—	—
'Exponential'	"Exponential Distribution" on page B-35	μ: mean	—	—
'Extreme Value'	"Extreme Value Distribution" on page B-39	μ: location parameter	σ: scale parameter	—
'F'	"F Distribution" on page B-45	ν_1: numerator degrees of freedom	ν_2: denominator degrees of freedom	—
'Gamma'	"Gamma Distribution" on page B-48	α: shape parameter	b: scale parameter	—
'Generalized Extreme Value'	"Generalized Extreme Value Distribution" on page B-54	k: shape parameter	σ: scale parameter	μ: location parameter
'Generalized Pareto'	"Generalized Pareto Distribution" on page B-60	k: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter
'Geometric'	"Geometric Distribution" on page B-65	p: probability parameter	—	—
'Hypergeometri	"Hypergeometric Distribution" on page B-74	m: size of the population	k: number of items with the desired characteristic in the population	n: number of samples drawn
'InverseGaussi	"Inverse Gaussian Distribution" on page B-77	μ: scale parameter	λ: shape parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'Logistic'	"Logistic Distribution" on page B-91	μ: mean	σ: scale parameter	—
'LogLogistic'	"Loglogistic Distribution" on page B-93	μ: log mean	σ: log scale parameter	—
'Lognormal'	"Lognormal Distribution" on page B-95	μ: log mean	σ: log standard deviation	—
'Nakagami'	"Nakagami Distribution" on page B-113	μ: shape parameter	ω: scale parameter	—
'Negative Binomial'	"Negative Binomial Distribution" on page B-115	r: number of successes	p: probability of success in a single trial	—
'Noncentral F'	"Noncentral F Distribution" on page B-123	ν_1: numerator degrees of freedom	ν_2: denominator degrees of freedom	δ: noncentrality parameter
'Noncentral t'	"Noncentral t Distribution" on page B-126	ν: degrees of freedom	δ: noncentrality parameter	—
'Noncentral Chi-square'	"Noncentral Chi-Square Distribution" on page B-120	ν: degrees of freedom	δ: noncentrality parameter	—
'Normal'	"Normal Distribution" on page B-130	μ: mean	σ: standard deviation	—
'Poisson'	"Poisson Distribution" on page B-138	λ: mean	—	—
'Rayleigh'	"Rayleigh Distribution" on page B-141	b: scale parameter	—	—
'Rician'	"Rician Distribution" on page B-144	s: noncentrality parameter	σ: scale parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'T'	"Student's t Distribution" on page B-146	ν: degrees of freedom	—	—
'tLocationScal	"t Location-Scale Distribution" on page B-154	μ: location parameter	σ: scale parameter	ν: shape parameter
'Uniform'	"Uniform Distribution (Continuous)" on page B-163	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'Discrete Uniform'	"Uniform Distribution (Discrete)" on page B-169	n: maximum observable value	—	—
'Weibull'	"Weibull Distribution" on page B-172	a: scale parameter	b: shape parameter	—

x — Values at which to evaluate pdf

scalar value | array of scalar values

Values at which to evaluate the pdf, specified as a scalar value, or an array of scalar values.

- If x is a scalar value, and if you specify distribution parameters A, B, or C as arrays, then `cdf` expands x into a constant matrix the same size as `A` and `B`.
- If x is an array, and if you specify distribution parameters A, B, or C as arrays, then x, A, B, and C must all be the same size.

Example: `[0.1,0.25,0.5,0.75,0.9]`

Data Types: `single` | `double`

A — First probability distribution parameter

scalar value | array of scalar values

First probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x and A are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A. If A is a scalar, then `cdf` expands it into a constant matrix the same size as x.

Data Types: `single` | `double`

`B` — Second probability distribution parameter

scalar value | array of scalar values

Second probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x, A, and B are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A and B. If A or B are scalars, then `cdf` expands them into constant matrices the same size as x

Data Types: `single` | `double`

`C` — Third probability distribution parameter

scalar value | array of scalar values

Third probability distribution parameter, specified as a scalar value, or an array of scalar values.

If x, A, B, and C are arrays, they must be the same size. If x is a scalar, then `cdf` expands it into a constant matrix the same size as A, B, and C. If any of A, B or C are scalars, then `cdf` expands them into constant matrices the same size as x.

Data Types: `single` | `double`

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object created using one of the following.

`makedist`	Create a probability distribution object using specified parameter values.
`fitdist`	Fit a probability distribution object to sample data.
`dfittool`	Fit a probability distribution object to sample data using the interactive Distribution Fitting app.
`paretotails`	Create a Pareto tails object.

`gmdistribution`	Create a Gaussian mixture distribution object.

Output Arguments

y — Probability density function

array

Probability density function of the specified probability distribution, returned as an array.

- If you specify distribution parameters A, B, or C, then y is the common size of x, A, B, and C after any necessary scalar expansion.
- If you specify a probability distribution object, pd, then y has the same dimensions as x.

See Also

`cdf` | `icdf` | `mle` | `random`

pdf

Class: gmdistribution

Probability density function for Gaussian mixture distribution

Syntax

```
y = pdf(obj,X)
```

Description

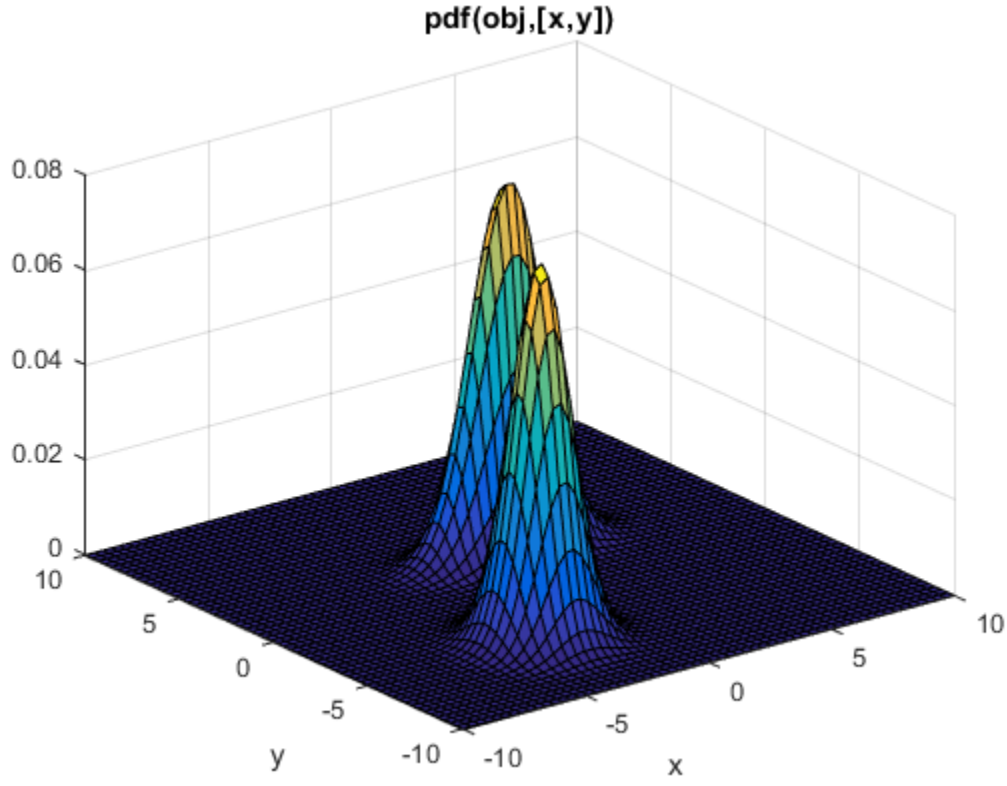
`y = pdf(obj,X)` returns a vector `y` of length n containing the values of the probability density function (pdf) for the `gmdistribution` object `obj`, evaluated at the n-by-d data matrix `X`, where n is the number of observations and d is the dimension of the data. `obj` is an object created by `gmdistribution` or `fitgmdist`. `y(I)` is the pdf of observation `I`.

Examples

Construct a Gaussian Mixture Distribution

Create a `gmdistribution` distribution defining a two-component mixture of bivariate Gaussian distributions.

```
mu = [1 2;-3 -5];
sigma = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(mu,sigma,p);

ezsurf(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
```



See Also

`gmdistribution` | `fitgmdist` | `cdf` | `mvnpdf`

pdf

Class: piecewisedistribution

Probability density function for piecewise distribution

Syntax

```
P = pdf(obj,X)
```

Description

`P = pdf(obj,X)` returns an array `P` of values of the probability density function for the piecewise distribution object `obj`, evaluated at the values in the array `X`.

Note: For a Pareto tails object, the pdf is computed using the generalized Pareto distribution in the tails. In the center, the pdf is computed using the slopes of the cdf, which are interpolated between a set of discrete values. Therefore the pdf in the center is piecewise constant. It is noisy for a *`cdffun`* specified in `paretotails` via the `'ecdf'` option, and somewhat smoother for the `'kernel'` option, but generally not a good estimate of the underlying density of the original data.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);
[p,q] = boundary(obj)
p =
    0.1000
    0.9000
q =
   -1.7766
    1.8432
```

```
pdf(obj,q)
ans =
    0.2367
    0.1960
```

See Also

paretotails | cdf

pdf

Class: ProbDist

Return probability density function (PDF) for ProbDist object

Syntax

```
Y = pdf(PD, X)
```

Description

`Y = pdf(PD, X)` returns `Y`, an array containing the probability density function (PDF) for the ProbDist object `PD`, evaluated at values in `X`.

Input Arguments

`PD`	An object of the class `ProbDistUnivParam` or `ProbDistUnivKernel`.
`X`	A numeric array of values where you want to evaluate the PDF.

Output Arguments

`Y`	An array containing the probability density function (PDF) for the ProbDist object `PD`.

See Also

`pdf`

pdf

Class: prob.TruncatableDistribution
Package: prob

Probability density function of probability distribution object

Syntax

```
y = pdf(pd,x)
```

Description

`y = pdf(pd,x)` returns the probability density function (pdf) of the continuous probability distribution pd at the values in x. For discrete distributions, pdf returns the probability mass function.

Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

x — Values at which to calculate pdf

array

Values at which to calculate pdf, specified as an array.

Data Types: `single` | `double`

Output Arguments

y — Probability density function

array

Probability density function of pd, evaluated at the values in data vector x, returned as a array. y has the same dimensions as input x.

Examples

Plot the pdf of a Standard Normal Distribution

Create a standard normal distribution object.

```
pd = makedist('Normal')
```

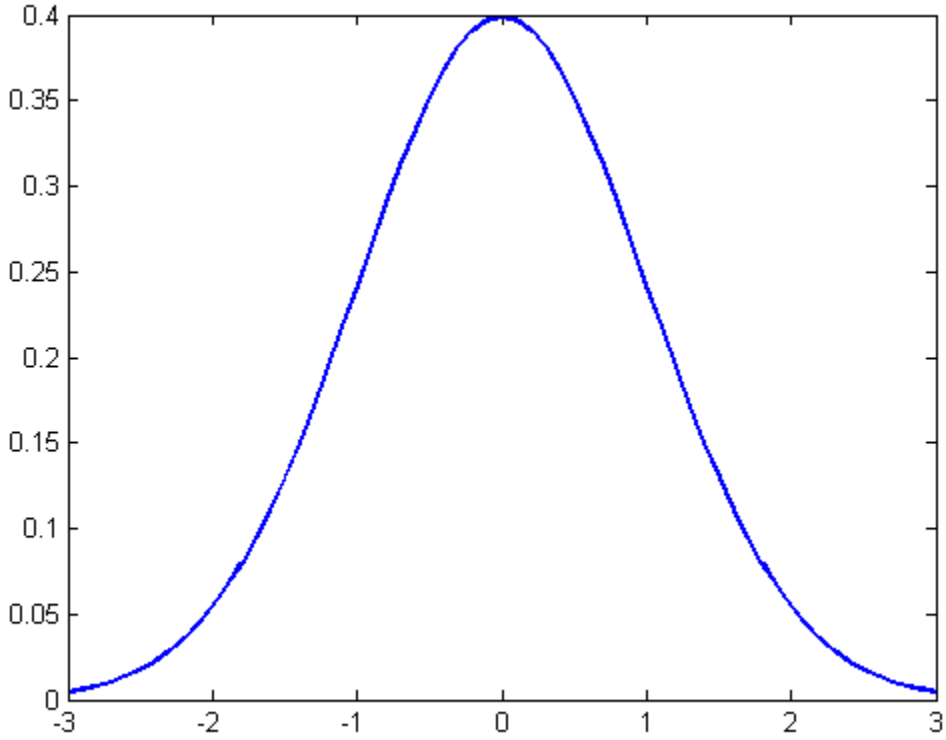
```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Specify the `x` values and compute the pdf.

```
x = -3:.1:3;
pdf_normal = pdf(pd,x);
```

Plot the pdf.

```
plot(x,pdf_normal,'LineWidth',2)
```



Plot the pdf of a Weibull Distribution

Create a Weibull probability distribution object.

```
pd = makedist('Weibull','a',5,'b',2)
```

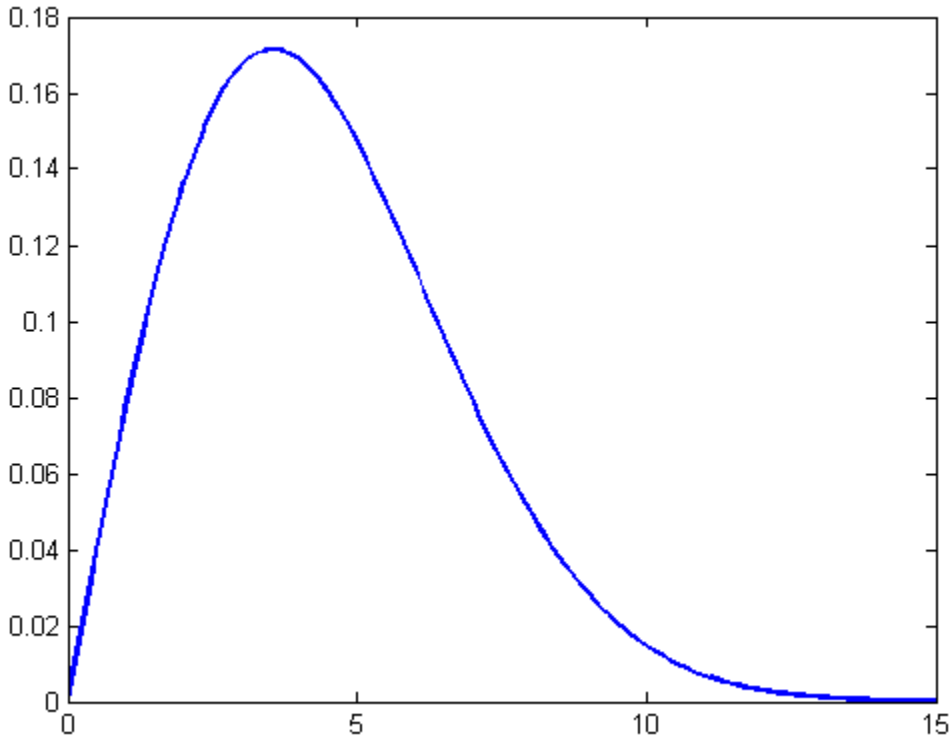
```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Specify the `x` values and compute the pdf.

```
x = 0:.1:15;
y = pdf(pd,x);
```

Plot the pdf.

```
plot(x,y,'LineWidth',2)
```



See Also

cdf | dfittool | fitdist | icdf | makedist | pdf

pdist

Pairwise distance between pairs of objects

Syntax

```
D = pdist(X)
D = pdist(X,distance)
```

Description

`D = pdist(X)` computes the Euclidean distance between pairs of objects in m-by-n data matrix `X`. Rows of `X` correspond to observations, and columns correspond to variables. `D` is a row vector of length $m(m-1)/2$, corresponding to pairs of observations in `X`. The distances are arranged in the order (2,1), (3,1), ..., (m,1), (3,2), ..., (m,2), ..., (m,m–1)). `D` is commonly used as a dissimilarity matrix in clustering or multidimensional scaling.

To save space and computation time, `D` is formatted as a vector. However, you can convert this vector into a square matrix using the `squareform` function so that element i, j in the matrix, where $i < j$, corresponds to the distance between objects i and j in the original data set.

`D = pdist(X,distance)` computes the distance between objects in the data matrix, `X`, using the method specified by *`distance`*, which can be any of the following character strings.

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in X is scaled by dividing by the corresponding element of the standard deviation `S=nanstd(X)`. To specify another value for `S`, use `D=pdist(X,'seuclidean',S)`.
`'cityblock'`	City block metric.
`'minkowski'`	Minkowski distance. The default exponent is 2. To specify a different exponent, use `D = pdist(X,'minkowski',P)`, where `P` is a scalar positive value of the exponent.

Metric	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist(X,'mahalanobis',C)`, where the matrix `C` is symmetric and positive definite.
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ.

custom distance function	A distance function specified using @:
	`D = pdist(X,@distfun)`
	
	A distance function must be of form
	
	`d2 = distfun(XI,XJ)`
	taking as arguments a 1-by-n vector `XI`, corresponding to a single row of `X`, and an $m2$-by-n matrix `XJ`, corresponding to multiple rows of `X`. `distfun` must accept a matrix `XJ` with an arbitrary number of rows. `distfun` must return an $m2$-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

The output `D` is arranged in the order of ((2,1),(3,1),..., (m,1),(3,2),...(m,2),.....(m,m–1)), i.e. the lower left triangle of the full m-by-m distance matrix in column order. To get the distance between the ith and jth observations ($i < j$), either use the formula $D((i–1)*(m–i/2)+j–i)$, or use the helper function `Z = squareform(D)`, which returns an m-by-m square symmetric matrix, with the (i,j) entry equal to distance between observation i and observation j.

Metrics

Given an m-by-n data matrix X, which is treated as m (1-by-n) row vectors x_1, x_2, ..., x_m, the various distances between the vector x_s and x_t are defined as follows:

- Euclidean distance

  $$d_{st}^2 = (x_s - x_t)(x_s - x_t)'$$

  Notice that the Euclidean distance is a special case of the Minkowski metric, where p = 2.

- Standardized Euclidean distance

  $$d_{st}^2 = (x_s - x_t)V^{-1}(x_s - x_t)'$$

  where V is the n-by-n diagonal matrix whose jth diagonal element is $S(j)^2$, where S is the vector of standard deviations.

- Mahalanobis distance

  $$d_{st}^2 = (x_s - x_t)C^{-1}(x_s - x_t)'$$

  where C is the covariance matrix.

- City block metric

  $$d_{st} = \sum_{j=1}^{n} \left| x_{sj} - x_{tj} \right|$$

  Notice that the city block distance is a special case of the Minkowski metric, where p=1.

- Minkowski metric

  $$d_{st} = \sqrt[p]{\sum_{j=1}^{n} \left| x_{sj} - x_{tj} \right|^p}$$

Notice that for the special case of p = 1, the Minkowski metric gives the city block metric, for the special case of p = 2, the Minkowski metric gives the Euclidean distance, and for the special case of p = ∞, the Minkowski metric gives the Chebychev distance.

- Chebychev distance

$$d_{st} = \max_j \left\{ \left| x_{sj} - x_{tj} \right| \right\}$$

Notice that the Chebychev distance is a special case of the Minkowski metric, where p = ∞.

- Cosine distance

$$d_{st} = 1 - \frac{x_s x_t'}{\sqrt{(x_s x_s')(x_t x_t')}}$$

- Correlation distance

$$d_{st} = 1 - \frac{(x_s - \bar{x}_s)(x_t - \bar{x}_t)'}{\sqrt{(x_s - \bar{x}_s)(x_s - \bar{x}_s)'}\sqrt{(x_t - \bar{x}_t)(x_t - \bar{x}_t)'}}$$

where

$$\bar{x}_s = \frac{1}{n}\sum_j x_{sj} \quad \text{and} \quad \bar{x}_t = \frac{1}{n}\sum_j x_{tj}$$

- Hamming distance

$$d_{st} = (\#(x_{sj} \neq x_{tj}) / n)$$

- Jaccard distance

$$d_{st} = \frac{\#\left[\left(x_{sj} \neq x_{tj}\right) \cap \left(\left(x_{sj} \neq 0\right) \cup \left(x_{tj} \neq 0\right)\right)\right]}{\#\left[\left(x_{sj} \neq 0\right) \cup \left(x_{tj} \neq 0\right)\right]}$$

- Spearman distance

$$d_{st} = 1 - \frac{(r_s - \bar{r}_s)(r_t - \bar{r}_t)'}{\sqrt{(r_s - \bar{r}_s)(r_s - \bar{r}_s)'}\sqrt{(r_t - \bar{r}_t)(r_t - \bar{r}_t)'}}$$

  where

  - r_{sj} is the rank of x_{sj} taken over x_{1j}, x_{2j}, ...x_{mj}, as computed by `tiedrank`
  - r_s and r_t are the coordinate-wise rank vectors of x_s and x_t, i.e., $r_s = (r_{s1}, r_{s2}, \ldots r_{sn})$
  - $\bar{r}_s = \frac{1}{n}\sum_j r_{sj} = \frac{(n+1)}{2}$
  - $\bar{r}_t = \frac{1}{n}\sum_j r_{tj} = \frac{(n+1)}{2}$

Examples

Generate random data and find the unweighted Euclidean distance and then find the weighted distance using two different methods:

```
% Compute the ordinary Euclidean distance.
X = randn(100, 5);
D = pdist(X,'euclidean');  % euclidean distance

% Compute the Euclidean distance with each coordinate
% difference scaled by the standard deviation.
Dstd = pdist(X,'seuclidean');

% Use a function handle to compute a distance that weights
% each coordinate contribution differently.
Wgts = [.1 .3 .3 .2 .1];     % coordinate weights
weuc = @(XI,XJ,W)(sqrt(bsxfun(@minus,XI,XJ).^2 * W'));
Dwgt = pdist(X, @(Xi,Xj) weuc(Xi,Xj,Wgts));
```

See Also

`cluster` | `clusterdata` | `cmdscale` | `cophenet` | `dendrogram` | `inconsistent` | `linkage` | `pdist2` | `silhouette` | `squareform`

pdist2

Pairwise distance between two sets of observations

Syntax

```
D = pdist2(X,Y)
D = pdist2(X,Y,distance)
D = pdist2(X,Y,'minkowski',P)
D = pdist2(X,Y,'mahalanobis',C)
D = pdist2(X,Y,distance,'Smallest',K)
D = pdist2(X,Y,distance,'Largest',K)
[D,I] = pdist2(X,Y,distance,'Smallest',K)
[D,I] = pdist2(X,Y,distance,'Largest',K)
```

Description

`D = pdist2(X,Y)` returns a matrix `D` containing the Euclidean distances between each pair of observations in the *mx*-by-*n* data matrix `X` and *my*-by-*n* data matrix `Y`. Rows of `X` and `Y` correspond to observations, columns correspond to variables. `D` is an *mx*-by-*my* matrix, with the (*i*,*j*) entry equal to distance between observation *i* in `X` and observation *j* in `Y`. The (*i*,*j*) entry will be `NaN` if observation *i* in `X` or observation *j* in `Y` contain `NaN`s.

`D = pdist2(X,Y,distance)` computes `D` using `distance`. Choices are:

Metric	Description
`'euclidean'`	Euclidean distance (default).
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between rows in `X` and `Y` is scaled by dividing by the corresponding element of the standard deviation computed from `X`, `S=nanstd(X)`. To specify another value for `S`, use `D = PDIST2(X,Y,'seuclidean',S)`.
`'cityblock'`	City block metric.
`'minkowski'`	Minkowski distance. The default exponent is 2. To compute the distance with a different exponent, use `D =`

Metric	Description
	`pdist2(X,Y,'minkowski',P)`, where the exponent `P` is a scalar positive value.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'mahalanobis'`	Mahalanobis distance, using the sample covariance of `X` as computed by `nancov`. To compute the distance with a different covariance, use `D = pdist2(X,Y,'mahalanobis',C)` where the matrix `C` is symmetric and positive definite.
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors).
`'correlation'`	One minus the sample correlation between points (treated as sequences of values).
`'spearman'`	One minus the sample Spearman's rank correlation between observations, treated as sequences of values.
`'hamming'`	Hamming distance, the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
function	A distance function specified using @: `D = pdist2(X,Y,@distfun)`. A distance function must be of the form `function D2 = distfun(ZI, ZJ)` taking as arguments a 1-by-*n* vector `ZI` containing a single observation from `X` or `Y`, an *m2*-by-*n* matrix `ZJ` containing multiple observations from `X` or `Y`, and returning an *m2*-by-1 vector of distances `D2`, whose `J`th element is the distance between the observations `ZI` and `ZJ(J,:)`. If your data is not sparse, generally it is faster to use a built-in `distance` than to use a function handle.

`D = pdist2(X,Y,distance,'Smallest',K)` returns a `K`-by-*my* matrix `D` containing the `K` smallest pairwise distances to observations in `X` for each observation in `Y`. `pdist2` sorts the distances in each column of `D` in ascending order. `D = pdist2(X,Y,distance,'Largest',K)` returns the `K` largest pairwise distances sorted in descending order. If `K` is greater than *mx*, `pdist2` returns an *mx*-by-*my* distance

matrix. For each observation in Y, pdist2 finds the K smallest or largest distances by computing and comparing the distance values to all the observations in X.

[D,I] = pdist2(X,Y,distance,'Smallest',K) returns a K-by-*my* matrix I containing indices of the observations in X corresponding to the K smallest pairwise distances in D. [D,I] = pdist2(X,Y,distance,'Largest',K) returns indices corresponding to the K largest pairwise distances.

Metrics

Given an *mx*-by-*n* data matrix X, which is treated as *mx* (1-by-*n*) row vectors x_1, x_2, ..., x_{mx}, and *my*-by-*n* data matrix Y, which is treated as *my* (1-by-*n*) row vectors y_1, y_2, ...,y_{my}, the various distances between the vector x_s and y_t are defined as follows:

- Euclidean distance

  $$d_{st}^2 = (x_s - y_t)(x_s - y_t)'$$

  Notice that the Euclidean distance is a special case of the Minkowski metric, where p=2.

- Standardized Euclidean distance

  $$d_{st}^2 = (x_s - y_t)V^{-1}(x_s - y_t)'$$

  where V is the *n*-by-*n* diagonal matrix whose *j*th diagonal element is $S(j)^2$, where S is the vector of standard deviations.

- Mahalanobis distance

  $$d_{st}^2 = (x_s - y_t)C^{-1}(x_s - y_t)'$$

  where C is the covariance matrix.

- City block metric

  $$d_{st} = \sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|$$

Notice that the city block distance is a special case of the Minkowski metric, where p=1.

- Minkowski metric

$$d_{st} = \sqrt[p]{\sum_{j=1}^{n} \left| x_{sj} - y_{tj} \right|^p}$$

Notice that for the special case of p = 1, the Minkowski metric gives the City Block metric, for the special case of p = 2, the Minkowski metric gives the Euclidean distance, and for the special case of p=∞, the Minkowski metric gives the Chebychev distance.

- Chebychev distance

$$d_{st} = \max_j \left\{ \left| x_{sj} - y_{tj} \right| \right\}$$

Notice that the Chebychev distance is a special case of the Minkowski metric, where p=∞.

- Cosine distance

$$d_{st} = \left(1 - \frac{x_s y_t'}{\sqrt{(x_s x_s')(y_t y_t')}} \right)$$

- Correlation distance

$$d_{st} = 1 - \frac{(x_s - \bar{x}_s)(y_t - \bar{y}_t)'}{\sqrt{(x_s - \bar{x}_s)(x_s - \bar{x}_s)'} \sqrt{(y_t - \bar{y}_t)(y_t - \bar{y}_t)'}}$$

where

$\bar{x}_s = \frac{1}{n} \sum_j x_{sj}$ and

$$\bar{y}_t = \frac{1}{n}\sum_j y_{tj}$$

- Hamming distance

$$d_{st} = (\#(x_{sj} \neq y_{tj}) / n)$$

- Jaccard distance

$$d_{st} = \frac{\#\left[\left(x_{sj} \neq y_{tj}\right) \cap \left(\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right)\right]}{\#\left[\left(x_{sj} \neq 0\right) \cup \left(y_{tj} \neq 0\right)\right]}$$

- Spearman distance

$$d_{st} = 1 - \frac{(r_s - \bar{r}_s)(r_t - \bar{r}_t)'}{\sqrt{(r_s - \bar{r}_s)(r_s - \bar{r}_s)'}\sqrt{(r_t - \bar{r}_t)(r_t - \bar{r}_t)'}}$$

  where

  - r_{sj} is the rank of x_{sj} taken over x_{1j}, x_{2j}, ...$x_{mx,j}$, as computed by `tiedrank`
  - r_{tj} is the rank of y_{tj} taken over y_{1j}, y_{2j}, ...$y_{my,j}$, as computed by `tiedrank`
  - r_s and r_t are the coordinate-wise rank vectors of x_s and y_t, i.e. $r_s = (r_{s1}, r_{s2}, \ldots r_{sn})$ and $r_t = (r_{t1}, r_{t2}, \ldots r_{tn})$
  - $$\bar{r}_s = \frac{1}{n}\sum_j r_{sj} = \frac{(n+1)}{2}$$
  - $$\bar{r}_t = \frac{1}{n}\sum_j r_{tj} = \frac{(n+1)}{2}$$

Examples

Generate random data and find the unweighted Euclidean distance, then find the weighted distance using two different methods:

```
% Compute the ordinary Euclidean distance
X = randn(100, 5);
Y = randn(25, 5);
D = pdist2(X,Y,'euclidean'); % euclidean distance

% Compute the Euclidean distance with each coordinate
% difference scaled by the standard deviation
Dstd = pdist2(X,Y,'seuclidean');

% Use a function handle to compute a distance that weights
% each coordinate contribution differently.
Wgts = [.1 .3 .3 .2 .1];
weuc = @(XI,XJ,W)(sqrt(bsxfun(@minus,XI,XJ).^2 * W'));
Dwgt = pdist2(X,Y, @(Xi,Xj) weuc(Xi,Xj,Wgts));
```

See Also

pdist | createns | knnsearch | KDTreeSearcher | ExhaustiveSearcher

pearsrnd

Pearson system random numbers

Syntax

```
r = pearsrnd(mu,sigma,skew,kurt,m,n)
r = pearsrnd(mu,sigma,skew,kurt)
r = pearsrnd(mu,sigma,skew,kurt,m,n,...)
r = pearsrnd(mu,sigma,skew,kurt,[m,n,...])
[r,type] = pearsrnd(...)
[r,type,coefs] = pearsrnd(...)
```

Description

`r = pearsrnd(mu,sigma,skew,kurt,m,n)` returns an `m`-by-`n` matrix of random numbers drawn from the distribution in the Pearson system with mean `mu`, standard deviation `sigma`, skewness `skew`, and kurtosis `kurt`. The parameters `mu`, `sigma`, `skew`, and `kurt` must be scalars.

Note: Because `r` is a random sample, its sample moments, especially the skewness and kurtosis, typically differ somewhat from the specified distribution moments.

`pearsrnd` uses the definition of kurtosis for which a normal distribution has a kurtosis of 3. Some definitions of kurtosis subtract 3, so that a normal distribution has a kurtosis of 0. The `pearsrnd` function does not use this convention.

Some combinations of moments are not valid; in particular, the kurtosis must be greater than the square of the skewness plus 1. The kurtosis of the normal distribution is defined to be 3.

`r = pearsrnd(mu,sigma,skew,kurt)` returns a scalar value.

`r = pearsrnd(mu,sigma,skew,kurt,m,n,...)` or `r = pearsrnd(mu,sigma,skew,kurt,[m,n,...])` returns an `m`-by-`n`-by-... array.

`[r,type] = pearsrnd(...)` returns the type of the specified distribution within the Pearson system. `type` is a scalar integer from `0` to `7`. Set `m` and `n` to `0` to identify the distribution type without generating any random values.

The seven distribution types in the Pearson system correspond to the following distributions:

- `0` — Normal distribution
- `1` — Four-parameter beta distribution
- `2` — Symmetric four-parameter beta distribution
- `3` — Three-parameter gamma distribution
- `4` — Not related to any standard distribution. The density is proportional to: $(1 + ((x - a)/b)^2)^{-c} \exp(-d \arctan((x - a)/b))$.
- `5` — Inverse gamma location-scale distribution
- `6` — F location-scale distribution
- `7` — Student's t location-scale distribution

`[r,type,coefs] = pearsrnd(...)` returns the coefficients `coefs` of the quadratic polynomial that defines the distribution via the differential equation

$$\frac{d}{dx}\log(p(x)) = \frac{-(a+x)}{c(0) + c(1)x + c(2)x^2}.$$

Examples

Generate random values from the standard normal distribution:

```
r = pearsrnd(0,1,0,3,100,1);  % Equivalent to randn(100,1)
```

Determine the distribution type:

```
[r,type] = pearsrnd(0,1,1,4,0,0);
r =
     []
type =
     1
```

References

[1] Johnson, N.L., S. Kotz, and N. Balakrishnan (1994) Continuous Univariate Distributions, Volume 1, Wiley-Interscience, Pg 15, Eqn 12.33.

See Also

`random` | `johnsrnd`

perfcurve

Receiver operating characteristic (ROC) curve or other performance curve for classifier output

Syntax

```
[X,Y] = perfcurve(labels,scores,posclass)
[X,Y,T] = perfcurve(labels,scores,posclass)
[X,Y,T,AUC] = perfcurve(labels,scores,posclass)
[X,Y,T,AUC,OPTROCPT] = perfcurve(labels,scores,posclass)
[X,Y,T,AUC,OPTROCPT,SUBY] = perfcurve(labels,scores,posclass)
[X,Y,T,AUC,OPTROCPT,SUBY,SUBYNAMES] = perfcurve(labels,scores,
posclass)
[ ___ ] = perfcurve(labels,scores,posclass,Name,Value)
```

Description

`[X,Y] = perfcurve(labels,scores,posclass)` returns the X and Y coordinates of an ROC curve for a vector of classifier predictions, scores, given true class labels, labels, and the positive class label, posclass. You can visualize the performance curve using `plot(X,Y)`.

`[X,Y,T] = perfcurve(labels,scores,posclass)` returns an array of thresholds on classifier scores for the computed values of X and Y.

`[X,Y,T,AUC] = perfcurve(labels,scores,posclass)` returns the area under the curve for the computed values of X and Y.

`[X,Y,T,AUC,OPTROCPT] = perfcurve(labels,scores,posclass)` returns the optimal operating point of the ROC curve.

`[X,Y,T,AUC,OPTROCPT,SUBY] = perfcurve(labels,scores,posclass)` returns the Y values for negative subclasses.

`[X,Y,T,AUC,OPTROCPT,SUBY,SUBYNAMES] = perfcurve(labels,scores,posclass)` returns the negative class names.

`[ ___ ] = perfcurve(labels,scores,posclass,Name,Value)` returns the coordinates of a ROC curve and any other output argument from the previous syntaxes, with additional options specified by one or more Name,Value pair arguments.

For example, you can provide a list of negative classes, change the X or Y criterion, compute pointwise confidence bounds using cross validation or bootstrap, specify the misclassification cost, or compute the confidence bounds in parallel.

Examples

Plot ROC Curve for Classification by Logistic Regression

Load the sample data.

```
load fisheriris
```

Use only the first two features as predictor variables. Define a binary classification problem by using only the measurements that correspond to the species versicolor and virginica.

```
pred = meas(51:end,1:2);
```

Define the binary response variable.

```
resp = (1:100)'>50;  % Versicolor = 0, virginica = 1
```

Fit a logistic regression model.

```
mdl = fitglm(pred,resp,'Distribution','binomial','Link','logit');
```

Compute the ROC curve. Use the probability estimates from the logistic regression model as scores.

```
scores = mdl.Fitted.Probability;
[X,Y,T,AUC] = perfcurve(species(51:end,:),scores,'virginica');
```

`perfcurve` stores the threshold values in the array `T`.

Display the area under the curve.

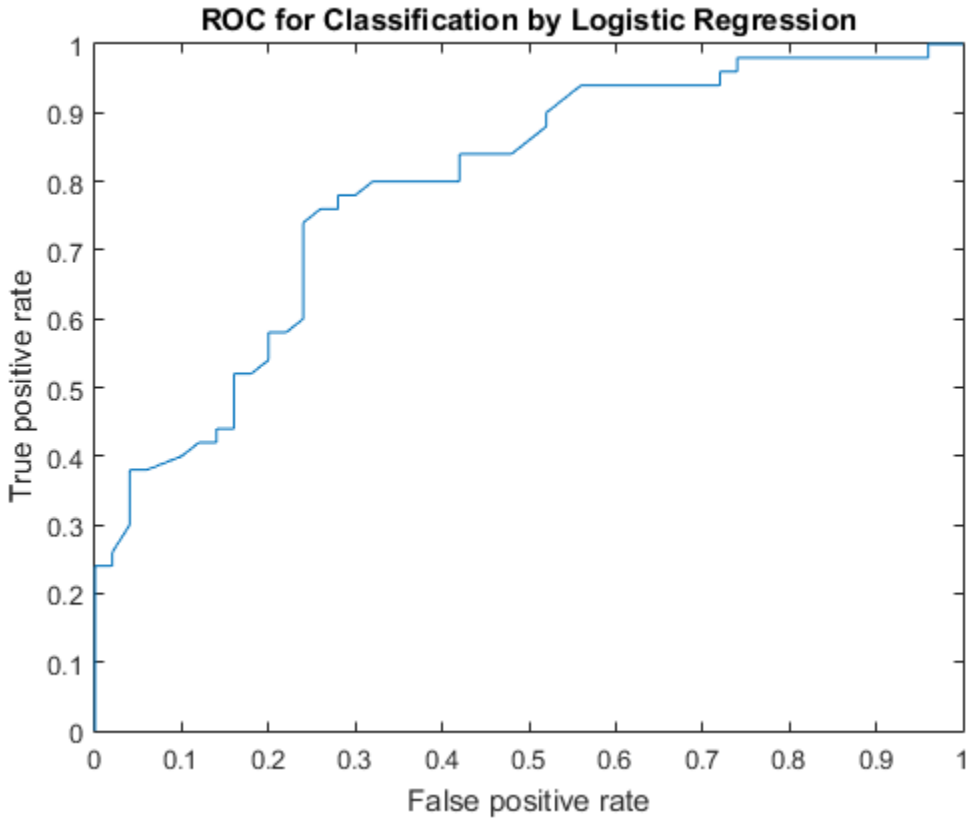
```
AUC
```

```
AUC =

    0.7918
```

The area under the curve is 0.7918. The maximum AUC is 1, which corresponds to a perfect classifier. Larger AUC values indicate better classifier performance.

Plot the ROC curve.

```
plot(X,Y)
xlabel('False positive rate')
ylabel('True positive rate')
title('ROC for Classification by Logistic Regression')
```



Compare Classification Methods Using ROC Curve

Load the sample data.

```
load ionosphere
```

`X` is a 351x34 real-valued matrix of predictors. `Y` is a character array of class labels: `'b'` for bad radar returns and `'g'` for good radar returns.

Reformat the response to fit a logistic regression. Use the predictor variables 3 through 34.

```
resp = strcmp(Y,'b'); % resp = 1, if Y = 'b', or 0 if Y = 'g'
```

```
pred = X(:,3:34);
```

Fit a logistic regression model to estimate the posterior probabilities for an iris to be a virginica.

```
mdl = fitglm(pred,resp,'Distribution','binomial','Link','logit');
score_log = mdl.Fitted.Probability; % Probability estimates
```

Compute the standard ROC curve using the probabilities for scores.

```
[Xlog,Ylog,Tlog,AUClog] = perfcurve(resp,score_log,'true');
```

Train an SVM classifier on the same sample data. Standardize the data.

```
mdlSVM = fitcsvm(pred,resp,'Standardize',true);
```

Compute the posterior probabilities (scores).

```
mdlSVM = fitPosterior(mdlSVM);
[~,score_svm] = resubPredict(mdlSVM);
```

The second column of `score_svm` contains the posterior probabilities of bad radar returns.

Compute the standard ROC curve using the scores from the SVM model.

```
[Xsvm,Ysvm,Tsvm,AUCsvm] = perfcurve(resp,score_svm(:,mdlSVM.ClassNames),'true');
```

Fit a naive Bayes classifier on the same sample data.

```
mdlNB = fitcnb(pred,resp);
```

Compute the posterior probabilities (scores).

```
[~,score_nb] = resubPredict(mdlNB);
```

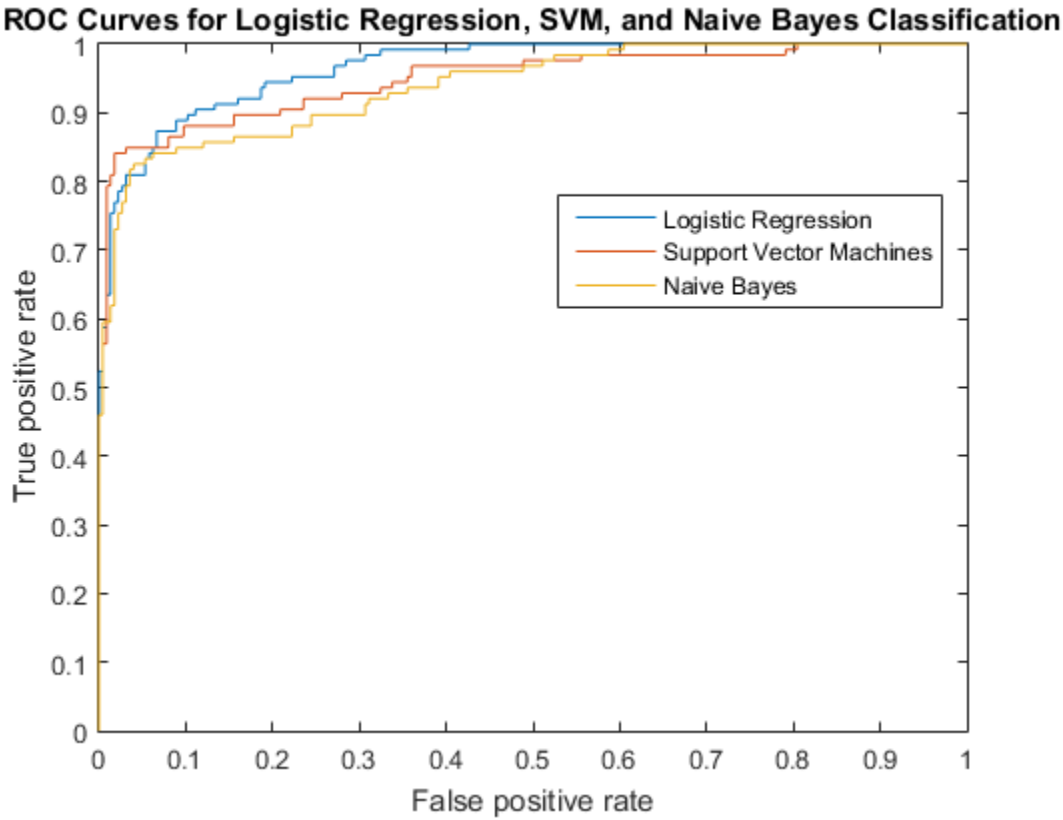
Compute the standard ROC curve using the scores from the naive Bayes classification.

```
[Xnb,Ynb,Tnb,AUCnb] = perfcurve(resp,score_nb(:,mdlNB.ClassNames),'true');
```

Plot the ROC curves on the same graph.

```
plot(Xlog,Ylog)
hold on
```

```
plot(Xsvm,Ysvm)
plot(Xnb,Ynb)
legend('Logistic Regression','Support Vector Machines','Naive Bayes','Location','Best')
xlabel('False positive rate'); ylabel('True positive rate');
title('ROC Curves for Logistic Regression, SVM, and Naive Bayes Classification')
hold off
```



Although SVM produces better ROC values for higher thresholds, logistic regression is usually better at distinguishing the bad radar returns from the good ones. The ROC curve for naive Bayes is generally lower than the other two ROC curves, which indicates worse in-sample performance than the other two classifier methods.

Compare the area under the curve for all three classifiers.

```
AUClog
AUCsvm
AUCnb


AUClog =

    0.9659


AUCsvm =

    0.9488


AUCnb =

    0.9393
```

Logistic regression has the highest AUC measure for classification and naive Bayes has the lowest. This result suggests that logistic regression has better in-sample average performance for this sample data.

Determine the Parameter Value for Custom Kernel Function

Generate a random set of points within the unit circle.

```
rng(1);  % For reproducibility
n = 100; % Number of points per quadrant

r1 = sqrt(rand(2*n,1));                     % Random radii
t1 = [pi/2*rand(n,1); (pi/2*rand(n,1)+pi)]; % Random angles for Q1 and Q3
X1 = [r1.*cos(t1) r1.*sin(t1)];             % Polar-to-Cartesian conversion

r2 = sqrt(rand(2*n,1));
t2 = [pi/2*rand(n,1)+pi/2; (pi/2*rand(n,1)-pi/2)]; % Random angles for Q2 and Q4
X2 = [r2.*cos(t2) r2.*sin(t2)];
```

Define the predictor variables. Label points in the first and third quadrants as belonging to the positive class, and those in the second and fourth quadrants in the negative class.

```
pred = [X1; X2];
```

```
resp = ones(4*n,1);
resp(2*n + 1:end) = -1; % Labels
```

Create the function `mysigmoid.m`, which accepts two matrices in the feature space as inputs, and transforms them into a Gram matrix using the sigmoid kernel.

```
function G = mysigmoid(U,V)
% Sigmoid kernel function with slope gamma and intercept c
gamma = 1;
c = -1;
G = tanh(gamma*U*V' + c);
end
```

Train an SVM classifier using the sigmoid kernel function. It is good practice to standardize the data.

```
SVMModel1 = fitcsvm(pred,resp,'KernelFunction','mysigmoid',...
    'Standardize',true);
SVMModel1 = fitPosterior(SVMModel1);
[~,scores1] = resubPredict(SVMModel1);
```

Set `gamma = 0.5`; within `mysigmoid.m`. Then, train an SVM classifier using the adjusted sigmoid kernel.

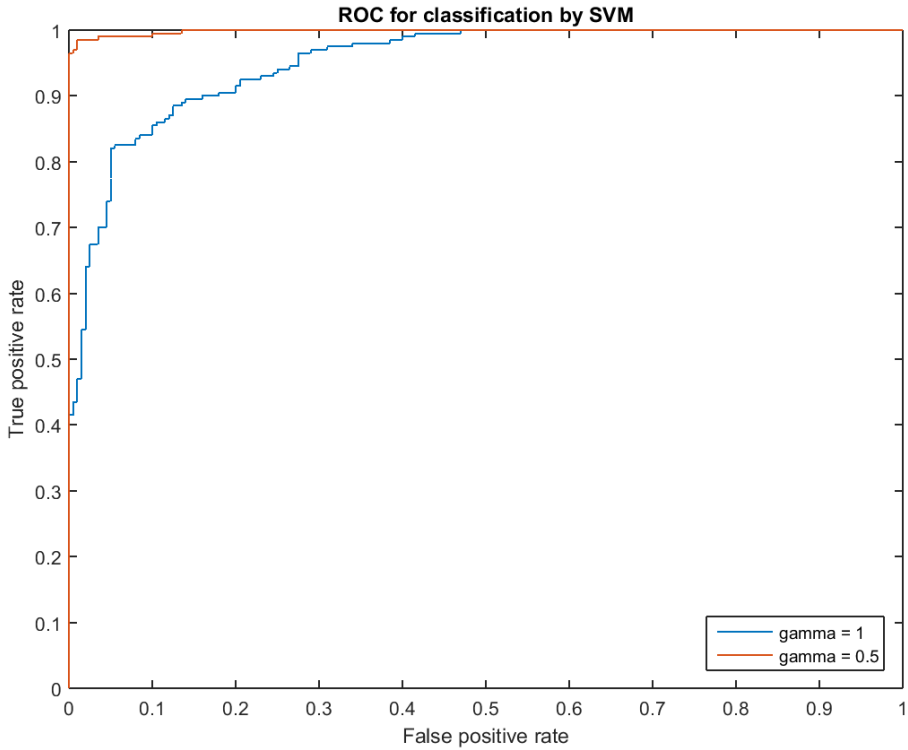
```
SVMModel2 = fitcsvm(pred,resp,'KernelFunction','mysigmoid',...
    'Standardize',true);
SVMModel2 = fitPosterior(SVMModel2);
[~,scores2] = resubPredict(SVMModel2);
```

Compute the ROC curves and the area under the curve (AUC) for both models.

```
[x1,y1,~,auc1] = perfcurve(resp,scores1(:,2),1);
[x2,y2,~,auc2] = perfcurve(resp,scores2(:,2),1);
```

Plot the ROC curves.

```
plot(x1,y1)
hold on
plot(x2,y2)
hold off
legend('gamma = 1','gamma = 0.5','Location','SE');
xlabel('False positive rate'); ylabel('True positive rate');
title('ROC for classification by SVM');
```



The kernel function with the gamma parameter set to 0.5 gives better in-sample results.

Compare the AUC measures.

```
auc1
auc2
```

```
auc1 =

    0.9518
auc2 =

    0.9985
```

The area under the curve for gamma set to 0.5 is higher than that for gamma set to 1. This also confirms that gamma parameter value of 0.5 produces better results. For visual

comparison of the classification performance with these two gamma parameter values, see “Train SVM Classifiers Using a Custom Kernel” on page 16-183.

Plot ROC Curve for Classification Tree

Load the sample data.

```
load fisheriris
```

The column vector, `species`, consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: sepal length, sepal width, petal length, and petal width. All measures are in centimeters.

Train a classification tree using the sepal length and width as the predictor variables. It is a good practice to specify the class names.

```
Model = fitctree(meas(:,1:2),species,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

Predict the class labels and scores for the species based on the tree `Model`.

```
[~,score] = resubPredict(Model);
```

The scores are the posterior probabilities that an observation (a row in the data matrix) belongs to a class. The columns of `score` correspond to the classes specified by `'ClassNames'`. So, the first column corresponds to setosa, the second corresponds to versicolor, and the third column corresponds to virginica.

Compute the ROC curve for the predictions that an observation belongs to versicolor, given the true class labels `species`. Also compute the optimal operating point and y values for negative subclasses. Return the names of the negative classes.

```
[X,Y,T,~,OPTROCPT,suby,subnames] = perfcurve(species,...
    score(:,2),'versicolor');
```

`X`, by default, is the false positive rate (fallout or 1-specificity) and `Y`, by default, is the true positive rate (recall or sensitivity). The positive class label is `versicolor`. Because a negative class is not defined, `perfcurve` assumes that the observations that do not belong to the positive class are in one class. The function accepts it as the negative class.

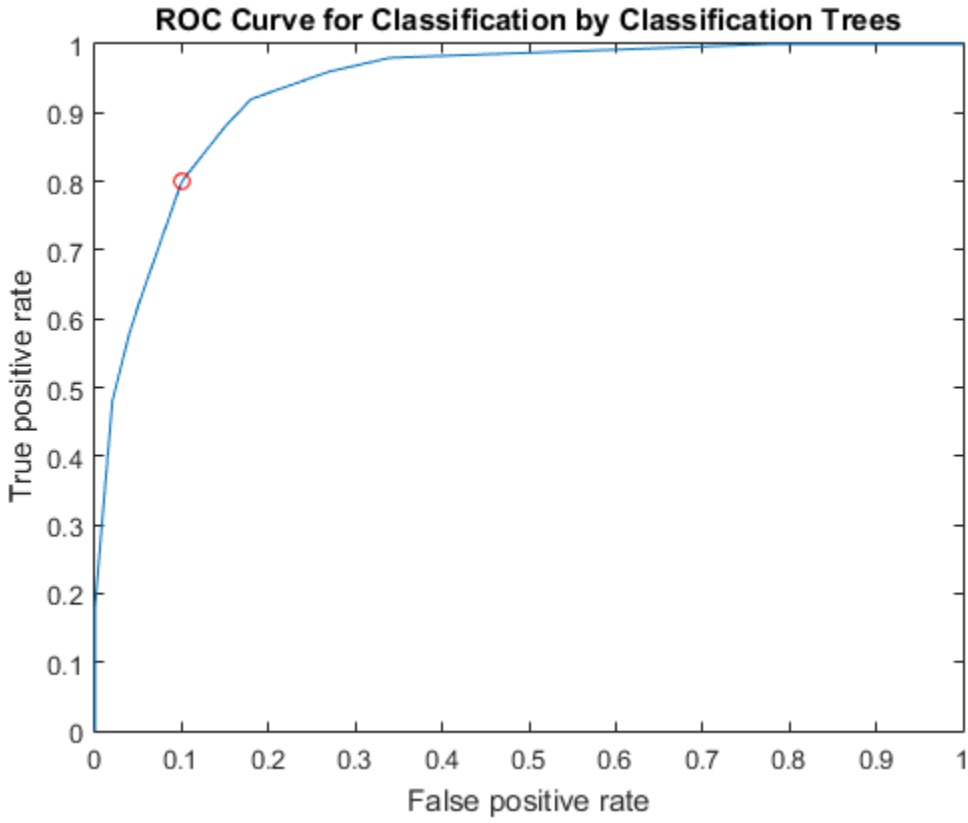
```
OPTROCPT
```

```
suby
subnames
```

```
OPTROCPT =

    0.1000    0.8000


suby =

         0         0
    0.1800    0.1800
    0.4800    0.4800
    0.5800    0.5800
    0.6200    0.6200
    0.8000    0.8000
    0.8800    0.8800
    0.9200    0.9200
    0.9600    0.9600
    0.9800    0.9800
    1.0000    1.0000
    1.0000    1.0000


subnames =

    'setosa'    'virginica'
```

Plot the ROC curve and the optimal operating point on the ROC curve.

```
plot(X,Y)
hold on
plot(OPTROCPT(1),OPTROCPT(2),'ro')
xlabel('False positive rate')
ylabel('True positive rate')
title('ROC Curve for Classification by Classification Trees')
hold off
```



Find the threshold that corresponds to the optimal operating point.

```
T((X==OPTROCPT(1))&(Y==OPTROCPT(2)))
```

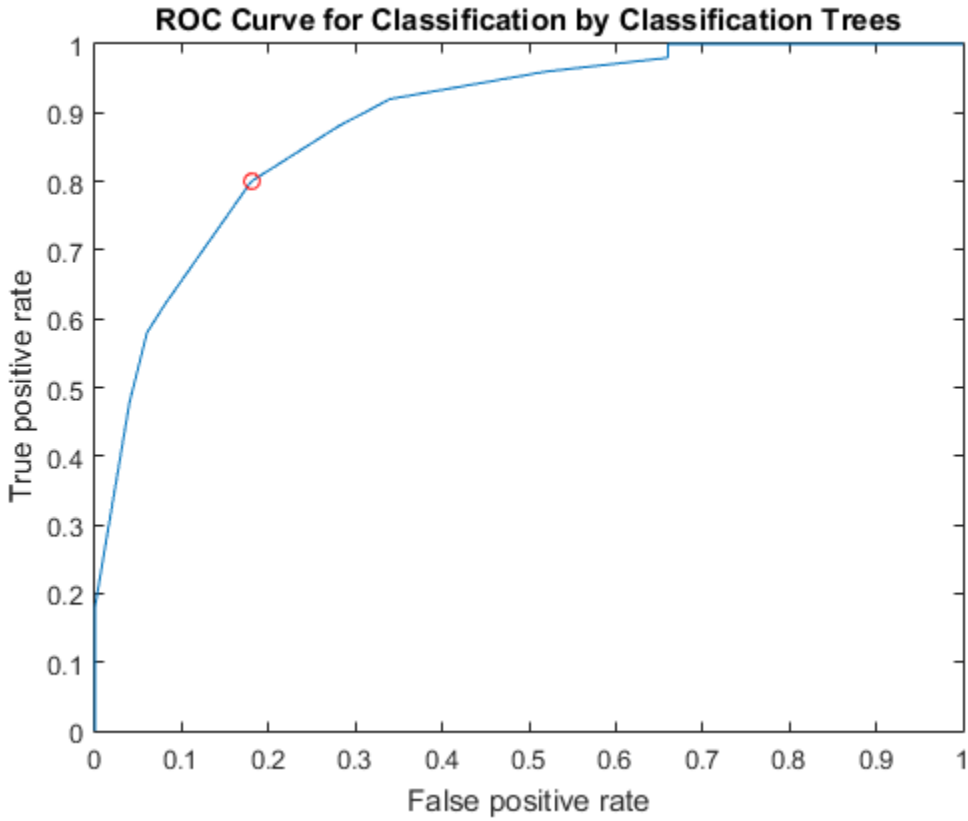
```
ans =

    0.6429
```

Specify `virginica` as the negative class and compute and plot the ROC curve for `versicolor`.

```
[X,Y,~,~,OPTROCPT] = perfcurve(species,score(:,2),...
```

```
    'versicolor','negClass','virginica');
OPTROCPT
plot(X,Y)
hold on
plot(OPTROCPT(1),OPTROCPT(2),'ro')
xlabel('False positive rate')
ylabel('True positive rate')
title('ROC Curve for Classification by Classification Trees')
hold off
```

```
OPTROCPT =

    0.1800    0.8000
```



Compute Pointwise Confidence Intervals for ROC Curve

Load the sample data.

```
load fisheriris
```

The column vector `species` consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: sepal length, sepal width, petal length, and petal width. All measures are in centimeters.

Use only the first two features as predictor variables. Define a binary problem by using only the measurements that correspond to the versicolor and virginica species.

```
pred = meas(51:end,1:2);
```

Define the binary response variable.

```
resp = (1:100)'>50;  % Versicolor = 0, virginica = 1
```

Fit a logistic regression model.

```
mdl = fitglm(pred,resp,'Distribution','binomial','Link','logit');
```

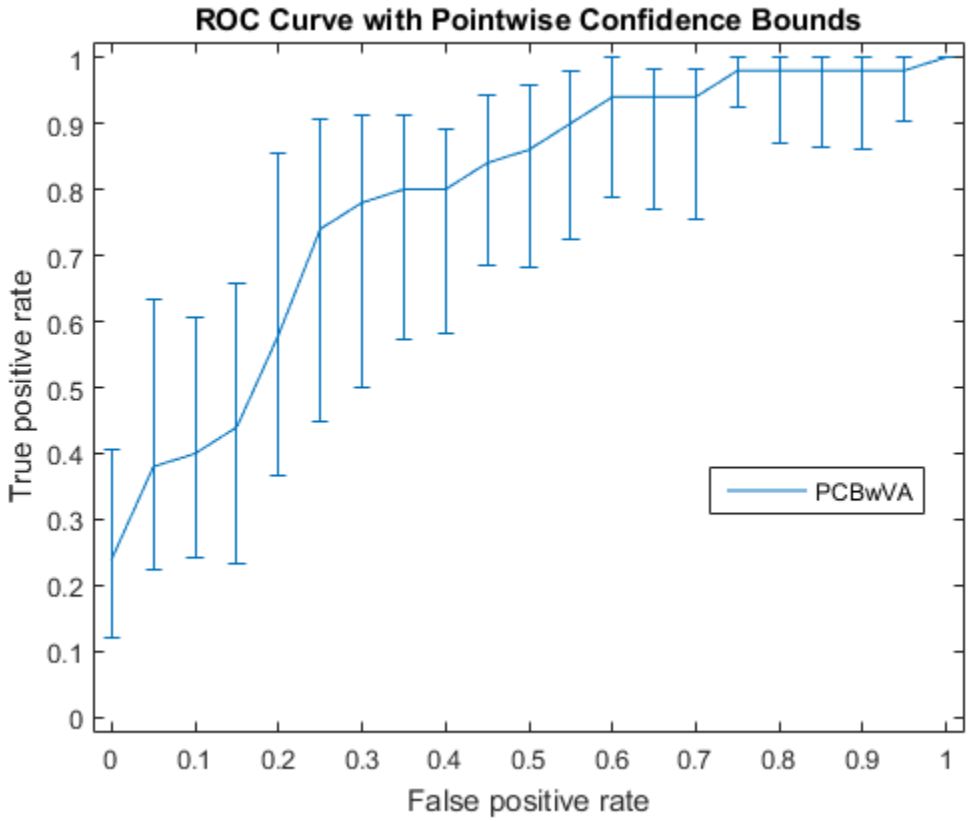
Compute the pointwise confidence intervals on the true positive rate (TPR) by vertical averaging (VA) and sampling using bootstrap.

```
[X,Y,T] = perfcurve(species(51:end,:),mdl.Fitted.Probability,...
       'virginica','NBoot',1000,'XVals',[0:0.05:1]);
```

`'NBoot',1000` sets the number of bootstrap replicas to 1000. `'XVals','All'` prompts `perfcurve` to return `X`, `Y`, and `T` values for all scores, and average the `Y` values (true positive rate) at all `X` values (false positive rate) using vertical averaging. If you do not specify `XVals`, then `perfcurve` computes the confidence bounds using threshold averaging by default.

Plot the pointwise confidence intervals.

```
errorbar(X,Y(:,1),Y(:,1)-Y(:,2),Y(:,3)-Y(:,1));
xlim([-0.02,1.02]); ylim([-0.02,1.02]);
xlabel('False positive rate')
ylabel('True positive rate')
title('ROC Curve with Pointwise Confidence Bounds')
legend('PCBwVA','Location','Best')
```



It might not always be possible to control the false positive rate (FPR, the `X` value in this example). So you might want to compute the pointwise confidence intervals on true positive rates (TPR) by threshold averaging.

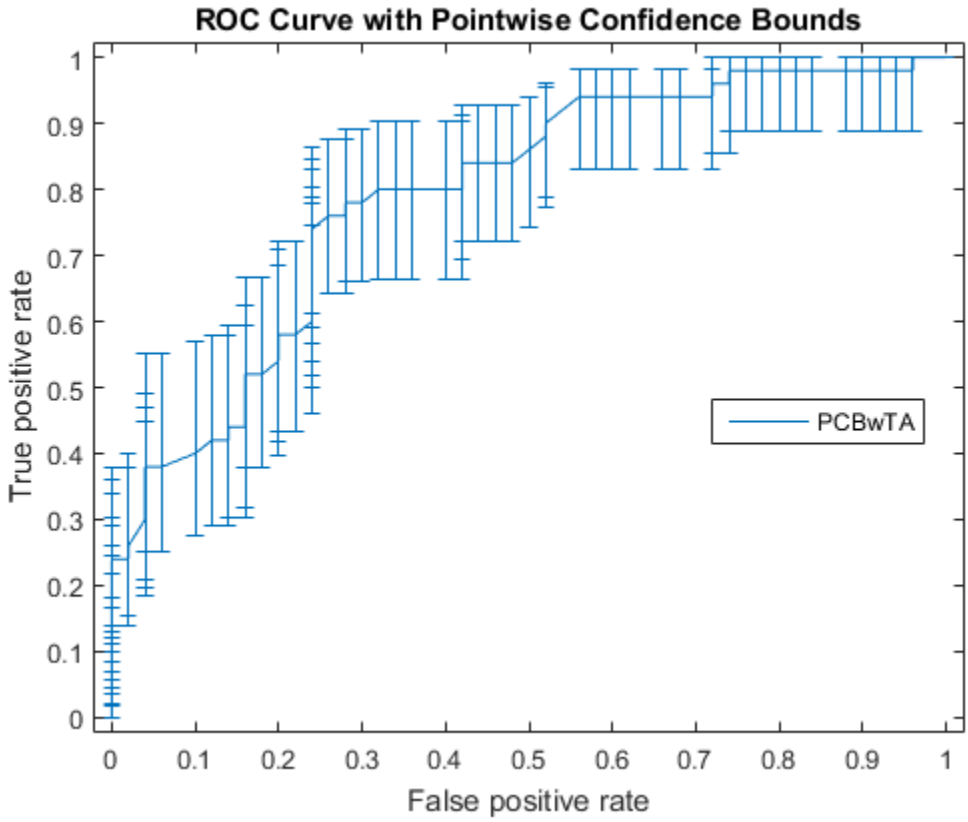
```
[X1,Y1,T1] = perfcurve(species(51:end,:),mdl.Fitted.Probability,...
    'virginica','NBoot',1000);
```

If you set `'TVals'` to `'All'`, or if you do not specify `'TVals'` or `'Xvals'`, then `perfcurve` returns `X`, `Y`, and `T` values for all scores and computes pointwise confidence bounds for `X` and `Y` using threshold averaging.

Plot the confidence bounds.

```
figure()
```

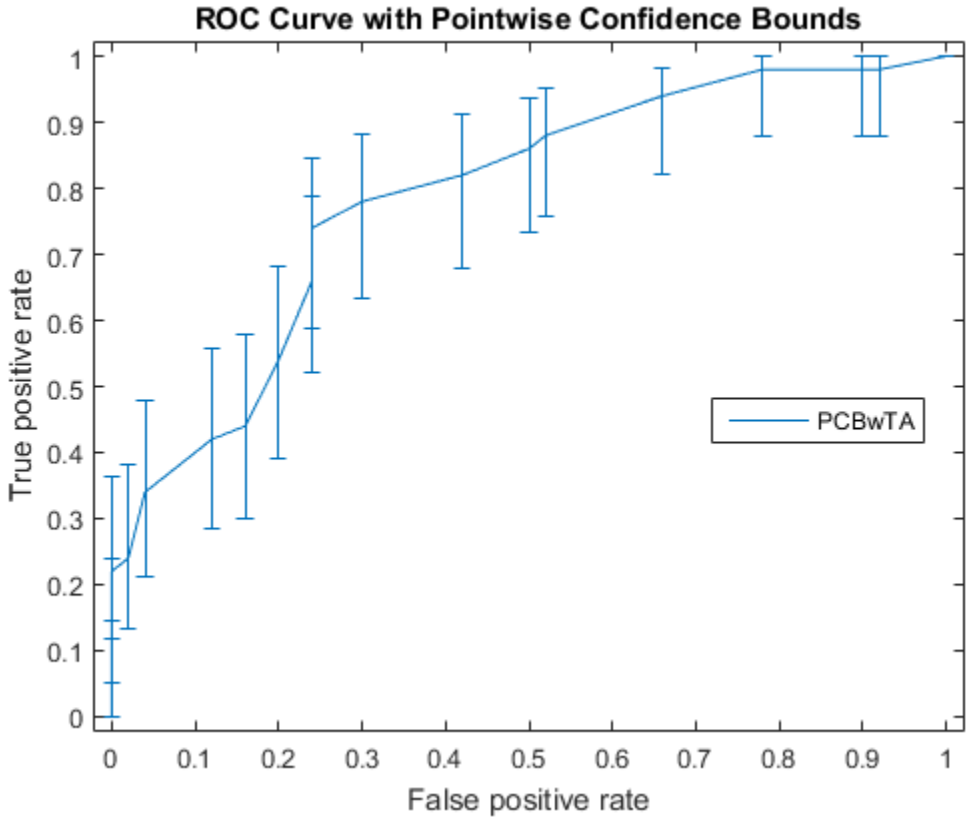
```
errorbar(X1(:,1),Y1(:,1),Y1(:,1)-Y1(:,2),Y1(:,3)-Y1(:,1));
xlim([-0.02,1.02]); ylim([-0.02,1.02]);
xlabel('False positive rate')
ylabel('True positive rate')
title('ROC Curve with Pointwise Confidence Bounds')
legend('PCBwTA','Location','Best')
```



Specify the threshold values to fix and compute the ROC curve. Then plot the curve.

```
[X1,Y1,T1] = perfcurve(species(51:end,:),mdl.Fitted.Probability,...
    'virginica','NBoot',1000,'TVals',0:0.05:1);
figure()
errorbar(X1(:,1),Y1(:,1),Y1(:,1)-Y1(:,2),Y1(:,3)-Y1(:,1));
xlim([-0.02,1.02]); ylim([-0.02,1.02]);
```

```
xlabel('False positive rate')
ylabel('True positive rate')
title('ROC Curve with Pointwise Confidence Bounds')
legend('PCBwTA','Location','Best')
```



Input Arguments

`labels` — True class labels

numeric vector | logical vector | character matrix | cell array of strings | categorical array

True class labels, specified as a numeric vector, a logical vector, a character matrix, a cell array of strings, or a categorical array. For more information, see “Grouping Variables” on page 2-52.

Example: `{'hi','mid','hi','low',...,'mid'}`

Example: `['H','M','H','L',...,'M']`

Data Types: `single` | `double` | `logical` | `char` | `cell`

`scores` — Scores returned by a classifier

vector of floating points

Scores returned by a classifier for some sample data, specified as a vector of floating points. scores must have the same number of elements as labels.

Data Types: `single` | `double`

`posclass` — Positive class label

numeric value | logical value | character array | cell array of strings | categorical value

Positive class label, specified as a numeric value, a logical value, a character array, or a cell array of strings. The positive class must be a member of the input labels. The value of posclass that you can specify depends on the value of labels.

`labels` value	`posclass` value
Numeric vector	Numeric scalar
Logical vector	Logical scalar
Character matrix	Character string
Cell array of strings	Character string or cell containing character string
Categorical vector	Categorical scalar

For example, in a cancer diagnosis problem, if a malignant tumor is the positive class, then specify `posclass` as `'malignant'`.

Data Types: `single` | `double` | `logical` | `char` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example:
`'NegClass','versicolor','XCrit','fn','NBoot',1000,'BootType','per'`
specifies the species versicolor as the negative class, the criterion for the X-coordinate as false negative, the number of bootstrap samples as 1000. It also specifies that the pointwise confidence bounds are computed using the percentile method.

`'NegClass'` — List of negative classes

`'all'` (default) | numeric array | categorical array

List of negative classes, specified as the comma-separated pair consisting of `'NegClass'`, and a numeric array or a categorical array. By default, `perfcurve` sets NegClass to `'all'` and considers all nonpositive classes found in the input array of labels to be negative.

If NegClass is a subset of the classes found in the input array of labels, then `perfcurve` discards the instances with labels that do not belong to either positive or negative classes.

Example: `'nNegClass',{'versicolor','setosa'}`

Data Types: `single` | `double`

`'XCrit'` — Criterion to compute for X

`'fpr'` (default) | `'fnr'` | `'tnr'` | `'ppv'` | `'ecost'` | ...

Criterion to compute for X, specified as the comma-separated pair consisting of `'XCrit'` and one of the following.

Criterion	Description
`tp`	Number of true positive instances
`fn`	Number of false negative instances.
`fp`	Number of false positive instances.
`tn`	Number of true negative instances.
`tp+fp`	Sum of true positive and false positive instances.
`rpp`	Rate of positive predictions. `rpp = (tp+fp)/(tp+fn+fp+tn)`
`rnp`	Rate of negative predictions.

Criterion	Description
	`rnp = (tn+fn)/(tp+fn+fp+tn)`
`accu`	Accuracy. `accu = (tp+tn)/(tp+fn+fp+tn)`
`tpr`, or `sens`, or `reca`	True positive rate, or sensitivity, or recall. `tpr= sens = reca = tp/(tp+fn)`
`fnr`, or `miss`	False negative rate, or miss. `fnr = miss = fn/(tp+fn)`
`fpr`, or `fall`	False positive rate, or fallout, or 1 – specificity. `fpr = fall = fp/(tn+fp)`
`tnr`, or `spec`	True negative rate, or specificity. `tnr = spec = tn/(tn+fp)`
`ppv`, or `prec`	Positive predictive value, or precision. `ppv = prec = tp/(tp+fp)`
`npv`	Negative predictive value. `npv = tn/(tn+fn)`
`ecost`	Expected cost. `ecost = (tp*Cost(P|P)+fn*Cost(N|P)+fp*Cost(P|N)+tn*Cost(N|N))/(tp+fn+fp+tn)`
Custom criterion	A custom-defined function with the input arguments `(C,scale,cost)`, where `C` is a 2-by-2 confusion matrix, `scale` is a 2-by-1 array of class scales, and `cost` is a 2-by-2 misclassification cost matrix.

Caution Some of these criteria return `NaN` values at one of the two special thresholds, `'reject all'` and `'accept all'`.

Example: `'XCrit','ecost'`

`'YCrit'` — Criterion to compute for `Y`

`tpr` (default) | same criteria options for X

Criterion to compute for Y, specified as the comma-separated pair consisting of `'YCrit'` and one of the same criteria options as for X. This criterion does not have to be a monotone function of the positive class score.

Example: 'YCrit','ecost'

'XVals' — Values for the X criterion

'all' (default) | numeric array

Values for the X criterion, specified as the comma-separated pair consisting of 'XVals' and a numeric array.

- If you specify XVals, then perfcurve computes X and Y and the pointwise confidence bounds for Y (when applicable) only for the specified XVals.
- If you do not specify XVals, then perfcurve, computes X and Y and the values for all scores by default.

Note: You cannot set XVals and TVals at the same time.

Example: 'XVals',[0:0.05:1]

Data Types: single | double

'TVals' — Thresholds for the positive class score

'all' (default) | numeric array

Thresholds for the positive class score, specified as the comma-separated pair consisting of 'TVals' and either 'all' or a numeric array.

- If TVals is set to 'all' or not specified, and XVals is not specified, then perfcurve returns X, Y, and T values for all scores and computes pointwise confidence bounds for X and Y using threshold averaging.
- If TVals is set to a numeric array, then perfcurve returns X, Y, and T values for the specified thresholds and computes pointwise confidence bounds for X and Y at these thresholds using threshold averaging.

Note: You cannot set XVals and TVals at the same time.

Example: 'TVals',[0:0.05:1]

Data Types: single | double

`'UseNearest'` — Indicator to use the nearest values in the data

`'on'` (default) | `'off'`

Indicator to use the nearest values in the data instead of the specified numeric `XVals` or `TVals`, specified as the comma-separated pair consisting of `'UseNearest'` and either `'on'` or `'off'`.

- If you specify numeric XVals and set UseNearest to `'on'`, then `perfcurve` returns the nearest unique X values found in the data, and it returns the corresponding values of Y and T.
- If you specify numeric XVals and set UseNearest to `'off'`, then `perfcurve` returns the sorted XVals.
- If you compute confidence bounds by cross validation or bootstrap, then this parameter is always `'off'`.

Example: `'UseNearest','off'`

`'ProcessNaN'` — `perfcurve` method for processing `NaN` scores

`'ignore'` (default) | `'addtofalse'`

`perfcurve` method for processing `NaN` scores, specified as the comma-separated pair consisting of `'ProcessNaN'` and `'ignore'` or `'addtofalse'`.

- If ProcessNaN is `'ignore'`, then `perfcurve` removes observations with `NaN` scores from the data.
- If ProcessNaN is `'addtofalse'`, then `perfcurve` adds instances with `NaN` scores to false classification counts in the respective class. That is, `perfcurve` always counts instances from the positive class as false negative (FN), and it always counts instances from the negative class as false positive (FP).

Example: `'ProcessNaN','addtofalse'`

`'Prior'` — Prior probabilities for positive and negative classes

`'empirical'` (default) | `'uniform'` | array with two elements

Prior probabilities for positive and negative classes, specified as the comma-separated pair consisting of `'Prior'` and `'empirical'`, `'uniform'`, or an array with two elements.

If Prior is `'empirical'`, then `perfcurve` derives prior probabilities from class frequencies.

If Prior is `'uniform'` , then `perfcurve` sets all prior probabilities to be equal.

Example: `'Prior',[0.3,0.7]`

Data Types: `single` | `double` | `char`

`'Cost'` — Misclassification costs

`[0 0.5;0.5 0]` (default) | 2-by-2 matrix

Misclassification costs, specified as the comma-separated pair consisting of `'Cost'` and a 2-by-2 matrix, containing `[Cost(P|P),Cost(N|P);Cost(P|N),Cost(N|N)]`.

`Cost(N|P)` is the cost of misclassifying a positive class as a negative class. `Cost(P|N)` is the cost of misclassifying a negative class as a positive class. Usually, `Cost(P|P)` = 0 and `Cost(N|N)` = 0, but `perfcurve` allows you to specify nonzero costs for correct classification as well.

Example: `'Cost',[0 0.7;0.3 0]`

Data Types: `single` | `double`

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 through 1

Confidence level for the confidence bounds, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range 0 through 1. `perfcurve` computes 100*(1 – *a*) percent pointwise confidence bounds for X, Y, T, and AUC for a confidence level of *a*.

Example: `'Alpha',0.01` specifies 99% confidence bounds

Data Types: `single` | `double`

`'Weights'` — Observation weights

(default) | vector of nonnegative scalar values | cell array of vectors of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a vector of nonnegative scalar values. This vector must have as many elements as scores or labels do.

If scores and labels are in cell arrays and you need to supply Weights, the weights must be in a cell array as well. In this case, every element in Weights must be a numeric vector with as many elements as the corresponding element in scores. For example, `numel(weights{1}) == numel(scores{1})`.

When `perfcurve` computes the X, Y and T or confidence bounds using cross-validation, it uses these observation weights instead of observation counts.

When `perfcurve` computes confidence bounds using bootstrap, it samples *N* out of *N* observations with replacement, using these weights as multinomial sampling probabilities.

Data Types: `single` | `double` | `cell`

`'NBoot'` — Number of bootstrap replicas

0 (default) | positive integer

Number of bootstrap replicas for computation of confidence bounds, specified as the comma-separated pair consisting of `'NBoot'` and a positive integer. The default value 0 means the confidence bounds are not computed.

If labels and scores are cell arrays, this parameter must be 0 because `perfcurve` can use either cross-validation or bootstrap to compute confidence bounds.

Example: `'NBoot',500`

Data Types: `single` | `double`

`'BootType'` — Confidence interval type for `bootci`

`'bca'` (default) | `'norm` | `'per'` | `'cper'` | `'stud'`

Confidence interval type for `bootci` to use to compute confidence bounds, specified as the comma-separated pair consisting of `'BootType'` and one of the following:

- `'bca'` — Bias corrected and accelerated percentile method
- `'norm` or `'normal'` — Normal approximated interval with bootstrapped bias and standard error
- `'per'` or `'percentile'` — Percentile method
- `'cper'` or `'corrected percentile'` — Bias corrected percentile method
- `'stud'` or `'student'` — Studentized confidence interval

Example: `'BootType','cper'`

`'BootArg'` — Optional input arguments for `bootci`

[ ] (default) |

Optional input arguments for `bootci` to compute confidence bounds, specified as the comma-separated pair consisting of `'BootArg'` and one of the inputs or name-value pair arguments that `bootci` accepts.

Example: `'BootArg',{'stderr',stderr}` specifies the standard error of the bootstrap statistics

`'Options'` — Options for controlling the computation of confidence intervals

`[ ]` (default) | structure array returned by `statset`

Options for controlling the computation of confidence intervals, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`. These options require Parallel Computing Toolbox. `perfcurve` uses this argument for computing pointwise confidence bounds only. To compute these bounds, you must pass cell arrays for labels and scores or set NBoot to a positive integer.

This table summarizes the available options.

Option	Description
`'UseParallel'`	• `false` — Serial computation (default). • `true` — Parallel computation. You need Parallel Computing Toolbox for this option to work.
`'UseSubstreams'`	• `false` — Do not use a separate substream for each iteration (default). • `true` — Use a separate substream for each iteration to compute in parallel in a reproducible fashion. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
`'Streams'`	A `RandStream` object, or a cell array of such objects. If you specify `Streams`, use a single object, except when: • You have an open parallel pool. • `UseParallel` is `true`. • `UseSubstreams` is `false`.

Option	Description
	In that case, use a cell array of the same size as the parallel pool. If a parallel pool is not open, then `Streams` must supply a single random number stream.

If `'UseParallel'` is `true` and `'UseSubstreams'` is `false`, then the length of `'Streams'` must equal the number of workers used by `perfcurve`. If a parallel pool is already open, then the length of `'Streams'` is the size of the parallel pool. If a parallel pool is not already open, then MATLAB might open a pool for you, depending on your installation and preferences. To ensure more predictable results, use `parpool` and explicitly create a parallel pool before invoking `perfcurve` and setting `'Options',statset('UseParallel',true)`.

Example: `'Options',statset('UseParallel',true)`

Data Types: `struct`

Output Arguments

X — *x*-coordinates for the performance curve

vector, `fpr` (default) | *m*-by-3 matrix

x-coordinates for the performance curve, returned as a vector or an *m*-by-3 matrix. By default, X values are the false positive rate, FPR (fallout or 1 – specificity). To change X, use the XCrit name-value pair argument.

- If `perfcurve` does not compute the pointwise confidence bounds, or if it computes them using vertical averaging, then X is a vector.
- If `perfcurve` computes the confidence bounds using threshold averaging, then X is an *m*-by-3 matrix, where *m* is the number of fixed threshold values. The first column of X contains the mean value. The second and third columns contain the lower bound and the upper bound, respectively, of the pointwise confidence bounds.

Y — *y*-coordinates for the performance curve

vector, `tpr` (default) | *m*-by-3 matrix

y-coordinates for the performance curve, returned as a vector or an *m*-by-3 matrix. By default, Y values are the true positive rate, TPR (recall or sensitivity). To change Y, use YCrit name-value pair argument.

- If `perfcurve` does not compute the pointwise confidence bounds, then Y is a vector.
- If `perfcurve` computes the confidence bounds, then Y is an *m*-by-3 matrix, where *m* is the number of fixed X values or thresholds (T values). The first column of Y contains the mean value. The second and third columns contain the lower bound and the upper bound, respectively, of the pointwise confidence bounds.

`T` — Thresholds on classifier scores

vector | *m*-by-3 matrix

Thresholds on classifier scores for the computed values of X and Y, returned as a vector or *m*-by-3 matrix.

- If `perfcurve` does not compute the pointwise confidence bounds, or computes them using threshold averaging, then T is a vector.
- If `perfcurve` computes the confidence bounds using vertical averaging, T is an *m*-by-3 matrix, where *m* is the number of fixed X values. The first column of T contains the mean value. The second and third columns contain the lower bound, and the upper bound, respectively, of the pointwise confidence bounds.

For each threshold, `TP` is the count of true positive observations with scores greater than or equal to this threshold, and `FP` is the count of false positive observations with scores greater than or equal to this threshold. `perfcurve` defines negative counts, `TN` and `FN`, in a similar way. The function then sorts the thresholds in the descending order that corresponds to the ascending order of positive counts.

For the *m* distinct thresholds found in the array of scores, `perfcurve` returns the X, Y and T arrays with *m* + 1 rows. `perfcurve` sets elements `T(2:`*m*`+1)` to the distinct thresholds, and `T(1)` replicates `T(2)`. By convention, `T(1)` represents the highest `'reject all'` threshold, and `perfcurve` computes the corresponding values of X and Y for `TP = 0` and `FP = 0`. The `T(end)` value is the lowest `'accept all'` threshold for which `TN = 0` and `FN = 0`.

`AUC` — Area under the curve

scalar value | 3-by-1 vector

Area under the curve (AUC) for the computed values of X and Y, returned as a scalar value or a 3-by-1 vector.

- If `perfcurve` does not compute the pointwise confidence bounds, AUC is a scalar value.

- If `perfcurve` computes the confidence bounds using vertical averaging, AUC is a 3-by-1 vector. The first column of AUC contains the mean value. The second and third columns contain the lower bound and the upper bound, respectively, of the confidence bound.

For a perfect classifier, AUC = 1. For a classifier that randomly assigns observations to classes, AUC = 0.5.

If you set XVals to `'all'` (default), then `perfcurve` computes AUC using the returned X and Y values.

If XVals is a numeric array, then `perfcurve` computes AUC using X and Y values from all distinct scores in the interval, which are specified by the smallest and largest elements of XVals. More precisely, `perfcurve` finds X values for all distinct thresholds as if XVals were set to `'all'`, and then uses a subset of these (with corresponding Y values) between `min(XVals)` and `max(XVals)` to compute AUC.

`perfcurve` uses trapezoidal approximation to estimate the area. If the first or last value of X or Y are `NaN`s, then `perfcurve` removes them to allow calculation of AUC. This takes care of criteria that produce `NaN`s for the special `'reject all'` or `'accept all'` thresholds, for example, positive predictive value (PPV) or negative predictive value (NPV).

`OPTROCPT` — Optimal operating point of the ROC curve

1-by-2 array

Optimal operating point of the ROC curve, returned as a 1-by-2 array with false positive rate (FPR) and true positive rate (TPR) values for the optimal ROC operating point.

`perfcurve` computes OPTROCPT for the standard ROC curve only, and sets to `NaN`s otherwise. To obtain the optimal operating point for the ROC curve, `perfcurve` first finds the slope, S, using

$$S = \frac{\text{Cost}(P \mid N) - \text{Cost}(N \mid N)}{\text{Cost}(N \mid P) - \text{Cost}(P \mid P)} * \frac{N}{P}$$

- $\text{Cost}(N \mid P)$ is the cost of misclassifying a positive class as a negative class. $\text{Cost}(P \mid N)$ is the cost of misclassifying a negative class as a positive class.
- $P = TP + FN$ and $N = TN + FP$. They are the total instance counts in the positive and negative class, respectively.

`perfcurve` then finds the optimal operating point by moving the straight line with slope S from the upper left corner of the ROC plot (`FPR = 0`, `TPR = 1`) down and to the right, until it intersects the ROC curve.

SUBY — Values for negative subclasses

array

Values for negative subclasses, returned as an array.

- If you specify only one negative class, then SUBY is identical to Y.
- If you specify k negative classes, then SUBY is a matrix of size m-by-k, where m is the number of returned values for X and Y, and k is the number of negative classes. `perfcurve` computes Y values by summing counts over all negative classes.

SUBY gives values of the Y criterion for each negative class separately. For each negative class, `perfcurve` places a new column in SUBY and fills it with Y values for true negative (TN) and false positive (FP) counted just for this class.

SUBYNAMES — Negative class names

cell array

Negative class names, returned as a cell array.

- If you provide an input array of negative class names, , NegClass, then `perfcurve` copies names into SUBYNAMES.
- If you do not provide NegClass, then `perfcurve` extracts SUBYNAMES from the input labels. The order of SUBYNAMES is the same as the order of columns in SUBY. That is, `SUBY(:,1)` is for negative class `SUBYNAMES{1}`, `SUBY(:,2)` is for negative class `SUBYNAMES{2}`, and so on.

More About

Algorithms

Pointwise Confidence Bounds

If you supply cell arrays for labels and scores, or if you set NBoot to a positive integer, then `perfcurve` returns pointwise confidence bounds for X,Y,T, and AUC. You cannot

supply cell arrays for labels and scores and set NBoot to a positive integer at the same time.

`perfcurve` resamples data to compute confidence bounds using either cross validation or bootstrap.

- Cross-validation — If you supply cell arrays for labels and scores, then `perfcurve` uses cross-validation and treats elements in the cell arrays as cross-validation folds. labels can be a cell array of numeric vectors, logical vectors, character matrices, cell arrays of strings, or categorical vectors. All elements in `labels` must have the same type. scores can be a cell array of numeric vectors. The cell arrays for labels and scores must have the same number of elements. The number of labels in cell *j* of `labels` must be equal to the number of scores in cell *j* of `scores` for any *j* in the range from 1 to the number of elements in scores.
- Bootstrap — If you set NBoot to a positive integer *n*, `perfcurve` generates *n* bootstrap replicas to compute pointwise confidence bounds. If you use XCrit or YCrit to set the criterion for X or Y to an anonymous function, `perfcurve` can compute confidence bounds only using bootstrap.

`perfcurve` estimates the confidence bounds using one of two methods:

- Vertical averaging (VA) — `perfcurve` estimates confidence bounds on Y and T at fixed values of X. That is, `perfcurve` takes samples of the ROC curves for fixed X values, averages the corresponding Y and T values, and computes the standard errors. You can use the XVals name-value pair argument to fix the X values for computing confidence bounds. If you do not specify XVals, then `perfcurve` computes the confidence bounds at all X values.
- Threshold averaging (TA) — `perfcurve` takes samples of the ROC curves at fixed thresholds T for the positive class score, averages the corresponding X and Y values, and estimates the confidence bounds. You can use the TVals name-value pair argument to use this method for computing confidence bounds. If you set TVals to `'all'` or do not specify TVals or XVals, then `perfcurve` returns X, Y, and T values for all scores and computes pointwise confidence bounds for Y and X using threshold averaging.

When you compute the confidence bounds, Y is an *m*-by-3 array, where *m* is the number of fixed X values or thresholds (T values). The first column of Y contains the mean value. The second and third columns contain the lower bound and the upper bound, respectively, of the pointwise confidence bounds. AUC is a row vector with three elements, following the same convention. If `perfcurve` computes the confidence bounds

using VA, then T is an *m*-by-3 matrix, and X is a column vector. If `perfcurve` uses TA, then X is an *m*-by-3 matrix and T is a column-vector.

`perfcurve` returns pointwise confidence bounds. It does not return a simultaneous confidence band for the entire curve.

- "Performance Curves" on page 15-35

References

[1] T. Fawcett. "ROC Graphs: Notes and Practical Considerations for Researchers", 2004.

[2] Zweig, M., and G. Campbell. "Receiver-Operating Characteristic (ROC) Plots: A Fundamental Evaluation Tool in Clinical Medicine." *Clin. Chem*. 1993, 39/4, pp. 561–577 .

[3] Davis, J., and M. Goadrich. "The Relationship Between Precision-Recall and ROC Curves." *Proceedings of ICML '06*, 2006, pp. 233–240.

[4] Moskowitz, C., and M. Pepe. "Quantifying and comparing the predictive accuracy of continuous prognostic factors for binary outcomes." *Biostatistics*, 2004, 5, pp. 113–127.

[5] Huang, Y., M. Pepe, and Z. Feng. "Evaluating the Predictiveness of a Continuous Marker." *U. Washington Biostatistics Paper Series*, 2006, 250–261.

[6] Briggs, W., and R. Zaretzki. "The Skill Plot: A Graphical Technique for Evaluating Continuous Diagnostic Tests." *Biometrics*, 2008, 63, pp. 250 – 261.

[7] R. Bettinger. "Cost-Sensitive Classifier Selection Using the ROC Convex Hull Method." *SAS Institute*.

See Also

`bootci` | `classify` | `fitcnb` | `fitctree` | `fitrtree` | `glmfit` | `mnrfit`

perms

Enumeration of permutations

Syntax

```
P = perms(v)
```

Description

`P = perms(v)`, where `v` is a row vector of length `n`, creates a matrix whose rows consist of all possible permutations of the `n` elements of `v`. The matrix `P` contains `n!` rows and `n` columns.

`perms` is only practical when `n` is less than about 11 (for `n = 11`, the output takes over 3 gigabytes).

Examples

```
perms([2 4 6])

ans =

   6   4   2
   6   2   4
   4   6   2
   4   2   6
   2   4   6
   2   6   4
```

See Also

`combnk`

piecewisedistribution class

Piecewise-defined distributions

Construction

`piecewisedistribution` is an abstract class. To construct a `piecewisedistribution` object, use the subclass constructor, `paretotails`.

Methods

boundary	Piecewise distribution boundaries
cdf	Cumulative distribution function for piecewise distribution
disp	Display piecewisedistribution object
display	Display piecewisedistribution object
icdf	Inverse cumulative distribution function for piecewise distribution
nsegments	Number of segments
pdf	Probability density function for piecewise distribution
random	Random numbers from piecewise distribution
segment	Segments containing values

Properties

Objects of the `piecewisedistribution` class have no properties accessible by dot indexing, `get` methods, or `set` methods. To obtain information about a `piecewisedistribution` object, use the appropriate method.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

piecewisedistribution

Class: piecewisedistribution

Create piecewise distribution object

Description

`piecewisedistribution` is an abstract class, and you cannot create instances of it directly. You can create `paretotails` objects that are derived from this class.

See Also

`paretotails`

prob.PiecewiseLinearDistribution class

Package: prob
Superclasses: prob.ParametricTruncatableDistribution

Piecewise linear probability distribution object

Description

`prob.PiecewiseLinearDistribution` is an object consisting of a model description for a piecewise linear probability distribution. Create a probability distribution object with specified parameters using `makedist`.

Construction

`pd = makedist('PiecewiseLinear')` creates a piecewise linear probability distribution object using the default parameter values.

`pd = makedist('PiecewiseLinear','x',x,'Fx',Fx)` creates a piecewise linear probability distribution object using the specified values.

Input Arguments

x — Data values

1 (default) | vector of scalar values

Data values at which the cumulative distribution function (cdf) changes slope, specified as a vector of scalar values.

Data Types: `single` | `double`

Fx — cdf value

1 (default) | vector of scalar values

cdf value at each value in x, specified as a vector of scalar values. x and Fx must be the same size. The first value in the vector `Fx` must be `0`, and the last element must be `1`. `Fx` increases linearly between `x`(*j*) and `x`(*j*+1), for all *j*.

Data Types: `single` | `double`

Properties

x — Data values

vector of scalar values

Data values at which the cumulative distribution function (cdf) changes slope, stored as a vector of scalar values.

Data Types: `single | double`

Fx — cdf value

vector of scalar values

cdf value at each value in `x`, stored as a vector of scalar values.

Data Types: `single | double`

DistributionName — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

IsTruncated — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

NumParameters — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

ParameterDescription — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object

median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Piecewise Linear Distribution

The piecewise linear distribution is a nonparametric probability distribution created using a piecewise linear representation of the cumulative distribution function (cdf). The options specified for the piecewise linear distribution specify the form of the cdf. The probability density function (pdf) is a step function.

Examples

Create a Piecewise Linear Distribution Object Using Default Parameters

Create a piecewise linear distribution object using the default parameter values.

```
pd = makedist('PiecewiseLinear')
```

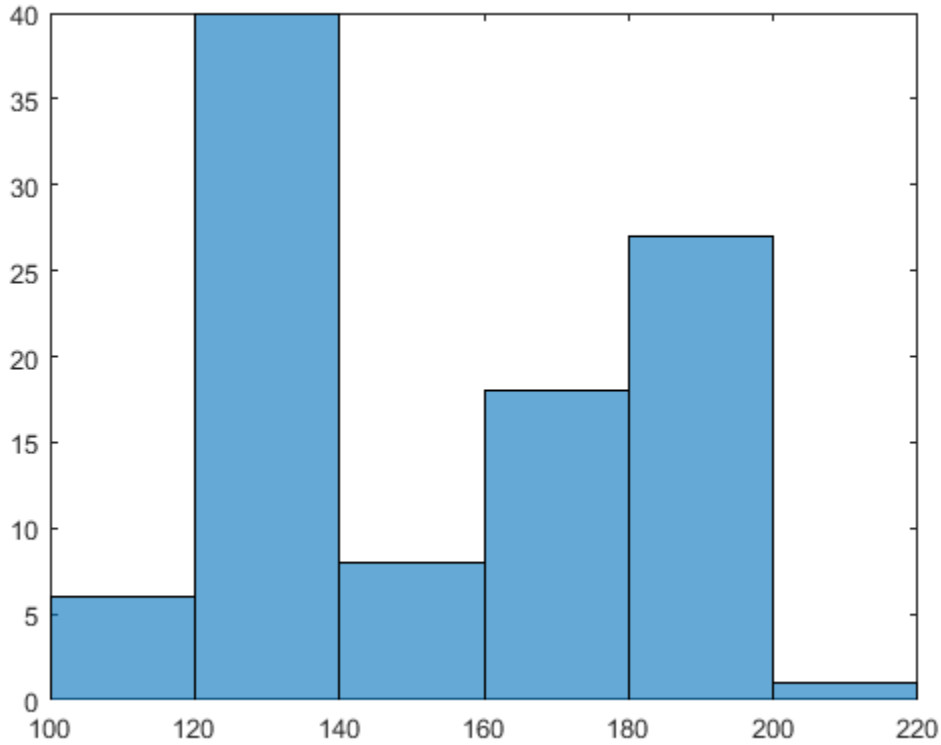
```
pd =
```

```
  PiecewiseLinearDistribution

F(0) = 0
F(1) = 1
```

Create a Piecewise Linear Distribution Object Using Specified Parameters

Load the sample data. Visualize the patient weight data using a histogram.

```
load hospital
histogram(hospital.Weight)
```



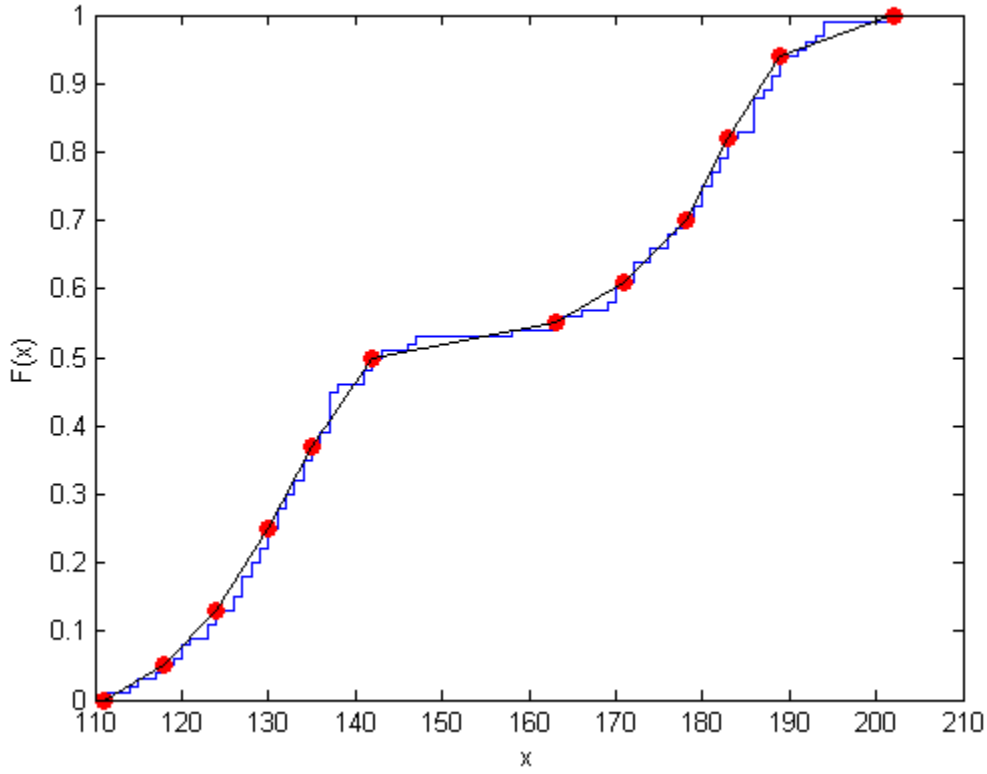
The histogram shows that the data has two modes, one for female patients and one for male patients.

Compute the empirical cumulative distribution function (ecdf) for the data.

```
[f,x] = ecdf(hospital.Weight);
```

Construct a piecewise linear approximation to the ecdf and plot both functions.

```
f = f(1:5:end); % keep a less dense grid of points
x = x(1:5:end);

figure;
ecdf(hospital.Weight)
hold on
plot(x,f,'ro','MarkerFace','r') % overlay grid
plot(x,f,'k') % show interpolation
```



Create a piecewise linear probability distribution object using the piecewise approximation of the ecdf.

```
pd = makedist('PiecewiseLinear','x',x,'Fx',f)
```

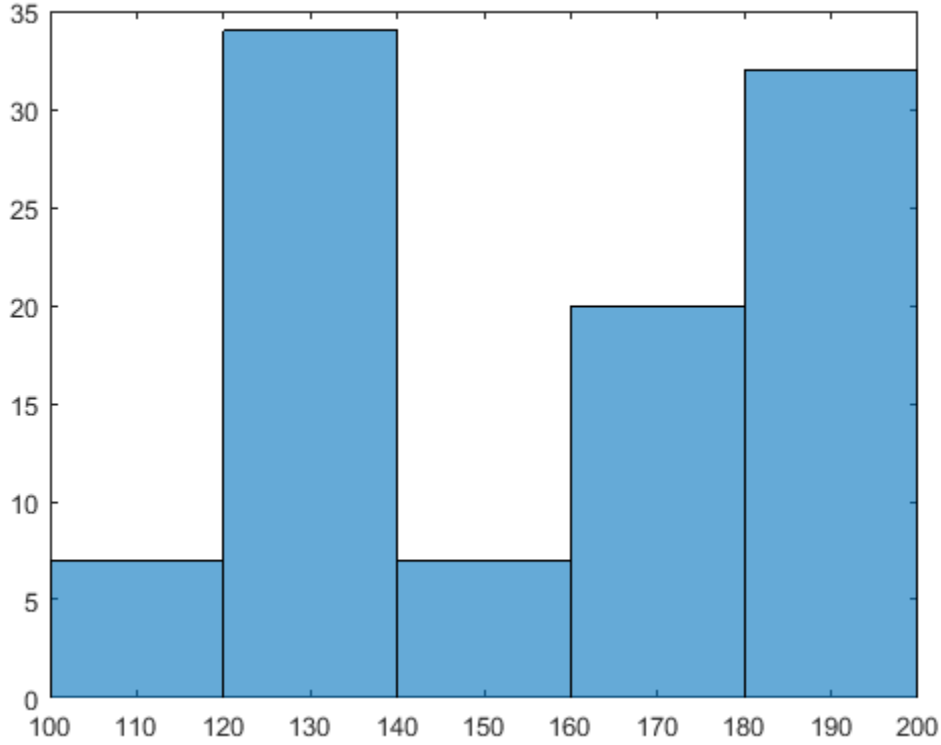
```
pd =

  PiecewiseLinearDistribution

F(111) = 0
F(118) = 0.05
F(124) = 0.13
F(130) = 0.25
F(135) = 0.37
F(142) = 0.5
F(163) = 0.55
F(171) = 0.61
F(178) = 0.7
F(183) = 0.82
F(189) = 0.94
F(202) = 1
```

Generate 100 random numbers from the distribution.

```
rng default  % For reproducibility
rw = random(pd,100,1);
```

Plot the random numbers to visually compare their distribution to the original data.

```
figure;
histogram(rw)
```



The random numbers generated from the piecewise linear distribution have the same bimodal distribution as the original data.

See Also

`makedist`

More About

- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Supported Distributions" on page 5-17

- "Piecewise Linear Distribution"
- Class Attributes
- Property Attributes

plot

Class: clustering.evaluation.ClusterCriterion
Package: clustering.evaluation

Plot clustering evaluation object criterion values

Syntax

```
plot(eva)
h = plot(eva)
```

Description

`plot(eva)` displays a plot of the criterion values versus the number of clusters, based on the values stored in the clustering evaluation object eva.

`h = plot(eva)` returns a handle to the plot line.

Input Arguments

`eva` — Clustering evaluation data

clustering evaluation object

Clustering evaluation data, specified as a clustering evaluation object. Create a clustering evaluation object using `evalclusters`.

Output Arguments

`h` — Handle to plot line

scalar value

Handle to the plot line, returned as a scalar value.

Examples

Plot the Clustering Evaluation Criterion Values

Plot the criterion values versus the number of clusters for each clustering solution stored in a clustering evaluation object.

Load the sample data.

```
load fisheriris;
```

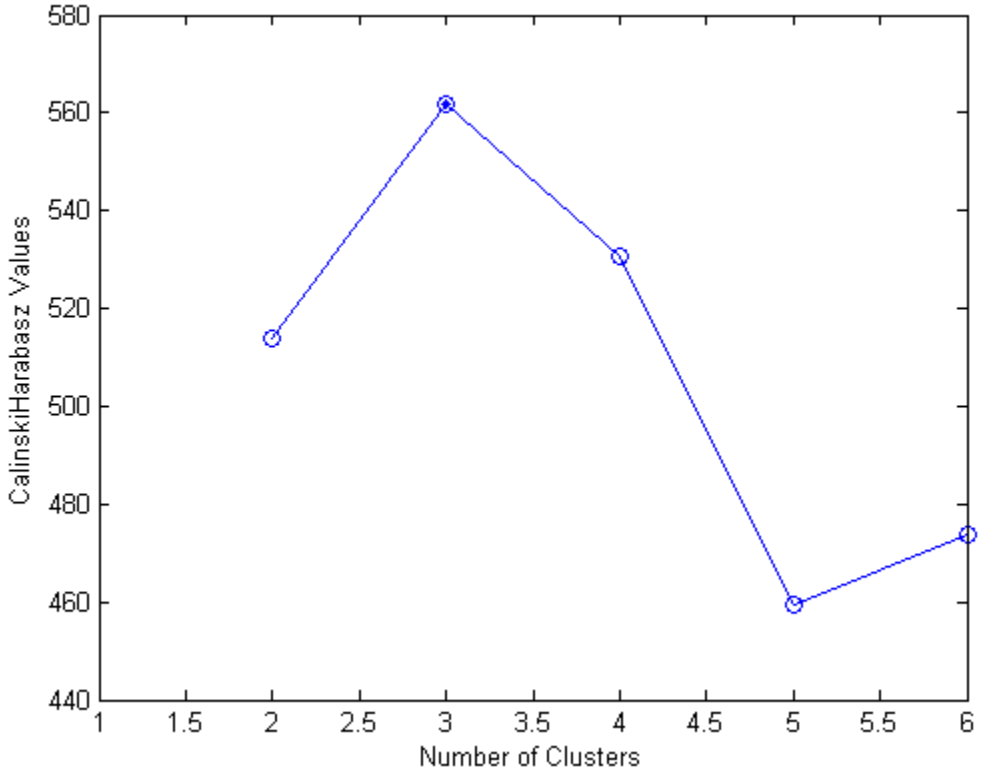
The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Create a clustering evaluation object. Cluster the data using `kmeans`, and evaluate the optimal number of clusters using the Calinski-Harabasz criterion.

```
rng('default');  % For reproducibility
eva = evalclusters(meas,'kmeans','CalinskiHarabasz','KList',[1:6]);
```

Plot the Calinski-Harabasz criterion values for each number of clusters tested.

```
figure;
plot(eva);
```



The plot shows that the highest Calinski-Harabasz value occurs at three clusters, suggesting that the optimal number of clusters is three.

See Also

`evalclusters`

plot

Class: LinearModel

Scatter plot or added variable plot of linear model

Syntax

```
plot(mdl)
h = plot(mdl)
```

Description

`plot(mdl)` creates a plot of the fitted linear model. The plot type depends on the number of predictor variables.

- If there is just one predictor variable, `plot` creates a scatter plot of the data along with a fitted curve and confidence bounds.
- If there are multiple predictor variables, `plot` creates an added variable plot.
- If there are no predictors, `plot` creates a histogram of the residuals.

`h = plot(mdl)` returns handles to the lines in the plot.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

Output Arguments

`h`

Vector of handles to lines or patches in the plot.

Definitions

Added Variable Plot, Adjusted Response

An added variable plot illustrates the incremental effect on the response of specified terms by removing the effects of all other terms. The slope of the fitted line is the coefficient of the linear combination of the specified terms projected onto the best-fitting direction. The adjusted response includes the constant (intercept) terms, and averages out all other terms.

Examples

Create an Added Variable Plot

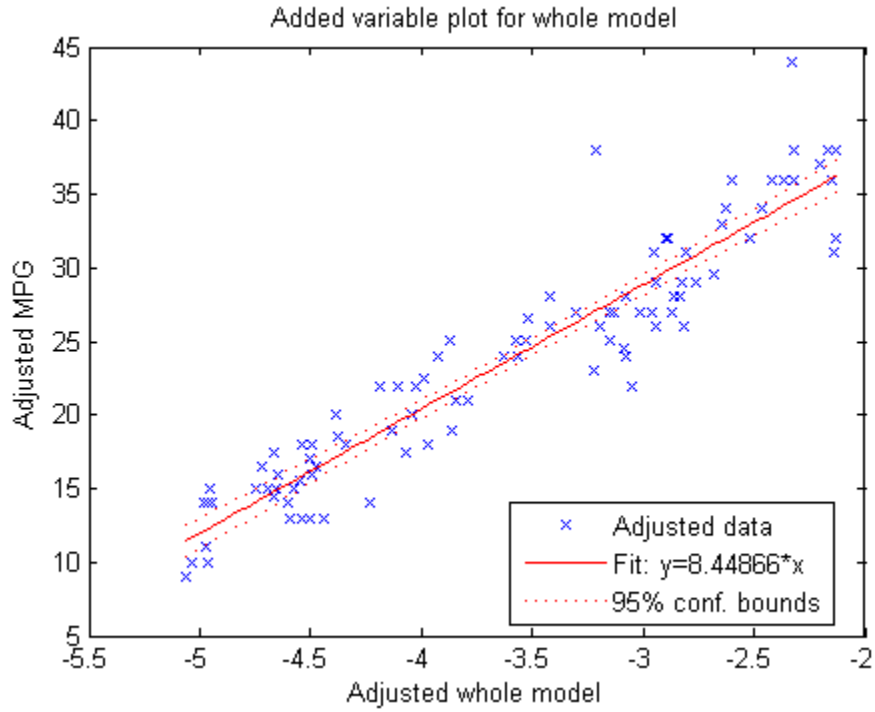
Create a model of car mileage as a function of weight and model year. Then create a plot to see the significance of the model.

Create a linear model of mileage from the `carsmall` data.

```
load carsmall
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
mdl = fitlm(tbl,'MPG ~ Year + Weight^2');
```

Create an added variable plot.

```
plot(mdl)
```



The plot illustrates that the model is significant—a horizontal line does not fit between the confidence bounds.

Alternatives

Use `plotAdded` to select particular predictors for an added variable plot.

See Also

`plotAdded` | `LinearModel`

How To

- “Linear Regression” on page 9-11

plot

Class: RepeatedMeasuresModel

Plot data with optional grouping

Syntax

```
plot(rm)
plot(rm,Name,Value)
H = plot( ___ )
```

Description

`plot(rm)` plots the measurements in the repeated measures model rm for each subject as a function of time. If there is a single numeric within-subjects factor, `plot` uses the values of that factor as the time values. Otherwise, `plot` uses the discrete values 1 through *r* as the time values, where *r* is the number of repeated measurements.

`plot(rm,Name,Value)` also plots the measurements in the repeated measures model rm, with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the factors to group by or change the line colors.

`H = plot( ___ )` returns handles, `H`, to the plotted lines.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Group'` — Name of between-subject factor or factors

string | cell array of strings

Name of between-subject factor or factors, specified as the comma-separated pair consisting of `'Group'` and a string or cell array of strings. This name-value pair argument groups the lines according to the factor values.

For example, if you have two between-subject factors, drug and sex, and you want to group the lines in the plot according to them, you can specify these factors as follows.

Example: `'Group',{'Drug','Sex'}`

Data Types: `char | cell`

`'Marker'` — Marker to use for each group

cell array of strings

Marker to use for each group, specified as the comma-separated pair consisting of `'Marker'` and a cell array of strings.

For example, if you have two between-subject factors, drug and sex, with each having two groups, you can specify `o` as the marker for the groups of drug and `x` as the marker for the groups of sex as follows.

Example: `'Marker',{'o','o','x','x'}`

Data Types: `cell`

`'Color'` — Color for each group

string | cell array of strings | rows of a three-column RGB matrix

Color for each group, specified as the comma-separated pair consisting of `'Color'` and a string, cell array of strings, or rows of a three-column RGB matrix.

For example, if you have two between-subject factors, drug and sex, with each having two groups, you can specify red as the color for the groups of drug and blue as the color for the groups of sex as follows.

Example: `'Color','rrbb'`

Data Types: `single | double | cell`

`'LineStyle'` — Line style for each group

cell array of strings

Line style for each group, specified as the comma-separated pair consisting of `'LineStyle'` and a cell array of strings.

For example, if you have two between-subject factors, drug and sex, with each having two groups, you can specify `-` as the line style of one group and `:` as the line style for the other group as follows.

Example: `'LineStyle',{'-' ':' '-' ':'}`

Data Types: `cell`

Output Arguments

`H` — Handle to plotted lines

handle

Handle to plotted lines, returned as a handle.

Examples

Plot Data by Group

Load the sample data.

```
load fisheriris
```

The column vector `species` consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
```

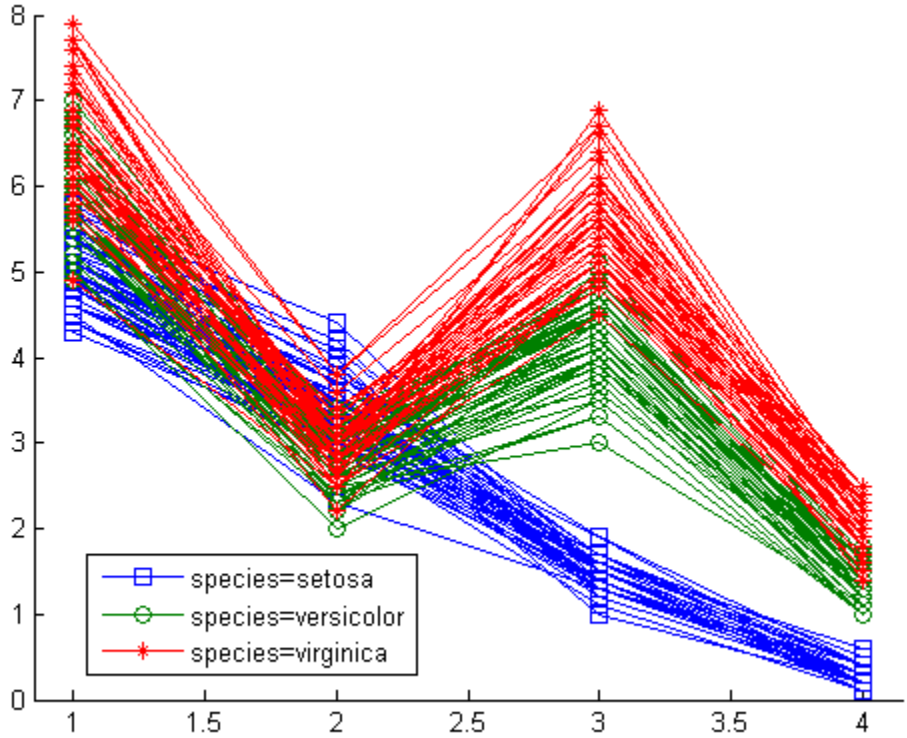
```
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

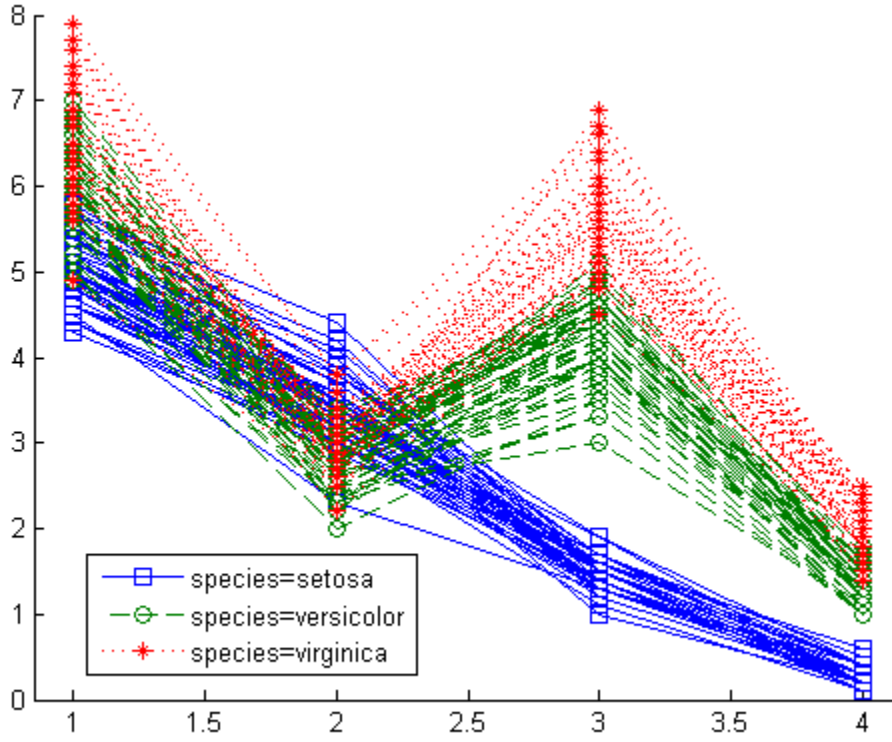
Plot data grouped by the factor species.

```
plot(rm,'group','species')
```



Change the line style for each group.

```
plot(rm,'group','species','LineStyle',{'-','--',':'})
```



Plot Data Grouped by Two Factors

Load the sample data.

```
load repeatedmeas
```

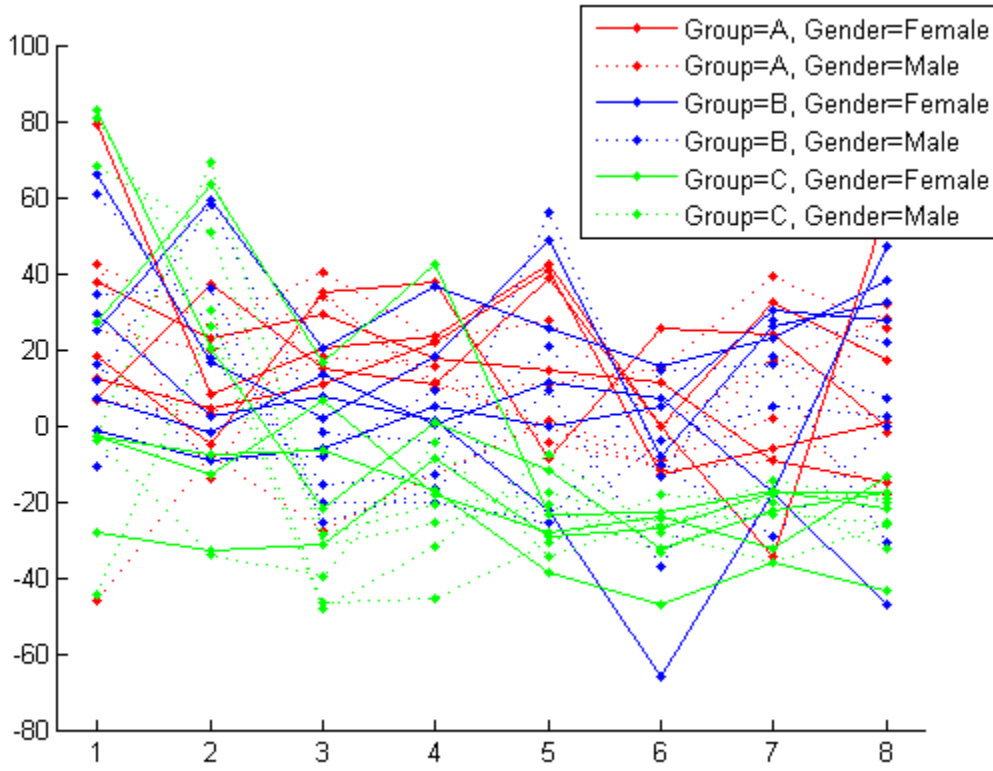
The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ through $y8$ as responses. The table `within` includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ through $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Plot data with `Group` coded by color and `Gender` coded by line type.

```
plot(R,'group',{'Group' 'Gender'},'Color','rrbbgg',...
               'LineStyle',{'-' ':' '-' ':' '-' ':'},'Marker','.')
```



See Also

`fitrm` | `multcompare` | `plotprofile`

plotAdded

Class: LinearModel

Added variable plot or leverage plot for linear model

Syntax

```
plotAdded(mdl)
plotAdded(mdl,coef)
h = plotAdded(mdl,...)
h = plotAdded(mdl,coef,Name,Value)
```

Description

`plotAdded(mdl)` produces a generalized added variable plot for all terms in `mdl` except the constant term.

`plotAdded(mdl,coef)` produces an added variable plot for the `coef` terms in `mdl`, after adjusting for all other terms.

`h = plotAdded(mdl,...)` returns handles to the lines in the plot.

`h = plotAdded(mdl,coef,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`coef`

Coefficients in `mdl`. Represent as:

- String giving a single coefficient name
- Vector of coefficient numbers in the `mdl.CoefficientNames` property

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerFaceColor'`

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

'MarkerSize'

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

Output Arguments

h

Vector of handles to lines or patches in the plot.

Definitions

Added Variable Plot, Adjusted Response

An added variable plot illustrates the incremental effect on the response of specified terms by removing the effects of all other terms. The slope of the fitted line is the coefficient of the linear combination of the specified terms projected onto the best-fitting direction. The adjusted response includes the constant (intercept) terms, and averages out all other terms.

Examples

Create an Added Variable Plot

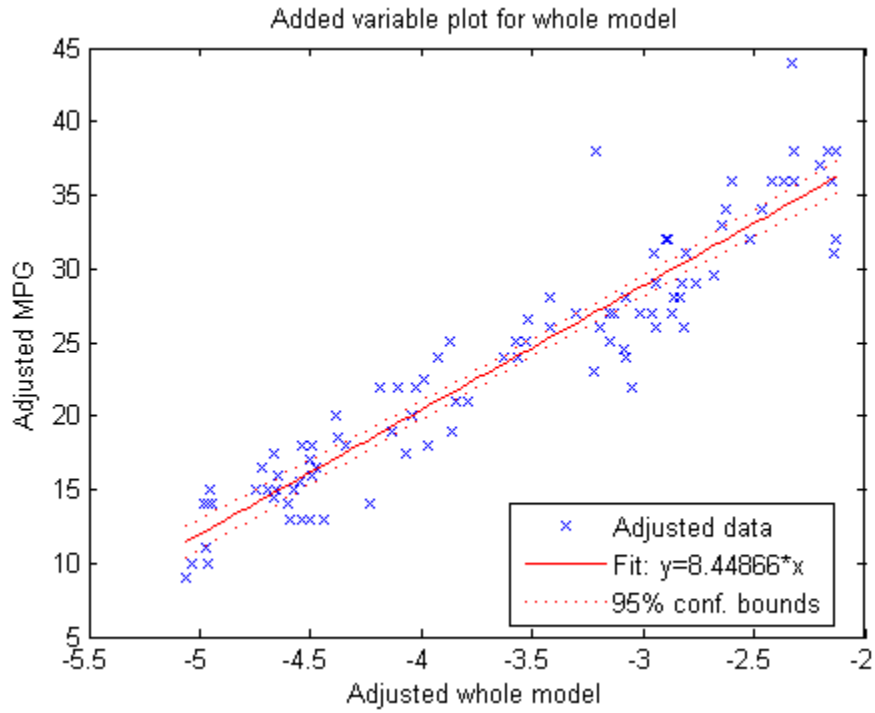
Create a model of car mileage as a function of weight and model year. Then create a plot to see the significance of the model.

Create a linear model of mileage from the `carsmall` data.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
mdl = fitlm(ds,'MPG ~ Year + Weight^2');
```

Create an added variable plot.

```
plotAdded(mdl)
```



The plot illustrates that the model is significant—a horizontal line does not fit between the confidence bounds.

Create an Added Variable Plot for Particular Variables

Create a model of car mileage as a function of weight and model year. Then create a plot to see the effect of the weight terms (`Weight` and `Weight^2`).

Create a linear model of mileage from the `carsmall` data.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
mdl = fitlm(ds,'MPG ~ Year + Weight^2');
```

Find the terms in the model corresponding to the `Weight` and `Weight^2`.

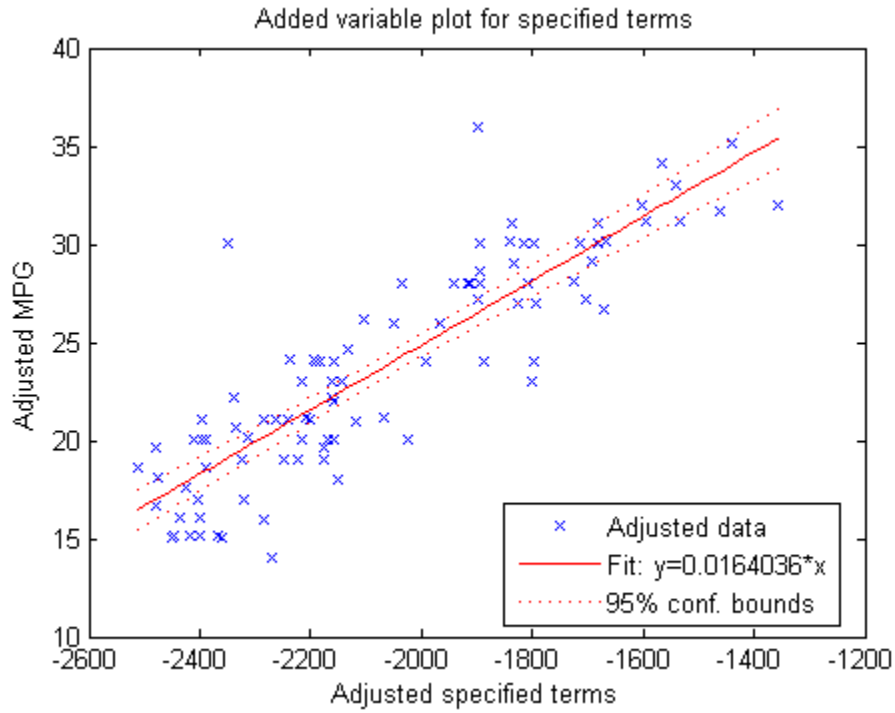
```
mdl.CoefficientNames
```

```
ans =

    '(Intercept)' 'Weight' 'Year_76' 'Year_82' 'Weight^2'
```

The weight terms are 2 and 5.

Create an added variable plot with the weight terms.

```
coef = [2 5];
plotAdded(mdl,coef)
```



The plot illustrates that the weight terms are significant—a horizontal line does not fit between the confidence bounds.

- “Plots to Understand Terms Effects” on page 9-33

See Also

`plot` | `LinearModel`

How To

- “Linear Regression” on page 9-11

plotAdjustedResponse

Class: LinearModel

Adjusted response plot for linear regression model

Syntax

```
plotAdjustedResponse(mdl,var)
h = plotAdjustedResponse(mdl,var)
h = plotAdjustedResponse(mdl,var,Name,Value)
```

Description

`plotAdjustedResponse(mdl,var)` gives an adjusted response plot for the variable `var` in the `mdl` regression model.

`h = plotAdjustedResponse(mdl,var)` returns handles to the lines in the plot.

`h = plotAdjustedResponse(mdl,var,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`var`

Variable name, or scalar index of variable in `mdl.CoefficientNames`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerFaceColor'`

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerSize'`

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

Output Arguments

h

Vector of handles to lines or patches in the plot.

Definitions

Adjusted Response Plot

The adjusted response plot shows the fitted response as a function of `var`, with the other predictors averaged out by averaging the fitted values over the data used in the fit. Adjusted data points are computed by adding the residual to the adjusted fitted value for each observation.

Examples

Plot Adjusted Responses

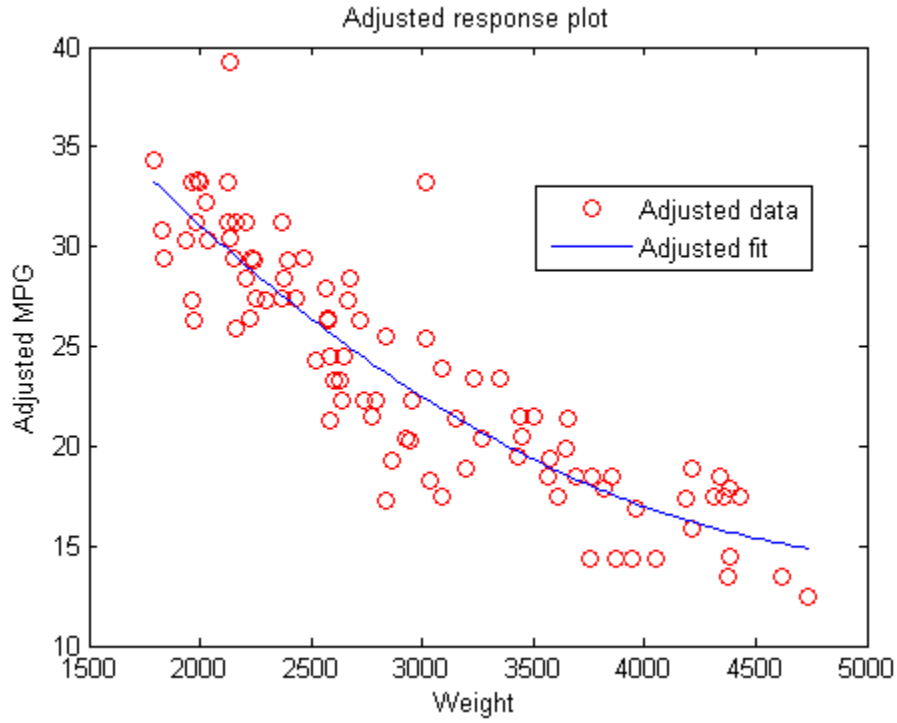
Plot the adjusted responses of a fitted linear model.

Load the `carsmall` data and fit a linear model of the mileage as a function of model year, weight, and weight squared.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
mdl = fitlm(ds,'MPG ~ Year + Weight^2');
```

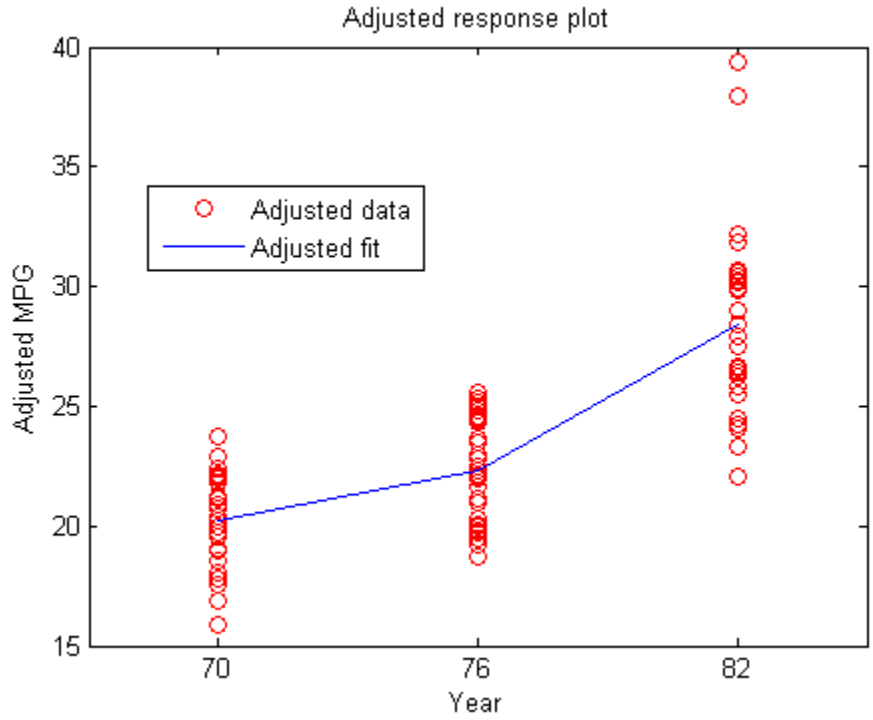
Plot the effect of `'Weight'` averaged over `Year` values.

```
plotAdjustedResponse(mdl,'Weight')
```



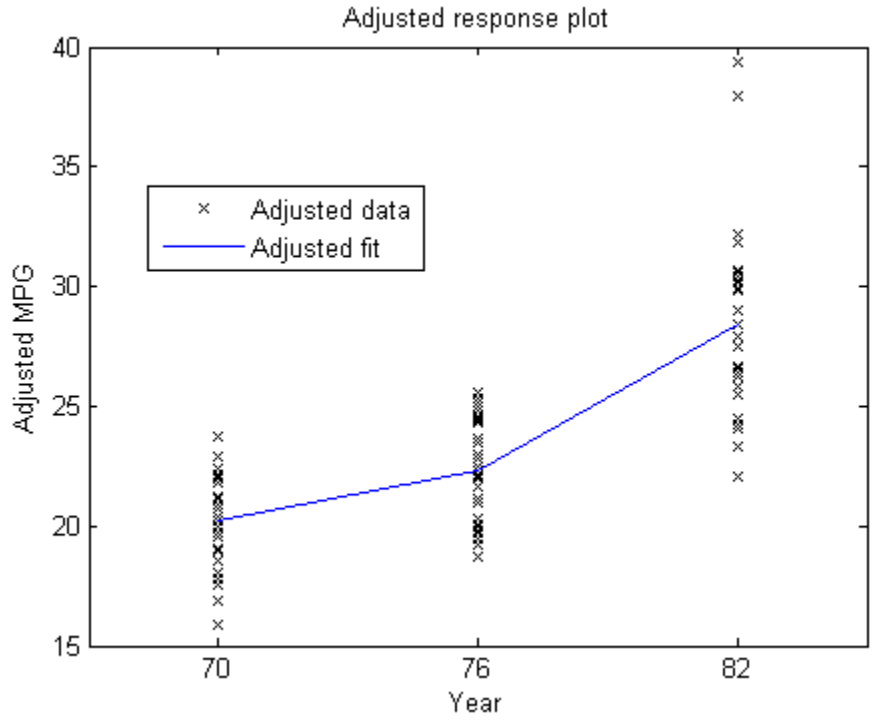
Plot the effect of `Year` averaged over `'Weight'` values. Include the `h` output.

```
h = plotAdjustedResponse(mdl,'Year');
```



Change the adjusted data to black `x` instead of red `o`.

```
set(h(1),'Marker','x','Color','k')
```



See Also

`plotAdded` | `LinearModel` | `plotEffects` | `plotInteraction`

How To

- “Linear Regression” on page 9-11

plotDiagnostics

Class: GeneralizedLinearModel

Plot diagnostics of generalized linear regression model

Syntax

```
plotDiagnostics(mdl)
plotDiagnostics(mdl,plottype)
h = plotDiagnostics(...)
h = plotDiagnostics(mdl,plottype,Name,Value)
```

Description

`plotDiagnostics(mdl)` plots diagnostics from the `mdl` linear model using leverage as the plot type.

`plotDiagnostics(mdl,plottype)` plots diagnostics from the `mdl` generalized linear model in a plot of type `plottype`.

`h = plotDiagnostics(...)` returns handles to the lines in the plot.

`h = plotDiagnostics(mdl,plottype,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`plottype`

String specifying the type of plot:

`'contour'`	Residual vs. leverage with overlayed Cook's contours
`'cookd'`	Cook's distance
`'leverage'`	Leverage (diagonal of Hat matrix)

Default: `'leverage'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

'MarkerFaceColor'

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

'MarkerSize'

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

Output Arguments

h

Vector of handles to lines or patches in the plot.

Definitions

Hat Matrix

The *hat matrix H* is defined in terms of the data matrix X and a diagonal weight matrix W:
$H = X(X^TWX)^{-1}X^TW^T$.

W has diagonal elements w_i:

$$w_i = \frac{g'(\mu_i)}{\sqrt{V(\mu_i)}},$$

where

- g is the link function mapping y_i to x_ib.
- g' is the derivative of the link function g.
- V is the variance function.

- μ_i is the ith mean.

The diagonal elements H_{ii} satisfy

$$0 \le h_{ii} \le 1$$
$$\sum_{i=1}^{n} h_{ii} = p,$$

where n is the number of observations (rows of X), and p is the number of coefficients in the regression model.

Leverage

The *leverage* of observation i is the value of the ith diagonal term, h_{ii}, of the hat matrix H. Because the sum of the leverage values is p (the number of coefficients in the regression model), an observation i can be considered to be an outlier if its leverage substantially exceeds p/n, where n is the number of observations.

Cook's Distance

The Cook's distance D_i of observation i is

$$D_i = w_i \frac{e_i^2}{p\hat{\varphi}} \frac{h_{ii}}{\left(1-h_{ii}\right)^2},$$

where

- $\hat{\varphi}$ is the dispersion parameter (estimated or theoretical).
- e_i is the linear predictor residual, $g\left(y_i\right) - x_i\hat{\beta}$, where
  - g is the link function.
  - y_i is the observed response.
  - x_i is the observation.

  - $\hat{\beta}$ is the estimated coefficient vector.
- p is the number of coefficients in the regression model.
- h_{ii} is the ith diagonal element of the Hat Matrix H.

Examples

Diagnostic Plots for Generalized Linear Models

Create leverage and Cook's distance plots of a fitted generalized linear model.

Generate artificial data for the model, Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

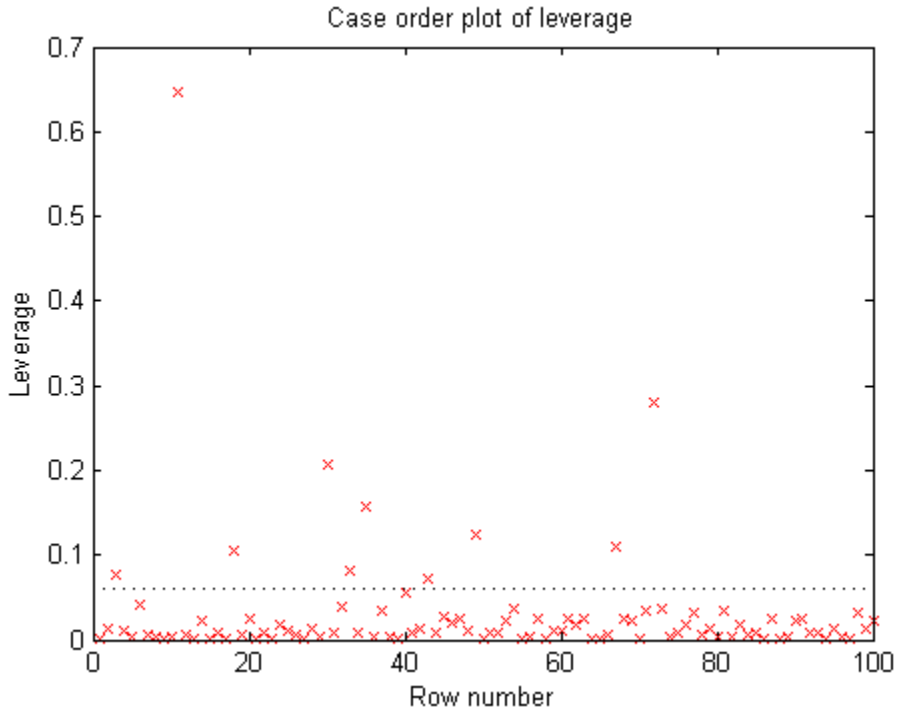
```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data.

```
mdl = fitglm(X,y,...
    'y ~ x1 + x2','distr','poisson');
```

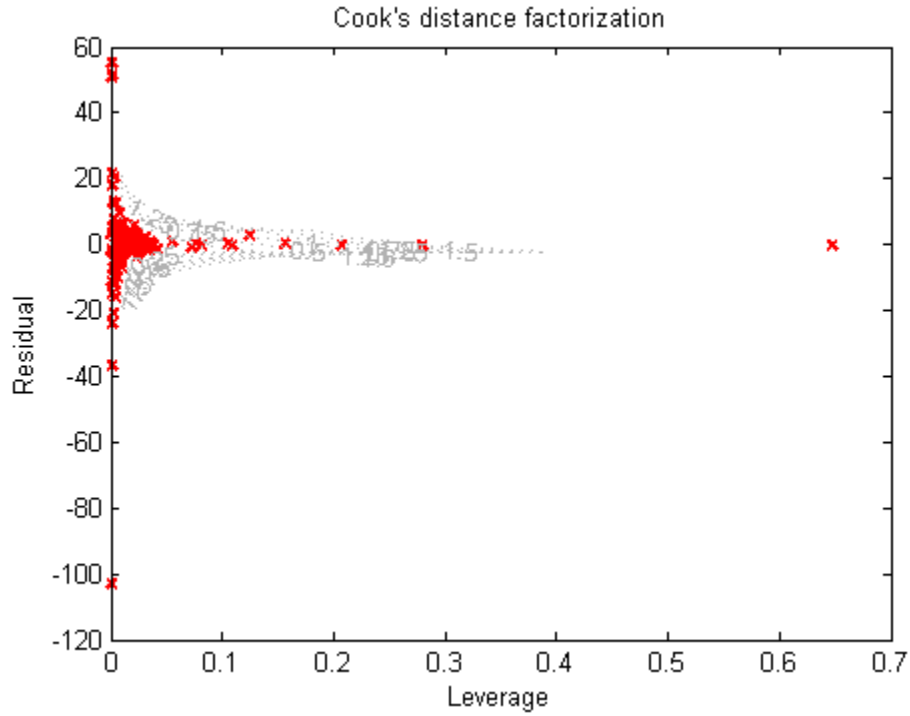
Create a leverage plot.

```
plotDiagnostics(mdl)
```



Create a contour plot with Cook's distance.

```
plotDiagnostics(mdl,'contour')
```



- “Diagnostic Plots” on page 10-25

References

[1] Neter, J., M. H. Kutner, C. J. Nachtsheim, and W. Wasserman. *Applied Linear Statistical Models*, Fourth Edition. Irwin, Chicago, 1996.

See Also

`GeneralizedLinearModel`

More About

- “Generalized Linear Models” on page 10-12

plotDiagnostics

Class: LinearModel

Plot diagnostics of linear regression model

Syntax

```
plotDiagnostics(mdl)
plotDiagnostics(mdl,plottype)
h = plotDiagnostics(...)
h = plotDiagnostics(mdl,plottype,Name,Value)
```

Description

`plotDiagnostics(mdl)` plots diagnostics from the `mdl` linear model using scaled delete-1 fitted values.

`plotDiagnostics(mdl,plottype)` plots diagnostics in a plot of type `plottype`.

`h = plotDiagnostics(...)` returns handles to the lines in the plot.

`h = plotDiagnostics(mdl,plottype,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`plottype`

String specifying the type of plot:

`'contour'`	Residual vs. leverage with overlayed Cook's contours
`'cookd'`	Cook's distance
`'covratio'`	Delete-1 ratio of determinant of covariance
`'dfbetas'`	Scaled delete-1 coefficient estimates
`'dffits'`	Scaled delete-1 fitted values
`'leverage'`	Leverage
`'s2_i'`	Delete-1 variance estimate

Delete-1 means compute a new model without the current observation. If the delete-1 calculation differs significantly from the model using all observations, then the observation is influential.

Default: `'leverage'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerFaceColor'`

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerSize'`

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

Output Arguments

`h`

Vector of handles to lines or patches in the plot.

Definitions

Hat Matrix

The *hat matrix H* is defined in terms of the data matrix *X*:
$H = X(X^TX)^{-1}X^T$.

The diagonal elements H_{ii} satisfy

$$0 \le h_{ii} \le 1$$

$$\sum_{i=1}^{n} h_{ii} = p,$$

where n is the number of observations (rows of X), and p is the number of coefficients in the regression model.

Leverage

The *leverage* of observation i is the value of the ith diagonal term, h_{ii}, of the hat matrix H. Because the sum of the leverage values is p (the number of coefficients in the regression model), an observation i can be considered to be an outlier if its leverage substantially exceeds p/n, where n is the number of observations.

Cook's Distance

Cook's distance is the scaled change in fitted values. Each element in `CooksDistance` is the normalized change in the vector of coefficients due to the deletion of an observation. The Cook's distance, D_i, of observation i is

$$D_i = \frac{\sum_{j=1}^{n} \left(\hat{y}_j - \hat{y}_{j(i)}\right)^2}{p\,MSE},$$

where

- $\hat{y}_j$ is the jth fitted response value.
- $\hat{y}_{j(i)}$ is the jth fitted response value, where the fit does not include observation i.
- MSE is the mean squared error.
- p is the number of coefficients in the regression model.

Cook's distance is algebraically equivalent to the following expression:

$$D_i = \frac{r_i^2}{p\,MSE}\left(\frac{h_{ii}}{\left(1-h_{ii}\right)^2}\right),$$

where r_i is the ith residual, and h_{ii} is the ith leverage value.

`CooksDistance` is an n-by-1 column vector in the `Diagnostics` table of the `LinearModel` object.

Examples

Leverage Plot of Linear Model

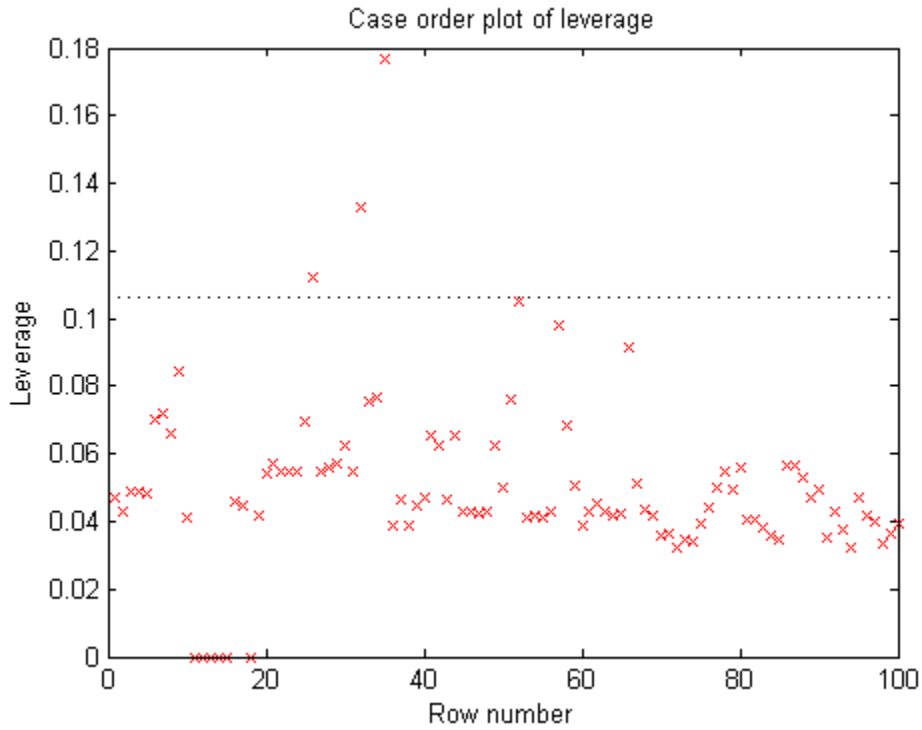
Plot the leverage values of observations in a fitted model.

Load the `carsmall` data and fit a linear model of the mileage as a function of model year, weight, and weight squared.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
mdl = fitlm(ds,'MPG ~ Year + Weight^2');
```

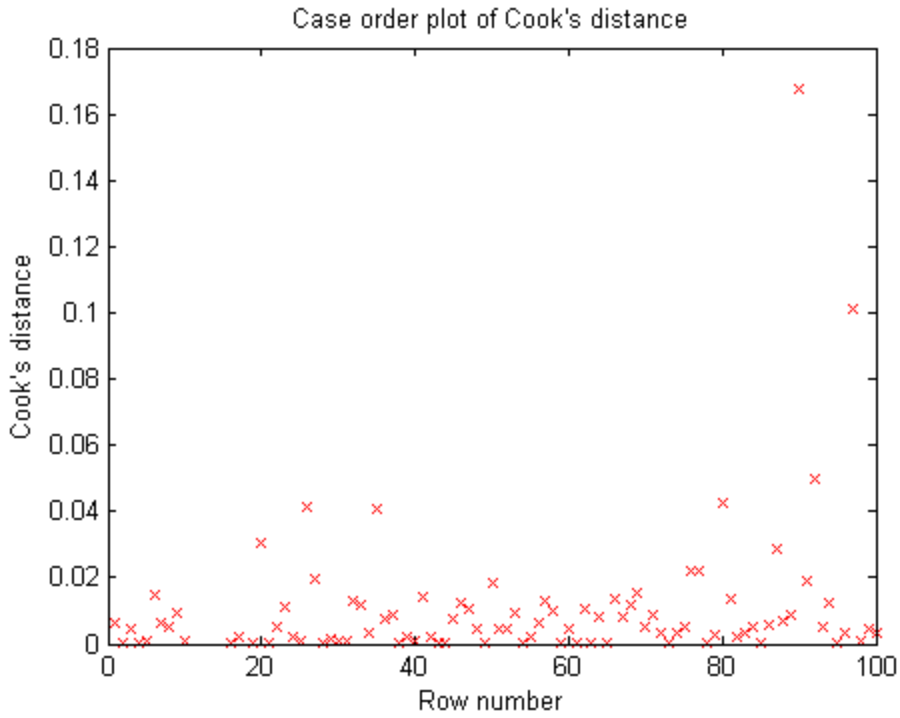
Plot the leverage values.

```
plotDiagnostics(mdl)
```



Plot the Cook's distance.

```
plotDiagnostics(mdl,'cookd')
```



The two diagnostic plots give different results.

- "Diagnostic Plots" on page 9-22

References

[1] Neter, J., M. H. Kutner, C. J. Nachtsheim, and W. Wasserman. *Applied Linear Statistical Models*, Fourth Edition. Irwin, Chicago, 1996.

Alternatives

The `mdl.Diagnostics` property contains the information that `plotDiagnostics` uses to create plots.

See Also

`LinearModel`

How To

- “Linear Regression” on page 9-11

plotDiagnostics

Class: NonLinearModel

Plot diagnostics of nonlinear regression model

Syntax

```
plotDiagnostics(mdl)
plotDiagnostics(mdl,plottype)
h = plotDiagnostics(...)
h = plotDiagnostics(mdl,plottype,Name,Value)
```

Description

`plotDiagnostics(mdl)` plots diagnostics from the `mdl` linear model using leverage as the plot type.

`plotDiagnostics(mdl,plottype)` plots diagnostics in a plot of type `plottype`.

`h = plotDiagnostics(...)` returns handles to the lines in the plot.

`h = plotDiagnostics(mdl,plottype,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

`plottype`

String specifying the type of plot:

`'contour'`	Residual vs. leverage with overlayed Cook's contours
`'cookd'`	Cook's distance
`'leverage'`	Leverage (diagonal of Hat matrix)

Default: `'leverage'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

'MarkerFaceColor'

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

'MarkerSize'

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

Output Arguments

h

Vector of handles to lines or patches in the plot.

Definitions

Hat Matrix

The *hat matrix H* is defined in terms of the data matrix X and the Jacobian matrix J:

$$J_{i,j} = \left.\frac{\partial f}{\partial \beta_j}\right|_{x_i,\beta}$$

Here f is the nonlinear model function, and β is the vector of model coefficients.

The Hat Matrix H is
$H = J(J^TJ)^{-1}J^T$.

The diagonal elements H_{ii} satisfy

$$0 \le h_{ii} \le 1$$

$$\sum_{i=1}^{n} h_{ii} = p,$$

where n is the number of observations (rows of X), and p is the number of coefficients in the regression model.

Leverage

The *leverage* of observation i is the value of the ith diagonal term, h_{ii}, of the hat matrix H. Because the sum of the leverage values is p (the number of coefficients in the regression model), an observation i can be considered to be an outlier if its leverage substantially exceeds p/n, where n is the number of observations.

Cook's Distance

The Cook's distance D_i of observation i is

$$D_i = \frac{\sum_{j=1}^{n} \left(\hat{y}_j - \hat{y}_{j(i)}\right)^2}{p\,MSE},$$

where

- $\hat{y}_j$ is the jth fitted response value.
- $\hat{y}_{j(i)}$ is the jth fitted response value, where the fit does not include observation i.
- MSE is the mean squared error.
- p is the number of coefficients in the regression model.

Cook's distance is algebraically equivalent to the following expression:

$$D_i = \frac{r_i^2}{p\,MSE}\left(\frac{h_{ii}}{\left(1-h_{ii}\right)^2}\right),$$

where e_i is the ith residual.

Examples

Nonlinear Model Leverage Plot

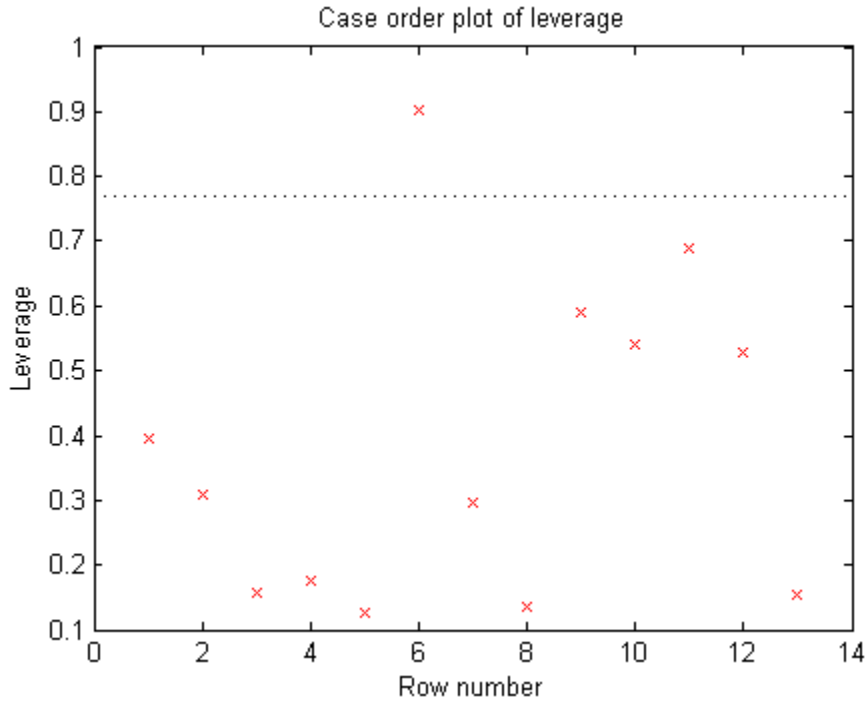
Create a leverage plot of a fitted nonlinear model, and find the points with high leverage.

Load the reaction data and fit a model of the reaction rate as a function of reactants.

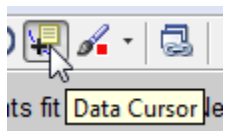
```
load reaction
mdl = fitnlm(reactants,rate,@hougen,[1 .05 .02 .1 2]);
```

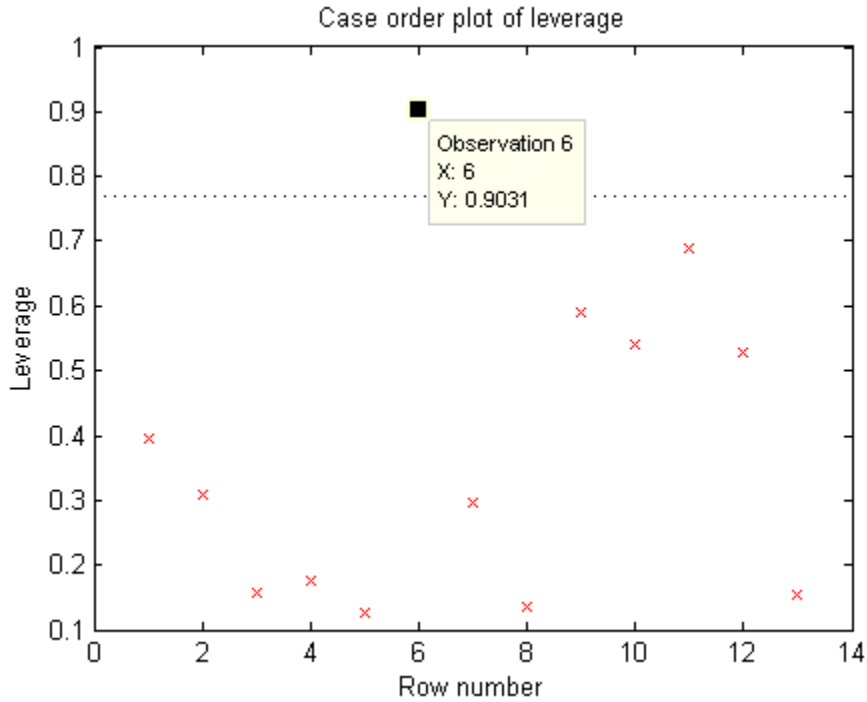
Create a leverage plot of the fitted model.

```
plotDiagnostics(mdl)
```



To examine the observation with high leverage, activate the Data Cursor and click the observation.





Alternatively, find the high-leverage observation at the command line.

```
find(mdl.Diagnostics.Leverage > 0.8)
```

```
ans =

     6
```

- "Examine Quality and Adjust the Fitted Nonlinear Model" on page 11-7
- "Nonlinear Regression Workflow" on page 11-14

References

[1] Neter, J., M. H. Kutner, C. J. Nachtsheim, and W. Wasserman. *Applied Linear Statistical Models*, Fourth Edition. Irwin, Chicago, 1996.

See Also

`NonLinearModel` | `plotResiduals`

More About

- “Nonlinear Regression” on page 11-2

plotEffects

Class: LinearModel

Plot main effects of each predictor in linear regression model

Syntax

```
plotEffects(mdl)
h = plotEffects(mdl)
```

Description

`plotEffects(mdl)` produces an effects plot for the predictors in the `mdl` regression model. The plot shows the estimated effect on the response from changing each predictor value, averaging out the effects of the other predictors. `plotEffects` chooses values to produce a relatively large effect on the response.

`h = plotEffects(mdl)` returns handles to the lines in the plot.

Tips

- For many plots, the Data Cursor tool in the figure window displays the x and y values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

Output Arguments

h

Vector of handles to lines or patches in plot. `h(1)` is a handle to the circles that represent the main effect estimates. `h(j+1)` is a handle to the line that defines the confidence interval for the effect of predictor `j`.

Examples

Effects Plot

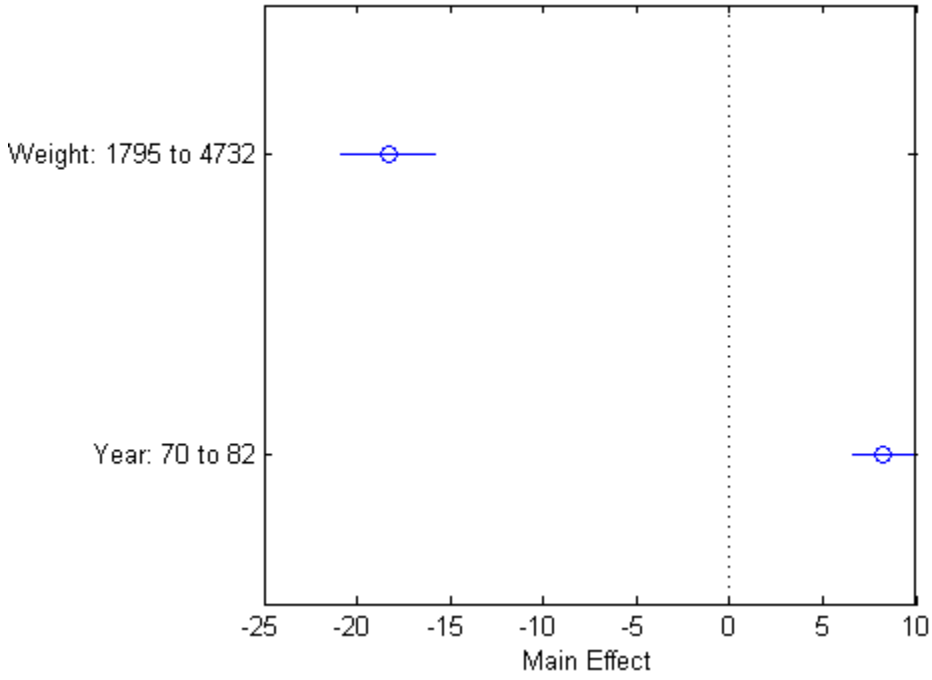
Plot the effects of two predictors in a fitted linear model.

Load the `carsmall` data and fit a linear model of the mileage as a function of model year, weight, and weight squared.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
mdl = fitlm(ds,'MPG ~ Year + Weight^2');
```

Create an effects plot.

```
plotEffects(mdl)
```



The width of each horizontal line in the figure shows a confidence interval for the effect on the response of the listed change in each predictor. The estimated effect of changing `Year` from `70` to `82` is an increase of about 8, and is between 6 and 10 with 95% confidence.

- "Plots to Understand Predictor Effects" on page 9-28

Alternatives

Use `plotInteraction` for an effects plot of the interactions of two specified variables.

See Also

`LinearModel` | `plotAdjustedResponse` | `plotInteraction`

How To

- “Linear Regression” on page 9-11

plotInteraction

Class: LinearModel

Plot interaction effects of two predictors in linear regression model

Syntax

```
plotInteraction(mdl,var1,var2)
plotInteraction(mdl,var1,var2,ptype)
h = plotInteraction(...)
```

Description

`plotInteraction(mdl,var1,var2)` creates a plot of the interaction effects of the predictors `var1` and `var2` in `mdl`. The plot shows the estimated effect on the response from changing each predictor value, averaging out the effects of the other predictors. The plot also shows the estimated effect with the other predictor fixed at certain values. `plotInteraction` chooses values to produce a relatively large effect on the response. The plot lets you examine whether the effect of one predictor depends on the value of the other predictor.

`plotInteraction(mdl,var1,var2,ptype)` returns a plot of the type specified in `ptype`.

`h = plotInteraction(...)` returns handles to the lines in the plot.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`var1`

String naming the variable for plot. `plotInteraction` chooses values of `var1` to create relatively large changes in the response. When you set `ptype` = `'predictions'`, the plot shows curves as a function of `var2` with various fixed values of `var1`.

`var2`

String naming the variable for plot. `plotInteraction` chooses values of `var2` to create relatively large changes in the response. When you set `ptype` = `'predictions'`, the plot shows curves as a function of `var2` various fixed values of `var1`.

`ptype`

String naming the plot type.

- `'effects'` — The plot shows each effect as a circle, with a horizontal bar showing the confidence interval for the estimated effect. `plotInteraction` computes the effect values from the adjusted response curve, as shown by the `plotAdjustedResponse` function.
- `'predictions'` — The plot shows the adjusted response curve as a function of `var2`, with `var1` fixed at certain values.

Default: `'effects'`

Output Arguments

`h`

Vector of handles to lines or patches in the plot.

Examples

Interaction Plot

Create a model of car mileage as a function of weight and model year. Then create a plot to see if the predictors have interactions.

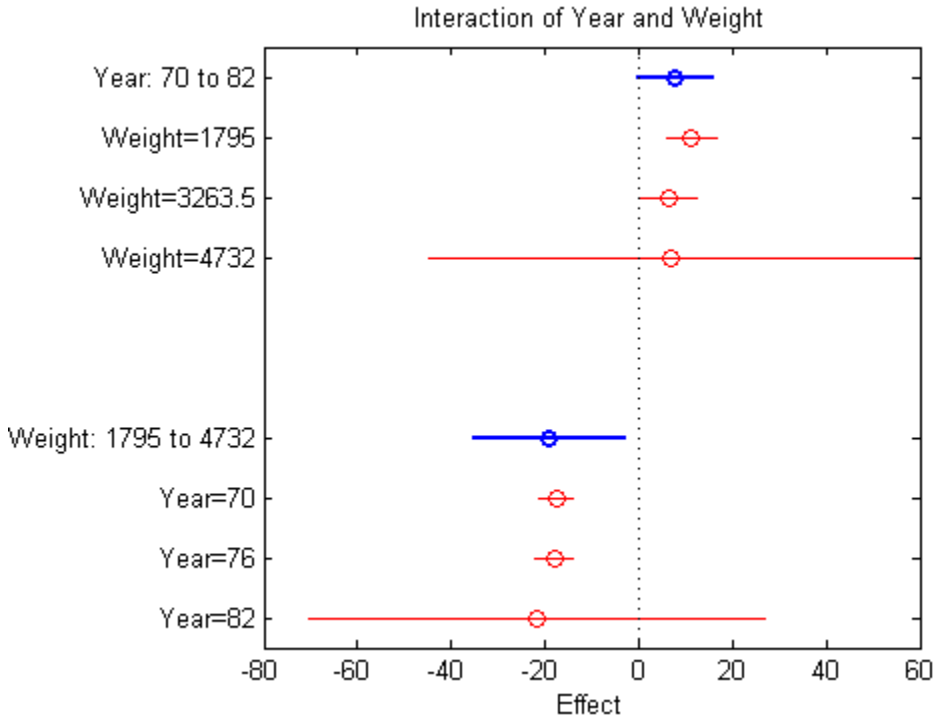
Create a linear model of mileage from the `carsmall` data.

```
load carsmall
```

```
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
var1 = 'Year';
var2 = 'Weight';
mdl = fitlm(ds,'MPG ~ Year * Weight^2');
```

Create an interaction plot.

```
plotInteraction(mdl,var1,var2)
```



The plot might show an interaction, because the groups of points are not perfectly vertical. But the error bars seem large enough that a vertical line could pass within all of the confidence intervals for each group, possibly indicating no interaction.

Prediction Curve Interaction Plot

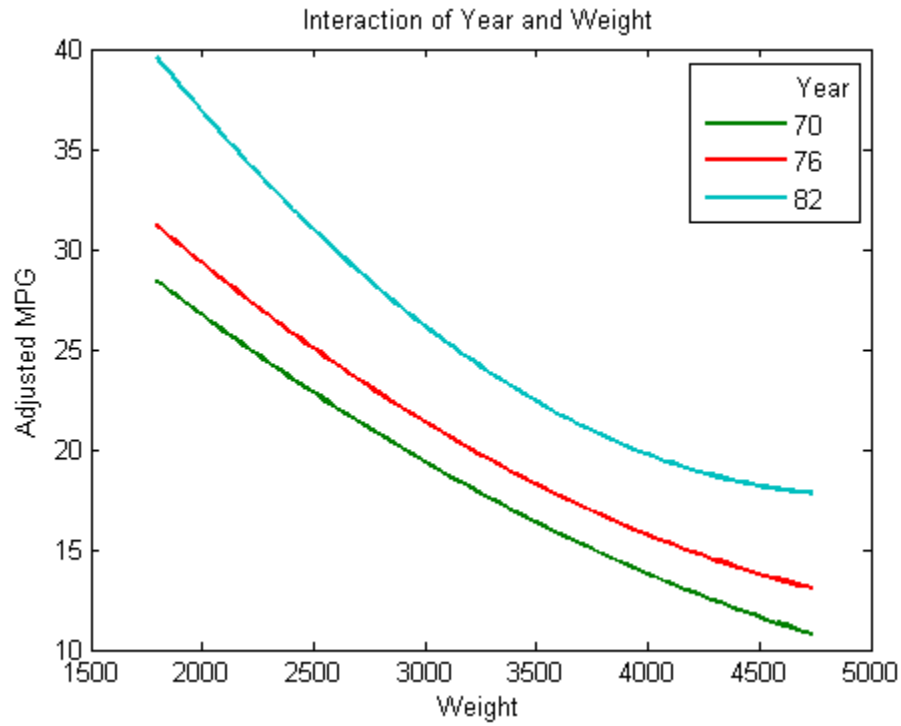
Create a model of car mileage as a function of weight and model year. Then create an interaction curve plot to see if the predictors have interactions.

Create a linear model of mileage from the `carsmall` data.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
var1 = 'Year';
var2 = 'Weight';
mdl = fitlm(ds,'MPG ~ Year * Weight^2');
```

Create an interaction plot with type `'predictions'`.

```
plotInteraction(mdl,var1,var2,'predictions')
```



The curves are not parallel. This indicates interactions between the predictors. The effect is subtle enough not to definitively indicate a interaction.

- “Plots to Understand Predictor Effects” on page 9-28

Alternatives

Use `plotEffects` for an effects plot showing separate effects for all predictors.

See Also

`plotEffects` | `LinearModel` | `plotAdjustedResponse`

How To

- “Linear Regression” on page 9-11

plotprofile

Class: RepeatedMeasuresModel

Plot expected marginal means with optional grouping

Syntax

```
plotprofile(rm,X)
plotprofile(rm,Name,Value)
H = plotprofile( ___ )
```

Description

`plotprofile(rm,X)` plots the expected marginal means computed from the repeated measures model rm as a function of the variable X.

`plotprofile(rm,Name,Value)` plots the expected marginal means computed from the repeated measures model rm with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the factors to group by or change the line colors.

`H = plotprofile( ___ )` returns handles, `H`, to the plotted lines.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`X` — Name of between-subjects or within-subjects factor

string

Name of a between-subjects or within-subjects factor, specified as a string.

For example, if you want to plot the marginal means as a function of the groups of a between-subjects variable drug, you can specify it as follows.

Example: `'Drug'`

Data Types: `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Group'` — Name of between-subject factor or factors

string | cell array of strings

Name of between-subject factor or factors, specified as the comma-separated pair consisting of `'Group'` and a string or cell array of strings. This name-value pair argument groups the lines according to the factor values.

For example, if you have two between-subject factors, drug and sex, and you want to group the lines in the plot according to them, you can specify these factors as follows.

Example: `'Group',{'Drug','Sex'}`

Data Types: `char | cell`

`'Marker'` — Marker to use for each group

cell array of strings

Marker to use for each group, specified as the comma-separated pair consisting of `'Marker'` and a cell array of strings.

For example, if you have two between-subject factors, drug and sex, with each having two groups, you can specify `o` as the marker for the groups of drug and `x` as the marker for the groups of sex as follows.

Example: `'Marker',{'o','o','x','x'}`

Data Types: `cell`

`'Color'` — Color for each group

string | cell array of strings | rows of a three-column RGB matrix

Color for each group, specified as the comma-separated pair consisting of `'Color'` and a string, cell array of strings, or rows of a three-column RGB matrix.

For example, if you have two between-subject factors, drug and sex, with each having two groups, you can specify red as the color for the groups of drug and blue as the color for the groups of sex as follows.

Example: `'Color','rrbb'`

Data Types: `single | double | cell`

`'LineStyle'` — Line style for each group

cell array of strings

Line style for each group, specified as the comma-separated pair consisting of `'LineStyle'` and a cell array of strings.

For example, if you have two between-subject factors, drug and sex, with each having two groups, you can specify `-` as the line style of one group and `:` as the line style for the other group as follows.

Example: `'LineStyle',{'-' ':' '-' ':'}`

Data Types: `cell`

Output Arguments

`H` — Handle to plotted lines

handle

Handle to plotted lines, returned as a handle.

Examples

Plot Expected Marginal Means

Load the sample data.

```
load fisheriris
```

The column vector `species`consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

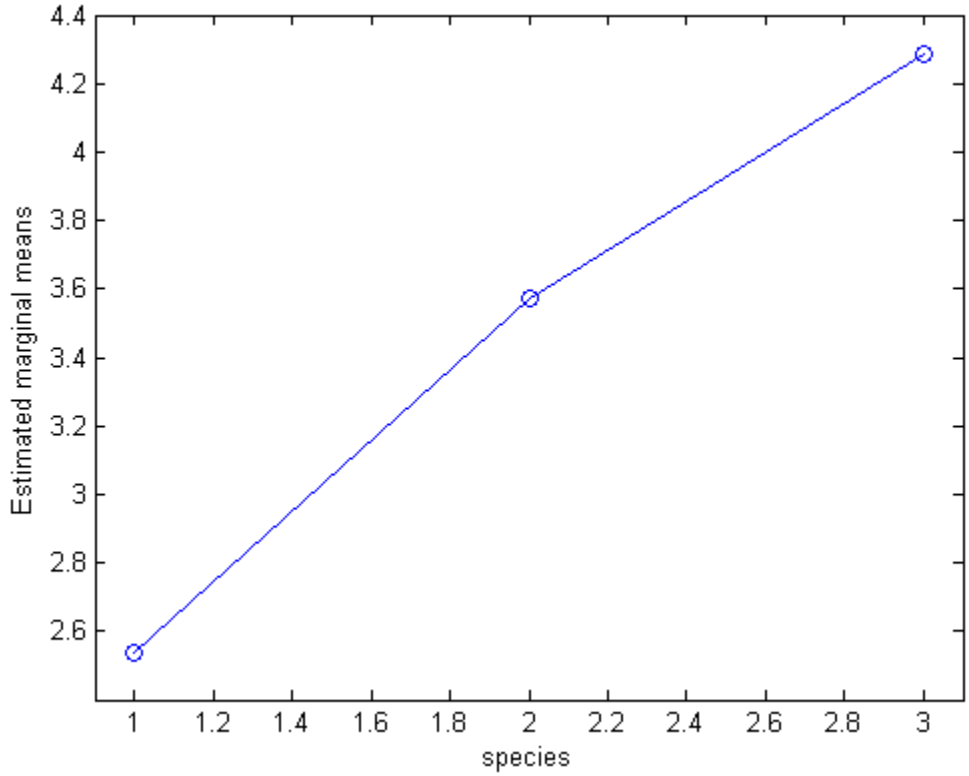
```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform data grouped by the factor species.

```
plotprofile(rm,'species')
```



The estimated marginal means seem to differ with group. You can compute the standard error and the 95% confidence intervals for the marginal means using the `margmean` method.

Plot Marginal Means for Two Groups

Load the sample data.

```
load repeatedmeas
```

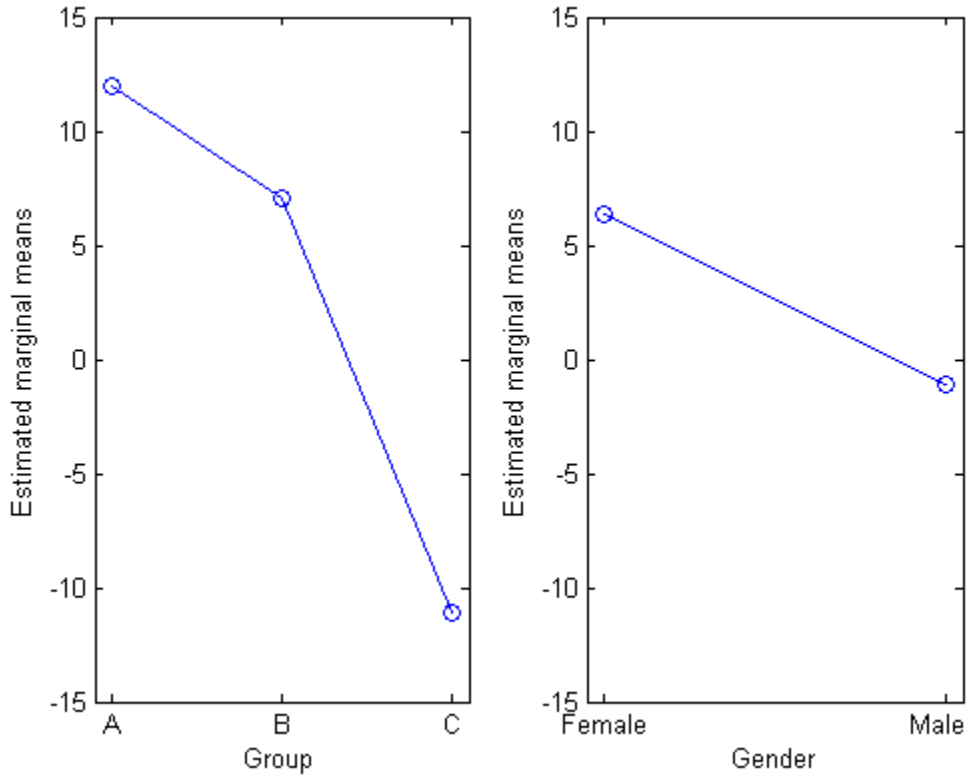
The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ through $y8$ as responses. The table `within` includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ through $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

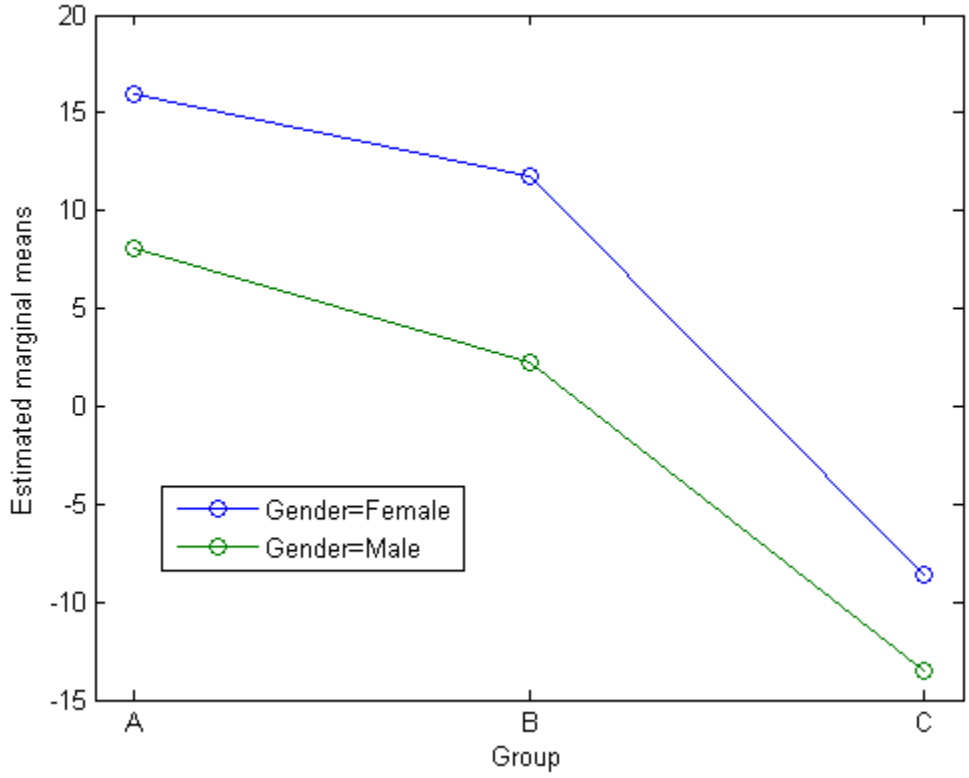
Plot the estimated marginal means based on the factors `Group` and `Gender`.

```
ax1 = subplot(1,2,1);
plotprofile(R,'Group')
ax2 = subplot(1,2,2);
plotprofile(R,'Gender')
linkaxes([ax1 ax2],'y')
```



Plot the estimated marginal means based on the factor `Group` and grouped by `Gender`.

```
figure()
plotprofile(R,'Group','Group','Gender')
```



See Also

`fitrm` | `margmean` | `plot`

plotResiduals

Class: GeneralizedLinearModel

Plot residuals of generalized linear regression model

Syntax

```
plotResiduals(mdl)
plotResiduals(mdl,plottype)
h = plotResiduals(...)
h = plotResiduals(mdl,plottype,Name,Value)
```

Description

`plotResiduals(mdl)` gives a histogram plot of the residuals of the `mdl` nonlinear model.

`plotResiduals(mdl,plottype)` plots residuals in a plot of type `plottype`.

`h = plotResiduals(...)` returns handles to the lines in the plot.

`h = plotResiduals(mdl,plottype,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`plottype`

String specifying the type of plot:

`'caseorder'`	Residuals vs. case (row) order
`'fitted'`	Residuals vs. fitted values
`'histogram'`	Histogram
`'lagged'`	Residuals vs. lagged residual ($r(t)$ vs. $r(t–1)$)
`'probability'`	Normal probability plot
`'symmetry'`	Symmetry plot

Default: `'histogram'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerFaceColor'`

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerSize'`

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

`'ResidualType'`

String giving type of residual used in the plot.

`'Raw'`	Observed minus fitted values
`'LinearPredictor'`	Residuals on the linear predictor scale, equal to the adjusted response value minus the fitted linear combination of the predictors
`'Pearson'`	Raw residuals divided by RMSE
`'Anscombe'`	Residuals defined on transformed data with the transformation chosen to remove skewness
`'Deviance'`	Residuals based on the contribution of each observation to the deviance

Default: `'Raw'`

Output Arguments

`h`

Vector of handles to lines or patches in the plot.

Definitions

Deviance

Deviance is twice the log likelihood of the model. Because this overall log likelihood is a sum of log likelihoods for each observation, the residual plot of deviance type shows the log likelihood per observation.

Examples

Residual Plots for Generalized Linear Models

Create residual plots of a fitted generalized linear model.

Generate artificial data for the model, Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

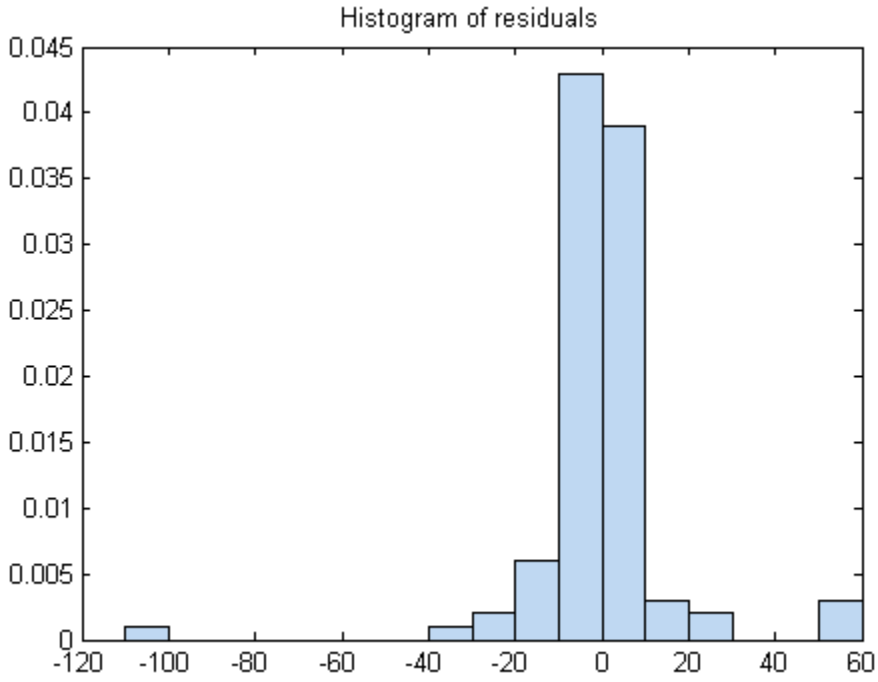
```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data.

```
mdl = fitglm(X,y,'y ~ x1 + x2','distr','poisson');
```

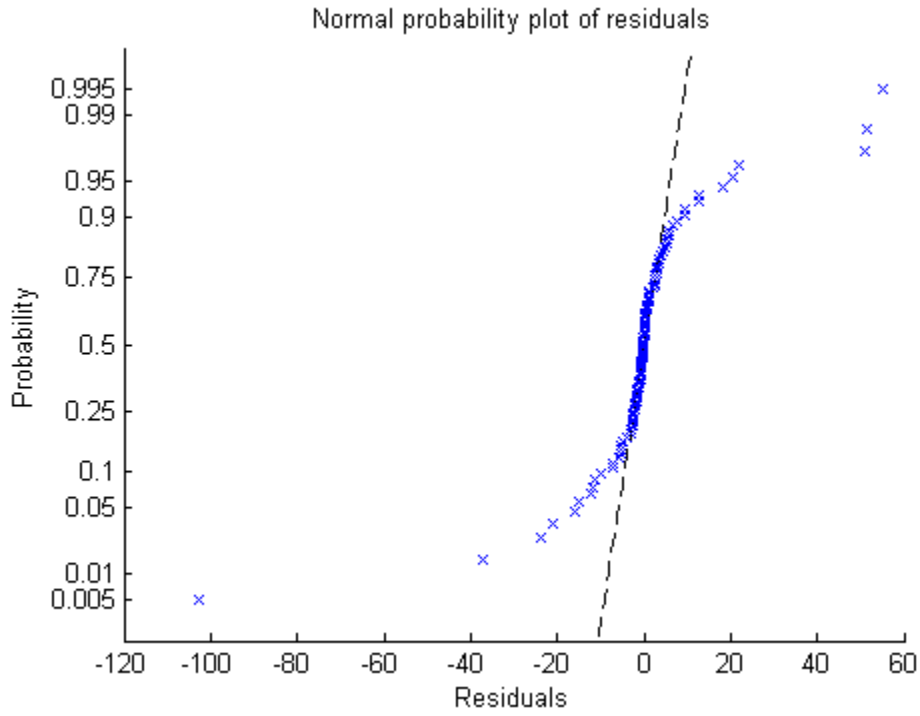
Create a default residuals plot.

```
plotResiduals(mdl)
```



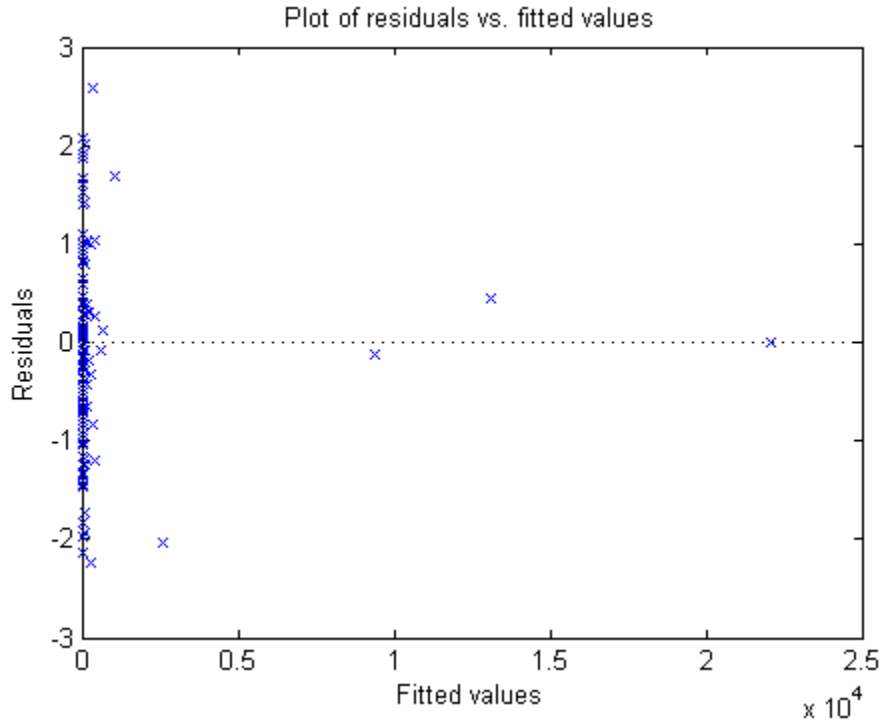
Create a probability plot.

```
plotResiduals(mdl,'probability')
```



The residuals do not match a normal distribution in the tails—they are more spread out.

Create a plot of the fitted residuals of Anscombe type.



- "Residuals — Model Quality for Training Data" on page 10-27

See Also

`GeneralizedLinearModel`

More About

- "Generalized Linear Models" on page 10-12

plotResiduals

Class: GeneralizedLinearMixedModel

Plot residuals of generalized linear mixed-effects model

Syntax

```
plotResiduals(glme,plottype)
plotResiduals(glme,plottype,Name,Value)

h = plotResiduals( ___ )
```

Description

`plotResiduals(glme,plottype)` plots the raw conditional residuals of the generalized linear mixed-effects model glme in a plot of the type specified by plottype.

`plotResiduals(glme,plottype,Name,Value)` plots the conditional residuals of glme using additional options specified by one or more `Name,Value` pair arguments. For example, you can specify to plot the Pearson residuals.

`h = plotResiduals( ___ )` returns a handle, h, to the lines or patches in the plot of residuals.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

`plottype` — Type of residual plot

`'histogram'` (default) | `'caseorder'` | `'fitted'` | `'lagged'` | `'probability'` | `'symmetry'`

Type of residual plot, specified as one of the following strings.

`'histogram'`	Histogram of residuals
`'caseorder'`	Residuals versus case order. Case order is the same as the row order used in the input data `tbl` when fitting the model using `fitglme`.
`'fitted'`	Residuals versus fitted values
`'lagged'`	Residuals versus lagged residual ($r(t)$ versus $r(t-1)$)
`'probability'`	Normal probability plot
`'symmetry'`	Symmetry plot

Example: `plotResiduals(glme,'lagged')`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'ResidualType'` — Residual type

`'raw'` (default) | `'Pearson'`

Residual type, specified by the comma-separated pair consisting of `ResidualType` and one of the following.

Residual Type	Formula
`'raw'`	$r_{ci} = y_i - g^{-1}\left(x_i^T\hat{\beta} + z_i^T\hat{b} + \delta_i\right)$
`'Pearson'`	$r_{ci}^{pearson} = \dfrac{r_{ci}}{\sqrt{\dfrac{\widehat{\sigma^2}}{w_i}v_i\left(\mu_i\left(\hat{\beta},\hat{b}\right)\right)}}$

In each of these equations:

- y_i is the ith element of the n-by-1 response vector, y, where $i = 1, ..., n$.
- g^{-1} is the inverse link function for the model.
- x_i^T is the ith row of the fixed-effects design matrix X.
- z_i^T is the ith row of the random-effects design matrix Z.
- δ_i is the ith offset value.
- σ^2 is the dispersion parameter.
- w_i is the ith observation weight.
- v_i is the variance term for the ith observation.
- μ_i is the mean of the response for the ith observation.
- $\hat{\beta}$ and $\hat{b}$ are estimated values of β and b.

Raw residuals from a generalized linear mixed-effects model have nonconstant variance. Pearson residuals are expected to have an approximately constant variance, and are generally used for analysis.

Example: `'ResidualType','Pearson'`

Output Arguments

h — Handle to residual plot

graphics object

Handle to the residual plot, returned as a graphics object. You can use dot notation to change certain property values of the object, including face color for a histogram, and marker style and color for a scatterplot. For more information, see “Access Property Values”.

Examples

Create Plots of Residuals

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

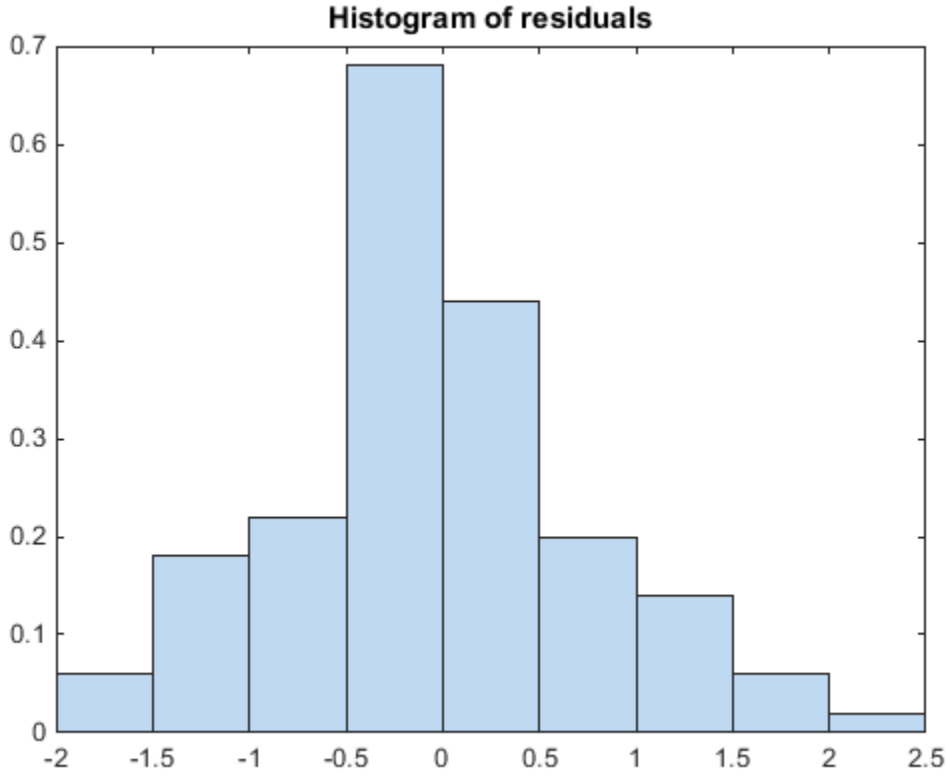
- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Create diagnostic plots using Pearson residuals to test the model assumptions.

Plot a histogram to visually confirm that the mean of the Pearson residuals is equal to 0. If the model is correct, we expect the Pearson residuals to be centered at 0.

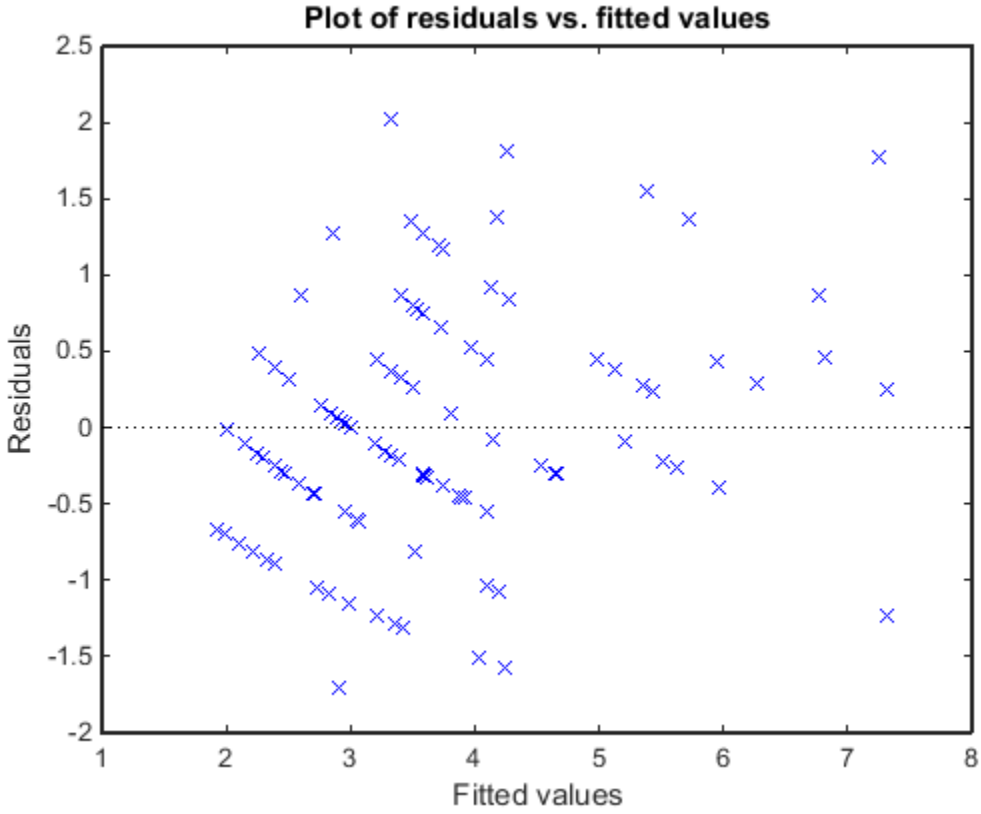
```
plotResiduals(glme,'histogram','ResidualType','Pearson')
```



The histogram shows that the Pearson residuals are centered at 0.

Plot the Pearson residuals versus the fitted values, to check for signs of nonconstant variance among the residuals (heteroscedasticity). We expect the conditional Pearson residuals to have a constant variance. Therefore, a plot of conditional Pearson residuals versus conditional fitted values should not reveal any systematic dependence on the conditional fitted values.

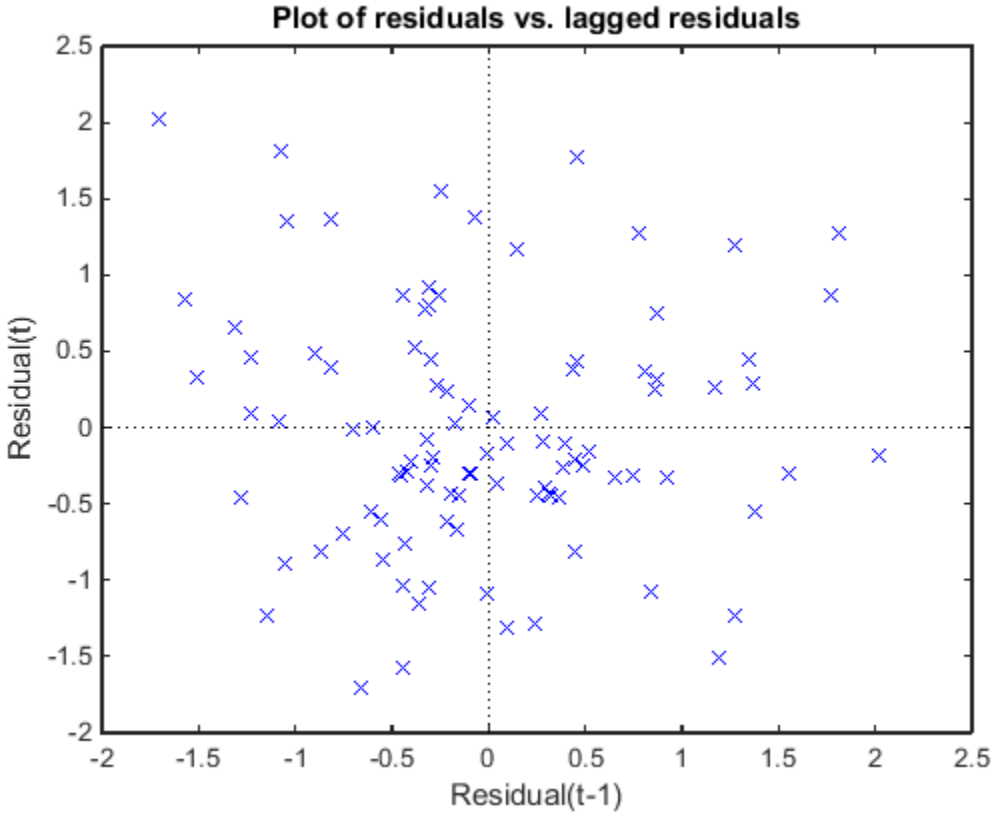
```
plotResiduals(glme,'fitted','ResidualType','Pearson')
```



The plot does not show a systematic dependence on the fitted values, so there are no signs of nonconstant variance among the residuals.

Plot the Pearson residuals versus lagged residuals, to check for correlation among the residuals. The conditional independence assumption in GLME implies that the conditional Pearson residuals are approximately uncorrelated.

```
plotResiduals(glme,'lagged','ResidualType','Pearson')
```



There is no pattern to the plot, so there are no signs of correlation among the residuals.

See Also

`GeneralizedLinearMixedModel` | `fitglme` | `fitted` | `plot` | `residuals`

plotResiduals

Class: LinearModel

Plot residuals of linear regression model

Syntax

```
plotResiduals(mdl)
plotResiduals(mdl,plottype)
h = plotResiduals(...)
h = plotResiduals(mdl,plottype,Name,Value)
```

Description

`plotResiduals(mdl)` gives a histogram plot of the residuals of the `mdl` linear model.

`plotResiduals(mdl,plottype)` plots residuals in a plot of type `plottype`.

`h = plotResiduals(...)` returns handles to the lines in the plot.

`h = plotResiduals(mdl,plottype,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`plottype`

String specifying the type of plot:

`'caseorder'`	Residuals vs. case (row) order
`'fitted'`	Residuals vs. fitted values
`'histogram'`	Histogram
`'lagged'`	Residuals vs. lagged residual ($r(t)$ vs. $r(t–1)$)
`'probability'`	Normal probability plot
`'symmetry'`	Symmetry plot

Default: `'histogram'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerFaceColor'`

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerSize'`

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

`'ResidualType'`

Type of residual used in the plot:

`'Raw'`	Observed minus fitted values
`'Pearson'`	Raw residuals divided by RMSE
`'Standardized'`	Raw residuals divided by their estimated standard deviation
`'Studentized'`	Raw residuals divided by an independent (delete-1) estimate of their standard deviation

Default: `'Raw'`

Output Arguments

`h`

Vector of handles to lines or patches in the plot.

Examples

Linear Residuals Plot

Plot the residuals of a fitted linear model.

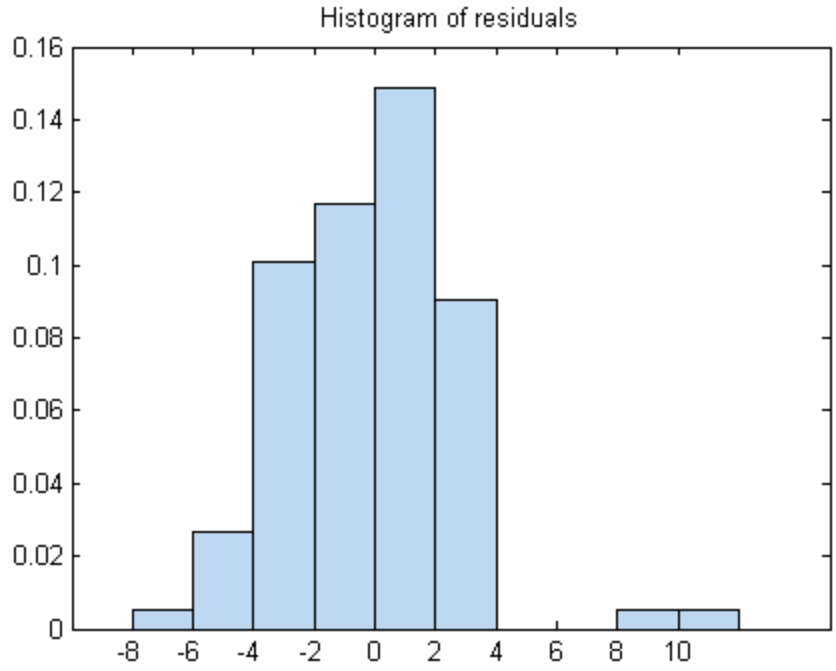
Load the `carsmall` data and fit a linear model of the mileage as a function of model year, weight, and weight squared.

```
load carsmall
```

```
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
mdl = fitlm(tbl,'MPG ~ Year + Weight^2');
```

Plot the raw residuals.

```
plotResiduals(mdl)
```



Residual Probability Plot

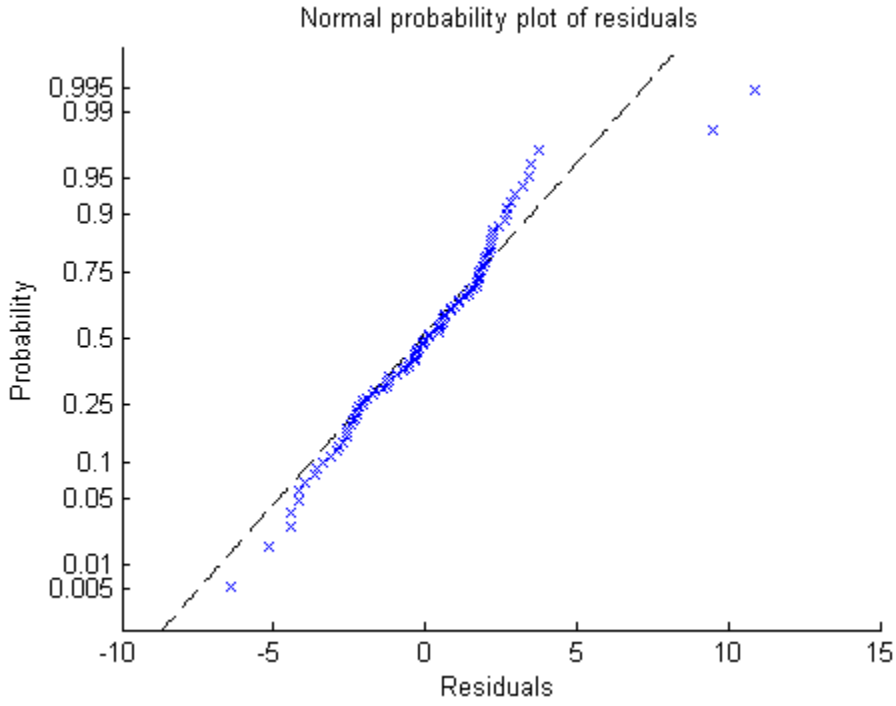
Create a normal probability plot of the residuals of a fitted linear model.

Load the `carsmall` data and fit a linear model of the mileage as a function of model year, weight, and weight squared.

```
load carsmall
X = [Weight,Model_Year];
mdl = fitlm(X,MPG,...
    'y ~ x2 + x1^2','Categorical',2);
```

Create a normal probability plot of the residuals of the fitted model.

```
plotResiduals(mdl,'probability')
```



- "Residuals — Model Quality for Training Data" on page 9-23
- "Linear Regression Workflow" on page 9-41
- "Compare large and small stepwise models" on page 9-124
- "Robust Regression versus Standard Least-Squares Fit" on page 9-128

Alternatives

The `mdl.Residuals` table contains the information in residual plots.

See Also

`LinearModel` | `plotDiagnostics`

How To

- “Linear Regression” on page 9-11

plotResiduals

Class: LinearMixedModel

Plot residuals of linear mixed-effects model

Syntax

```
plotResiduals(lme,plottype)
plotResiduals(lme,plottype,Name,Value)

h = plotResiduals( ___ )
```

Description

`plotResiduals(lme,plottype)` plots the raw conditional residuals of the linear mixed-effects model `lme` in a plot of the type specified by `plottype`.

`plotResiduals(lme,plottype,Name,Value)` also plots the residuals of the linear mixed-effects model `lme` with additional options specified by one or more name-value pair arguments. For example, you can specify the residual type to plot.

`plotResiduals` also accepts some other name-value pair arguments that specify the properties of the primary line in the plot. For those name-value pairs, see `plot`.

`h = plotResiduals( ___ )` returns a handle, `h`, to the lines or patches in the plot of residuals.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

`plottype` — Type of residual plot

`'histogram'` (default) | `'caseorder'` | `'fitted'` | `'lagged'` | `'probability'` | `'symmetry'`

Type of residual plot, specified as one of the following strings.

`'histogram'`	Default. Histogram of residuals
`'caseorder'`	Residuals versus case (row) order
`'fitted'`	Residuals versus fitted values
`'lagged'`	Residuals versus lagged residual ($r(t)$ versus $r(t-1)$)
`'probability'`	Normal probability plot
`'symmetry'`	Symmetry plot

Example: `plotResiduals(lme,'lagged')`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'ResidualType'` — Residual type

`'Raw'` (default) | `'Pearson'` | `'Standardized'`

Residual type, specified by the comma-separated pair consisting of `ResidualType` and one of the following.

Residual Type	Conditional	Marginal
`'Raw'`	$r_i^C = \left[y - X\hat{\beta} - Z\hat{b} \right]_i$	$r_i^M = \left[y - X\hat{\beta} \right]_i$
`'Pearson'`	$pr_i^C = \frac{r_i^C}{\sqrt{\left[\widehat{Var}_{y,b}\left(y - X\beta\right.\right.}}$	$pr_i^M = \frac{r_i^M}{\sqrt{\left[\widehat{Var}_y\left(y - X\beta\right) \right]_{ii}}}$

Residual Type	Conditional	Marginal
`'Standardized'`	$st_i^C = \frac{r_i^C}{\sqrt{\left[\widehat{Var}_y\left(r^C\right)\right]_{ii}}}$	$st_i^M = \frac{r_i^M}{\sqrt{\left[\widehat{Var}_y\left(r^M\right)\right]_{ii}}}$

For more information on the conditional and marginal residuals and residual variances, see `Definitions` at the end of this page.

Example: `'ResidualType','Standardized'`

Output Arguments

h — Handle to residual plot

handle

Handle to the residual plot, returned as a handle.

Examples

Examine Residuals

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

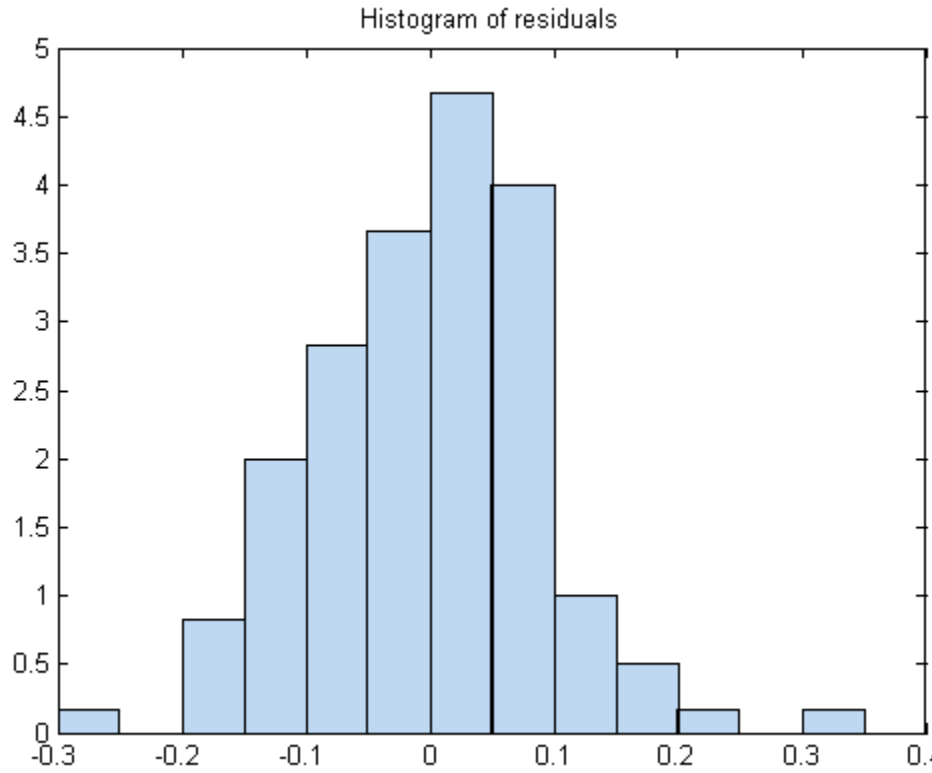
```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)');
```

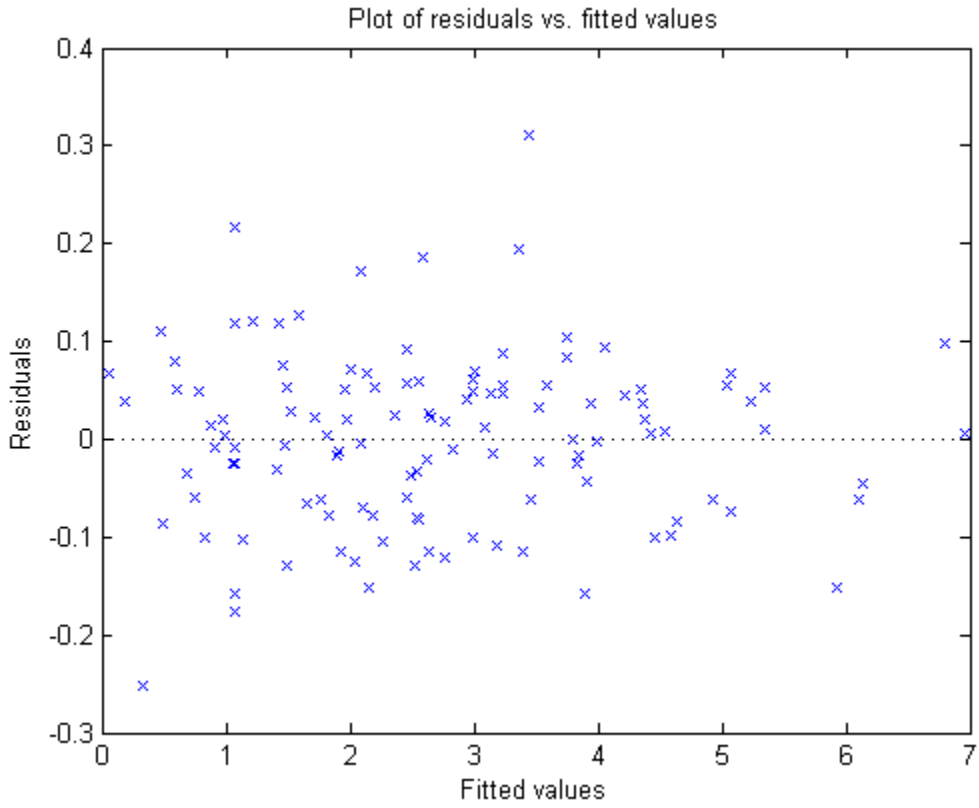
Plot the histogram of the raw residuals.

```
plotResiduals(lme)
```



Plot the residuals versus the fitted values.

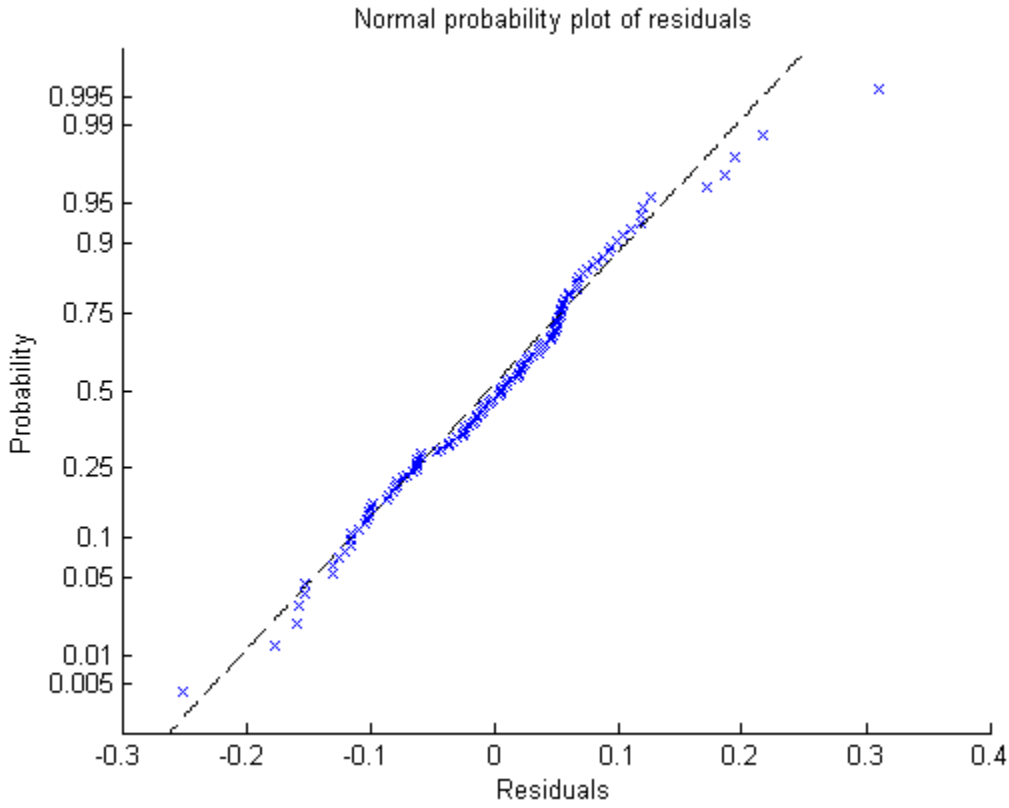
```
figure();
plotResiduals(lme,'fitted')
```



There is no obvious pattern, so there are no immediate signs of heteroscedasticity.

Create the normal probability plot of residuals.

```
figure();
plotResiduals(lme,'probability')
```



Data appears to be normal.

Find the observation number for the data that appears to be an outlier to the right of the plot.

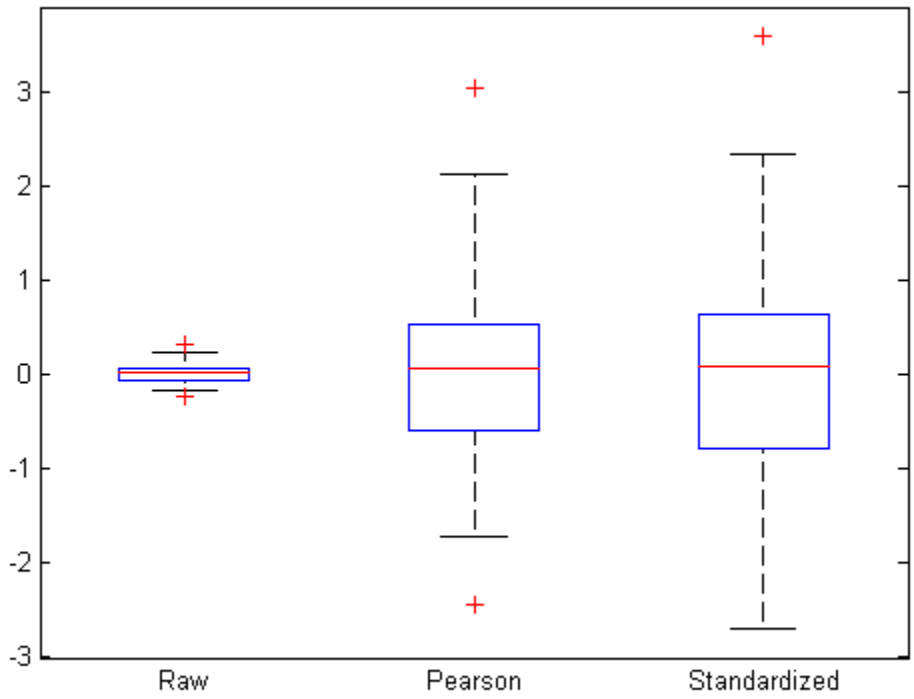
```
find(residuals(lme)>0.25)
```

```
ans =

   101
```

Create a box plot of the raw, Pearson, and standardized residuals.

```
r = residuals(lme);
```

```
pr = residuals(lme,'ResidualType','Pearson');
st = residuals(lme,'ResidualType','Standardized');
X = [r pr st];
boxplot(X,'labels',{'Raw','Pearson','Standardized'});
```



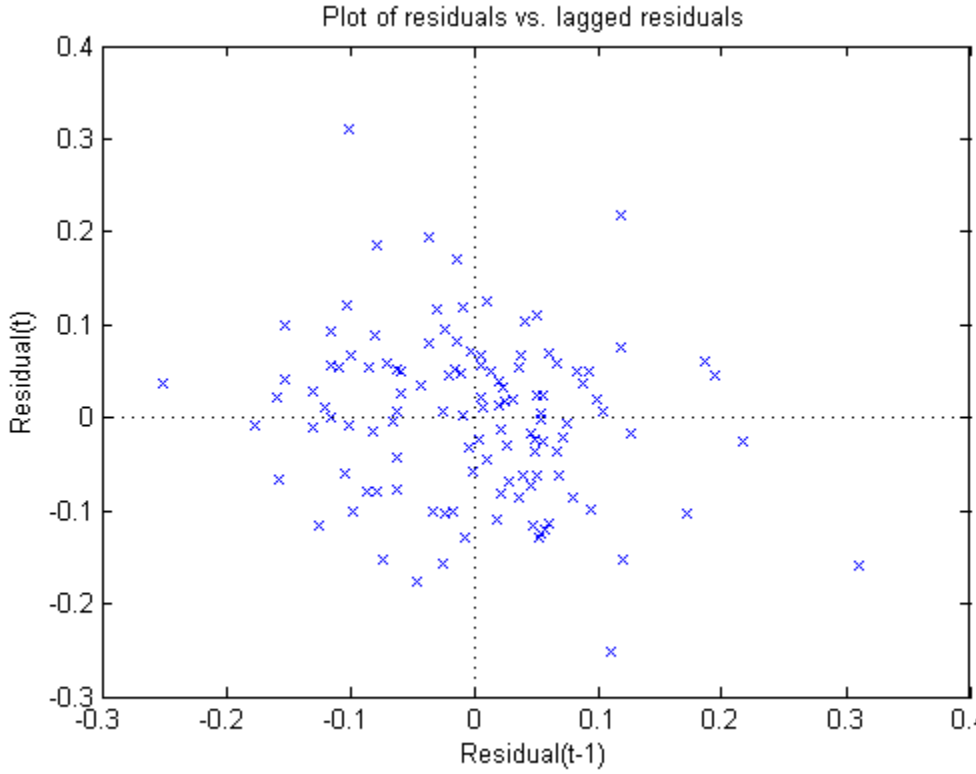
All three box plots point out the outlier on the right tail of the distribution. The box plots of raw and Pearson residuals also point out a second possible outlier on the left tail. Find the corresponding observation number.

```
find(pr<-2)
```

```
ans =

    10
```

Plot the raw residuals versus lagged residuals.

```
plotResiduals(lme,'lagged')
```



There is no obvious pattern in the graph. The residuals do not appear to be correlated.

See Also

`fitted` | `LinearMixedModel` | `residuals`

plotResiduals

Class: NonLinearModel

Plot residuals of nonlinear regression model

Syntax

```
plotResiduals(mdl)
plotResiduals(mdl,plottype)
h = plotResiduals(...)
h = plotResiduals(mdl,plottype,Name,Value)
```

Description

`plotResiduals(mdl)` gives a histogram plot of the residuals of the `mdl` nonlinear model.

`plotResiduals(mdl,plottype)` plots residuals in a plot of type `plottype`.

`h = plotResiduals(...)` returns handles to the lines in the plot.

`h = plotResiduals(mdl,plottype,Name,Value)` plots with additional options specified by one or more Name,Value pair arguments.

Tips

- For many plots, the Data Cursor tool in the figure window displays the *x* and *y* values for any data point, along with the observation name or number.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

`plottype`

String specifying the type of plot:

`'caseorder'`	Residuals vs. case (row) order
`'fitted'`	Residuals vs. fitted values
`'histogram'`	Histogram
`'lagged'`	Residuals vs. lagged residual ($r(t)$ vs. $r(t-1)$)
`'probability'`	Normal probability plot
`'symmetry'`	Symmetry plot

Default: `'histogram'`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Note: The plot property name-value pairs apply to the first returned handle `h(1)`.

`'Color'`

Color of the line or marker, a string or `ColorSpec` specification. For details, see `linespec`.

`'LineStyle'`

Type of line, a string or Chart Line Properties specification. For details, see `linespec`.

`'LineWidth'`

Width of the line or edges of filled area, in points, a positive scalar. One point is 1/72 inch.

Default: `0.5`

`'MarkerEdgeColor'`

Color of the marker or edge color for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerFaceColor'`

Color of the marker face for filled markers, a string or `ColorSpec` specification. For details, see `linespec`.

`'MarkerSize'`

Size of the marker in points, a strictly positive scalar. One point is 1/72 inch.

`'ResidualType'`

Type of residual used in the plot:

`'Raw'`	Observed minus fitted values
`'Pearson'`	Raw residuals divided by RMSE
`'Standardized'`	Raw residuals divided by their estimated standard deviation
`'Studentized'`	Raw residuals divided by an independent (delete-1) estimate of their standard deviation

Default: `'Raw'`

Output Arguments

`h`

Vector of handles to lines or patches in the plot.

Examples

Residual Plot

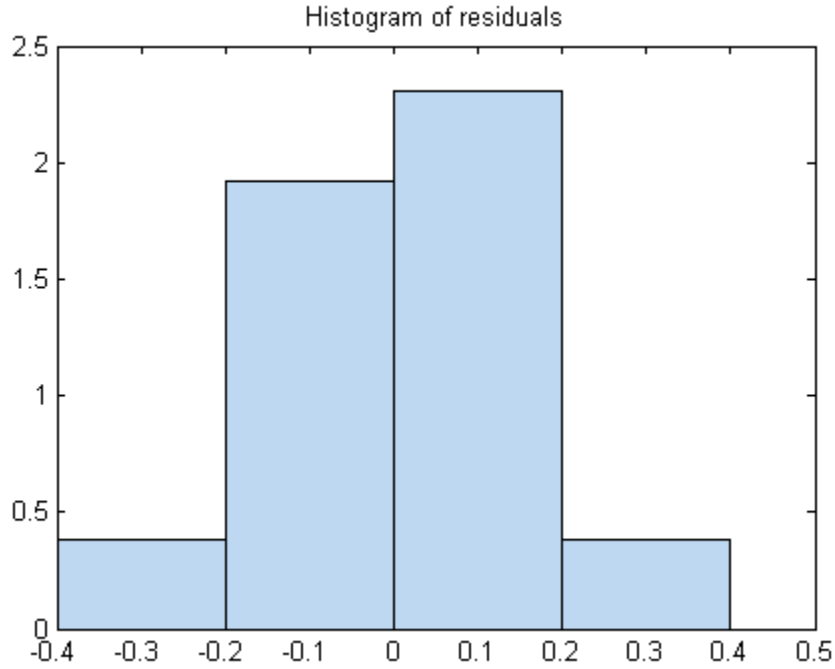
Plot the residuals of a fitted nonlinear model.

Load the `reaction` data and fit a model of the reaction rate as a function of reactants.

```
load reaction
mdl = fitnlm(reactants,rate,@hougen,[1 .05 .02 .1 2]);
```

Plot the residuals of the fitted model.

```
plotResiduals(mdl)
```



Residual Probability Plot

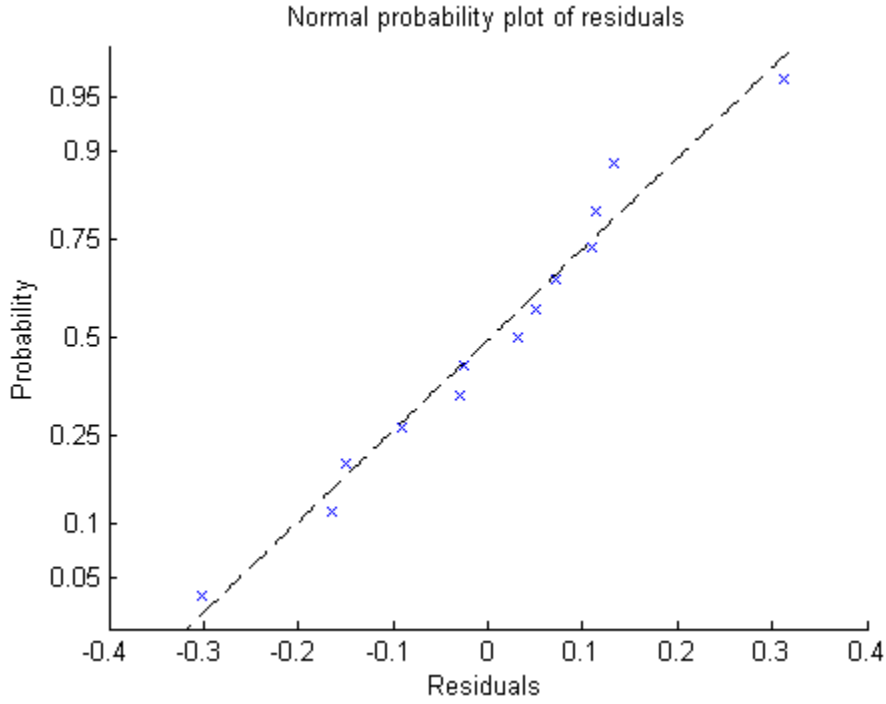
Create a normal probability plot of the residuals of a fitted nonlinear model.

Load the `reaction` data and fit a model of the reaction rate as a function of reactants.

```
load reaction
mdl = fitnlm(reactants,rate,@hougen,[1 .05 .02 .1 2]);
```

Create a normal probability plot of the residuals of the fitted model.

```
plotResiduals(mdl,'probability')
```



- "Examine Quality and Adjust the Fitted Nonlinear Model" on page 11-7
- "Nonlinear Regression Workflow" on page 11-14

See Also

`NonLinearModel` | `plotDiagnostics`

More About

- "Nonlinear Regression" on page 11-2

plotSlice

Class: GeneralizedLinearModel

Plot of slices through fitted generalized linear regression surface

Syntax

```
plotSlice(mdl)
h = plotSlice(mdl)
```

Description

`plotSlice(mdl)` creates a new figure containing a series of plots, each representing a slice through the regression surface predicted by `mdl`. For each plot, the surface slice is shown as a function of a single predictor variable, with the other predictor variables held constant.

`h = plotSlice(mdl)` returns handles to the lines in the plot.

Tips

- If there are more than eight predictors, `plotSlice` selects the first five for plotting. Use the **Predictors** menu to control which predictors are plotted.
- The **Bounds** menu lets you choose between simultaneous or non-simultaneous bounds, and between bounds on the function or bounds on a new observation.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

Output Arguments

h

Vector of handles to lines or patches in the plot.

Examples

Slice Plot of Generalized Linear Regression Model

Create a slice plot of a Poisson generalized linear model.

Generate artificial data for the model using Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

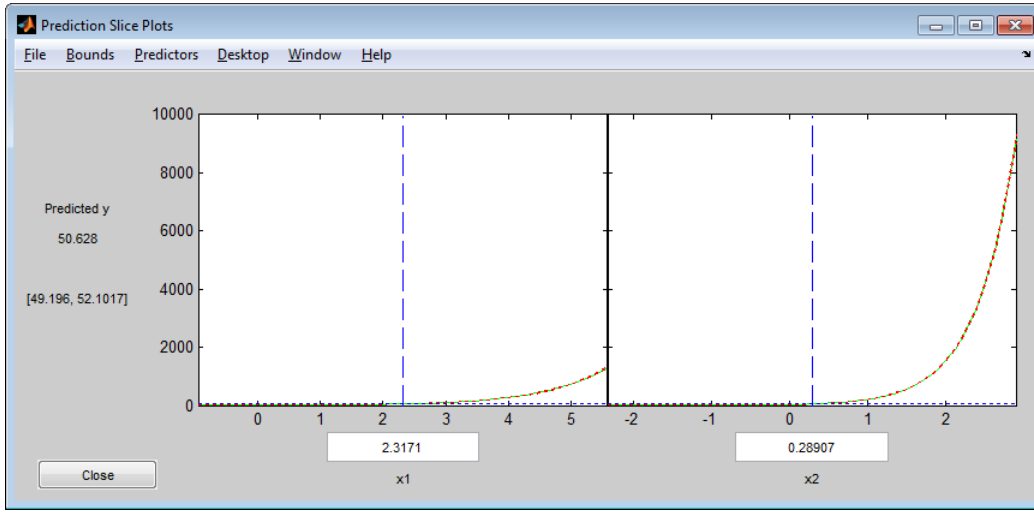
```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data.

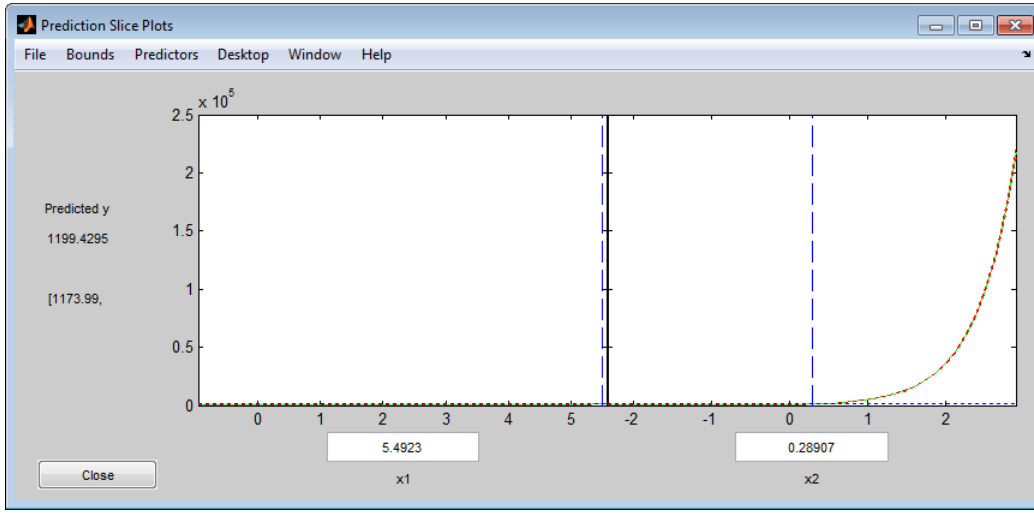
```
mdl = fitglm(X,y,'y ~ x1 + x2','distr','poisson');
```

Create the slice plot.

```
plotSlice(mdl)
```



Drag the `x1` prediction line to the right and view the changes in the prediction and the response curve for the `x2` predictor.



- "Diagnostic Plots" on page 10-25
- "Plots to Understand Predictor Effects and How to Modify a Model" on page 10-30

See Also

`GeneralizedLinearModel` | `predict`

More About

- “Generalized Linear Models” on page 10-12

plotSlice

Class: LinearModel

Plot of slices through fitted linear regression surface

Syntax

```
plotSlice(mdl)
h = plotSlice(mdl)
```

Description

`plotSlice(mdl)` creates a new figure containing a series of plots, each representing a slice through the regression surface predicted by `mdl`. For each plot, the surface slice is shown as a function of a single predictor variable, with the other predictor variables held constant.

`h = plotSlice(mdl)` returns handles to the lines in the plot.

Tips

- If there are more than eight predictors, `plotSlice` selects the first five for plotting. Use the **Predictors** menu to control which predictors are plotted.
- The **Bounds** menu lets you choose between simultaneous or non-simultaneous bounds, and between bounds on the function or bounds on a new observation.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

Output Arguments

h

Vector of handles to lines or patches in the plot.

Examples

Slice Plot

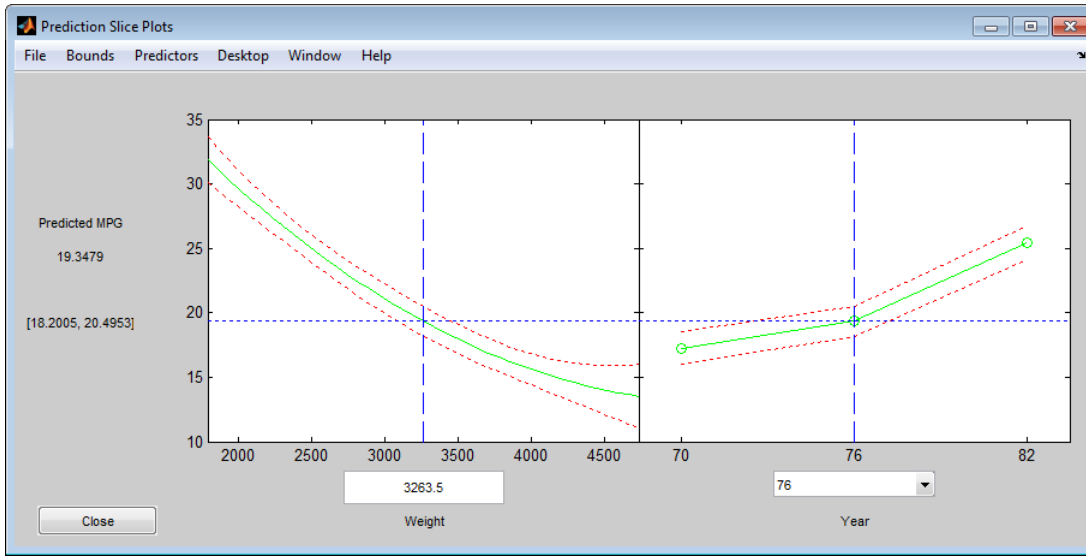
Plot the slices through a fitted linear model.

Load the `carsmall` data and fit a linear model of the mileage as a function of model year, weight, and weight squared.

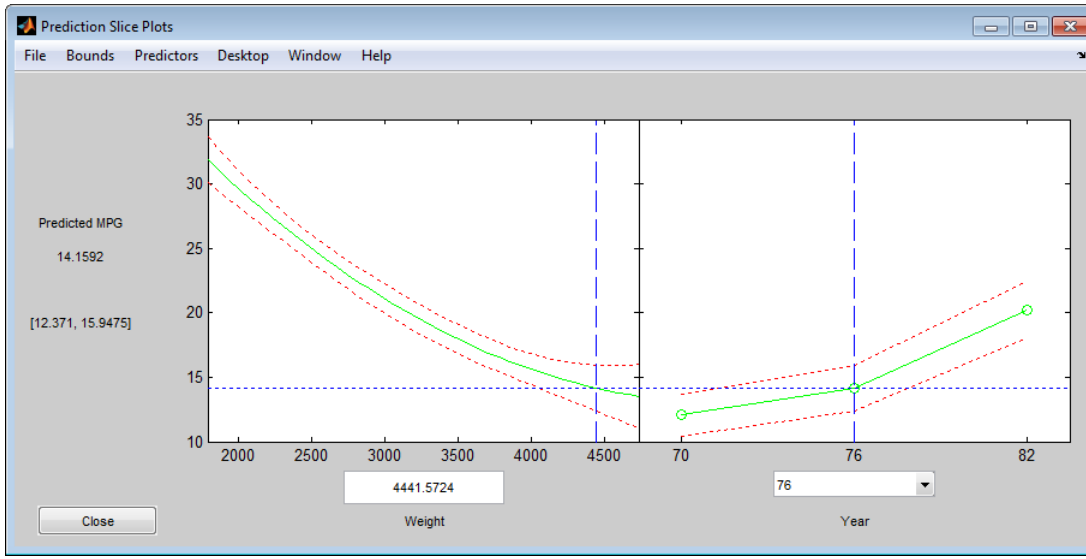
```
load carsmall
tbl = table(MPG,Weight);
tbl.Year = ordinal(Model_Year);
mdl = fitlm(tbl,'MPG ~ Year + Weight^2');
```

Create a slice plot.

```
plotSlice(mdl)
```



Drag the `Weight` prediction line to the right and observe the change in the predicted `MPG` and the response curve for `Year`.



- "Plots to Understand Predictor Effects" on page 9-28

See Also

`predict` | `LinearModel`

How To

- "Linear Regression" on page 9-11

plotSlice

Class: NonLinearModel

Plot of slices through fitted nonlinear regression surface

Syntax

```
plotSlice(mdl)
h = plotSlice(mdl)
```

Description

`plotSlice(mdl)` creates a new figure containing a series of plots, each representing a slice through the regression surface predicted by `mdl`. For each plot, the surface slice is shown as a function of a single predictor variable, with the other predictor variables held constant.

`h = plotSlice(mdl)` returns handles to the lines in the plot.

Tips

- If there are more than eight predictors, `plotSlice` selects the first five for plotting. Use the **Predictors** menu to control which predictors are plotted.
- The **Bounds** menu lets you choose between simultaneous or non-simultaneous bounds, and between bounds on the function or bounds on a new observation.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

Output Arguments

h

Vector of handles to lines or patches in the plot.

Examples

Slice Plot

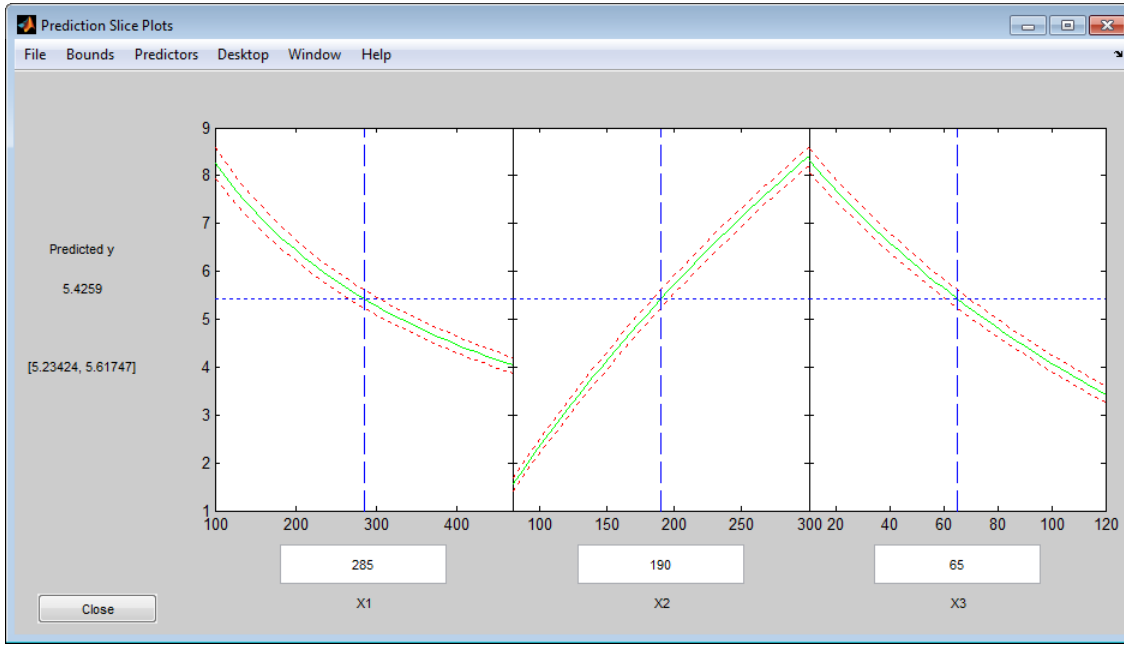
Plot slices of a fitted nonlinear model.

Load the `reaction` data and fit a model of the reaction rate as a function of reactants.

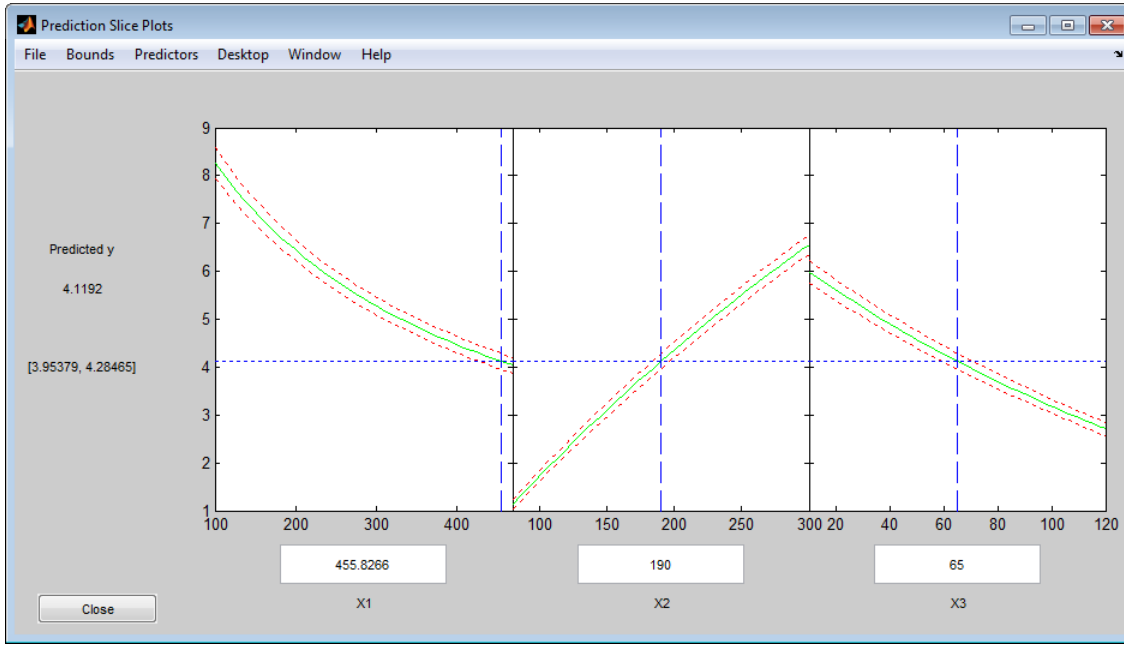
```
load reaction
mdl = fitnlm(reactants,...
    rate,@hougen,[1 .05 .02 .1 2]);
```

Create a slice plot

```
plotSlice(mdl)
```



Drag the `X1` prediction line to the right, and observe the change in the predicted response `y` and in the predicted response curves to `X2` and `X3`.



- "Examine Quality and Adjust the Fitted Nonlinear Model" on page 11-7
- "Predict or Simulate Responses Using a Nonlinear Model" on page 11-10
- "Nonlinear Regression Workflow" on page 11-14

See Also

`NonLinearModel | predict`

More About

- "Nonlinear Regression" on page 11-2

plsregress

Partial least-squares regression

Syntax

```
[XL,YL] = plsregress(X,Y,ncomp)
[XL,YL,XS] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS,BETA] = PLSREGRESS(X,Y,ncomp,...)
[XL,YL,XS,YS,BETA,PCTVAR] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS,BETA,PCTVAR,MSE] = plsregress(X,Y,ncomp)
[XL,YL,XS,YS,BETA,PCTVAR,MSE] =
plsregress(...,param1,val1,param2,val2,...)
[XL,YL,XS,YS,BETA,PCTVAR,MSE,stats] = PLSREGRESS(X,Y,ncomp,...)
```

Description

`[XL,YL] = plsregress(X,Y,ncomp)` computes a partial least-squares (PLS) regression of `Y` on `X`, using `ncomp` PLS components, and returns the predictor and response loadings in `XL` and `YL`, respectively. `X` is an n-by-p matrix of predictor variables, with rows corresponding to observations and columns to variables. `Y` is an n-by-m response matrix. `XL` is a p-by-`ncomp` matrix of predictor loadings, where each row contains coefficients that define a linear combination of PLS components that approximate the original predictor variables. `YL` is an m-by-`ncomp` matrix of response loadings, where each row contains coefficients that define a linear combination of PLS components that approximate the original response variables.

`[XL,YL,XS] = plsregress(X,Y,ncomp)` returns the predictor scores `XS`, that is, the PLS components that are linear combinations of the variables in `X`. `XS` is an n-by-`ncomp` orthonormal matrix with rows corresponding to observations and columns to components.

`[XL,YL,XS,YS] = plsregress(X,Y,ncomp)` returns the response scores `YS`, that is, the linear combinations of the responses with which the PLS components `XS` have maximum covariance. `YS` is an n-by-`ncomp` matrix with rows corresponding to observations and columns to components. `YS` is neither orthogonal nor normalized.

`plsregress` uses the SIMPLS algorithm, first centering `X` and `Y` by subtracting off column means to get centered variables `X0` and `Y0`. However, it does not rescale the columns. To perform PLS with standardized variables, use `zscore` to normalize `X` and `Y`.

If `ncomp` is omitted, its default value is `min(size(X,1)-1,size(X,2))`.

The relationships between the scores, loadings, and centered variables `X0` and `Y0` are:

`XL = (XS\X0)' = X0'*XS`,

`YL = (XS\Y0)' = Y0'*XS`,

`XL` and `YL` are the coefficients from regressing `X0` and `Y0` on `XS`, and `XS*XL'` and `XS*YL'` are the PLS approximations to `X0` and `Y0`.

`plsregress` initially computes `YS` as:

`YS = Y0*YL = Y0*Y0'*XS`,

By convention, however, `plsregress` then orthogonalizes each column of `YS` with respect to preceding columns of `XS`, so that `XS'*YS` is lower triangular.

`[XL,YL,XS,YS,BETA] = PLSREGRESS(X,Y,ncomp,...)` returns the PLS regression coefficients `BETA`. `BETA` is a (p+1)-by-m matrix, containing intercept terms in the first row:

`Y = [ones(n,1),X]*BETA + Yresiduals`,

`Y0 = X0*BETA(2:end,:) + Yresiduals`. Here `Yresiduals` is the vector of response residuals.

`[XL,YL,XS,YS,BETA,PCTVAR] = plsregress(X,Y,ncomp)` returns a 2-by-`ncomp` matrix `PCTVAR` containing the percentage of variance explained by the model. The first row of `PCTVAR` contains the percentage of variance explained in `X` by each PLS component, and the second row contains the percentage of variance explained in `Y`.

`[XL,YL,XS,YS,BETA,PCTVAR,MSE] = plsregress(X,Y,ncomp)` returns a 2-by-(`ncomp`+1) matrix `MSE` containing estimated mean-squared errors for PLS models with `0:ncomp` components. The first row of `MSE` contains mean-squared errors for the predictor variables in `X`, and the second row contains mean-squared errors for the response variable(s) in `Y`.

`[XL,YL,XS,YS,BETA,PCTVAR,MSE] = plsregress(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs from the following table to control the calculation of `MSE`.

Parameter	Value
`'cv'`	The method used to compute `MSE`. • When the value is a positive integer `k`, `plsregress` uses `k`-fold cross-validation. • When the value is an object of the `cvpartition` class, other forms of cross-validation can be specified. • When the value is `'resubstitution'`, `plsregress` uses `X` and `Y` both to fit the model and to estimate the mean-squared errors, without cross-validation. The default is `'resubstitution'`.
`'mcreps'`	A positive integer indicating the number of Monte-Carlo repetitions for cross-validation. The default value is `1`. The value must be `1` if the value of `'cv'` is `'resubstitution'`.
`options`	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the `options` structure with `statset`. Option fields: • `UseParallel` — Set to `true` to compute in parallel. Default is `false`. • `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `plsregress` uses the default stream.

`[XL,YL,XS,YS,BETA,PCTVAR,MSE,stats] = PLSREGRESS(X,Y,ncomp,...)` returns a structure `stats` with the following fields:

- `W` — A p-by-`ncomp` matrix of PLS weights so that `XS = XO*W`.
- `T2` — The T^2 statistic for each point in `XS`.
- `Xresiduals` — The predictor residuals, that is, `XO-XS*XL'`.
- `Yresiduals` — The response residuals, that is, `YO-XS*YL'`.

Examples

Perform Partial Least-Squares Regression

Load data on near infrared (NIR) spectral intensities of 60 samples of gasoline at 401 wavelengths, and their octane ratings.

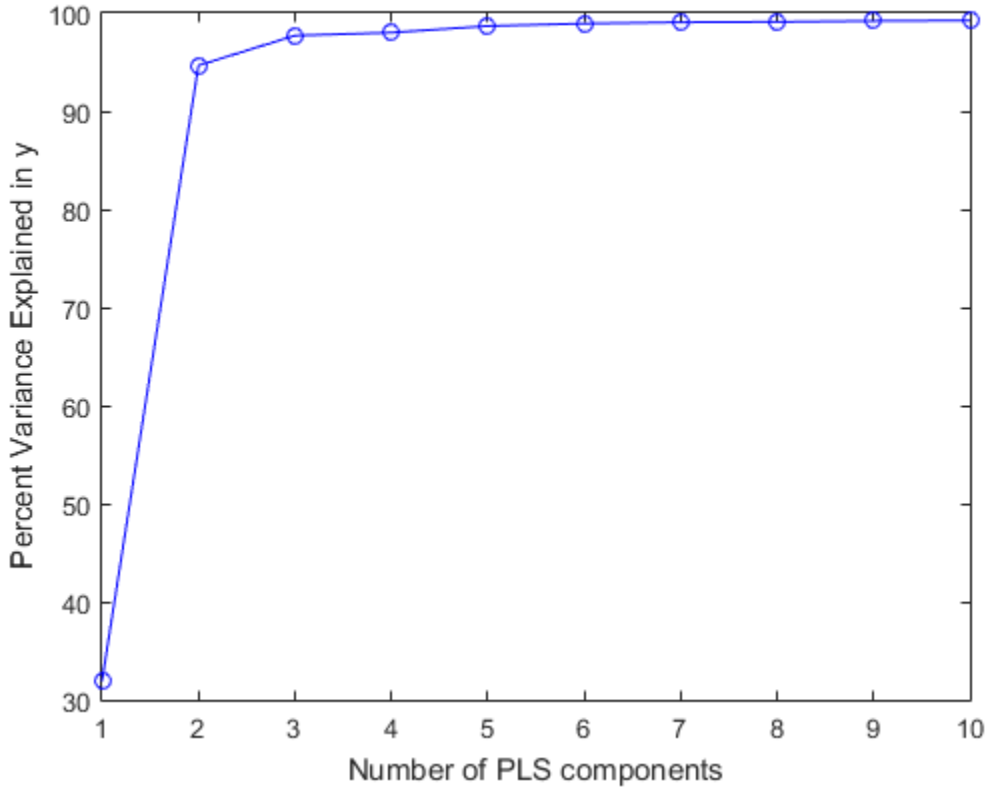
```
load spectra
X = NIR;
y = octane;
```

Perform PLS regression with ten components.

```
[XL,yl,XS,YS,beta,PCTVAR] = plsregress(X,y,10);
```

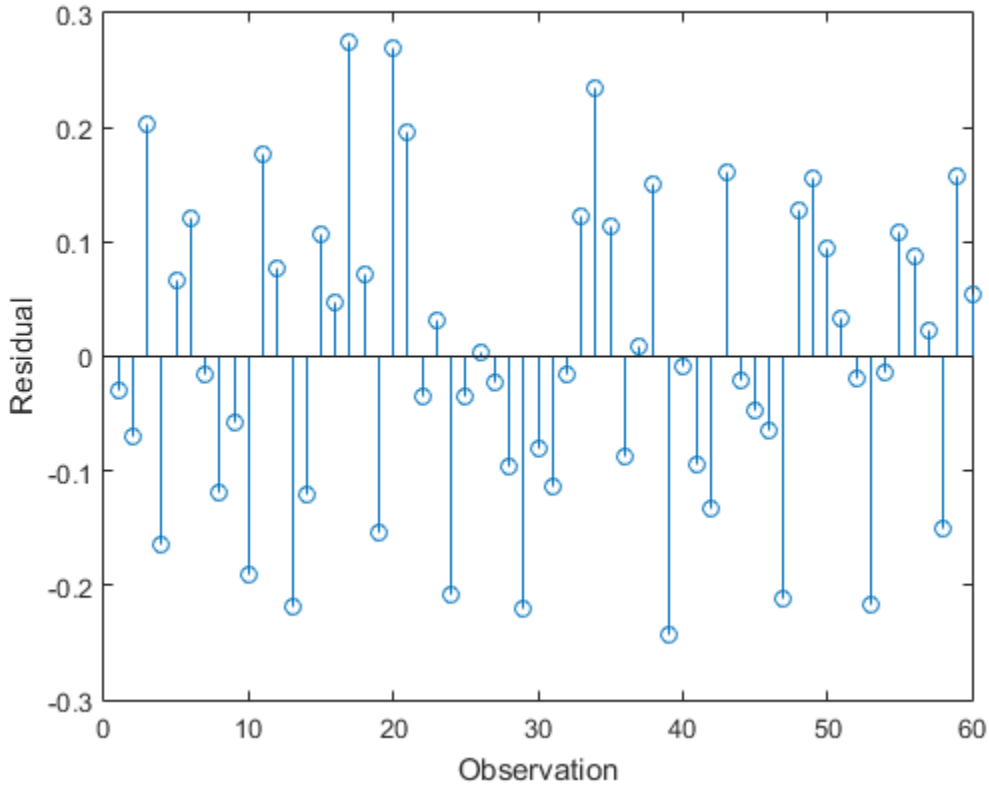
Plot the percent of variance explained in the response variable as a function of the number of components.

```
plot(1:10,cumsum(100*PCTVAR(2,:)),'-bo');
xlabel('Number of PLS components');
ylabel('Percent Variance Explained in y');
```



Compute the fitted response and display the residuals.

```
yfit = [ones(size(X,1),1) X]*beta;
residuals = y - yfit;
stem(residuals)
xlabel('Observation');
ylabel('Residual');
```



References

[1] de Jong, S. "SIMPLS: An Alternative Approach to Partial Least Squares Regression." *Chemometrics and Intelligent Laboratory Systems*. Vol. 18, 1993, pp. 251–263.

[2] Rosipal, R., and N. Kramer. "Overview and Recent Advances in Partial Least Squares." *Subspace, Latent Structure and Feature Selection: Statistical and Optimization Perspectives Workshop (SLSFS 2005), Revised Selected Papers (Lecture Notes in Computer Science 3940)*. Berlin, Germany: Springer-Verlag, 2006, pp. 34–51.

See Also

`regress` | `sequentialfs`

PointOrder property

Class: sobolset

Point generation method

Description

The `PointOrder` property contains a string that specifies the order in which the Sobol sequence points are produced. The property value must be one of `'standard'` or `'graycode'`. When set to `'standard'` the points produced match the original Sobol sequence implementation. When set to `'graycode'`, the sequence is generated using an implementation that uses the Gray code of the index instead of the index itself.

PointSet property

Class: qrandstream

Point set from which stream is drawn

Description

The `PointSet` property contains a copy of the point set from which the stream is providing points. The point set is specified during construction of a quasi-random stream and cannot subsequently be altered.

Examples

```
Q = qrandstream('sobol', 5, 'Skip', 8);
% Create a new stream based on the same sequence as that in Q
Q2 = qrandstream(Q.PointSet);
u1 = qrand(Q, 10)
u2 = qrand(Q2, 10) % contains exactly the same values as u1
```

poisscdf

Poisson cumulative distribution function

Syntax

```
p = poisscdf(x,lambda)
p = poisscdf(x,lambda,'upper')
```

Description

`p = poisscdf(x,lambda)` returns the Poisson cdf at each value in `x` using the corresponding mean parameters in `lambda`. `x` and `lambda` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `lambda` must be positive.

`p = poisscdf(x,lambda,'upper')` returns the complement of the Poisson cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The Poisson cdf is

$$p = F(x \mid \lambda) = e^{-\lambda} \sum_{i=0}^{floor(x)} \frac{\lambda^i}{i!}$$

Examples

Compute Poisson Distribution cdf

For example, consider a Quality Assurance department that performs random tests of individual hard disks. Their policy is to shut down the manufacturing process if an inspector finds more than four bad sectors on a disk. What is the probability of shutting down the process if the mean number of bad sectors (λ) is two?

```
probability = 1-poisscdf(4,2)
```

```
probability =
  0.0527
```

About 5% of the time, a normally functioning manufacturing process produces more than four flaws on a hard disk.

Suppose the average number of flaws (λ) increases to four. What is the probability of finding fewer than five flaws on a hard drive?

```
probability = poisscdf(4,4)
```

```
probability =
  0.6288
```

This means that this faulty manufacturing process continues to operate after this first inspection almost 63% of the time.

More About

- "Poisson Distribution" on page B-138

See Also

`cdf` | `poisspdf` | `poissinv` | `poisstat` | `poissfit` | `poissrnd`

poissfit

Poisson parameter estimates

Syntax

```
lambdahat = poissfit(data)
[lambdahat,lambdaci] = poissfit(data)
[lambdahat,lambdaci] = poissfit(data,alpha)
```

Description

`lambdahat = poissfit(data)` returns the maximum likelihood estimate (MLE) of the parameter of the Poisson distribution, λ, given the data `data`.

`[lambdahat,lambdaci] = poissfit(data)` also gives 95% confidence intervals in `lamdaci`.

`[lambdahat,lambdaci] = poissfit(data,alpha)` gives `100(1 - alpha)`% confidence intervals. For example `alpha = 0.001` yields 99.9% confidence intervals.

The sample mean is the MLE of λ.

$$\hat{\lambda} = \frac{1}{n}\sum_{i=1}^{n} x_i$$

Examples

```
r = poissrnd(5,10,2);
[l,lci] = poissfit(r)
l =
    7.4000    6.3000
lci =
    5.8000    4.8000
    9.1000    7.9000
```

More About

- "Poisson Distribution" on page B-138

See Also

`mle` | `poisspdf` | `poisscdf` | `poissinv` | `poisstat` | `poissrnd`

poissinv

Poisson inverse cumulative distribution function

Syntax

```
X = poissinv(P,lambda)
```

Description

`X = poissinv(P,lambda)` returns the smallest value `X` such that the Poisson cdf evaluated at `X` equals or exceeds `P`, using mean parameters in `lambda`. `P` and `lambda` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input.

Examples

If the average number of defects (λ) is two, what is the 95th percentile of the number of defects?

```
poissinv(0.95,2)
ans =
   5
```

What is the median number of defects?

```
median_defects = poissinv(0.50,2)
median_defects =
   2
```

More About

- “Poisson Distribution” on page B-138

See Also

`icdf` | `poisscdf` | `poisspdf` | `poisstat` | `poissfit` | `poissrnd`

prob.PoissonDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Poisson probability distribution object

Description

`prob.PoissonDistribution` is an object consisting of parameters, a model description, and sample data for a Poisson probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Poisson')` creates a Poisson probability distribution object using the default parameter values.

`pd = makedist('Poisson','lambda',lambda)` creates a Poisson distribution object using the specified parameter value.

Input Arguments

`lambda` — Mean
1 (default) | nonnegative scalar value

Mean of the Poisson distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

Properties

`lambda` — Mean
nonnegative scalar value

Mean of the Poisson distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The `(i,j)` element is the covariance between

the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters

proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Poisson Distribution

The Poisson distribution is appropriate for applications that involve counting the number of times a random event occurs in a given amount of time, distance, area, etc. If the number of counts follows the Poisson distribution, then the interval between individual counts follows the exponential distribution.

The Poisson distribution uses the following parameters.

Parameter	Description	Support
`lambda`	Mean	$\lambda \geq 0$

The probability density function of the Poisson distribution is

$$f(x \mid \lambda) = \frac{\lambda^x}{x!} e^{-\lambda} \quad ; \quad x = 0,1,2,\ldots,\infty .$$

Examples

Create a Poisson Distribution Object Using Default Parameters

Create a Poisson distribution object using the default parameter values.

```
pd = makedist('Poisson')
```

```
pd =

  PoissonDistribution

  Poisson distribution
    lambda = 1
```

Create a Poisson Distribution Object Using Specified Parameters

Create a Poisson distribution object by specifying the parameter values.

```
pd = makedist('Poisson','lambda',5)
```

```
pd =

  PoissonDistribution

  Poisson distribution
    lambda = 5
```

Compute the variance of the distribution.

```
v = var(pd)
```

```
v =

     5
```

For the Poisson distribution, both the mean and variance are equal to the parameter lambda.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Poisson Distribution"
- Class Attributes
- Property Attributes

poisspdf

Poisson probability density function

Syntax

```
Y = poisspdf(X,lambda)
```

Description

`Y = poisspdf(X,lambda)` computes the Poisson pdf at each of the values in `X` using mean parameters in `lambda`. `X` and `lambda` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other input. The parameters in `lambda` must all be positive.

The Poisson pdf is

$$f(x \mid \lambda) = \frac{\lambda^x}{x!} e^{-\lambda}; x = 0,1,2,\ldots,\infty .$$

The density function is zero unless x is an integer.

Examples

A computer hard disk manufacturer has observed that flaws occur randomly in the manufacturing process at the average rate of two flaws in a 4 GB hard disk and has found this rate to be acceptable. What is the probability that a disk will be manufactured with no defects?

In this problem, $\lambda = 2$ and $x = 0$.

```
p = poisspdf(0,2)
p =
  0.1353
```

More About

- "Poisson Distribution" on page B-138

See Also

`pdf` | `poisscdf` | `poissinv` | `poisstat` | `poissfit` | `poissrnd`

poissrnd

Poisson random numbers

Syntax

```
R = poissrnd(lambda)
R = poissrnd(lambda,m,n,...)
R = poissrnd(lambda,[m,n,...])
```

Description

`R = poissrnd(lambda)` generates random numbers from the Poisson distribution with mean parameter `lambda`. `lambda` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `lambda`.

`R = poissrnd(lambda,m,n,...)` or `R = poissrnd(lambda,[m,n,...])` generates an `m`-by-`n`-by-... array. The `lambda` parameter can be a scalar or an array of the same size as `R`.

Examples

Generate a random sample of 10 pseudo-observations from a Poisson distribution with $\lambda = 2$.

```
lambda = 2;

random_sample1 = poissrnd(lambda,1,10)
random_sample1 =
   1   0   1   2   1   3   4   2   0   0

random_sample2 = poissrnd(lambda,[1 10])
random_sample2 =
   1   1   1   5   0   3   2   2   3   4

random_sample3 = poissrnd(lambda(ones(1,10)))
random_sample3 =
```

```
    3     2     1     1     0     0     4     0     2     0
```

More About

- "Poisson Distribution" on page B-138

See Also

`random` | `poisspdf` | `poisscdf` | `poissinv` | `poisstat` | `poissfit`

poisstat

Poisson mean and variance

Syntax

```
M = poisstat(lambda)
[M,V] = poisstat(lambda)
```

Description

`M = poisstat(lambda)` returns the mean of the Poisson distribution using mean parameters in `lambda`. The size of `M` is the size of `lambda`.

`[M,V] = poisstat(lambda)` also returns the variance `V` of the Poisson distribution.

For the Poisson distribution with parameter λ, both the mean and variance are equal to λ.

Examples

Find the mean and variance for the Poisson distribution with λ = 2.

```
[m,v] = poisstat([1 2; 3 4])
m =
   1   2
   3   4
v =
   1   2
   3   4
```

More About

- "Poisson Distribution" on page B-138

See Also

`poisspdf` | `poisscdf` | `poissinv` | `poissfit` | `poissrnd`

polyconf

Polynomial confidence intervals

Syntax

```
Y = polyconf(p,X)
[Y,DELTA] = polyconf(p,X,S)
[Y,DELTA] = polyconf(p,X,S,param1,val1,param2,val2,...)
```

Description

`Y = polyconf(p,X)` evaluates the polynomial `p` at the values in `X`. `p` is a vector of coefficients in descending powers.

`[Y,DELTA] = polyconf(p,X,S)` takes outputs `p` and `S` from `polyfit` and generates 95% prediction intervals `Y ± DELTA` for new observations at the values in `X`.

`[Y,DELTA] = polyconf(p,X,S,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs chosen from the following list.

Parameter	Value
`'alpha'`	A value between 0 and 1 specifying a confidence level of `100*(1-alpha)`%. The default is `0.05`.
`'mu'`	A two-element vector containing centering and scaling parameters. With this option, `polyconf` uses `(X-mu(1))/mu(2)` in place of `X`.
`'predopt'`	Either `'observation'` (the default) to compute prediction intervals for new observations at the values in `X`, or `'curve'` to compute confidence intervals for the fit evaluated at the values in `X`. See below.
`'simopt'`	Either `'off'` (the default) for nonsimultaneous bounds, or `'on'` for simultaneous bounds. See below.

The `'predopt'` and `'simopt'` parameters can be understood in terms of the following functions:

- $p(x)$ — the unknown mean function estimated by the fit
- $l(x)$ — the lower confidence bound
- $u(x)$ — the upper confidence bound

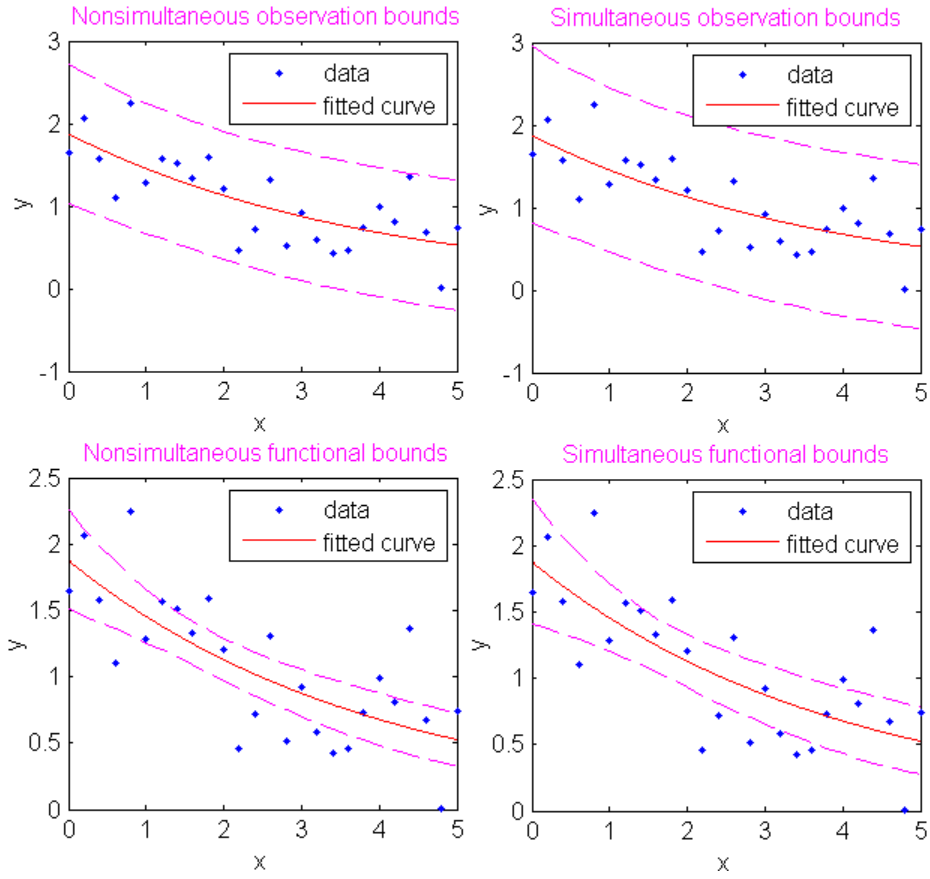
Suppose you make a new observation y_{n+1} at x_{n+1}, so that $y_{n+1}(x_{n+1}) = p(x_{n+1}) + \varepsilon_{n+1}$

By default, the interval $[l_{n+1}(x_{n+1}), u_{n+1}(x_{n+1})]$ is a 95% confidence bound on $y_{n+1}(x_{n+1})$.

The following combinations of the `'predopt'` and `'simopt'` parameters allow you to specify other bounds.

`'simopt'`	`'predopt'`	Bounded Quantity
`'off'`	`'observation'`	$y_{n+1}(x_{n+1})$ (default)
`'off'`	`'curve'`	$p(x_{n+1})$
`'on'`	`'observation'`	$y_{n+1}(x)$, for all x
`'on'`	`'curve'`	$p(x)$, for all x

In general, `'observation'` intervals are wider than `'curve'` intervals, because of the additional uncertainty of predicting a new response value (the curve plus random errors). Likewise, simultaneous intervals are wider than nonsimultaneous intervals, because of the additional uncertainty of bounding values for all predictors x.



Examples

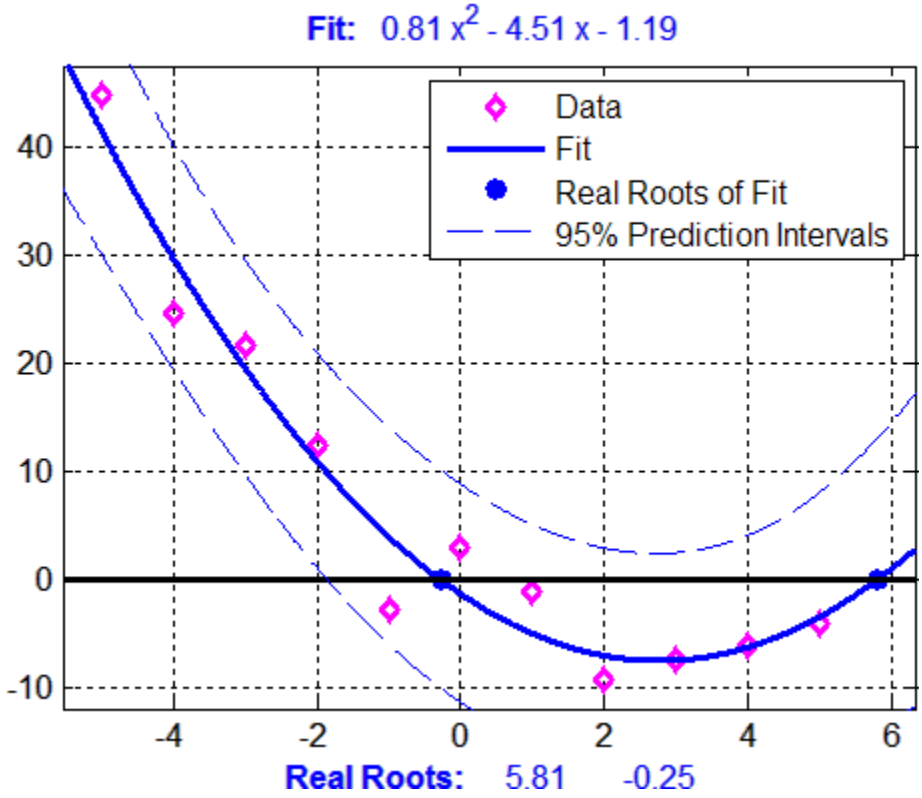
This example uses code from the documentation example function `polydemo`, and calls the documentation example function `polystr` to convert the coefficient vector `p` into a string for the polynomial expression displayed in the figure title. It combines the functions `polyfit`, `polyval`, `roots`, and `polyconf` to produce a formatted display of data with a polynomial fit.

Note: Statistics and Machine Learning Toolbox documentation example files are located in the `\help\toolbox\stats\examples` subdirectory of your MATLAB root folder (`matlabroot`). This subdirectory is not on the MATLAB path at installation. To use the files in this subdirectory, either add the subdirectory to the MATLAB path (`addpath`) or make the subdirectory your current working folder (`cd`).

Display simulated data with a quadratic trend, a fitted quadratic polynomial, and 95% prediction intervals for new observations:

```
xdata = -5:5;
ydata = xdata.^2 - 5*xdata - 3 + 5*randn(size(xdata));

degree = 2;  % Degree of the fit
alpha = 0.05; % Significance level

% Compute the fit and return the structure used by
% POLYCONF.
[p,S] = polyfit(xdata,ydata,degree);

% Compute the real roots and determine the extent of the
% data.
r = roots(p)';        % Roots as a row vector.
real_r = r(imag(r) == 0);  % Real roots.

% Assure that the data are row vectors.
xdata = reshape(xdata,1,length(xdata));
ydata = reshape(ydata,1,length(ydata));

% Extent of the data.
mx = min([real_r,xdata]);
Mx = max([real_r,xdata]);
my = min([ydata,0]);
My = max([ydata,0]);

% Scale factors for plotting.
sx = 0.05*(Mx-mx);
sy = 0.05*(My-my);

% Plot the data, the fit, and the roots.
hdata = plot(xdata,ydata,'md','MarkerSize',5,...
  'LineWidth',2);
hold on
xfit = mx-sx:0.01:Mx+sx;
```

```
yfit = polyval(p,xfit);
hfit = plot(xfit,yfit,'b-','LineWidth',2);
hroots = plot(real_r,zeros(size(real_r)),...
              'bo','MarkerSize',5,...
              'LineWidth',2,...
              'MarkerFaceColor','b');
grid on
plot(xfit,zeros(size(xfit)),'k-','LineWidth',2)
axis([mx-sx Mx+sx my-sy My+sy])

% Add prediction intervals to the plot.
[Y,DELTA] = polyconf(p,xfit,S,'alpha',alpha);
hconf = plot(xfit,Y+DELTA,'b--');
plot(xfit,Y-DELTA,'b--')

% Display the polynomial fit and the real roots.
approx_p = round(100*p)/100; % Round for display.
htitle = title(['{\bf Fit:   }',...
  texlabel(polystr(approx_p))]);
set(htitle,'Color','b')
approx_real_r = round(100*real_r)/100; % Round for display.
hxlabel = xlabel(['{\bf Real Roots:     }',...
    num2str(approx_real_r)]);
set(hxlabel,'Color','b')

% Add a legend.
legend([hdata,hfit,hroots,hconf],...
        'Data','Fit','Real Roots of Fit',...
        '95% Prediction Intervals')
```



See Also

`polyfit` | `polytool` | `polyval`

polytool

Interactive polynomial fitting

Syntax

```
polytool(x,y)
polytool(x,y,n)
polytool(x,y,n,alpha)
polytool(x,y,n,alpha,xname,yname)
h = polytool(...)
```

Description

`polytool(x,y)` fits a line to the vectors `x` and `y` and displays an interactive plot of the result in a graphical interface. You can use the interface to explore the effects of changing the parameters of the fit and to export fit results to the workspace.

`polytool(x,y,n)` initially fits a polynomial of degree `n`. The default is `1`, which produces a linear fit.

`polytool(x,y,n,alpha)` initially plots `100(1 - alpha)`% confidence intervals on the predicted values. The default is `0.05` which results in 95% confidence intervals.

`polytool(x,y,n,alpha,xname,yname)` labels the `x` and `y` values on the graphical interface using the strings `xname` and `yname`. Specify `n` and `alpha` as `[]` to use their default values.

`h = polytool(...)` outputs a vector of handles, `h`, to the line objects in the plot. The handles are returned in the degree: data, fit, lower bounds, upper bounds.

Examples

Interactive polynomial fitting

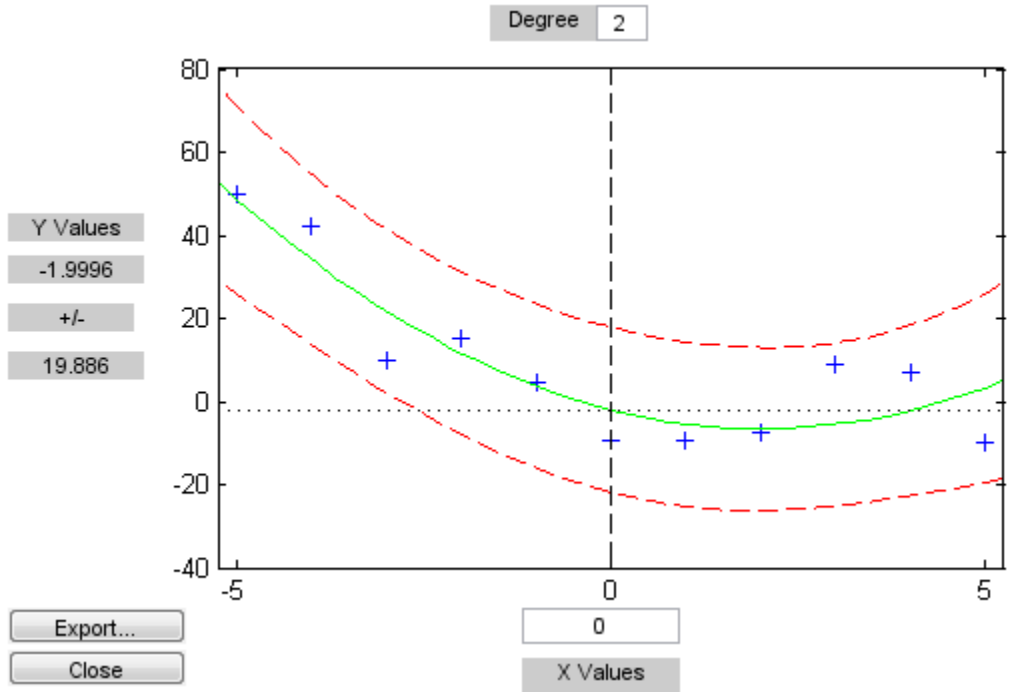
This example shows how to start an interactive fitting session with `polytool`.

Generate data from a quadratic curve with added noise.

```
rng('default') % for reproducibility
x = -5:5;
y = x.^2 - 5*x - 3 + 5*randn(size(x));
```

Fit a quadratic (degree-2) model with `0.90` confidence intervals.

```
n = 2;
alpha = 0.1;
polytool(x,y,n,alpha)
```



See Also

`polyfit` | `polyconf` | `invpred` | `polyval`

posterior

Class: gmdistribution

Posterior probabilities of components

Syntax

```
P = posterior(obj,X)
[P,nlogl] = posterior(obj,X)
```

Description

`P = posterior(obj,X)` returns the posterior probabilities of each of the k components in the Gaussian mixture distribution defined by `obj` for each observation in the data matrix `X`. `X` is n-by-d, where n is the number of observations and d is the dimension of the data. `obj` is an object created by `gmdistribution` or `fitgmdist`. `P` is n-by-k, with `P(I,J)` the probability of component `J` given observation `I`.

`posterior` treats `NaN` values as missing data. Rows of `X` with `NaN` values are excluded from the computation.

`[P,nlogl] = posterior(obj,X)` also returns `nlogl`, the negative log-likelihood of the data.

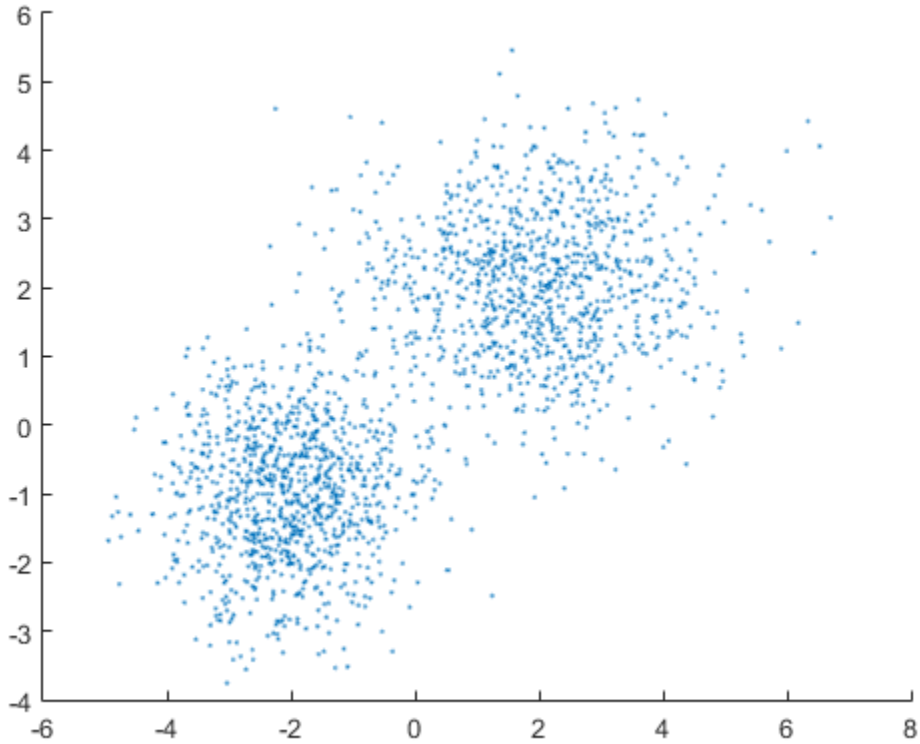
Examples

Compute Posterior Probabilities for Gaussian Mixture Variates

Generate data from a mixture of two bivariate Gaussian distributions using the `mvnrnd` function.

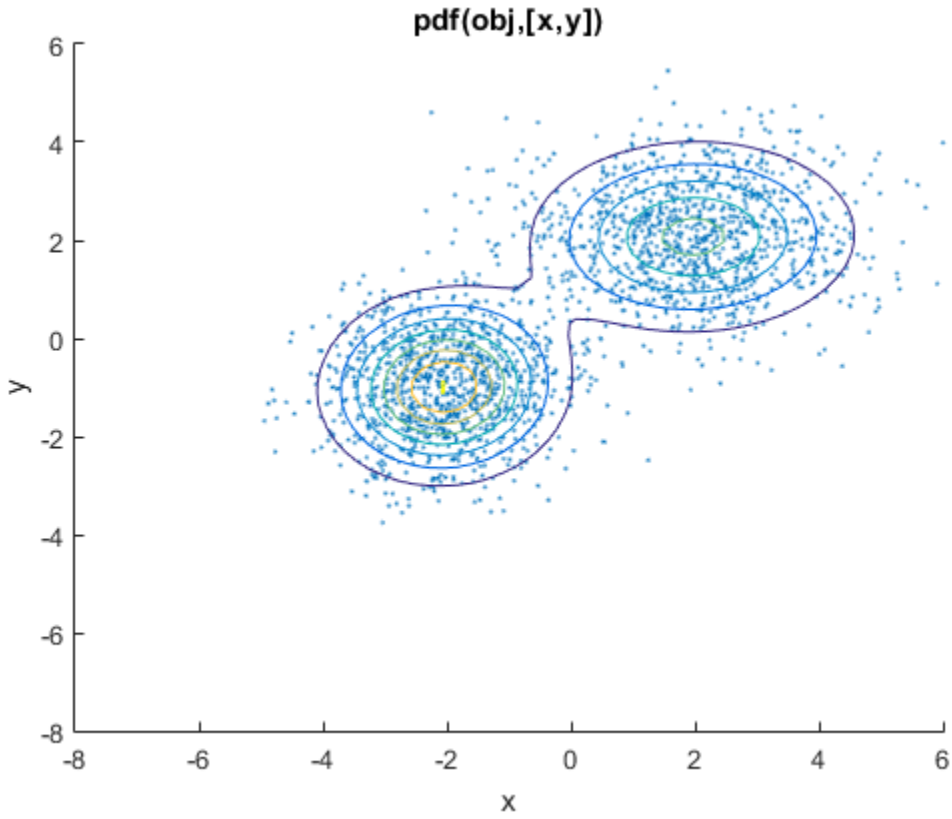
```
MU1 = [2 2];
SIGMA1 = [2 0; 0 1];
MU2 = [-2 -1];
```

```
SIGMA2 = [1 0; 0 1];
rng(1); % For reproducibility
X = [mvnrnd(MU1,SIGMA1,1000);mvnrnd(MU2,SIGMA2,1000)];

scatter(X(:,1),X(:,2),10,'.')
hold on
```



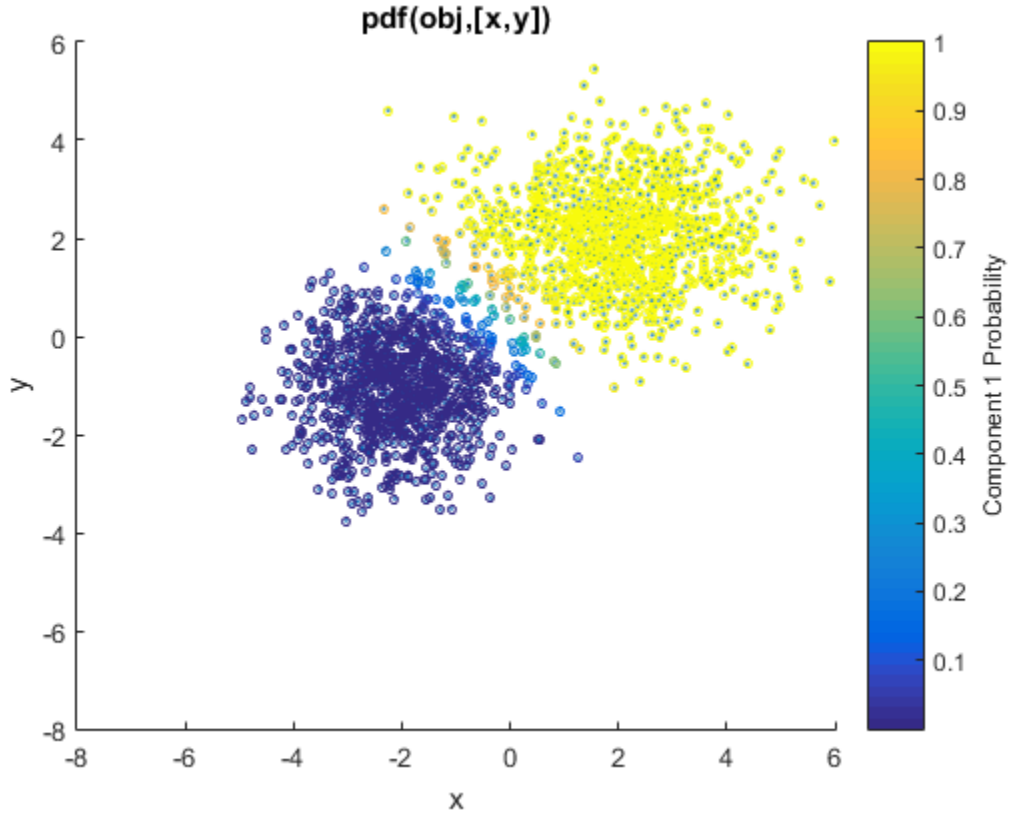
Fit a two-component Gaussian mixture model.

```
obj = fitgmdist(X,2);
h = ezcontour(@(x,y)pdf(obj,[x y]),[-8 6],[-8 6]);
```



Compute posterior probabilities of the components.

```
P = posterior(obj,X);

delete(h)
scatter(X(:,1),X(:,2),10,P(:,1))
hb = colorbar;
ylabel(hb,'Component 1 Probability')
```



See Also

`gmdistribution` | `mahal` | `fitgmdist` | `cluster`

posterior

Class: NaiveBayes

Compute posterior probability of each class for test data

Syntax

```
post = posterior(nb,test)
[post,cpre] = posterior(nb,test)
[post,cpre,logp] = posterior(nb,test)
[...] = posterior(..., 'HandleMissing',val)
```

Description

`post = posterior(nb,test)` returns the posterior probability of the observations in `test` according to the `NaiveBayes` object `nb`. `test` is a `N`-by-`nb.ndims` matrix, where `N` is the number of observations in the test data. Rows of `test` correspond to points, columns of `test` correspond to features. `post` is a `N`-by-`nb.nclasses` matrix containing the posterior probability of each observation for each class. `post(i,j)` is the posterior probability of point I belonging to class `j`. Classes are ordered the same as `nb.clevels`, i.e., column `j` of `post` corresponds to the `j`th class in `nb.clevels`. The posterior probabilities corresponding to any empty classes are `NaN`.

`[post,cpre] = posterior(nb,test)` returns `cpre`, an `N`-by-1 vector, containing the class to which each row of `test` has been assigned. `cpre` has the same type as `nb.CLevels`.

`[post,cpre,logp] = posterior(nb,test)` returns `logp`, an `N`-by-1 vector containing estimates of the log of the probability density function (PDF). `logp(i)` is the log of the PDF of point `i`. The PDF value of point `i` is the sum of `Prob(point I | class J) * Pr{class J}` taken over all classes.

`[...] = posterior(..., 'HandleMissing',val)` specifies how `posterior` treats NaN (missing values). `val` can be one of the following:

`'off'` (default)	Observations with `NaN` in any of the columns are not classified into any class. The corresponding rows in `post` and `logp` are `NaN`. The

	corresponding rows in `cpre` are `NaN` (if `obj.clevels` is numeric or logical), empty strings (if `obj.clevels` is char or cell array of strings) or `<undefined>` (if `obj.clevels` is categorical).
`'on'`	For observations having `NaN` in some (but not all) columns, `post` and `cpre` are computed using the columns with non-`NaN` values. Corresponding `logp` values are `NaN`.

See Also

`NaiveBayes` | `fitNaiveBayes` | `predict`

prctile

Percentiles of a data set

Syntax

```
Y = prctile(X,p)
Y = prctile(X,p,dim)
```

Description

`Y = prctile(X,p)` returns percentiles of the values in a data vector or matrix `X` for the percentages `p` in the interval [0,100].

- If `X` is a vector, then `Y` is a scalar or a vector with the same length as the number of percentiles required (`length(p)`). `Y(i)` contains the `p(i)` percentile.
- If `X` is a matrix, then `Y` is a row vector or a matrix, where the number of rows of `Y` is equal to the number of percentiles required (`length(p)`). The `i`th row of `Y` contains the `p(i)` percentiles of each column of `X`.
- For multidimensional arrays, `prctile` operates along the first nonsingleton dimension of `X`.

`Y = prctile(X,p,dim)` returns percentiles along dimension `dim`.

Examples

Percentiles of a Data Vector

Generate a data set of size 10.

```
rng('default'); % for reproducibility
x = normrnd(5,2,1,10)
```

```
x =
    6.0753    8.6678    0.4823    6.7243    5.6375    2.3846    4.1328    5.6852    12.
```

Calculate the 42nd percentile.

```
Y = prctile(x,42)
```

```
Y =
    5.6709
```

Percentiles of a Data Matrix

Calculate the percentiles along the columns and rows of a data matrix for specified percentages.

Generate a 5-by-5 data matrix.

```
X = (1:5)'*(2:6)
```

```
X =
     2     3     4     5     6
     4     6     8    10    12
     6     9    12    15    18
     8    12    16    20    24
    10    15    20    25    30
```

Calculate the 25th, 50th, and 75th percentiles along the columns of `X`.

```
Y = prctile(X,[25 50 75],1)
```

```
Y =
    3.5000    5.2500    7.0000    8.7500   10.5000
    6.0000    9.0000   12.0000   15.0000   18.0000
    8.5000   12.7500   17.0000   21.2500   25.5000
```

The rows of `Y` correspond to the percentiles of columns of `X`. For example, the 25th, 50th, and 75th percentiles of the third column of `X` with elements (4, 8, 12, 16, 20) are 7, 12, and 17, respectively. `Y = prctile(X,[25 50 75])` returns the same percentile matrix.

Calculate the 25th, 50th, and 75th percentiles along the rows of `X`.

```
Y = prctile(X,[25 50 75],2)
```

```
Y =

    2.7500    4.0000    5.2500
    5.5000    8.0000   10.5000
    8.2500   12.0000   15.7500
   11.0000   16.0000   21.0000
```

```
   13.7500   20.0000   26.2500
```

The rows of `Y` correspond to the percentiles of rows of `X`. For example, the 25th, 50th, and 75th percentiles of the first row of `X` with elements (2, 3, 4, 5, 6) are 2.75, 4, and 5.25, respectively.

Input Arguments

`X` — Input data

vector | array

Input data, specified as a vector or array.

Data Types: `double` | `single`

`p` — Percentages

scalar | vector

Percentages for which to compute percentiles, returned as a scalar or vector of scalars from 0 to 100.

Example: 25

Example: [25, 50, 75]

Data Types: `double` | `single`

`dim` — Dimension

1 (default) | positive integer

Dimension along which the percentiles of `X` are required, specified as a positive integer. For example, for a matrix `X`, when `dim` = 1, `prctile` returns the quantile(s) of the columns of `X` and when `dim` = 2, quantile returns the quantile(s) of the rows of `X`. For a multidimensional array `X`, the length of the `dim`th dimension of `Y` is equal to the length of `p`.

Data Types: `double`

Output Arguments

`Y` — Percentiles

scalar | array

Percentiles of a data vector or array, specified as a scalar or array for one or more percentage values.

- If `X` is a vector, then `Y` is a scalar or a vector with the same length as the number of percentiles required (`length(p)`). `Y(i)` contains the `p(i)`th percentile.
- If `X` is a matrix, then `Y` is a vector or a matrix with the length of the `dim`th dimension equal to the number percentiles required (`length(p)`). When `dim` = 1, for example, the `i`th row of `Y` contains the `p(i)`th percentiles of columns of `X`.
- If `X` is an array of dimension *d*, then `Y` is an array with the length of the `dim`th dimension equal to the number of percentiles required (`length(p)`).

More About

Multidimensional Array

A *multidimensional array* is an array with more than two dimensions. For example, if X is a 1-by-3-by-4 array, then X is a 3-D array.

Nonsingleton Dimension

A *first nonsingleton dimension* is the first dimension of an array whose size is not equal to 1. For example, if X is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of X.

Linear Interpolation

Linear interpolation uses linear polynomials to find $y_i = f(x_i)$, the values of the underlying function $Y = f(X)$ at the points in the vector or array x. Given the data points (x_1, y_1) and (x_2, y_2), where $y_1 = f(x_1)$ and $y_2 = f(x_2)$, linear interpolation finds $y = f(x)$ for a given x between x_1 and x_2 as follows:

$$y = f(x) = y_1 + \frac{(x - x_1)}{(x_2 - x_1)}(y_2 - y_1).$$

Similarly, if the 100(1.5/n)th percentile is $y_{1.5/n}$ and the 100(2.5/n)th percentile is $y_{2.5/n}$, then linear interpolation finds the 100(2.3/n)th percentile, $y_{2.3/n}$ as:

$$y_{\frac{2.3}{n}} = y_{\frac{1.5}{n}} + \frac{\left(\frac{2.3}{n} - \frac{1.5}{n}\right)}{\left(\frac{2.5}{n} - \frac{1.5}{n}\right)}\left(y_{\frac{2.5}{n}} - y_{\frac{1.5}{n}}\right).$$

Algorithms

For an n-element vector `X`, `prctile` returns percentiles as follows:

1. The sorted values in `X` are taken as the 100(0.5/n)th, 100(1.5/n)th, ..., 100([n – 0.5]/n)th percentiles. For example:
   - For a data vector of five elements such as {6, 3, 2, 10, 1}, the sorted elements {1, 2, 3, 6, 10} respectively correspond to the 10th, 30th, 50th, 70th, and 90th percentiles.
   - For a data vector of six elements such as {6, 3, 2, 10, 8, 1}, the sorted elements {1, 2, 3, 6, 8, 10} respectively correspond to the (50/6)th, (150/6)th, (250/6)th, (350/6)th, (450/6)th, and (550/6)th percentiles.
2. `prctile` uses linear interpolation to compute percentiles for percentages between 100(0.5/n) and 100([n – 0.5]/n).
3. `prctile` assigns the minimum or maximum values in `X` to the percentiles corresponding to the percentages outside that range.

`prctile` treats `NaN`s as missing values and removes them.

- "Quantiles and Percentiles" on page 3-7

References

[1] Langford, E. "Quartiles in Elementary Statistics", *Journal of Statistics Education*. Vol. 14, No. 3, 2006.

See Also

`iqr` | `median` | `quantile`

predict

Class: ClassificationKNN

Predict *k*-nearest neighbor classification

Syntax

```
label = predict(mdl,Xnew)
[label,score] = predict(mdl,Xnew)
[label,score,cost] = predict(mdl,Xnew)
```

Description

`label = predict(mdl,Xnew)` returns a vector of predicted class labels for a matrix `Xnew`, based on `mdl`, a `ClassificationKNN` model.

`[label,score] = predict(mdl,Xnew)` returns a matrix of scores, indicating the likelihood that a label comes from a particular class.

`[label,score,cost] = predict(mdl,Xnew)` returns a matrix of costs; `label` is the vector of minimal costs for each row of `cost`

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

`Xnew` — Prediction points
matrix

Points at which `mdl` predicts classifications. Each row of `Xnew` is one point. The number of columns in `Xnew` must equal the number of predictors in `mdl`.

If you specified to standardize the predictor data, that is, `mdl.Mu` and `mdl.Sigma` are not empty (`[]`), then `predict` standardizes `Xnew` before predicting labels.

Output Arguments

`label`

Predicted class labels for the points in `Xnew`, a vector with length equal to the number of rows of `Xnew`. The label is the class with minimal expected cost. See "Predicted Class Label" on page 22-3653.

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in `Xnew`, and `K` is the number of classes (in `mdl.ClassNames`). `score(i,j)` is the posterior probability that row `i` of `Xnew` is of class `j`. See "Posterior Probability" on page 22-3654.

`cost`

Matrix of expected costs of size `N`-by-`K`, where `N` is the number of observations (rows) in `Xnew`, and `K` is the number of classes (in `mdl.ClassNames`). `cost(i,j)` is the cost of classifying row `i` of `X` as class `j`. See "Expected Cost" on page 22-3655.

Definitions

Predicted Class Label

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

Posterior Probability

For a vector (single query point) `Xnew` and model `mdl`, let:

- `K` be the number of nearest neighbors used in prediction, `mdl.NumNeighbors`
- `nbd(mdl,Xnew)` be the `K` nearest neighbors to `Xnew` in `mdl.X`
- `Y(nbd)` be the classifications of the points in `nbd(mdl,Xnew)`, namely `mdl.Y(nbd)`
- `W(nbd)` be the weights of the points in `nbd(mdl,Xnew)`
- `prior` be the priors of the classes in `mdl.Y`

If there is a vector of prior probabilities, then the observation weights `W` are normalized by class to sum to the priors. This might involve a calculation for the point `Xnew`, because weights can depend on the distance from `Xnew` to the points in `mdl.X`.

The posterior probability $p(j \mid \texttt{Xnew})$ is

$$p(j \mid \text{Xnew}) = \frac{\sum_{i \in \text{nbd}} W(i) 1_{Y(X(i)=j)}}{\sum_{i \in \text{nbd}} W(i)}.$$

Here, $1_{Y(X(i)=j)}$ means `1` when `mdl.Y(i) = j`, and `0` otherwise.

True Misclassification Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation.

You can set the true misclassification cost per class in the `Cost` name-value pair when you run `fitcknn`. `Cost(i,j)` is the cost of classifying an observation into class `j` if its

true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

Expected Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation. The third output of `predict` is the expected misclassification cost per observation.

Suppose you have `Nobs` observations that you want to classify with a trained classifier `mdl`. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row. The command

```
[label,score,cost] = predict(mdl,Xnew)
```

returns, among other outputs, a `cost` matrix of size `Nobs`-by-`K`. Each row of the `cost` matrix contains the expected (average) cost of classifying the observation into each of the `K` classes. `cost(n,k)` is

$$\sum_{i=1}^{K}\hat{P}(i\mid Xnew(n))C(k\mid i),$$

where

- K is the number of classes.
- $\hat{P}(i\mid Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.
- $C(k\mid i)$ is the true misclassification cost of classifying an observation as k when its true class is i.

Examples

k-Nearest Neighbor Classification Predictions

Construct a k-nearest neighbor classifier for Fisher's iris data, where $k = 5$. Evaluate some model predictions on new data.

Load the data.

```
load fisheriris
X = meas;
Y = species;
```

Construct a classifier for 5-nearest neighbors. It is good practice to standardize non-categorical predictor data.

```
mdl = fitcknn(X,Y,'NumNeighbors',5,'Standardize',1);
```

Predict the classifications for flowers with minimum, mean, and maximum characteristics.

```
Xnew = [min(X);mean(X);max(X)];
[label,score,cost] = predict(mdl,Xnew)
```

```
label =

    'versicolor'
    'versicolor'
    'virginica'


score =

    0.4000    0.6000         0
         0    1.0000         0
         0         0    1.0000


cost =

    0.6000    0.4000    1.0000
    1.0000         0    1.0000
    1.0000    1.0000         0
```

The classifications have binary values for the score and cost matrices, meaning all five nearest neighbors of each of the three points have identical classifications.

- “Predict Classification Based on a KNN Classifier” on page 16-30

See Also

`ClassificationKNN` | `fitcknn`

More About

- "Classification Using Nearest Neighbors" on page 16-8

predict

Class: CompactClassificationDiscriminant

Predict classification

Syntax

```
label = predict(obj,X)
[label,score] = predict(obj,X)
[label,score,cost] = predict(obj,X)
```

Description

`label = predict(obj,X)` returns a vector of predicted class labels for a matrix `X`, based on `obj`, a trained full or compact classifier.

`[label,score] = predict(obj,X)` returns a matrix of scores (posterior probabilities).

`[label,score,cost] = predict(obj,X)` returns a matrix of costs; `label` is the vector of minimal costs for each row of `cost`.

Input Arguments

`obj`

Discriminant analysis classifier of class `ClassificationDiscriminant` or `CompactClassificationDiscriminant`, typically constructed with `fitcdiscr`.

`X`

Matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `obj`.

Output Arguments

`label`

Vector of class labels of the same type as the response data used in training obj. Each entry of `labels` corresponds to a predicted class label for the corresponding row of `X`; see "Predicted Class Label" on page 22-3660.

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in `X`, and `K` is the number of classes (in `obj.ClassNames`). `score(i,j)` is the posterior probability that row `i` of `X` is of class `j`; see "Posterior Probability" on page 22-3659.

`cost`

Matrix of expected costs of size `N`-by-`K`. `cost(i,j)` is the cost of classifying row `i` of `X` as class `j`. See "Cost" on page 22-3660.

Definitions

Posterior Probability

The posterior probability that a point z belongs to class j is the product of the prior probability and the multivariate normal density. The density function of the multivariate normal with mean μ_j and covariance Σ_j at a point z is

$$P(x \mid k) = \frac{1}{\left(2\pi|\Sigma_k|\right)^{1/2}} \exp\left(-\frac{1}{2}(x-\mu_k)^T \Sigma_k^{-1}(x-\mu_k) \right),$$

where $|\Sigma_k|$ is the determinant of Σ_k, and Σ_k^{-1} is the inverse matrix.

Let $P(k)$ represent the prior probability of class k. Then the posterior probability that an observation x is of class k is

$$\hat{P}(k \mid x) = \frac{P(x \mid k)P(k)}{P(x)},$$

where $P(x)$ is a normalization constant, the sum over k of $P(x \mid k)P(k)$.

Prior Probability

The prior probability is one of three choices:

- `'uniform'` — The prior probability of class `k` is one over the total number of classes.
- `'empirical'` — The prior probability of class `k` is the number of training samples of class `k` divided by the total number of training samples.
- Custom — The prior probability of class `k` is the `k`th element of the `prior` vector. See `fitcdiscr`.

After creating a classifier `obj`, you can set the prior using dot notation:

```
obj.Prior = v;
```

where `v` is a vector of positive elements representing the frequency with which each element occurs. You do not need to retrain the classifier when you set a new prior.

Cost

The matrix of expected costs per observation is defined in “Cost” on page 15-8.

Predicted Class Label

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.
- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

Examples

Examine predictions for a few rows in the Fisher iris data:

```
load fisheriris
obj = fitcdiscr(meas,species);
X = meas(99:102,:); % take four rows
[label score cost] = predict(obj,X)

label =
    'versicolor'
    'versicolor'
    'virginica'
    'virginica'

score =
    0.0000    1.0000    0.0000
    0.0000    0.9999    0.0001
    0.0000    0.0000    1.0000
    0.0000    0.0011    0.9989

cost =
    1.0000    0.0000    1.0000
    1.0000    0.0001    0.9999
    1.0000    1.0000    0.0000
    1.0000    0.9989    0.0011
```

See Also

`ClassificationDiscriminant` | `fitcdiscr` | `edge` | `loss` | `margin`

How To

- “Discriminant Analysis” on page 15-3

predict

Class: CompactClassificationECOC

Predict labels for error-correcting output code multiclass classifiers

Syntax

```
label = predict(Mdl,X)
label = predict(Mdl,X,Name,Value)
[label,NegLoss,PBScore] = predict(___)
[label,NegLoss,PBScore,Posterior] = predict(___)
```

Description

`label = predict(Mdl,X)` returns a vector of predicted class labels for the predictor data, based on the full or compact, trained error-correcting output code multiclass classifier `Mdl`. Each row of `X` is an observation.

The software predicts the classification of an observation by assigning the observation to the class yielding the largest negated average binary loss (or, equivalently, the smallest average binary loss).

`label = predict(Mdl,X,Name,Value)` returns predicted class labels with additional options specified by one or more Name,Value pair arguments.

For example, specify the posterior probability estimation method, decoding scheme, or verbosity level.

`[label,NegLoss,PBScore] = predict(___)` additionally returns negated average binary loss per class (`NegLoss`) for observations, and positive-class scores (`PBScore`) for the observations classified by each binary learner.

`[label,NegLoss,PBScore,Posterior] = predict(___)` additionally returns posterior class probability estimates for observations (`Posterior`).

To obtain posterior class probabilities, you must set `'FitPosterior',1` when training the ECOC model using `fitcecoc`. Otherwise, `predict` throws an error.

Input Arguments

`Mdl` — ECOC multiclass classifier

`ClassificationECOC` model | `CompactClassificationECOC` model

ECOC multiclass classifier, specified as a `ClassificationECOC` or `CompactClassificationECOC` model. You can create a:

- `ClassificationECOC` model by training the ECOC classifier using `fitcecoc`
- `CompactClassificationECOC` model by passing a `ClassificationECOC` classifier to `compact`

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also called an instance or example), and each column corresponds to one variable (also known as a feature). The variables composing the columns of `X` should be the same as the variables that trained the `Mdl` classifier.

If you trained `Mdl` specifying to standardize the predictor data, then the software standardizes the columns of `X` using the corresponding means and standard deviations that the software stored in `Mdl.BinaryLearner{j}.Mu` and `Mdl.BinaryLearner{j}.Sigma` for learner `j`.

Data Types: `double` | `single`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

  The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `Mdl.CodingMatrix`.
  - `s` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.
  - L is the number of binary learners.

  For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`
- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char | function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'NumKLInitializations'` — Number of random initial values

`0` (default) | nonnegative integer

Number of random initial values for fitting posterior probabilities by Kullback-Leibler divergence minimization, specified as the comma-separated pair consisting of `'NumKLInitializations'` and a nonnegative integer.

If you do not request the fourth output argument (Posterior) and set `'PosteriorMethod','kl'` (the default), then the software ignores the value of `NumKLInitializations`.

For more details, see “Posterior Estimation Using Kullback-Leibler Divergence” on page 22-3679.

Example: `'NumKLInitializations',5`

Data Types: `single | double`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'PosteriorMethod'` — Posterior probability estimation method

`'kl'` (default) | `'qp'`

Posterior probability estimation method, specified as the comma-separated pair consisting of `'PosteriorMethod'` and `'kl'` or `'qp'`.

- If `PosteriorMethod` is `'kl'`, then the software estimates multiclass posterior probabilities by minimizing the Kullback-Leibler divergence between the predicted and expected posterior probabilities returned by binary learners. For details, see "Posterior Estimation Using Kullback-Leibler Divergence".
- If `PosteriorMethod` is `'qp'`, then the software estimates multiclass posterior probabilities by solving a least-squares problem using quadratic programming. You need an Optimization Toolbox license to use this option. For details, see "Posterior Estimation Using Quadratic Programming".
- If you do not request the fourth output argument (Posterior), then the software ignores the value of `PosteriorMethod`.

Example: `'PosteriorMethod','qp'`

Data Types: `char`

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single` | `double`

Output Arguments

`label` — Predicted class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Predicted class labels, returned as a categorical or character array, logical or numeric vector, or cell array of strings.

`label`:

- Is the same data type as the Mdl.ClassNames
- Has length equal to the number of rows of X

The software predicts the classification of an observation by assigning the observation to the class yielding the largest negated average binary loss (or, equivalently, the smallest average binary loss).

`NegLoss` — Negated average binary losses

numeric matrix

Negated, average binary losses, returned as a numeric matrix. `NegLoss` is an `n`-by-`K` matrix, where `n` is the number of observations (`size(X,1)`) and `K` is the number of unique classes (`size(Mdl.ClassNames,1)`).

`PBScore` — Positive-class scores

numeric matrix

Positive-class scores for each binary learner, returned as a numeric matrix. `PBScore` is an `n`-by-`L` matrix, where `n` is the number of observations (`size(X,1)`) and `L` is the number of binary learners (`size(Mdl.CodingMatrix,2)`).

`Posterior` — Posterior class probabilities

numeric matrix

Posterior class probabilities, returned as a numeric matrix. `Posterior` is an `n`-by-`K` matrix, where `n` is the number of observations (`size(X,1)`) and `K` is the number of unique classes (`size(Mdl.ClassNames,1)`).

You must set `'FitPosterior',1` when training the ECOC model using `fitcecoc` to request `Posterior`. Otherwise, the software throws an error.

Definitions

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left|m_{kj}\right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Predict Test-Sample Labels of Training Data Using ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
classOrder = unique(Y);
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify a 30% holdout sample. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
```

```
CVMdl = fitcecoc(X,Y,'Holdout',0.30,'Learners',t,'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

Predict the test-sample labels. Print a random subset of true and predicted labels.

```
labels = predict(CMdl,XTest);
idx = randsample(sum(testInds),10);
table(YTest(idx),labels(idx),...
    'VariableNames',{'TrueLabels','PredictedLabels'})
```

```
ans =

    TrueLabels    PredictedLabels
    __________    _______________

    setosa        setosa
    versicolor    virginica
    setosa        setosa
    virginica     virginica
    versicolor    versicolor
    setosa        setosa
    virginica     virginica
    virginica     virginica
    setosa        setosa
    setosa        setosa
```

`Mdl` correctly labeled all except one of the test-sample observations with indices `idx`.

Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
```

```
classOrder = unique(Y); % Class order
K = numel(classOrder);  % Number of classes
rng(1); % For reproducibility
```

Train an ECOC model using SVM binary classifiers and specify a 30% holdout sample. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
CVMdl = fitcecoc(X,Y,'Holdout',0.30,'Learners',t,'ClassNames',classOrder);
CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVMdl` is a `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

SVM scores are signed distances from the observation to the decision boundary. Therefore, the domain is $(-\infty,\infty)$. Create a custom binary loss function that:

- Maps the coding design matrix (*M*) and positive-class classification scores (*s*) for each learner to the binary loss for each observation
- Uses linear loss
- Aggregates the binary learner loss using the median.

You can create a separate function for the binary loss function, and then save it on the MATLAB® path. Or, you can specify an anonymous binary loss function.

```
customBL = @(M,s)nanmedian(1 - bsxfun(@times,M,s),2)/2;
```

Predict test-sample labels and estimate the median binary loss per class. Print the median negative binary losses per class for a random set of 10 test-sample observations.

```
[label,NegLoss] = predict(CMdl,XTest,'BinaryLoss',customBL);

idx = randsample(sum(testInds),10);
classOrder
table(YTest(idx),label(idx),NegLoss(idx,:),'VariableNames',...
    {'TrueLabel','PredictedLabel','NegLoss'})
```

```
classOrder =

     setosa
     versicolor
     virginica


ans =

    TrueLabel     PredictedLabel                NegLoss
    __________    ______________    ____________________________________

    setosa        versicolor          0.1857       1.9878      -3.6735
    versicolor    virginica          -1.3316      -0.12333    -0.045053
    setosa        versicolor         0.13898       1.9261      -3.5651
    virginica     virginica          -1.5133      -0.38263      0.39592
    versicolor    versicolor        -0.87209       0.74777      -1.3757
    setosa        versicolor         0.48381       1.9972       -3.981
    virginica     virginica          -1.9364      -0.67508       1.1114
    virginica     virginica           -1.579      -0.83339      0.91235
    setosa        versicolor         0.51001       2.1208      -4.1308
    setosa        versicolor         0.36119       2.0594      -3.9206
```

The order of the columns corresponds to the elements of `classOrder`. The software predicts the label based on the maximum negated loss. The results seem to indicate that the median of the linear losses might not perform as well as other losses.

Estimate Posterior Probabilities Using ECOC Classifiers

Load Fisher's iris data set. Train the classifier using the petal dimensions as predictors.

```
load fisheriris
X = meas(:,3:4);
Y = species;
rng(1); % For reproducibility
```

Create an SVM template, and specify the Gaussian kernel. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1,'KernelFunction','gaussian');
```

`t` is an SVM template. Most of its properties are empty. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier using the SVM template. Transform classification scores to class posterior probabilities (which are returned by `predict` or `resubPredict`) using the `'FitPosterior'` name-value pair argument. Display diagnostic messages during the training using the `'Verbose'` name-value pair argument. It is good practice to specify the class order.

```
Mdl = fitcecoc(X,Y,'Learners',t,'FitPosterior',1,...
    'ClassNames',{'setosa','versicolor','virginica'},...
    'Verbose',2);
```

```
Training binary learner 1 (SVM) out of 3 with 50 negative and 50 positive observations.
Negative class indices: 2
Positive class indices: 1

Fitting posterior probabilities for learner 1 (SVM).
Training binary learner 2 (SVM) out of 3 with 50 negative and 50 positive observations.
Negative class indices: 3
Positive class indices: 1

Fitting posterior probabilities for learner 2 (SVM).
Training binary learner 3 (SVM) out of 3 with 50 negative and 50 positive observations.
Negative class indices: 3
Positive class indices: 2

Fitting posterior probabilities for learner 3 (SVM).
```

`Mdl` is a `ClassificationECOC` model. The same SVM template applies to each binary learner, but you can adjust options for each binary learner by passing in a cell vector of templates.

Predict the in-sample labels and class posterior probabilities. Display diagnostic messages during the computation of labels and class posterior probabilities using the `'Verbose'` name-value pair argument.

```
[label,~,~,Posterior] = resubPredict(Mdl,'Verbose',1);
Mdl.BinaryLoss
```

```
Predictions from all learners have been computed.
Loss for all observations has been computed.
Computing posterior probabilities...

ans =

quadratic
```

The software assigns an observation to the class that yields the smallest average binary loss. Since all binary learners are computing posterior probabilities, the binary loss function is `quadratic`.

Display a random set of results.

```
idx = randsample(size(X,1),10,1);
Mdl.ClassNames
table(Y(idx),label(idx),Posterior(idx,:),...
    'VariableNames',{'TrueLabel','PredLabel','Posterior'})
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

     TrueLabel       PredLabel                  Posterior
    ____________    ____________    ____________________________________

    'virginica'     'virginica'      0.0039321     0.0039869       0.99208
    'virginica'     'virginica'       0.017067      0.018263       0.96467
    'virginica'     'virginica'       0.014948      0.015856        0.9692
    'versicolor'    'versicolor'    2.2197e-14       0.87317       0.12683
    'setosa'        'setosa'             0.999    0.00025091    0.00074639
    'versicolor'    'virginica'     2.2195e-14      0.059429       0.94057
    'versicolor'    'versicolor'    2.2194e-14       0.97001      0.029986
    'setosa'        'setosa'             0.999     0.0002499    0.00074741
    'versicolor'    'versicolor'     0.0085646       0.98259      0.008849
    'setosa'        'setosa'             0.999    0.00025013    0.00074718
```

The columns of `Posterior` correspond to the class order of `Mdl.ClassNames`.

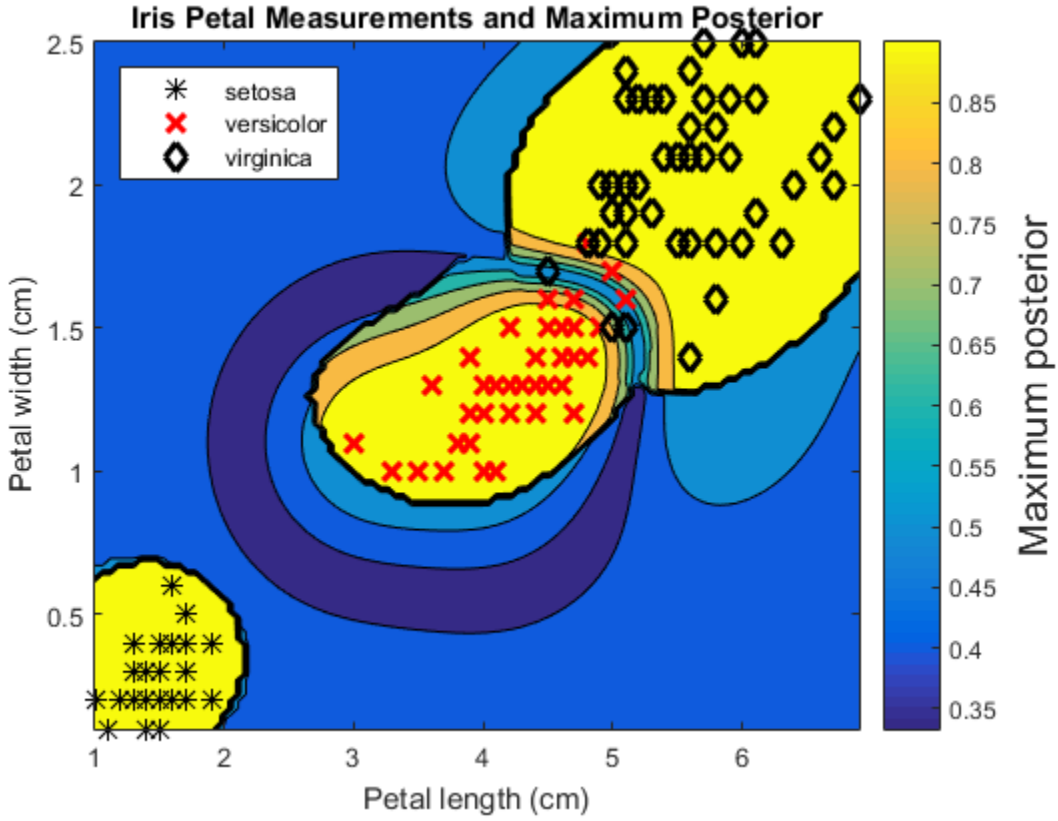
Define a grid of values in the observed predictor space. Predict the posterior probabilities for each instance in the grid.

```
xMax = max(X);
```

```
xMin = min(X);

x1Pts = linspace(xMin(1),xMax(1));
x2Pts = linspace(xMin(2),xMax(2));
[x1Grid,x2Grid] = meshgrid(x1Pts,x2Pts);

[~,~,~,PosteriorRegion] = predict(Mdl,[x1Grid(:),x2Grid(:)]);
```

For each coordinate on the grid, plot the maximum class posterior probability among all classes.

```
figure;
contourf(x1Grid,x2Grid,...
        reshape(max(PosteriorRegion,[],2),size(x1Grid,1),size(x1Grid,2)));
h = colorbar;
h.YLabel.String = 'Maximum posterior';
h.YLabel.FontSize = 15;
hold on
gh = gscatter(X(:,1),X(:,2),Y,'krk','*xd',8);
gh(2).LineWidth = 2;
gh(3).LineWidth = 2;

title 'Iris Petal Measurements and Maximum Posterior';
xlabel 'Petal length (cm)';
ylabel 'Petal width (cm)';
axis tight
legend(gh,'Location','NorthWest')
hold off
```



Estimate Test-Sample Posterior Probabilities Using Parallel Computing

Train an error-correcting output codes, multiclass model and estimate posterior probabilities using parallel computing.

Load the `arrhythmia` data set.

```
load arrhythmia
Y = categorical(Y);
tabulate(Y)
n = numel(Y);
K = numel(unique(Y));
```

```
  Value    Count   Percent
```

```
     1      245     54.20%
     2       44      9.73%
     3       15      3.32%
     4       15      3.32%
     5       13      2.88%
     6       25      5.53%
     7        3      0.66%
     8        2      0.44%
     9        9      1.99%
    10       50     11.06%
    14        4      0.88%
    15        5      1.11%
    16       22      4.87%
```

Several classes are not represented in the data, and many of the other classes have low relative frequencies.

Specify an ensemble learning template that uses the GentleBoost method and 50 weak, classification tree learners.

```
t = templateEnsemble('GentleBoost',50,'Tree');
```

`t` is a template object. Most of the options are empty ([ ]). The software uses default values for all empty options during training.

Since there are many classes, specify a sparse random coding design.

```
rng(1); % For reproducibility
Coding = designecoc(K,'sparserandom');
```

Train an ECOC model using parallel computing. Specify to hold out 15% of the data and fit posterior probabilities.

```
pool = parpool;                       % Invokes workers
options = statset('UseParallel',1);
CVMdl = fitcecoc(X,Y,'Learner',t,'Options',options,'Coding',Coding,...
    'FitPosterior',1,'Holdout',0.15);

CMdl = CVMdl.Trained{1};           % Extract trained, compact classifier
testInds = test(CVMdl.Partition);  % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

```
Starting parallel pool (parpool) using the 'local' profile ... connected to 4 workers.
```

`CVMdl` is a `ClassificationPartitionedECOC` model. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationECOC` model that the software trained using the training set.

The pool invokes four workers. The number of workers might vary among systems.

Estimate posterior probabilities, and display the posterior probability of being classified as not having arrhythmia (class 1) given the data for a random set of test-sample observations.

```
[~,~,~,posterior] = predict(CMdl,XTest,'Options',options);
idx = randsample(sum(testInds),10);
table(idx,YTest(idx),posterior(idx,1),...
    'VariableNames',{'TestSampleIndex','TrueLabel','PosteriorNoArrhythmia'})
```

```
ans =

    TestSampleIndex    TrueLabel    PosteriorNoArrhythmia
    _______________    _________    _____________________

    11                 6            0.60631
    41                 4            0.23674
    51                 2            0.13802
    33                 10           0.43831
    12                 1            0.94332
     8                 1            0.97278
    37                 1            0.62807
    24                 10           0.96876
    56                 16           0.29375
    30                 1            0.64512
```

- “Quick Start Parallel Computing for Statistics and Machine Learning Toolbox” on page 21-2

Algorithms

The software can estimate class posterior probabilities using quadratic programming or by minimizing the Kullback-Leibler divergence. For the following descriptions of the posterior estimation algorithms, let:

- m_{kj} be the element (k,j) of the coding design matrix M.

- I be the indicator function.
- $\hat{p}_k$ be the class posterior probability estimate for class k of an observation, $k = 1,...,K$.
- r_j be the positive-class posterior probability for binary learner j. That is, r_j is the probability that binary learner j classifies an observation into the positive class, given the training data.

Posterior Estimation Using Kullback-Leibler Divergence

By default, the software minimizes the Kullback-Leibler divergence to estimate class posterior probabilities. The Kullback-Leibler divergence between the expected and observed positive-class posterior probabilities is

$$\Delta(r,r) = \sum_{j=1}^{L} w_j \left[r_j \log \frac{r_j}{r_j} + \left(1 - r_j\right) \log \frac{1 - r_j}{1 - r_j} \right],$$

where $w_j = \sum_{S_j} w_i^*$ is the weight for binary learner j with S_j the set of observation indices that binary learner j is trained on and w_i^* is the weight of observation i. The software minimizes the divergence iteratively. The first step is to choose initial values $\hat{p}_k^{(0)};\ k = 1,...,K$ for the class posterior probabilities.

- If you do not specify NumKLIterations, then the software uses both sets of deterministic initial values described next, and uses the one that minimizes Δ.
  - $\hat{p}_k^{(0)} = 1/K;\ k = 1,...,K.$
  - $\hat{p}_k^{(0)};\ k = 1,...,K$ is the solution of the system

    $$M_{01}\hat{p}^{(0)} = r,$$

    where M_{01} is M with all $m_{kj} = -1$ replaced with 0, and r is a vector of positive-class posterior probabilities returned by the L binary learners [2]. The software uses `lsqnonneg` to solve the system.

- If you specify `'NumKLIterations',c`, where `c` is a natural number, then the software does the following to choose $\hat{p}_k^{(0)};\ k = 1,\ldots,K$, and uses the one that minimizes Δ.
  - The software chooses both sets of deterministic initial values as described previously.
  - The software randomly generates `c` vectors of length K using `rand`, and then normalizes each vector to sum to 1.

At iteration t, the software:

1. Computes

$$\hat{r}_j^{(t)} = \frac{\sum_{k=1}^{K} \hat{p}_k^{(t)} I(m_{kj} = +1)}{\sum_{k=1}^{K} \hat{p}_k^{(t)} I(m_{kj} = +1 \cup m_{kj} = -1)}.$$

2. Estimates the next class posterior probability using

$$\hat{p}_k^{(t+1)} = \hat{p}_k^{(t)} \frac{\sum_{j=1}^{L} w_j \left[r_j I\left(m_{kj} = +1\right) + \left(1 - r_j\right) I\left(m_{kj} = -1\right) \right]}{\sum_{j=1}^{L} w_j \left[\hat{r}_j^{(t)} I\left(m_{kj} = +1\right) + \left(1 - \hat{r}_j^{(t)}\right) I\left(m_{kj} = -1\right) \right]}.$$

3. Normalizes $\hat{p}_k^{(t+1)};\ k = 1,\ldots,K$ so that they sum to 1.

4. Checks for convergence.

For more details, see [5] and [7].

Posterior Estimation Using Quadratic Programming

Posterior probability estimation using quadratic programming requires an Optimization Toolbox license. To estimate posterior probabilities for an observation using this method, the software:

1 Estimates the positive-class posterior probabilities, r_j, for binary learners $j = 1,...,L$.

2 Using the relationship between r_j and $\hat{p}_k$ [6], minimizes

$$\sum_{j=1}^{L}\left[-r_j\sum_{k=1}^{K}\hat{p}_k I\left(m_{kj}=-1\right)+\left(1-r_j\right)\sum_{k=1}^{K}\hat{p}_k I\left(m_{kj}=+1\right)\right]^2$$

with respect to $\hat{p}_k$ and the restrictions

$$0 \le \hat{p}_k \le 1$$
$$\sum_k \hat{p}_k = 1.$$

The software performs minimization using `quadprog`.

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Dietterich, T., and G. Bakiri. "Solving Multiclass Learning Problems Via Error-Correcting Output Codes." *Journal of Artificial Intelligence Research*. Vol. 2, 1995, pp. 263–286.

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See Also

`ClassificationECOC` | `CompactClassificationECOC` | `fitcecoc` | `quadprog` | `resubPredict` | `statset`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

predict

Class: CompactClassificationEnsemble

Predict classification

Syntax

```
labels = predict(ens,X)
[labels,score] = predict(ens,X)
[labels,...] = predict(ens,X,Name,Value)
```

Description

`labels = predict(ens,X)` returns a vector of predicted class labels for a matrix `X`, based on `ens`, a trained full or compact classification ensemble.

`[labels,score] = predict(ens,X)` also returns scores for all classes.

`[labels,...] = predict(ens,X,Name,Value)` predicts classifications with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A classification ensemble created by `fitensemble`, or a compact classification ensemble created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `ens`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners `predict` uses for computation of responses, a numeric vector.

Default: `1:T`, where `T` is the number of weak learners in ens

`'UseObsForLearner'`

A logical matrix of size `N`-by-`T`, where:

- `N` is the number of rows of X.
- `T` is the number of weak learners in ens.

When `UseObsForLearner(i,j)` is `true`, learner `j` is used in predicting the class of row `i` of X.

Default: `true(N,T)`

Output Arguments

`labels`

Vector of classification labels. `labels` has the same data type as the labels used in training ens.

`score`

A matrix with one row per observation and one column per class. For each observation and each class, the score generated by each tree is the probability of this observation originating from this class computed as the fraction of observations of this class in a tree leaf. `predict` averages these scores over all trees in the ensemble.

Definitions

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Train a boosting ensemble for the `ionosphere` data, and predict the classification of the mean of the data:

```
load ionosphere;
ada = fitensemble(X,Y,'AdaBoostM1',100,'tree');
Xbar = mean(X);
[ypredict score] = predict(ada,Xbar)

ypredict =
    'g'

score =
   -2.9460    2.9460
```

See Also

`margin` | `edge` | `loss`

predict

Class: CompactClassificationNaiveBayes

Predict classification for naive Bayes models

Syntax

```
label = predict(Mdl,X)
[label,Posterior,Cost] = predict(Mdl,X)
```

Description

`label = predict(Mdl,X)` returns a vector of predicted class labels for predictor data (`X`), based on the trained, full or compact naive Bayes classifier `Mdl`.

`[label,Posterior,Cost] = predict(Mdl,X)` additionally returns posterior probabilities (`Posterior`) and predicted (expected) misclassification costs (`Cost`) corresponding to the observations (rows) in `X`.

Input Arguments

`Mdl` — Naive Bayes classifier

`ClassificationNaiveBayes` model | `CompactClassificationNaiveBayes` model

Naive Bayes classifier, specified as a `ClassificationNaiveBayes` model or `CompactClassificationNaiveBayes` model returned by `fitcnb` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained `Mdl`.

The length of `Y` and the number of rows of `X` must be equal.

Data Types: `double` | `single`

Notes:

- If `Mdl.DistributionNames` is `'mn'`, then the software returns `NaN`s corresponding to rows of X containing at least one `NaN`.
- If `Mdl.DistributionNames` is not `'mn'`, then the software ignores `NaN` values when estimating misclassification costs and posterior probabilities. Specifically, the software computes the conditional density of the predictors given the class by leaving out the factors corresponding to missing predictor values.
- For predictor distribution specified as `'mvmn'`, if X contains levels that are not represented in the training data (i.e., not in `Mdl.CategoricalLevels` for that predictor), then the conditional density of the predictors given the class is 0. For those observations, the software returns the corresponding value of `Posterior` as a `NaN`. The software determines the class label for such observations using the class prior probability, stored in `Mdl.Prior`.

Output Arguments

`label` — Predicted class labels

categorical vector | character array | logical vector | numeric vector | cell vector of strings

Predicted class labels, returned as a categorical vector, character array, logical or numeric vector, or cell vector of strings.

`label`:

- Is the same data type as the observed class labels (`Mdl.Y`) that trained Mdl
- Has length equal to the number of rows of Mdl.X
- Is the class yielding the lowest expected misclassification cost (Cost)

`Posterior` — Class posterior probabilities

numeric matrix

Class posterior probabilities, returned as a numeric matrix. `Posterior` has rows equal to the number of rows of X and columns equal to the number of distinct classes in the training data (`size(Mdl.ClassNames,1)`).

`Posterior(j,k)` is the predicted posterior probability of class `k` (i.e., in class `Mdl.ClassNames(k)`) given the observation in row `j` of `X`.

Data Types: `double`

`Cost` — Expected misclassification costs
numeric matrix

Expected misclassification costs, returned as a numeric matrix. `Cost` has rows equal to the number of rows of X and columns equal to the number of distinct classes in the training data (`size(Mdl.ClassNames,1)`).

`Cost(j,k)` is the expected misclassification cost of the observation in row `j` of `X` being predicted into class `k` (i.e., in class `Mdl.ClassNames(k)`).

Definitions

Misclassification Cost

A *misclassification cost* is the relative severity of a classifier labeling an observation into the wrong class.

There are two types of misclassification costs: true and expected. Let K be the number of classes.

- *True misclassification cost* — A K-by-K matrix, where element (i,j) indicates the misclassification cost of predicting an observation into class j if its true class is i. The software stores the misclassification cost in the property `Mdl.Cost`, and used in computations. By default, `Mdl.Cost(i,j)` = 1 if `i` ≠ `j`, and `Mdl.Cost(i,j)` = 0 if `i` = `j`. In other words, the cost is `0` for correct classification, and `1` for any incorrect classification.
- *Expected misclassification cost* — A K-dimensional vector, where element k is the weighted average misclassification cost of classifying an observation into class k, weighted by the class posterior probabilities. In other words,

$$c_k = \sum_{j=1}^{K} \hat{P}(Y = j \mid x_1,...,x_P)\texttt{Cost}_{jk}.$$

the software classifies observations to the class corresponding with the lowest expected misclassification cost.

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.
- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

  $$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Examples

Label Test Sample Observations of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);
```

Train a naive Bayes classifier and specify to holdout 30% of the data for a test sample. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
CVMdl = fitcnb(X,Y,'Holdout',0.30,...
    'ClassNames',{'setosa','versicolor','virginica'});
CMdl = CVMdl.Trained{1};          % Extract trained, compact classifier
testIdx = test(CVMdl.Partition); % Extract the test indices
XTest = X(testIdx,:);
YTest = Y(testIdx);
```

`CVMdl` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationNaiveBayes` classifier that the software trained using the training set.

Label the test sample observations. Display the results for a random set of 10 observations in the test sample.

```
idx = randsample(sum(testIdx),10);
label = predict(CMdl,XTest);
table(YTest(idx),label(idx),'VariableNames',...
    {'TrueLabel','PredictedLabel'})
```

```
ans =

     TrueLabel      PredictedLabel
    ____________    ______________

    'setosa'        'setosa'
    'versicolor'    'versicolor'
    'setosa'        'setosa'
    'virginica'     'virginica'
    'versicolor'    'versicolor'
    'setosa'        'setosa'
    'virginica'     'virginica'
    'virginica'     'virginica'
    'setosa'        'setosa'
    'setosa'        'setosa'
```

Estimate Posterior Probabilities and Misclassification Costs

A goal of classification is to estimate posterior probabilities of new observations using a trained algorithm. Many applications train algorithms on large data sets, which can use resources that are better used elsewhere. This example shows how to efficiently estimate posterior probabilities of new observations using a Naive Bayes classifier.

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);
```

Partition the data set into two sets: one in the training set, and the other is new unobserved data. Reserve 10 observations for the new data set.

```
n = size(X,1);
newInds = randsample(n,10);
inds = ~ismember(1:n,newInds);
XNew = X(newInds,:);
YNew = Y(newInds);
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label. Conserve memory by reducing the size of the trained SVM classifier.

```
Mdl = fitcnb(X(inds,:),Y(inds),...
    'ClassNames',{'setosa','versicolor','virginica'});
CMdl = compact(Mdl);
whos('Mdl','CMdl')
```

```
  Name      Size            Bytes  Class

  CMdl      1x1              4772  classreg.learning.classif.CompactClassificationNaive
  Mdl       1x1             12541  ClassificationNaiveBayes
```

The `CompactClassificationNaiveBayes` classifier (`CMdl`) uses less space than the `ClassificationNaiveBayes` classifier (`Mdl`) because the latter stores the data.

Predict the labels, posterior probabilities, and expected class misclassification costs. Since true labels are available, compare them with the predicted labels.

```
CMdl.ClassNames
[labels,PostProbs,MisClassCost] = predict(CMdl,XNew);
table(YNew,labels,PostProbs,'VariableNames',...
    {'TrueLabels','PredictedLabels',...
    'PosteriorProbabilities'})
MisClassCost
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'
```

```
ans =

     TrueLabels     PredictedLabels            PosteriorProbabilities
    ____________    _______________    ____________________________________

    'setosa'        'setosa'                    1     4.1259e-16     1.1846e-23
    'versicolor'    'versicolor'         1.0373e-60        0.99999     5.8053e-06
    'virginica'     'virginica'         4.8708e-211     0.00085645        0.99914
    'setosa'        'setosa'                    1     1.4053e-19     2.2672e-26
    'versicolor'    'versicolor'         2.9308e-75        0.99987     0.00012869
    'setosa'        'setosa'                    1      2.629e-18     4.4297e-25
    'versicolor'    'versicolor'         1.4238e-67        0.99999      9.733e-06
    'versicolor'    'versicolor'        2.0667e-110        0.94237       0.057625
    'setosa'        'setosa'                    1     4.3779e-19     3.5139e-26
    'setosa'        'setosa'                    1     1.1792e-17     2.2912e-24
```

```
MisClassCost =

    0.0000    1.0000    1.0000
    1.0000    0.0000    1.0000
    1.0000    0.9991    0.0009
    0.0000    1.0000    1.0000
    1.0000    0.0001    0.9999
    0.0000    1.0000    1.0000
    1.0000    0.0000    1.0000
    1.0000    0.0576    0.9424
    0.0000    1.0000    1.0000
    0.0000    1.0000    1.0000
```

`PostProbs` and `MisClassCost` are 15-by- 3 numeric matrices, where each row corresponds to a new observation and each column corresponds to a class. The order of the columns corresponds to the order of `CMdl.ClassNames`.

Plot Posterior Probability Regions for Naive Bayes Classifiers

Load Fisher's iris data set. Train the classifier using the petal lengths and widths.

```
load fisheriris
X = meas(:,3:4);
Y = species;
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
Mdl = fitcnb(X,Y,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationNaiveBayes` model. You can access its properties using dot notation.

Define a grid of values in the observed predictor space. Predict the posterior probabilities for each instance in the grid.

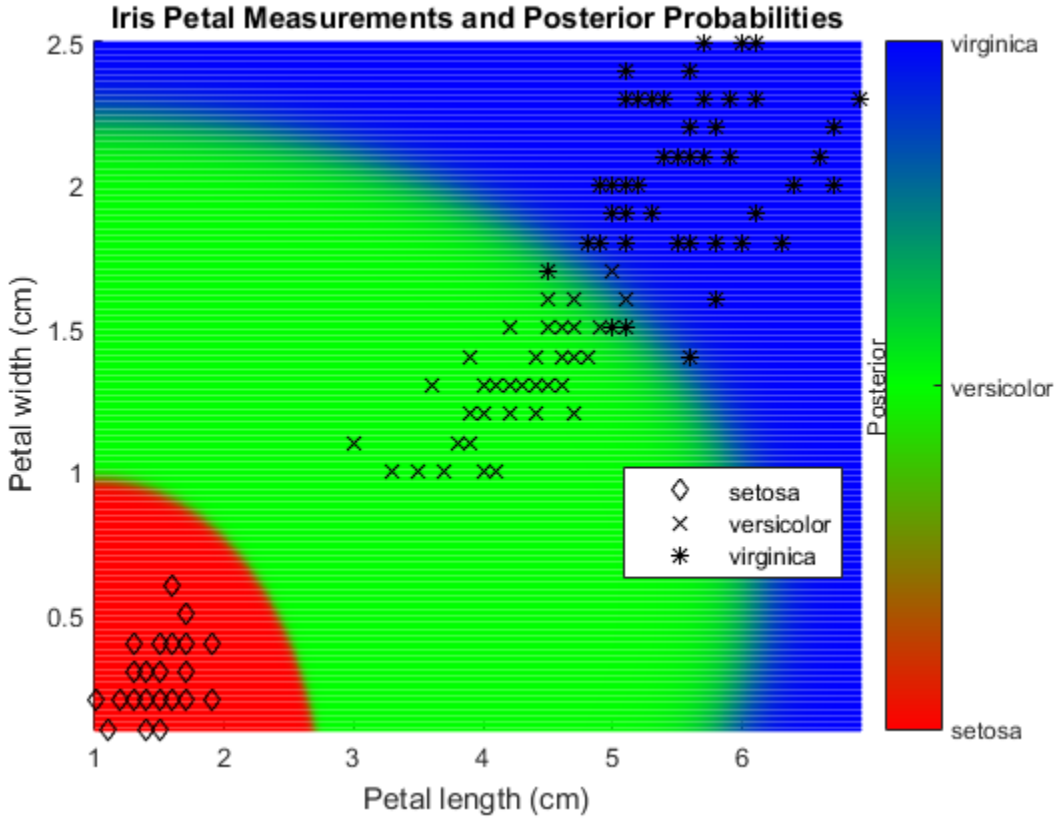
```
xMax = max(X);
xMin = min(X);
h = 0.01;
[x1Grid,x2Grid] = meshgrid(xMin(1):h:xMax(1),xMin(2):h:xMax(2));

[~,PosteriorRegion] = predict(Mdl,[x1Grid(:),x2Grid(:)]);
```

Plot the posterior probability regions and the training data.

```
figure;
% Plot posterior regions
scatter(x1Grid(:),x2Grid(:),1,PosteriorRegion);
% Adjust color bar options
h = colorbar;
h.Ticks = [0 0.5 1];
h.TickLabels = {'setosa','versicolor','virginica'};
h.YLabel.String = 'Posterior';
h.YLabel.Position = [-0.5 0.5 0];
% Adjust color map options
d = 1e-2;
cmap = zeros(201,3);
cmap(1:101,1) = 1:-d:0;
```

```
cmap(1:201,2) = [0:d:1 1-d:-d:0];
cmap(101:201,3) = 0:d:1;
colormap(cmap);
% Plot data
hold on
gh = gscatter(X(:,1),X(:,2),Y,'k','dx*');
title 'Iris Petal Measurements and Posterior Probabilities';
xlabel 'Petal length (cm)';
ylabel 'Petal width (cm)';
axis tight
legend(gh,'Location','Best')
hold off
```



References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `fitcnb` | `loss` | `resubPredict`

More About

- "Naive Bayes Classification" on page 15-31

- “Grouping Variables” on page 2-52

predict

Class: CompactClassificationSVM

Predict labels for support vector machine classifiers

Syntax

```
label = predict(SVMModel,X)
[label,Score] = predict(SVMModel,X)
```

Description

`label = predict(SVMModel,X)` returns a vector of predicted class labels for predictor data `X`, based on the full or compact, trained SVM classifier `SVMModel`.

`[label,Score] = predict(SVMModel,X)` additionally returns class likelihood measures, i.e., either scores or posterior probabilities.

Input Arguments

`SVMModel` — SVM classifier

`ClassificationSVM` classifier | `CompactClassificationSVM` classifier

SVM classifier, specified as a `ClassificationSVM` classifier or `CompactClassificationSVM` classifier returned by `fitcsvm` or `compact`, respectively.

`X` — Predictor data

numeric matrix

Predictor data, specified as a numeric matrix.

Each row of `X` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a feature). The variables making up the columns of `X` should be the same as the variables that trained the `SVMModel` classifier.

The length of Y and the number of rows of X must be equal.

If you set 'Standardize',true in fitcsvm to train SVMModel, then the software standardizes the columns of X using the corresponding means in SVMModel.Mu and standard deviations in SVMModel.Sigma.

Data Types: double | single

Output Arguments

label — Predicted class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Predicted class labels, returned as a categorical or character array, logical or numeric vector, or cell array of strings.

label:

- Is the same data type as the observed class labels (Y) that trained SVMModel
- Has length equal to the number of rows of X

For one-class learning, the elements of label are the one class represented in the observed class labels.

Score — Predicted class scores or posterior probabilities

numeric column vector | numeric matrix

Predicted class scores or posterior probabilities, returned as a numeric column vector or numeric matrix.

- For one-class learning, Score is a column vector with the same number of rows as the training observations (X). The elements are the positive class scores for the corresponding observations. You cannot obtain posterior probabilities for one-class learning.
- For two-class learning, Score is a two column matrix with the same number of rows as X.
    - If you fit the optimal score-to-posterior probability transformation function using fitPosterior or fitSVMPosterior, then Score contains class posterior

probabilities. That is, if the value of `SVMModel.ScoreTransform` is not `none`, then the elements of the first and second columns of `Score` are the negative class (`SVMModel.ClassNames{1}`) and positive class (`SVMModel.ClassNames{2}`) posterior probabilities for the corresponding observations, respectively.

- Otherwise, the elements of the first column are the negative class scores and the elements of the second column are the positive class scores for the corresponding observations.

If SVMModel`.KernelParameters.Function` is `'linear'`, then the software estimates the classification score for the observation x using

$$f(x) = (x / s)'\beta + b.$$

SVMModel stores β, b, s in the properties Beta, Bias, and KernelParameters`.Scale`, respectively.

Data Types: `double | single`

Definitions

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j,x) = x_j'x$ (the linear kernel), then the score function reduces to

$$f(x) = (x / s)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Posterior Probability

The probability that an observation belongs in a particular class, given the data.

For SVM, the posterior probability is a function of the score, $P(s)$, that observation j is in class $k = \{-1,1\}$.

- For separable classes, the posterior probability is the step function

$$P(s_j) = \begin{cases} 0; & s < \max_{y_k=-1} s_k \\ \pi; & \max_{y_k=-1} s_k \le s_j \le \min_{y_k=+1} s_k \\ 1; & s_j > \min_{y_k=+1} s_k \end{cases},$$

  where:

  - s_j is the score of observation j.
  - +1 and –1 denote the positive and negative classes, respectively.
  - π is the prior probability that an observation is in the positive class.
- For inseparable classes, the posterior probability is the sigmoid function

$$P(s_j) = \frac{1}{1 + \exp(As_j + B)},$$

  where the parameters A and B are the slope and intercept parameters.

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Examples

Label Test Sample Observations of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM classifier. Specify a 15% holdout sample for testing. It is good practice to specify the class order and standardize the data.

```
CVSVMModel = fitcsvm(X,Y,'Holdout',0.15,'ClassNames',{'b','g'},...
    'Standardize',true);
CompactSVMModel = CVSVMModel.Trained{1}; % Extract trained, compact classifier
testInds = test(CVSVMModel.Partition);   % Extract the test indices
XTest = X(testInds,:);
YTest = Y(testInds,:);
```

`CVSVMModel` is a `ClassificationPartitionedModel` classifier. It contains the property `Trained`, which is a 1-by-1 cell array holding a `CompactClassificationSVM` classifier that the software trained using the training set.

Label the test sample observations. Display the results for the first 10 observations in the test sample.

```
[label,score] = predict(CompactSVMModel,XTest);
table(YTest(1:10),label(1:10),score(1:10,2),'VariableNames',...
    {'TrueLabel','PredictedLabel','Score'})
```

```
ans =

    TrueLabel    PredictedLabel     Score
    _________    ______________    ________

    'b'          'b'               -1.7177
    'g'          'g'                2.0003
    'b'          'b'               -9.6841
    'g'          'g'                2.5618
    'b'          'b'                -1.548
    'g'          'g'                2.0984
    'b'          'b'               -2.7018
```

```
    'b'          'b'              -0.66291
    'g'          'g'                1.6046
    'g'          'g'                1.7731
```

Predict Labels and Posterior Probabilities of SVM Classifiers

A goal of classification is to predict labels of new observations using a trained algorithm. Many applications train algorithms on large data sets, which can use resources that are better used elsewhere. This example shows how to efficiently label new observations using an SVM classifier.

Load the ionosphere data set. Suppose that the last 10 observations become available after training the SVM classifier.

```
load ionosphere

n = size(X,1);       % Training sample size
isInds = 1:(n-10);   % In-sample indices
oosInds = (n-9):n;   % Out-of-sample indices
```

Train an SVM classifier. It is good practice to standardize the predictors and specify the order of the classes. Conserve memory by reducing the size of the trained SVM classifier.

```
SVMModel = fitcsvm(X(isInds,:),Y(isInds),'Standardize',true,...
    'ClassNames',{'b','g'});
CompactSVMModel = compact(SVMModel);
whos('SVMModel','CompactSVMModel')
```

```
  Name                 Size              Bytes  Class

  CompactSVMModel      1x1               29576  classreg.learning.classif.CompactClassif
  SVMModel             1x1              137550  ClassificationSVM
```

The positive class is `'g'`. The `CompactClassificationSVM` classifier (`CompactSVMModel`) uses less space than the `ClassificationSVM` classifier (`SVMModel`) because the latter stores the data.

Estimate the optimal score-to-posterior-probability-transformation function.

```
CompactSVMModel = fitPosterior(CompactSVMModel,...
    X(isInds,:),Y(isInds))
```

```
CompactSVMModel =

  classreg.learning.classif.CompactClassificationSVM
         PredictorNames: {1x34 cell}
           ResponseName: 'Y'
             ClassNames: {'b'  'g'}
         ScoreTransform: '@(S)sigmoid(S,-1.968452e+00,3.121267e-01)'
                  Alpha: [88x1 double]
                   Bias: -0.2143
       KernelParameters: [1x1 struct]
                     Mu: [1x34 double]
                  Sigma: [1x34 double]
         SupportVectors: [88x34 double]
    SupportVectorLabels: [88x1 double]
```

The optimal score transformation function (`CompactSVMModel.ScoreTransform`) is the sigmoid function because the classes are inseparable.

Predict the out-of-sample labels and positive class posterior probabilities. Since true labels are available, compare them with the predicted labels.

```
[labels,PostProbs] = predict(CompactSVMModel,X(oosInds,:));
table(Y(oosInds),labels,PostProbs(:,2),'VariableNames',...
    {'TrueLabels','PredictedLabels','PosClassPosterior'})
```

```
ans =

    TrueLabels    PredictedLabels    PosClassPosterior
    __________    _______________    _________________

    'g'           'g'                0.98419
    'g'           'g'                0.95545
    'g'           'g'                0.67792
    'g'           'g'                0.94448
    'g'           'g'                0.98744
    'g'           'g'                0.92482
    'g'           'g'                0.97111
    'g'           'g'                0.96986
    'g'           'g'                0.97803
    'g'           'g'                0.94361
```

`PostProbs` is a 10-by-2 matrix; its first column is the negative class posterior probabilities, and second column is the positive class posterior probabilities corresponding to the new observations.

- "Plot Posterior Probability Regions for SVM Classification Models" on page 16-201
- "Train SVM Classifiers Using a Custom Kernel" on page 16-183
- "Analyze Images Using Linear Support Vector Machines" on page 16-204

Algorithms

- By default, the software computes optimal posterior probabilities using Platt's method [1]:

  1. Performing 10-fold cross validation
  2. Fitting the sigmoid function parameters to the scores returned from the cross validation
  3. Estimating the posterior probabilities by entering the cross-validation scores into the fitted sigmoid function

- The software incorporates prior probabilities in the SVM objective function during training.
- For SVM, `predict` classifies observations into the class yielding the largest score (i.e., the largest posterior probability). The software accounts for misclassification costs by applying the average-cost correction before training the classifier. That is, given the class prior vector P, misclassification cost matrix C, and observation weight vector w, the software defines a new vector of observation weights (W) such that

$$W_j = w_j P_j \sum_{k=1}^{K} C_{jk}.$$

References

[1] Platt, J. "Probabilistic outputs for support vector machines and comparisons to regularized likelihood methods." *In Advances in Large Margin Classifiers*. MIT Press, 1999, pages 61–74.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm` | `fitSVMPosterior` | `loss`

More About

- "Support Vector Machines (SVM)" on page 16-170

predict

Class: CompactClassificationTree

Predict classification

Syntax

```
label = predict(tree,X)
[label,score] = predict(tree,X)
[label,score,node] = predict(tree,X)
[label,score,node,cnum] = predict(tree,X)
[label,...] = predict(tree,X,Name,Value)
```

Description

`label = predict(tree,X)` returns a vector of predicted class labels for a matrix `X`, based on `tree`, a trained full or compact classification tree.

`[label,score] = predict(tree,X)` returns a matrix of scores, indicating the likelihood that a label comes from a particular class.

`[label,score,node] = predict(tree,X)` returns a vector of predicted node numbers for the classification, based on `tree`.

`[label,score,node,cnum] = predict(tree,X)` returns a vector of predicted class number for the classification, based on `tree`.

`[label,...] = predict(tree,X,Name,Value)` returns labels with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

A classification tree created by `fitctree`, or a compact classification tree created by `compact`.

`X`

A matrix where each row represents an observation, and each column represents a predictor. The number of columns in `X` must equal the number of predictors in `tree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `CompactClassificationTree.predict` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`CompactClassificationTree.predict` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

Output Arguments

`label`

Vector of class labels of the same type as the response data used in training tree. Each entry of `label` corresponds to the class with minimal expected cost for the corresponding row of `X`. See “Predicted Class Label” on page 22-3708.

If `Subtrees` has `T` elements, and X has `N` rows, then labels is an `N`-by-`T` matrix. The `i`th column of `labels` contains the fitted values produced by the `Subtrees(I)` subtree.

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in `X`, and `K` is the number of classes (in `tree.ClassNames`). `score(i,j)` is the posterior probability that row `i` of `X` is of class `j`.

If `Subtrees` has `T` elements, and X has `N` rows, then score is an `N`-by-`K`-by-`T` array, and node and cnum are `N`-by-`T` matrices.

`node`

Numeric vector of node numbers for the predicted classes. Each entry corresponds to the predicted node in tree for the corresponding row of X.

`cnum`

Numeric vector of class numbers corresponding to the predicted labels. Each entry of `cnum` corresponds to a predicted class number for the corresponding row of `X`.

Definitions

Predicted Class Label

`predict` classifies so as to minimize the expected classification cost:

$$\hat{y} = \underset{y=1,\ldots,K}{\arg\min} \sum_{k=1}^{K} \hat{P}(k \mid x) C(y \mid k),$$

where

- $\hat{y}$ is the predicted classification.
- K is the number of classes.

- $\hat{P}(k \mid x)$ is the posterior probability of class k for observation x.
- $C(y \mid k)$ is the cost of classifying an observation as y when its true class is k.

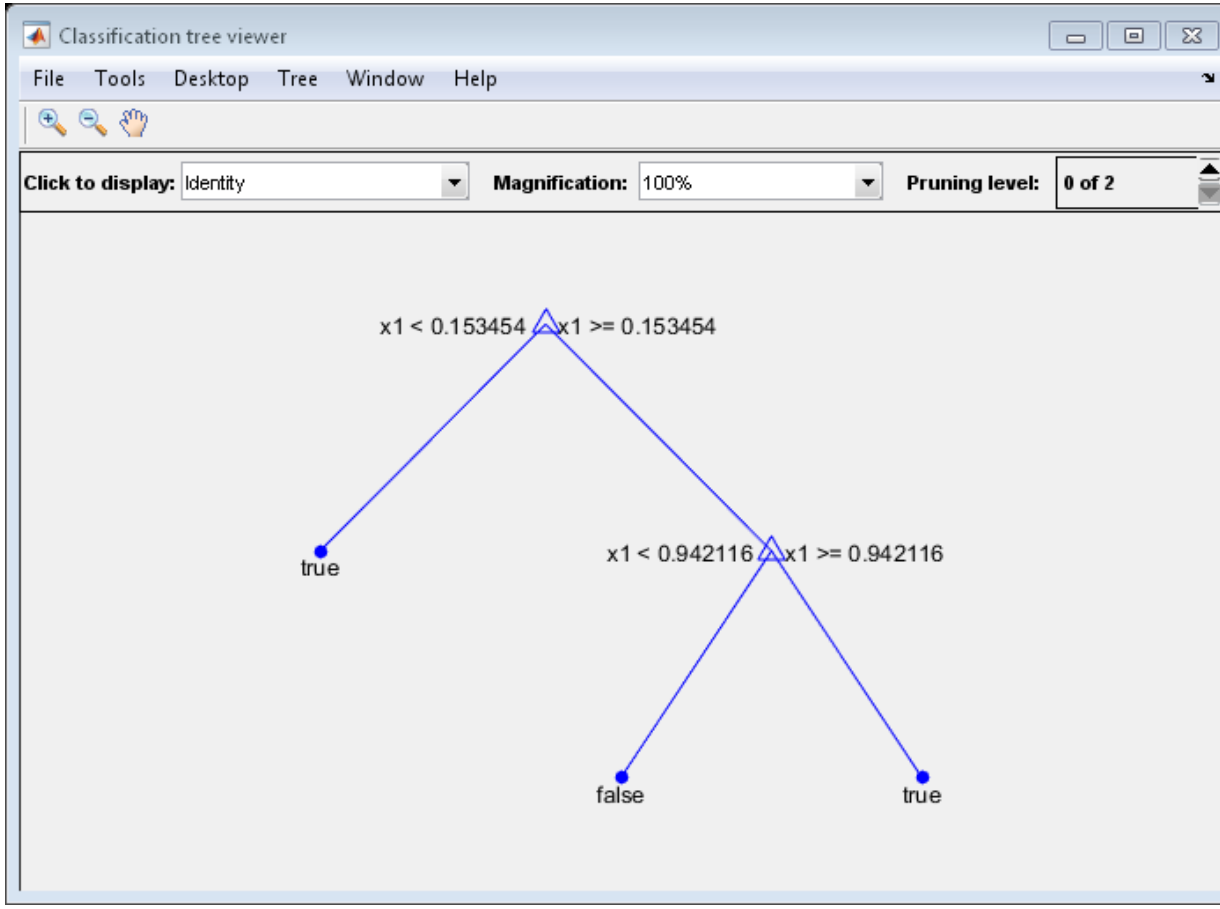
Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

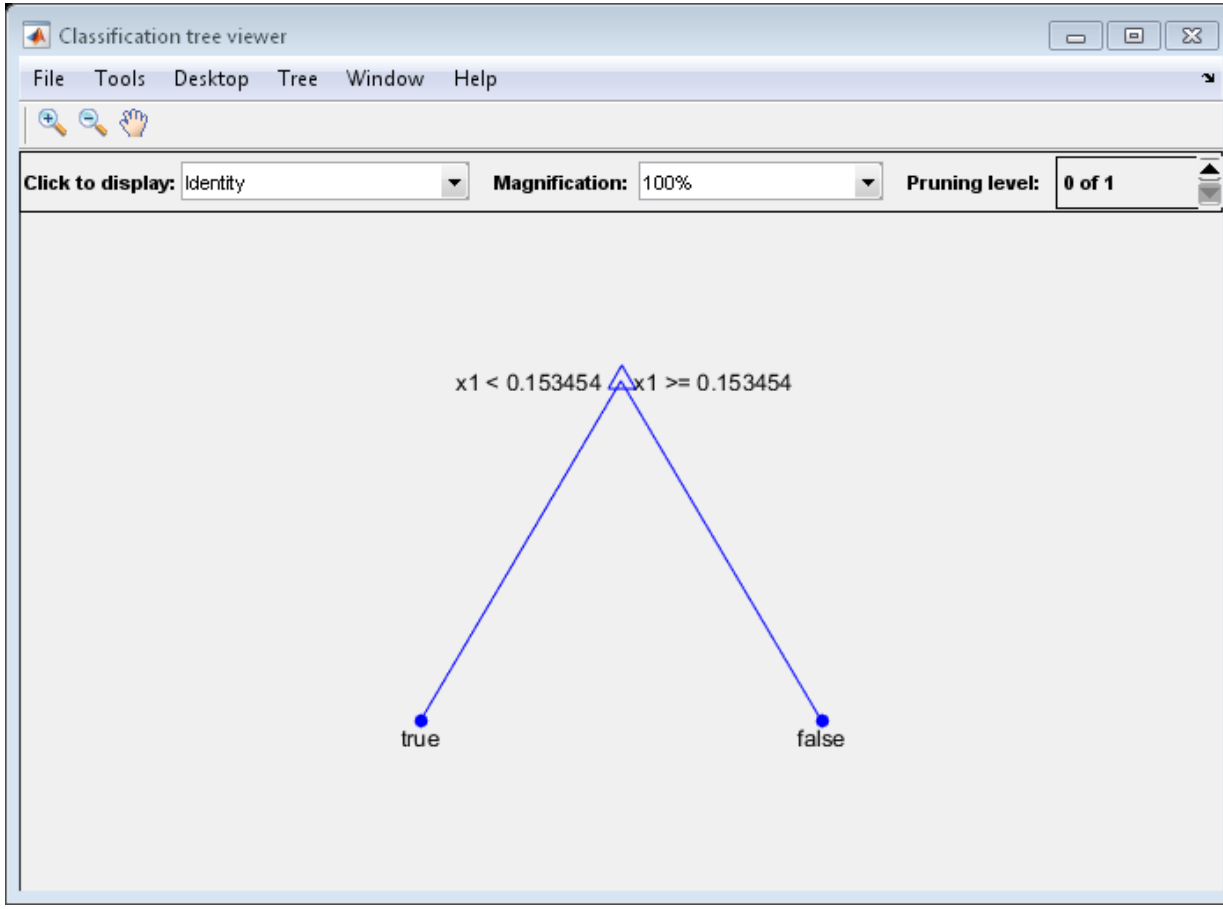
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

True Misclassification Cost

There are two costs associated with classification: the true misclassification cost per class, and the expected misclassification cost per observation.

You can set the true misclassification cost per class in the `Cost` name-value pair when you create the classifier using the `fitctree` method. `Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

Expected Cost

There are two costs associated with classification: the true misclassification cost per class, and the expected misclassification cost per observation.

Suppose you have `Nobs` observations that you want to classify with a trained classifier. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row.

The expected cost matrix `CE` has size `Nobs`-by-`K`. Each row of `CE` contains the expected (average) cost of classifying the observation into each of the `K` classes. `CE(n,k)` is

$$\sum_{i=1}^{K} \hat{P}(i \mid Xnew(n))C(k \mid i),$$

where

- K is the number of classes.
- $\hat{P}(i \mid Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.
- $C(k \mid i)$ is the true misclassification cost of classifying an observation as k when its true class is i.

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Examples

Predict Labels Using a Classification Tree

Examine predictions for a few rows in a data set left out of training.

Load Fisher's iris data set.

```
load fisheriris
```

Partition the data into training (50%) and validation (50%) sets.

```
n = size(meas,1);
rng(1) % For reproducibility
idxTrn = false(n,1);
idxTrn(randsample(n,round(0.5*n))) = true; % Training set logical indices
idxVal = idxTrn == false;                  % Validation set logical indices
```

Grow a classification tree using the training set.

```
Mdl = fitctree(meas(idxTrn,:),species(idxTrn));
```

Predict labels for the validation data. Count the number of misclassified observations.

```
label = predict(Mdl,meas(idxVal,:));
label(randsample(numel(label),5)) % Display several predicted labels
numMisclass = sum(~strcmp(label,species(idxVal)))
```

```
ans =

    'setosa'
    'setosa'
    'setosa'
    'virginica'
    'versicolor'


numMisclass =

     3
```

The software misclassifies three out-of-sample observations.

Estimate Class Posterior Probabilities Using a Classification Tree

Load Fisher's iris data set.

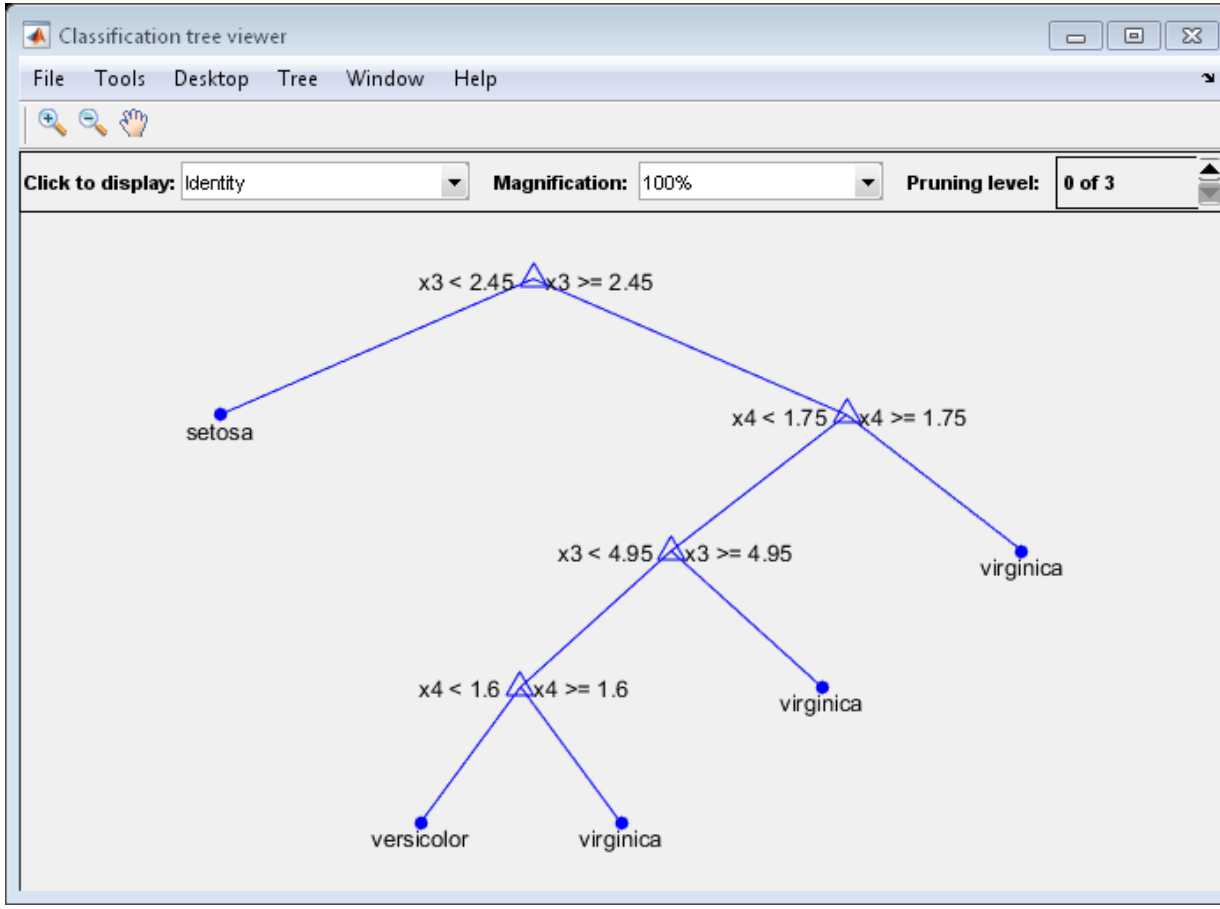
```
load fisheriris
```

Partition the data into training (50%) and validation (50%) sets.

```
n = size(meas,1);
rng(1) % For reproducibility
idxTrn = false(n,1);
idxTrn(randsample(n,round(0.5*n))) = true; % Training set logical indices
idxVal = idxTrn == false;                  % Validation set logical indices
```

Grow a classification tree using the training set, and then view it.

```
Mdl = fitctree(meas(idxTrn,:),species(idxTrn));
view(Mdl,'Mode','graph')
```



The resulting tree has four levels.

Estimate posterior probabilities for the test set using subtrees pruned to levels 1 and 3.

```
[~,Posterior] = predict(Mdl,meas(idxVal,:),'SubTrees',[1 3]);
Mdl.ClassNames
Posterior(randsample(size(Posterior,1),5),:,:),...
    % Display several posterior probabilities
```

```
ans =
```

```
    'setosa'
    'versicolor'
    'virginica'


ans(:,:,1) =

    1.0000         0         0
    1.0000         0         0
    1.0000         0         0
         0         0    1.0000
         0    0.8571    0.1429


ans(:,:,2) =

    0.3733    0.3200    0.3067
    0.3733    0.3200    0.3067
    0.3733    0.3200    0.3067
    0.3733    0.3200    0.3067
    0.3733    0.3200    0.3067
```

The elements of `Posterior` are class posterior probabilities:

- Rows correspond to observations in the validation set.
- Columns correspond to the classes as listed in `Mdl.ClassNames`.
- Pages correspond to the subtrees.

The subtree pruned to level 1 is more sure of its predictions than the subtree pruned to level 3 (i.e., the root node).

Algorithms

`predict` generates predictions by following the branches of `tree` until it reaches a leaf node or a missing value. If `predict` reaches a leaf node, it returns the classification of that node.

If `predict` reaches a node with a missing value for a predictor, its behavior depends on the setting of the `Surrogate` name-value pair when `fitctree` constructs `tree`.

- **`Surrogate = 'off'`** (default) — `predict` returns the label with the largest number of training samples that reach the node.
- **`Surrogate = 'on'`** — `predict` uses the best surrogate split at the node. If all surrogate split variables with positive *predictive measure of association* are missing, `predict` returns the label with the largest number of training samples that reach the node. For a definition, see “Predictive Measure of Association” on page 22-3713.

See Also

`fitctree` | `compact` | `loss` | `margin` | `prune` | `edge`

predict

Class: CompactRegressionEnsemble

Predict response of ensemble

Syntax

```
Yfit = predict(ens,Xdata)
Yfit = predict(ens,Xdata,Name,Value)
```

Description

`Yfit = predict(ens,Xdata)` returns predicted responses to the data in `Xdata`, based on the `ens` regression ensemble model.

`Yfit = predict(ens,Xdata,Name,Value)` predicts with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

Regression ensemble created by `fitensemble`, or by the `compact` method.

`Xdata`

Numeric array with the same number of columns as the array used for creating `ens`. Each row of `Xdata` corresponds to one data point, and each column corresponds to one predictor.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `ens.NumTrained`. `oobEdge` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'UseObsForLearner'`

A logical matrix of size `N`-by-`NumTrained`, where `N` is the number of observations in `ens.X`, and `NumTrained` is the number of weak learners. When `UseObsForLearner(I,J)` is `true`, `predict` uses learner `J` in predicting observation `I`.

Default: `true(N,NumTrained)`

Output Arguments

`Yfit`

A numeric column vector with the same number of rows as Xdata. Each row of `Yfit` gives the predicted response to the corresponding row of `Xdata`, based on the ens regression model.

Examples

Find the predicted mileage for a four-cylinder car, with 200 cubic inch engine displacement, 150 horsepower, weighing 3000 lbs, based on the `carsmall` data:

```
load carsmall
X = [Cylinders Displacement Horsepower Weight];
rens = fitensemble(X,MPG,'LSBoost',100,'Tree');
Mileage = predict(rens,[4 200 150 3000])

Mileage =
   20.4982
```

See Also

`loss` | `fitensemble`

predict

Class: CompactRegressionTree

Predict response of regression tree

Syntax

```
Yfit = predict(tree,Xdata)
[Yfit,node] = predict(tree,Xdata)
[Yfit,node] = predict(tree,Xdata,Name,Value)
```

Description

`Yfit = predict(tree,Xdata)` returns predicted responses to the data in `Xdata`, based on the `tree` regression tree.

`[Yfit,node] = predict(tree,Xdata)` returns the predicted node numbers of `tree` in response to `Xdata`.

`[Yfit,node] = predict(tree,Xdata,Name,Value)` predicts response with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

Regression tree created by `fitrtree`, or by the `compact` method.

`Xdata`

Numeric array with the same number of columns as the array used for creating `tree`. Each row of `Xdata` corresponds to one data point, and each column corresponds to one predictor.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `CompactRegressionTree.predict` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`CompactRegressionTree.predict` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

Output Arguments

`Yfit`

A numeric column vector with the same number of rows as Xdata. Each row of `Yfit` gives the predicted response to the corresponding row of `Xdata`, based on the tree regression model.

`node`

Numeric vector of node numbers for the predictions. Each entry corresponds to the predicted leaf node in tree for the corresponding row of Xdata.

Examples

Predict a Response Using a Regression Tree

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
X = [Displacement Horsepower Weight];
```

Grow a regression tree using the entire data set.

```
Mdl = fitrtree(X,MPG);
```

Predict the MPG for a car with 200 cubic inch engine displacement, 150 horsepower, and that weighs 3000 lbs.

```
X0 = [200 150 3000];
MPG0 = predict(Mdl,X0)
```

```
MPG0 =

   21.9375
```

The regression tree predicts the car's efficiency to be 21.94 mpg.

- “Predict Out-of-Sample Responses of Subtrees” on page 16-41

See Also

`compact` | `fitrtree` | `loss`

More About

- “What Are Classification Trees and Regression Trees?” on page 16-33
- “Predicting Responses With Classification and Regression Trees” on page 16-40

predict

Class: CompactTreeBagger

Predict response

Syntax

```
YFIT = predict(B,X)
[YFIT,stdevs] = predict(B,X)
[YFIT,scores] = predict(B,X)
[YFIT,scores,stdevs] = predict(B,X)
Y = predict(B,X,'param1',val1,'param2',val2,...)
```

Description

`YFIT = predict(B,X)` computes the predicted response of the trained ensemble `B` for predictors `X`. By default, `predict` takes a democratic (nonweighted) average vote from all trees in the ensemble. In `X`, rows represent observations and columns represent variables. `YFIT` is a cell array of strings for classification and a numeric array for regression.

For regression, `[YFIT,stdevs] = predict(B,X)` also returns standard deviations of the computed responses over the ensemble of the grown trees.

For classification, `[YFIT,scores] = predict(B,X)` returns scores for all classes. `scores` is a matrix with one row per observation and one column per class. For each observation and each class, the score generated by each tree is the probability of this observation originating from this class computed as the fraction of observations of this class in a tree leaf. `predict` averages these scores over all trees in the ensemble.

`[YFIT,scores,stdevs] = predict(B,X)` also returns standard deviations of the computed scores for classification. `stdevs` is a matrix with one row per observation and one column per class, with standard deviations taken over the ensemble of the grown trees.

`Y = predict(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Array of tree indices to use for computation of responses. Default is `'all'`.
`'treeweights'`	Array of `NTrees` weights for weighting votes from the specified trees.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees to use to make predictions for each observation. By default all trees are used for all observations.

See Also

`RegressionTree.predict` | `ClassificationTree.predict` | `TreeBagger.predict`

predict

Class: GeneralizedLinearModel

Predict response of generalized linear regression model

Syntax

```
ypred = predict(mdl,Xnew)
[ypred,yci] = predict(mdl,Xnew)
[ypred,yci] = predict(mdl,Xnew,Name,Value)
```

Description

`ypred = predict(mdl,Xnew)` returns the predicted response of the `mdl` generalized linear regression model to the points in `Xnew`.

`[ypred,yci] = predict(mdl,Xnew)` returns confidence intervals for the true mean responses.

`[ypred,yci] = predict(mdl,Xnew,Name,Value)` predicts responses with additional options specified by one or more Name,Value pair arguments.

Tips

- For predictions with added noise, use `random`.
- For a syntax that can be easier to use with models created from dataset arrays, try `feval`.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`Xnew`

Points at which `mdl` predicts responses.

- If `Xnew` is a table or dataset array, it must contain the predictor names in `mdl`.
- If `Xnew` is a numeric matrix, it must have the same number of variables (columns) as was used to create `mdl`. Furthermore, all variables used in creating `mdl` must be numeric.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'alpha'`

Positive scalar from `0` to `1`. Confidence level of `yci` is 100(1 – `alpha`)%.

Default: `0.05`, meaning a 95% confidence interval.

`'BinomialSize'`

Value of the binomial *n* parameter for each row in the training data. `BinomialSize` can be a vector the same length as `Xnew`, or a scalar that applies to each row. The default value `1` produces `ypred` values that are predicted proportions. Use `BinomialSize` only if `mdl` is fit to a binomial distribution.

Default: `1`

`'Offset'`

Value of the offset for each row in `Xnew`. `Offset` can be a vector the same length as `Xnew`, or a scalar that applies to each row. The offset is used as an additional predictor with a coefficient value fixed at `1`. In other words, if `b` is the fitted coefficient vector, and `link` is the link function,
`link(ypred) = Offset + Xnew * b`.

Default: `zeros(size(Xnew,1))`

`'Simultaneous'`

Logical value specifying whether the confidence bounds are for all predictor values simultaneously (`true`), or hold for each individual predictor value (`false`). Simultaneous bounds are wider than separate bounds, because it is more stringent to require that the entire curve be within the bounds than to require that the curve at a single predictor value be within the bounds.

For details, see `polyconf`.

Default: `false`

Output Arguments

`ypred`

Vector of predicted mean values at `Xnew`.

`yci`

Confidence intervals, a two-column matrix with each row providing one interval. The meaning of the confidence interval depends on the settings of the name-value pairs.

Examples

Generalized Linear Model Predictions

Create a generalized linear model, and predict its response to new data.

Generate artificial data for the model using Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data.

```
mdl = fitglm(X,y,'y ~ x1 + x2','distr','poisson');
```

Create points for prediction.

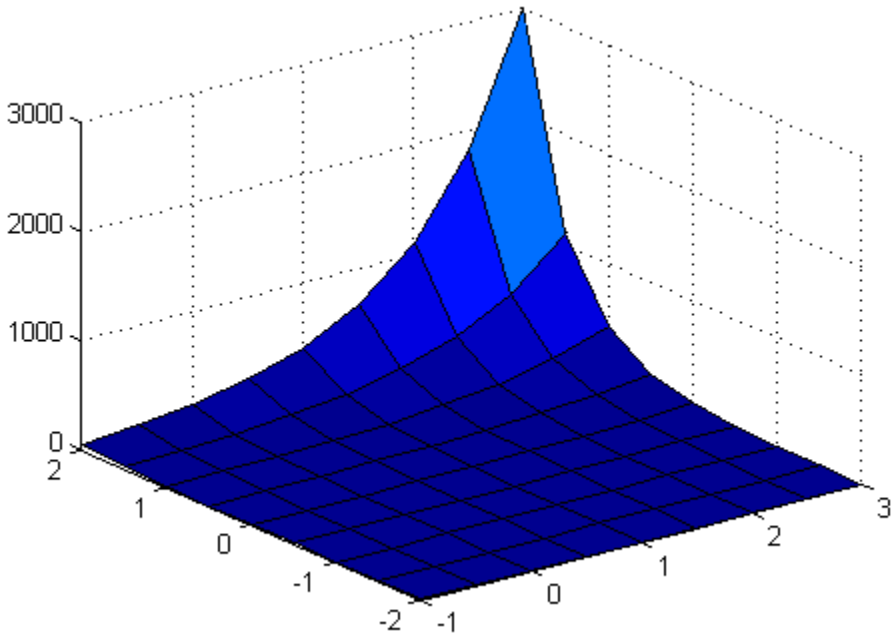
```
[Xtest1 Xtest2] = meshgrid(-1:.5:3,-2:.5:2);
Xnew = [Xtest1(:),Xtest2(:)];
```

Predict responses at the new points.

```
ypred = predict(mdl,Xnew);
```

Plot the predictions.

```
surf(Xtest1,Xtest2,reshape(ypred,9,9))
```



Create confidence intervals on the predictions.

```
[ypred yci] = predict(mdl,Xnew);
```

- “predict” on page 10-34

- “Generalized Linear Model Workflow” on page 10-39

Alternatives

`feval` gives the same predictions, but uses separate input arrays for each predictor, instead of one input array containing all predictors.

`random` predicts with added noise.

See Also

`GeneralizedLinearModel` | `random`

More About

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predict

Class: GeneralizedLinearMixedModel

Predict response of generalized linear mixed-effects model

Syntax

```
ypred = predict(glme)
ypred = predict(glme,tblnew)
ypred = predict( ___ ,Name,Value)
[ypred,ypredCI] = predict( ___ )
[ypred,ypredCI,DF] = predict( ___ )
```

Description

`ypred = predict(glme)` returns the predicted conditional means of the response, ypred, using the original predictor values used to fit the generalized linear mixed-effects model glme.

`ypred = predict(glme,tblnew)` returns the predicted conditional means using the new predictor values specified in tblnew.

If a grouping variable in `tblnew` has levels that are not in the original data, then the random effects for that grouping variable do not contribute to the `'Conditional'` prediction at observations where the grouping variable has new levels.

`ypred = predict( ___ ,Name,Value)` returns the predicted conditional means of the response using additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the confidence level, simultaneous confidence bounds, or contributions from only fixed effects. You can use any of the input arguments in the previous syntaxes.

`[ypred,ypredCI] = predict( ___ )` also returns 95% point-wise confidence intervals, ypredCI, for each predicted value.

`[ypred,ypredCI,DF] = predict( ___ )` also returns the degrees of freedom, DF, used to compute the confidence intervals.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

`tblnew` — New input data

table | `dataset` array

New input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or dataset array. The predictor variables can be continuous or grouping variables. tblnew must have the same variables as the original table or dataset array used in `fitglme` to fit the generalized linear mixed-effects model glme.

Data Types: `single` | `double` | `logical` | `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range [0,1]

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range [0,1]. For a value α, the confidence level is 100 × (1 – α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Conditional'` — Indicator for conditional predictions

`true` (default) | `false`

Indicator for conditional predictions, specified as the comma-separated pair consisting of `'Conditional'` and one of the following.

`true`	Contributions from both fixed effects and random effects (conditional)
`false`	Contribution from only fixed effects (marginal)

Example: `'Conditional',false`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'residual'` (default) | `'none'`

Method for computing approximate degrees of freedom, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'residual'`	The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'none'`	All degrees of freedom are set to infinity.

Example: `'DFMethod','none'`

`'Offset'` — Model offset

`zeros(m,1)` (default) | m-by-1 vector of scalar values

Model offset, specified as a vector of scalar values of length m, where m is the number of rows in tblnew. The offset is used as an additional predictor and has a coefficient value fixed at `1`.

`'Simultaneous'` — Type of confidence bounds

`false` (default) | `true`

Type of confidence bounds, specified as the comma-separated pair consisting of `'Simultaneous'` and either `false` or `true`.

- If `'Simultaneous'` is `false`, then `predict` computes nonsimultaneous confidence bounds.
- If `'Simultaneous'` is `true`, `predict` returns simultaneous confidence bounds.

Example: `'Simultaneous',true`

Output Arguments

`ypred` — Predicted responses

vector

Predicted responses, returned as a vector. If the 'Conditional' name-value pair argument is specified as `true`, ypred contains predictions for the conditional means of the responses given the random effects. Conditional predictions include contributions from both fixed and random effects. Marginal predictions include only contributions from fixed effects.

To compute marginal predictions, `predict` computes conditional predictions, but substitutes a vector of zeros in place of the empirical Bayes predictors (EBPs) of the random effects.

`ypredCI` — Point-wise confidence intervals

two-column matrix

Point-wise confidence intervals for the predicted values, returned as a two-column matrix. The first column of ypredCI contains the lower bound, and the second column contains the upper bound. By default, ypredCI contains the 95% nonsimultaneous confidence intervals for the predictions. You can change the confidence level using the Alpha name-value pair argument, and make them simultaneous using the Simultaneous name-value pair argument.

When fitting a GLME model using `fitglme` and one of the maximum likelihood fit methods (`'Laplace'` or `'ApproximateLaplace'`), `predict` computes the confidence intervals using the conditional mean squared error of prediction (CMSEP) approach conditional on the estimated covariance parameters and the observed response. Alternatively, you can interpret the confidence intervals as approximate Bayesian credible intervals conditional on the estimated covariance parameters and the observed response.

When fitting a GLME model using `fitglme` and one of the pseudo likelihood fit methods (`'MPL'` or `'REMPL'`), `predict` bases the computations on the fitted linear mixed-effects model from the final pseudo likelihood iteration.

`DF` — Degrees of freedom

vector | scalar value

Degrees of freedom used in computing the confidence intervals, returned as a vector or a scalar value.

- If 'Simultaneous' is `false`, then `DF` is a vector.
- If 'Simultaneous' is `true`, then `DF` is a scalar value.

Examples

Predict Responses at Original Design Values

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the

appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Predict the response values at the original design values. Display the first ten predictions along with the observed response values.

```
ypred = predict(glme);
[ypred(1:10),mfr.defects(1:10)]
```

```
ans =

    4.9883    6.0000
```

```
    5.9423    7.0000
    5.1318    6.0000
    5.6295    5.0000
    5.3499    6.0000
    5.2134    5.0000
    4.6430    4.0000
    4.5342    4.0000
    5.3903    9.0000
    4.6529    4.0000
```

Column 1 contains the predicted response values at the original design values. Column 2 contains the observed response values.

Predict Responses at Values in New Table

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Predict the response values at the original design values.

```
ypred = predict(glme);
```

Create a new table by copying the first 10 rows of `mfr` into `tblnew`.

```
tblnew = mfr(1:10,:);
```

The first 10 rows of `mfr` include data collected from trials 1 through 5 for factories 1 and 2. Both factories used the old process for all of their trials during the experiment, so `newprocess = 0` for all 10 observations.

Change the value of `newprocess` to `1` for the observations in `tblnew`.

```
tblnew.newprocess = ones(height(tblnew),1);
```

Compute predicted response values and nonsimultaneous 99% confidence intervals using `tblnew`. Display the first 10 rows of the predicted values based on `tblnew`, the predicted values based on `mfr`, and the observed response values.

```
[ypred_new,ypredCI] = predict(glme,tblnew,'Alpha',0.01);
[ypred_new,ypred(1:10),mfr.defects(1:10)]
```

```
ans =

    3.4536    4.9883    6.0000
    4.1142    5.9423    7.0000
    3.5530    5.1318    6.0000
    3.8976    5.6295    5.0000
    3.7040    5.3499    6.0000
    3.6095    5.2134    5.0000
    3.2146    4.6430    4.0000
    3.1393    4.5342    4.0000
    3.7320    5.3903    9.0000
    3.2214    4.6529    4.0000
```

Column 1 contains predicted response values based on the data in `tblnew`, where `newprocess = 1`. Column 2 contains predicted response values based on the original data in `mfr`, where `newprocess = 0`. Column 3 contains the observed response values in `mfr`. Based on these results, if all other predictors retain their original values, the predicted number of defects appears to be smaller when using the new process.

Display the 99% confidence intervals for rows 1 through 10 corresponding to the new predicted response values.

```
ypredCI(1:10,1:2)
```

```
    1.6983    7.0235
    1.9191    8.8201
    1.8735    6.7380
```

```
    2.0149    7.5395
    1.9034    7.2079
    1.8918    6.8871
    1.6776    6.1597
    1.5404    6.3976
    1.9574    7.1154
    1.6892    6.1436
```

References

[1] Booth, J.G., and J.P. Hobert. "Standard Errors of Prediction in Generalized Linear Mixed Models." *Journal of the American Statistical Association*, Vol. 93, 1998, pp. 262–272.

See Also

`GeneralizedLinearMixedModel` | `fitglme` | `fitted` | `random`

predict

Class: LinearModel

Predict response of linear regression model

Syntax

```
ypred = predict(mdl,Xnew)
[ypred,yci] = predict(mdl,Xnew)
[ypred,yci] = predict(mdl,Xnew,Name,Value)
```

Description

`ypred = predict(mdl,Xnew)` returns the predicted response of the `mdl` linear regression model to the points in `Xnew`.

`[ypred,yci] = predict(mdl,Xnew)` returns confidence intervals for the true mean responses.

`[ypred,yci] = predict(mdl,Xnew,Name,Value)` predicts responses with additional options specified by one or more Name,Value pair arguments.

Tips

- For predictions with added noise, use `random`.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`Xnew`

Points at which `mdl` predicts responses.

- If `Xnew` is a table or dataset array, it must contain the predictor names in `mdl`.
- If `Xnew` is a numeric matrix, it must have the same number of variables (columns) as was used to create `mdl`. Furthermore, all variables used in creating `mdl` must be numeric.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'alpha'`

Positive scalar from `0` to `1`. Confidence level of `yci` is 100(1 – `alpha`)%.

Default: `0.05`, meaning a 95% confidence interval.

`'Prediction'`

String specifying the type of prediction:

- `'curve'` — `predict` predicts confidence bounds for the fitted mean values.
- `'observation'` — `predict` predicts confidence bounds for the new observations. This results in wider bounds because the error in a new observation is equal to the error in the estimated mean value, plus the variability in the observation from the true mean.

For details, see `polyconf`.

Default: `'curve'`

`'Simultaneous'`

Logical value specifying whether the confidence bounds are for all predictor values simultaneously (`true`), or hold for each individual predictor value (`false`). Simultaneous bounds are wider than separate bounds, because it is more stringent to require that the entire curve be within the bounds than to require that the curve at a single predictor value be within the bounds.

For details, see `polyconf`.

Default: `false`

Output Arguments

`ypred`

Vector of predicted mean values at `Xnew`.

`yci`

Confidence intervals, a two-column matrix with each row providing one interval. The meaning of the confidence interval depends on the settings of the name-value pairs.

Examples

Predict Response to Data

Create a model of car mileage as a function of weight, and predict the response.

Create a quadratic model of car mileage as a function of weight from the `carsmall` data.

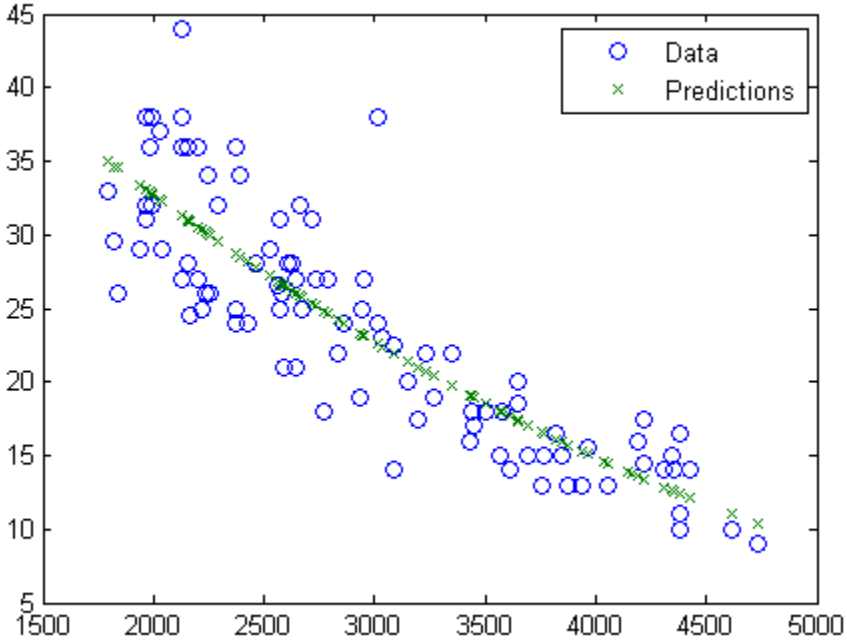
```
load carsmall
X = Weight;
y = MPG;
mdl = fitlm(X,y,'quadratic');
```

Create predicted responses to the data.

```
Xnew = X;
ypred = predict(mdl,Xnew);
```

Plot the original responses and the predicted responses to see how they differ.

```
plot(X,y,'o',Xnew,ypred,'x')
legend('Data','Predictions')
```



- “predict” on page 9-37
- “Linear Regression Workflow” on page 9-41

Alternatives

`feval` gives the same predictions, but uses multiple input arrays with one component in each input argument. `feval` can be simpler to use with a model created from a table or dataset array `tbl`. `feval` does not give confidence intervals on its predictions.

`random` predicts with added noise.

See Also

`random` | `stepwiselm` | `feval` | `LinearModel` | `fitlm`

How To

- “Linear Regression” on page 9-11

predict

Class: LinearMixedModel

Predict response of linear mixed-effects model

Syntax

```
ypred = predict(lme)
ypred = predict(lme,tblnew)
ypred = predict(lme,Xnew,Znew)
ypred = predict(lme,Xnew,Znew,Gnew)
ypred = predict(___,Name,Value)
[ypred,ypredCI] = predict(___)
[ypred,ypredCI,DF] = predict(___)
```

Description

`ypred = predict(lme)` returns a vector of conditional predicted responses `ypred` at the original predictors used to fit the linear mixed-effects model `lme`.

`ypred = predict(lme,tblnew)` returns a vector of conditional predicted responses `ypred` from the fitted linear mixed-effects model `lme` at the values in the new table or dataset array `tblnew`. Use a table or dataset array for `predict` if you use a table or dataset array for fitting the model lme.

If a particular grouping variable in `tblnew` has levels that are not in the original data, then the random effects for that grouping variable do not contribute to the `'Conditional'` prediction at observations where the grouping variable has new levels.

`ypred = predict(lme,Xnew,Znew)` returns a vector of conditional predicted responses `ypred` from the fitted linear mixed-effects model `lme` at the values in the new fixed- and random-effects design matrices, `Xnew` and `Znew`, respectively. `Znew` can also be a cell array of matrices. In this case, the grouping variable G is `ones(n,1)`, where n is the number of observations used in the fit.

Use the matrix format for `predict` if using design matrices for fitting the model `lme`.

`ypred = predict(lme,Xnew,Znew,Gnew)` returns a vector of conditional predicted responses `ypred` from the fitted linear mixed-effects model `lme` at the values in the new fixed- and random-effects design matrices, `Xnew` and `Znew`, respectively, and the grouping variable `Gnew`.

`Znew` and `Gnew` can also be cell arrays of matrices and grouping variables, respectively.

`ypred = predict( ___ ,Name,Value)` returns a vector of predicted responses `ypred` from the fitted linear mixed-effects model `lme` with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the confidence level, simultaneous confidence bounds, or contributions from only fixed effects.

`[ypred,ypredCI] = predict( ___ )` also returns confidence intervals `ypredCI` for the predictions `ypred` for any of the input arguments in the previous syntaxes.

`[ypred,ypredCI,DF] = predict( ___ )` also returns the degrees of freedom `DF` used in computing the confidence intervals for any of the input arguments in the previous syntaxes.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

`tblnew` — New input data

table | `dataset` array

New input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or dataset array. The predictor variables can be continuous or grouping variables. `tblnew` must have the same variables as in the original table or dataset array used to fit the linear mixed-effects model `lme`.

Data Types: `single` | `double` | `logical` | `char`

`Xnew` — New fixed-effects design matrix

n-by-*p* matrix

New fixed-effects design matrix, specified as an *n*-by-*p* matrix, where *n* is the number of observations and *p* is the number of fixed predictor variables. Each row of `X` corresponds to one observation and each column of `X` corresponds to one variable.

Data Types: `single` | `double`

`Znew` — New random-effects design

n-by-*q* matrix | cell array of length *R*

New random-effects design, specified as an *n*-by-*q* matrix or a cell array of *R* design matrices `Z{r}`, where *r* = 1, 2, ..., *R*. If `Znew` is a cell array, then each `Z{r}` is an *n*-by-*q*(*r*) matrix, where *n* is the number of observations, and *q*(*r*) is the number of random predictor variables.

Data Types: `single` | `double` | `logical` | `char` | `cell`

`Gnew` — New grouping variable or variables

vector | cell array of grouping variables of length *R*

New grouping variable or variables, specified as a vector or a cell array, of length *R*, of grouping variables with the same levels or groups as the original grouping variables used to fit the linear mixed-effects model lme.

Data Types: `single` | `double` | `logical` | `char` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 to 1

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range 0 to 1. For a value α, the confidence level is 100*(1–α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Conditional'` — Indicator for conditional predictions

True (default) | False

Indicator for conditional predictions, specified as the comma-separated pair consisting of `'Conditional'` and one of the following.

`True`	Contributions from both fixed effects and random effects (conditional)
`False`	Contribution from only fixed effects (marginal)

Example: `'Conditional','False'`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'Residual'` (default) | `'Satterthwaite'` | `'None'`

Method for computing approximate degrees of freedom to use in the confidence interval computation, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'Residual'`	Default. The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'Satterthwaite'`	Satterthwaite approximation.
`'None'`	All degrees of freedom are set to infinity.

For example, you can specify the Satterthwaite approximation as follows.

Example: `'DFMethod','Satterthwaite'`

`'Simultaneous'` — Type of confidence bounds

`false` (default) | `true`

Type of confidence bounds, specified as the comma-separated pair consisting of `'Simultaneous'` and one of the following.

`false`	Default. Nonsimultaneous bounds.
`true`	Simultaneous bounds.

Example: `'Simultaneous',true`

`'Prediction'` — Type of prediction
`'curve'` (default) | `'observation'`

Type of prediction, specified as the comma-separated pair consisting of `'Prediction'` and one of the following.

`'curve'`	Default. Confidence bounds for the predictions based on the fitted function.
`'observation'`	Variability due to observation error for the new observations is also included in the confidence bound calculations and this results in wider bounds.

Example: `'Prediction','observation'`

Output Arguments

`ypred` — Predicted responses
vector

Predicted responses, returned as a vector. `ypred` can contain the conditional or marginal responses, depending on the value choice of the 'Conditional' name-value pair argument. Conditional predictions include contributions from both fixed and random effects.

`ypredCI` — Point-wise confidence intervals
two-column matrix

Point-wise confidence intervals for the predicted values, returned as a two-column matrix. The first column of `yCI` contains the lower bounds, and the second column contains the upper bound. By default, `yCI` contains the 95% confidence intervals for the predictions. You can change the confidence level using the Alpha name-value pair

argument, make them simultaneous using the Simultaneous name-value pair argument, and also make them for a new observation rather than for the curve using the Prediction name-value pair argument.

`DF` — Degrees of freedom

vector | scalar value

Degrees of freedom used in computing the confidence intervals, returned as a vector or a scalar value.

- If the 'Simultaneous' name-value pair argument is `false`, then `DF` is a vector.
- If the 'Simultaneous' name-value pair argument is `true`, then `DF` is a scalar value.

Examples

Predict Responses at the Original Design Values

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Predict the response values at the original design values. Display the first five predictions with the observed response values.

```
yhat = predict(lme);
[yhat(1:5) ds.Yield(1:5)]
```

```
ans =

  115.4788  104.0000
  135.1455  136.0000
  152.8121  158.0000
  160.4788  174.0000
   58.0839   57.0000
```

Plot Predictions vs. Observed Responses

Load the sample data.

```
load carsmall
```

Fit a linear mixed-effects model, with a fixed effect for `Weight`, and a random intercept grouped by `Model_Year`. First, store the data in a table.

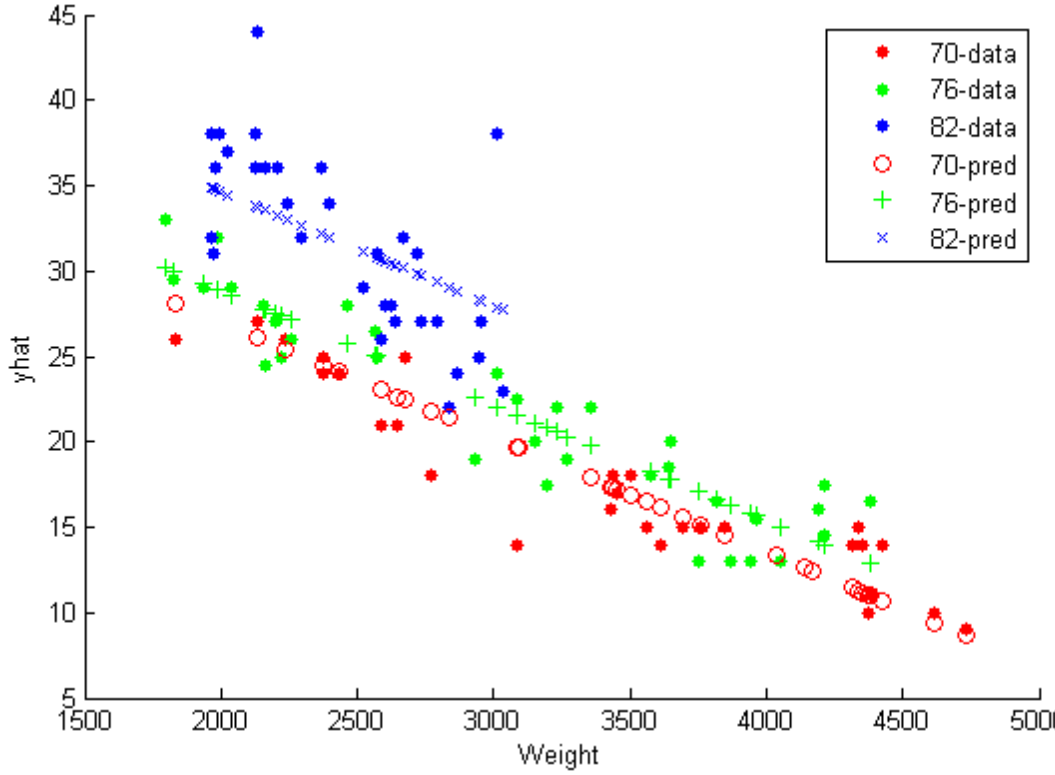
```
tbl = table(MPG,Weight,Model_Year);
lme = fitlme(tbl,'MPG ~ Weight + (1|Model_Year)');
```

Create predicted responses to the data.

```
yhat = predict(lme,tbl);
```

Plot the original responses and the predicted responses to see how they differ. Group them by model year.

```
figure()
gscatter(Weight,MPG,Model_Year)
hold on
gscatter(Weight,yhat,Model_Year,[],'o+x')
legend('70-data','76-data','82-data','70-pred','76-pred','82-pred')
hold off
```



Predict Responses at Values in a New Dataset Array

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and

plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Create a new dataset array with design values. The new dataset array must have the same variables as the original dataset array you use for fitting the model `lme`.

```
dsnew = dataset();
dsnew.Soil = nominal({'Sandy';'Silty'});
dsnew.Tomato = nominal({'Cherry';'Vine'});
dsnew. Fertilizer = nominal([2;2]);
```

Predict the conditional and marginal responses at the original design points.

```
yhatC = predict(lme,dsnew);
yhatM = predict(lme,dsnew,'Conditional',false);
[yhatC yhatM]
```

```
ans =

   92.7505  111.6667
   87.5891   82.6667
```

Predict Responses at the Values in New Design Matrices

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower, and cylinders, and potentially correlated random effects for intercept and acceleration grouped by model year.

First, prepare the design matrices for fitting the linear mixed-effects model.

```
X = [ones(406,1) Acceleration Horsepower];
Z = [ones(406,1) Acceleration];
Model_Year = nominal(Model_Year);
G = Model_Year;
```

Now, fit the model using `fitlmematrix` with the defined design matrices and grouping variables.

```
lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept','Acceleration'}},'RandomEffectGroups',{'Model_Year'});
```

Create the design matrices that contain the data at which to predict the response values. `Xnew` must have three columns as in `X`. The first column must be a column of 1s. And the values in the last two columns must correspond to `Acceleration` and `Horsepower`, respectively. The first column of `Znew` must be a column of 1s, and the second column must contain the same `Acceleration` values as in `Xnew`. The original grouping variable in `G` is the model year. So, `Gnew` must contain values for the model year. Note that `Gnew` must contain nominal values.

```
Xnew = [1,13.5,185; 1,17,205; 1,21.2,193];
Znew = [1,13.5; 1,17; 1,21.2]; % alternatively Znew = Xnew(:,1:2);
Gnew = nominal([73 77 82]);
```

Predict the responses for the data in the new design matrices.

```
yhat = predict(lme,Xnew,Znew,Gnew)
```

```
yhat =

    8.7063
    5.4423
   12.5384
```

Now, repeat the same for a linear mixed-effects model with uncorrelated random-effects terms for intercept and acceleration. First, change the original random effects design and the random effects grouping variables. Then, refit the model.

```
Z = {ones(406,1),Acceleration};
G = {Model_Year,Model_Year};

lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
```

```
{{'Intercept'},{'Acceleration'}},'RandomEffectGroups',{'Model_Year','Model_Year'})
```

Now, recreate the new random effects design, `Znew`, and the grouping variable design, `Gnew`, using which to predict the response values.

```
Znew = {[1;1;1],[13.5;17;21.2]};
MY = nominal([73 77 82]);
Gnew = {MY,MY};
```

Predict the responses using the new design matrices.

```
yhat = predict(lme,Xnew,Znew,Gnew)
```

```
yhat =

    8.6365
    5.9199
   12.1247
```

Compute Confidence Intervals for Predictions

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower, and cylinders, and potentially correlated random effects for intercept and acceleration grouped by model year. First, store the variables in a table.

```
tbl = table(MPG,Acceleration,Horsepower,Model_Year);
```

Now, fit the model using `fitlme` with the defined design matrices and grouping variables.

```
lme = fitlme(tbl,'MPG ~ Acceleration + Horsepower + (Acceleration|Model_Year)');
```

Create the new data and store it in a new table.

```
tblnew = table();
tblnew.Acceleration = linspace(8,25)';
tblnew.Horsepower = linspace(nanmin(Horsepower),nanmax(Horsepower))';
tblnew.Model_Year = repmat(70,100,1);
```

`linspace` creates 100 equally distanced values between the lower and the upper input limits. `Model_Year` is fixed at 70. You can repeat this for any model year.

Compute and plot the predicted values and 95% confidence limits (nonsimultaneous).

```
[ypred,yCI,DF] = predict(lme,tblnew);
figure();
h1 = line(tblnew.Acceleration,ypred);
hold on;
h2 = plot(tblnew.Acceleration,yCI,'g-.');
```

Display the degrees of freedom.

```
DF(1)
```

```
ans =

   389
```

Compute and plot the simultaneous confidence bounds.

```
[ypred,yCI,DF] = predict(lme,tblnew,'Simultaneous',true);
h3 = plot(tblnew.Acceleration,yCI,'r--');
```

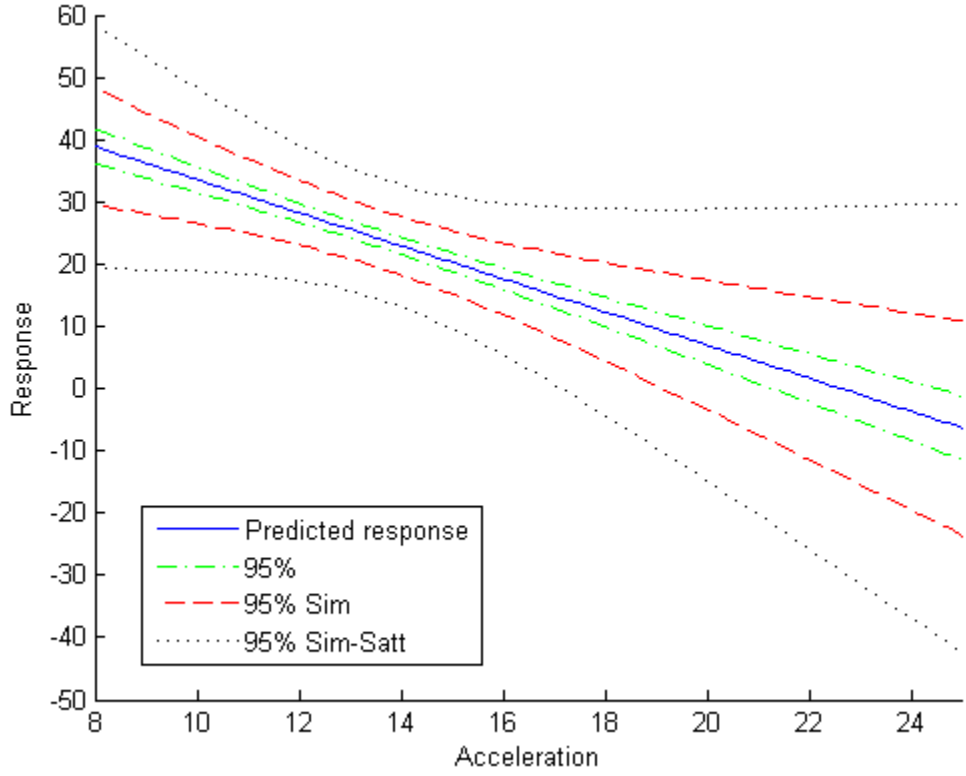
Display the degrees of freedom.

```
DF
```

```
DF =

   389
```

Compute the simultaneous confidence bounds using the Satterthwaite method to compute the degrees of freedom.

```
[ypred,yCI,DF] = predict(lme,tblnew,'Simultaneous',true,'DFMethod','Satterthwaite');
h4 = plot(tblnew.Acceleration,yCI,'k:');
hold off
xlabel('Acceleration')
ylabel('Response')
ylim([-50,60])
xlim([8,25])
legend([h1,h2(1),h3(1),h4(1)],'Predicted response','95%','95% Sim',...
'95% Sim-Satt','Location','Best')
```



Display the degrees of freedom.

```
DF
```

```
DF =
```

```
3.6001
```

Definitions

Conditional and Marginal Predictions

A conditional prediction includes contributions from both fixed and random effects, whereas a marginal model includes contribution from only fixed effects.

Suppose the linear mixed-effects model `lme` has an n-by-p fixed-effects design matrix `X` and an n-by-q random-effects design matrix `Z`. Also, suppose the estimated p-by-1 fixed-effects vector is $\hat{\beta}$, and the q-by-1 estimated best linear unbiased predictor (BLUP) vector of random effects is $\hat{b}$. The predicted conditional response is

$$\hat{y}_{Cond} = X\hat{\beta} + Z\hat{b},$$

which corresponds to the `'Conditional','true'` name-value pair argument.

The predicted marginal response is

$$\hat{y}_{Mar} = X\hat{\beta},$$

which corresponds to the `'Conditional','false'` name-value pair argument.

When making predictions, if a particular grouping variable has new levels (1s that were not in the original data), then the random effects for the grouping variable do not contribute to the `'Conditional'` prediction at observations where the grouping variable has new levels.

See Also

`fitted` | `LinearMixedModel` | `random`

predict

Class: NaiveBayes

Predict class label for test data

Syntax

```
cpre = predict(nb,test)
cpre = predict(...,'HandleMissing',val)
```

Description

`cpre = predict(nb,test)` classifies each row of data in `test` into one of the classes according to the `NaiveBayes` classifier `nb`, and returns the predicted class level `cpre`. `test` is an `N`-by-`nb.ndims` matrix, where `N` is the number of observations in the test data. Rows of `test` correspond to points, columns of `test` correspond to features. `cpre` is an `N`-by-1 vector of the same type as `nb.CLevels`, and it indicates the class to which each row of `test` has been assigned.

`cpre = predict(...,'HandleMissing',val)` specifies how `predict` treats `NaN` (missing values). `val` can be one of the following:

`'off'` (default)	Observations with `NaN` in any of the columns are not classified into any class. The corresponding rows in `cpre` are `NaN` (if `obj.clevels` is numeric or logical), empty strings (if `obj.clevels` is char or cell array of strings) or `<undefined>` (if `obj.clevels` is categorical).
`'on'`	For observations having `NaN` in some (but not all) columns, `predict` computes `cpre` using the columns with non-`NaN` values. Corresponding `cpre` values are `NaN`.

See Also

`NaiveBayes` | `fitNaiveBayes` | `posterior`

predict

Class: NonLinearModel

Predict response of nonlinear regression model

Syntax

```
ypred = predict(mdl,Xnew)
[ypred,yci] = predict(mdl,Xnew)
[ypred,yci] = predict(mdl,Xnew,Name,Value)
```

Description

`ypred = predict(mdl,Xnew)` returns the predicted response of the `mdl` nonlinear regression model to the points in `Xnew`.

`[ypred,yci] = predict(mdl,Xnew)` returns confidence intervals for the true mean responses.

`[ypred,yci] = predict(mdl,Xnew,Name,Value)` predicts responses with additional options specified by one or more Name,Value pair arguments.

Tips

- For predictions with added noise, use `random`.
- For a syntax that can be easier to use with models created from tables or dataset arrays, try `feval`.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

`Xnew`

Points at which `mdl` predicts responses.

- If `Xnew` is a table or dataset array, it must contain the predictor names in `mdl`.
- If `Xnew` is a numeric matrix, it must have the same number of variables (columns) as was used to create `mdl`. Furthermore, all variables used in creating `mdl` must be numeric.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'alpha'`

Positive scalar from `0` to `1`. Confidence level of `yci` is 100(1 – `alpha`)%.

Default: `0.05`, meaning a 95% confidence interval.

`'Prediction'`

String specifying the type of prediction:

- `'curve'` — `predict` predicts confidence bounds for the fitted mean values.
- `'observation'` — `predict` predicts confidence bounds for the new observations. This results in wider bounds because the error in a new observation is equal to the error in the estimated mean value, plus the variability in the observation from the true mean.

For details, see `polyconf`.

Default: `'curve'`

`'Simultaneous'`

Logical value specifying whether the confidence bounds are for all predictor values simultaneously (`true`), or hold for each individual predictor value (`false`). Simultaneous bounds are wider than separate bounds, because it is more stringent to require that the entire curve be within the bounds than to require that the curve at a single predictor value be within the bounds.

For details, see `polyconf`.

Default: `false`

`'Weights'`

Vector of real, positive value weights or a function handle.

- If you specify a vector, then it must have the same number of elements as the number of observations (or rows) in `Xnew`.
- If you specify a function handle, then the function must accept a vector of predicted response values as input, and return a vector of real positive weights as output.

Given weights, `W`, `predict` estimates the error variance at observation `i` by `MSE*(1/W(i))`, where MSE is the mean squared error.

Default: No weights

Output Arguments

`ypred`

Vector of predicted mean values at `Xnew`.

`yci`

Confidence intervals, a two-column matrix with each row providing one interval. The meaning of the confidence interval depends on the settings of the name-value pairs.

Examples

Predict Responses

Create a nonlinear model of car mileage as a function of weight, and predict the response.

Create an exponential model of car mileage as a function of weight from the `carsmall` data. Scale the weight by a factor of 1000 so all the variables are roughly equal in size.

```
load carsmall
X = Weight;
```

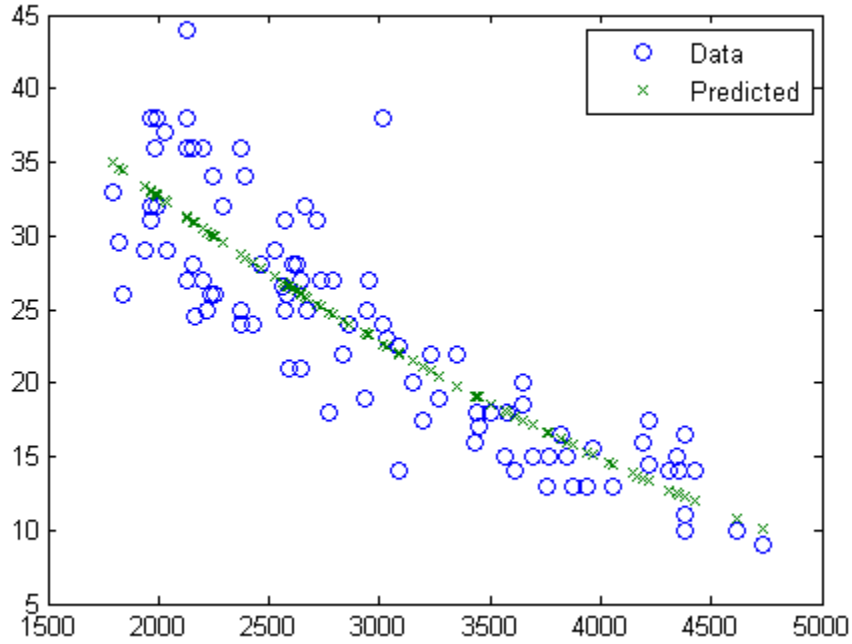
```
y = MPG;
modelfun = 'y ~ b1 + b2*exp(-b3*x/1000)';
beta0 = [1 1 1];
mdl = fitnlm(X,y,modelfun,beta0);
```

Create predicted responses to the data.

```
Xnew = X;
ypred = predict(mdl,Xnew);
```

Plot the original responses and the predicted responses to see how they differ.

```
plot(X,y,'o',X,ypred,'x')
legend('Data','Predicted')
```



Confidence Intervals for Predictions

Create a nonlinear model of car mileage as a function of weight, and examine confidence intervals of some responses.

Create an exponential model of car mileage as a function of weight from the `carsmall` data. Scale the weight by a factor of 1000 so all the variables are roughly equal in size.

```
load carsmall
X = Weight;
y = MPG;
modelfun = 'y ~ b1 + b2*exp(-b3*x/1000)';
beta0 = [1 1 1];
mdl = fitnlm(X,y,modelfun,beta0);
```

Create predicted responses to the smallest, mean, and largest data points.

```
Xnew = [min(X);mean(X);max(X)];
[ypred,yci] = predict(mdl,Xnew)
```

```
ypred =
   34.9469
   22.6868
   10.0617

yci =
   32.5212   37.3726
   21.4061   23.9674
    7.0148   13.1086
```

Simultaneous Confidence Intervals for Robust Fit Curve

Generate sample data from the nonlinear regression model

$$y = b_1 + b_2 \exp\{-b_3 x\} + \varepsilon,$$

where b_1, b_2, and b_3 are coefficients, and the error term is normally distributed with mean 0 and standard deviation 0.5.

```
modelfun = @(b,x)(b(1)+b(2)*exp(-b(3)*x));

rng('default') % for reproducibility
b = [1;3;2];
x = exprnd(2,100,1);
y = modelfun(b,x) + normrnd(0,0.5,100,1);
```

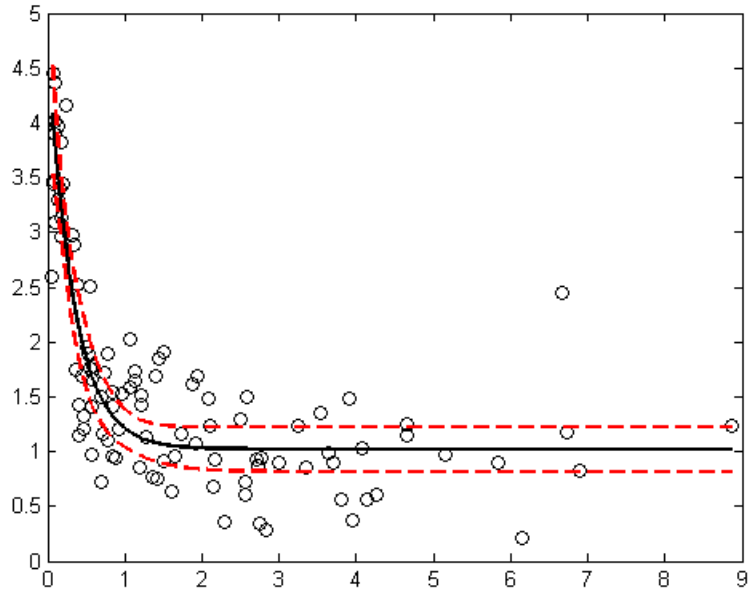
Fit the nonlinear model using robust fitting options.

```
opts = statset('nlinfit');
opts.RobustWgtFun = 'bisquare';
```

```
b0 = [2;2;2];
mdl = fitnlm(x,y,modelfun,b0,'Options',opts);
```

Plot the fitted regression model and simultaneous 95% confidence bounds.

```
xrange = [min(x):.01:max(x)]';
[ypred,yci] = predict(mdl,xrange,'Simultaneous',true);

figure()
plot(x,y,'ko') % observed data
hold on
plot(xrange,ypred,'k','LineWidth',2)
plot(xrange,yci','r--','LineWidth',1.5)
```



Confidence Interval Using Observation Weights

Load sample data.

```
S = load('reaction');
X = S.reactants;
```

```
y = S.rate;
beta0 = S.beta;
```

Specify a function handle for observation weights, then fit the Hougen-Watson model to the rate data using the specified observation weights function.

```
a = 1; b = 1;
weights = @(yhat) 1./((a + b*abs(yhat)).^2);
mdl = fitnlm(X,y,@hougen,beta0,'Weights',weights);
```

Compute the 95% prediction interval for a new observation with reactant levels `[100,100,100]` using the observation weight function.

```
[ypred,yci] = predict(mdl,[100,100,100],'Prediction','observation',...
                      'Weights',weights)
```

```
ypred =

    1.8149


yci =

    1.5264    2.1033
```

- "Predict or Simulate Responses Using a Nonlinear Model" on page 11-10
- "Nonlinear Regression Workflow" on page 11-14

References

[1] Lane, T. P. and W. H. DuMouchel. "Simultaneous Confidence Intervals in Multiple Regression." *The American Statistician*. Vol. 48, No. 4, 1994, pp. 315–321.

[2] Seber, G. A. F., and C. J. Wild. *Nonlinear Regression*. Hoboken, NJ: Wiley-Interscience, 2003.

See Also

`NonLinearModel` | `random`

More About

- "Nonlinear Regression" on page 11-2

predict

Class: RepeatedMeasuresModel

Compute predicted values given predictor values

Syntax

```
ypred = predict(rm,tnew)
ypred = predict(rm,tnew,Name,Value)
[ypred,yci] = predict( ___ )
```

Description

`ypred = predict(rm,tnew)` returns the predicted values from the repeated measures model rm using the predictor values from the table t.

`ypred = predict(rm,tnew,Name,Value)` returns the predicted values from the repeated measures model rm with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the within-subjects design matrix.

`[ypred,yci] = predict( ___ )` also returns the 95% confidence interval for the predicted values.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`tnew` — New data

table used to create `rm` (default) | table

New data including the values of the response variables and the between-subject factors used as predictors in the repeated measures model, rm, specified as a table. `tnew` must contain all of the between-subject factors used to create rm.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range of 0 through 1

Confidence level of the confidence intervals for the predicted values, specified as the comma-separated pair consisting of `'alpha'` and a scalar value in the range of 0 to 1. The confidence level is 100*(1–`alpha`)%.

Example: `'alpha',0.01`

Data Types: `double` | `single`

`'WithinModel'` — Model for within-subject factors

`'separatemeans'` | `'orthogonalcontrats'` | text string

Model for the within-subject factors, specified as the comma-separated pair consisting of `'WithinModel'` and one of the following:

- `'separatemeans'` — Compute a separate mean for each group.
- `'orthogonalcontrasts'` — Valid when the within-subject design consists of a single numeric factor T. This specifies a model consisting of orthogonal polynomials up to order $T^{(r-1)}$, where r is the number of repeated measures.
- A string that defines a model specification in the within-subject factors.

Example: `'WithinModel','orthogonalcontrasts'`

`'WithinDesign'` — Design for within-subject factors

vector | matrix | table

Design for within-subject factors, specified as the comma-separated pair consisting of `'WithinDesign'` and a vector, matrix, or a table. It provides the values of the within-subject factors in the same form as the `RM.WithinDesign` property.

Example: `'WithinDesign','Time'`

Data Types: `single | double | table`

Output Arguments

`ypred` — Predicted values

n-by-*r* matrix

Predicted values from the repeated measures model `rm`, returned as an *n*-by-*r* matrix, where *n* is the number of rows in tnew and *r* is the number of repeated measures in rm.

`yci` — Confidence intervals for predicted values

n-by-*r*-by-2 matrix

Confidence intervals for predicted values from the repeated measures model `rm`, returned as an *n*-by-*r*-by-2 matrix.

These are nonsimultaneous intervals for predicting the mean response at the specified predictor values. For predicted value `ypred(i,j)`, the lower limit of the interval is `yci(i,j,1)` and the upper limit is `yci(i,j,2)`.

Examples

Predict Response Values

Load the sample data.

```
load fisheriris
```

The column vector,`species`consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the `species` is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Predict responses for the three species.

```
Y = predict(rm,t([1 51 101],:))
```

```
Y =

    5.0060    3.4280    1.4620    0.2460
    5.9360    2.7700    4.2600    1.3260
    6.5880    2.9740    5.5520    2.0260
```

Predict Response Values and Plot Predictions

Navigate to the folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load('longitudinalData')
```

The matrix Y contains response data for 16 individuals. The response is the blood level of a drug measured at five time points (time = 0, 2, 4, 6, and 8). Each row of Y corresponds to an individual, and each column corresponds to a time point. The first eight subjects are female, and the second eight subjects are male. This is simulated data.

Define a variable that stores gender information.

```
Gender = ['F' 'F' 'F' 'F' 'F' 'F' 'F' 'F' 'M' 'M' 'M' 'M' 'M' 'M' 'M' 'M']';
```

Store the data in a proper table array format to perform repeated measures analysis.

```
t = table(Gender,Y(:,1),Y(:,2),Y(:,3),Y(:,4),Y(:,5),...
'VariableNames',{'Gender','t0','t2','t4','t6','t8'});
```

Define the within-subjects variable.

```
Time = [0 2 4 6 8]';
```

Fit a repeated measures model, where the blood levels are the responses and gender is the predictor variable.

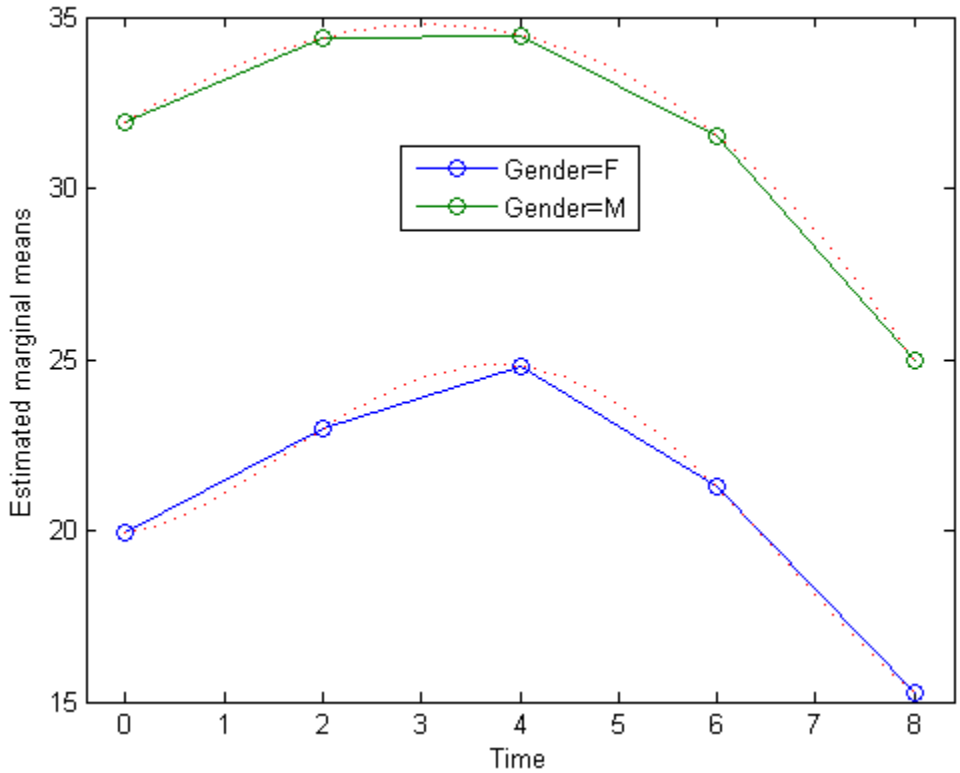
```
rm = fitrm(t,'t0-t8 ~ Gender','WithinDesign',Time);
```

Predict the responses at intermediate times.

```
time = linspace(0,8)';
Y = predict(rm,t([1 5 8 12],:), ...
    'WithinModel','orthogonalcontrasts','WithinDesign',time);
```

Plot the predictions along with the estimated marginal means.

```
plotprofile(rm,'Time','Group',{'Gender'})
hold on;
plot(time,Y,'Color','r','LineStyle',':');
hold off
```



Compute and Plot Confidence Intervals

Navigate to the folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load('longitudinalData')
```

The matrix Y contains response data for 16 individuals. The response is the blood level of a drug measured at five time points (time = 0, 2, 4, 6, and 8). Each row of Y corresponds to an individual, and each column corresponds to a time point. The first eight subjects are female, and the second eight subjects are male. This is simulated data.

Define a variable that stores gender information.

```
Gender = ['F' 'F' 'F' 'F' 'F' 'F' 'F' 'F' 'M' 'M' 'M' 'M' 'M' 'M' 'M' 'M']';
```

Store the data in a proper table array format to perform repeated measures analysis.

```
t = table(Gender,Y(:,1),Y(:,2),Y(:,3),Y(:,4),Y(:,5),...
'VariableNames',{'Gender','t0','t2','t4','t6','t8'});
```

Define the within-subjects variable.

```
Time = [0 2 4 6 8]';
```

Fit a repeated measures model, where the blood levels are the responses and gender is the predictor variable.

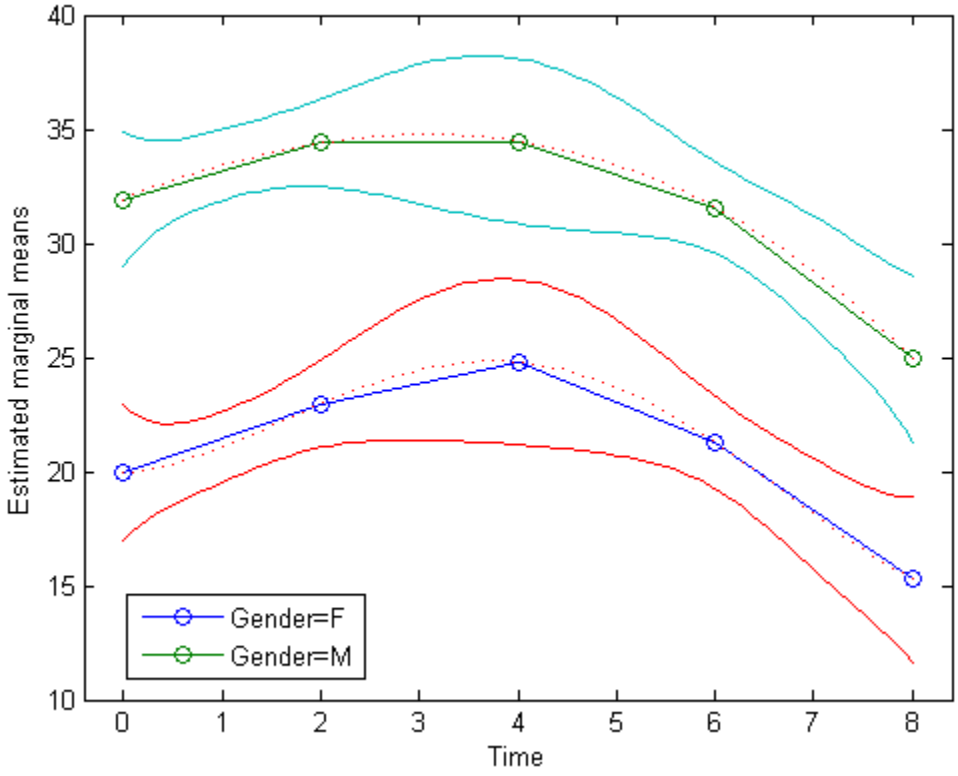
```
rm = fitrm(t,'t0-t8 ~ Gender','WithinDesign',Time);
```

Predict the responses at intermediate times.

```
time = linspace(0,8)';
[ypred,ypredci] = predict(rm,t([1 5 8 12],:), ...
    'WithinModel','orthogonalcontrasts','WithinDesign',time);
```

Plot the predictions and the confidence intervals for predictions along with the estimated marginal means.

```
plotprofile(rm,'Time','Group',{'Gender'})
hold on;
plot(time,ypred,'Color','r','LineStyle',':');
plot(time,ypredci(:,:,1))
plot(time,ypredci(:,:,2))
hold off
```



See Also

`fitrm` | `random`

predict

Class: TreeBagger

Predict response

Syntax

```
Y = predict(B,X)
[Y,stdevs] = predict(B,X)
[Y,scores] = predict(B,X)
[Y,scores,stdevs] = predict(B,X)
Y = predict(B,X,'param1',val1,'param2',val2,...)
```

Description

`Y = predict(B,X)` computes predicted response of the trained ensemble `B` for data `X`. The output has one prediction for each row of `X`. The returned `Y` is a cell array of strings for classification and a numeric array for regression.

For regression, `[Y,stdevs] = predict(B,X)` also returns standard deviations of the computed responses over the ensemble of the grown trees.

For classification, `[Y,scores] = predict(B,X)` returns scores for all classes. `scores` is a matrix with one row per observation and one column per class. For each observation and each class, the score generated by each tree is the probability of this observation originating from this class computed as the fraction of observations of this class in a tree leaf. `predict` averages these scores over all trees in the ensemble.

`[Y,scores,stdevs] = predict(B,X)` also returns standard deviations of the computed scores for classification. `stdevs` is a matrix with one row per observation and one column per class, with standard deviations taken over the ensemble of the grown trees.

`Y = predict(B,X,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'trees'`	Array of tree indices to use for computation of responses. Default is `'all'`.

`'treeweights'`	Array of `NTrees` weights for weighting votes from the specified trees.
`'useifort'`	Logical matrix of size `Nobs`-by-`NTrees` indicating which trees to use to make predictions for each observation. By default all trees are used for all observations.

See Also

`CompactTreeBagger.predict`

predictorImportance

Class: CompactClassificationEnsemble

Estimates of predictor importance

Syntax

```
imp = predictorImportance(ens)
[imp,ma] = predictorImportance(ens)
```

Description

`imp = predictorImportance(ens)` computes estimates of predictor importance for `ens` by summing these estimates over all weak learners in the ensemble. `imp` has one element for each input predictor in the data used to train this ensemble. A high value indicates that this predictor is important for `ens`.

`[imp,ma] = predictorImportance(ens)` returns a `P`-by-`P` matrix with predictive measures of association for `P` predictors, when the learners in `ens` contain surrogate splits. See "Definitions" on page 22-3778.

Input Arguments

`ens`

A classification ensemble created by `fitensemble`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in `ens.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

ma

A P-by-P matrix of predictive measures of association for P predictors. Element ma(I,J) is the predictive measure of association averaged over surrogate splits on predictor J for which predictor I is the optimal split predictor. predictorImportance averages this predictive measure of association over all trees in the ensemble.

Definitions

Predictor Importance

predictorImportance computes estimates of predictor importance for ens by summing changes in the *risk* due to splits on every predictor and dividing the sum by the number of branch nodes. If ens is grown without surrogate splits, this sum is taken over best splits found at each branch node. If ens is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. imp has one element for each input predictor in the data used to train ens. Predictor importance associated with this split is computed as the difference between the risk for the parent node and the total risk for the two children.

Impurity and Node Error

ClassificationTree splits nodes based on either *impurity* or *node error*.

Impurity means one of several things, depending on your choice of the SplitCriterion name-value pair argument:

- Gini's Diversity Index (gdi) — The Gini index of a node is

  $$1-\sum_i p^2(i),$$

  where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index 0; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.
- Deviance ('deviance') — With $p(i)$ defined the same as for the Gini index, the deviance of a node is

$$-\sum_i p(i)\log p(i).$$

A pure node has deviance `0`; otherwise, the deviance is positive.

- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

$$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.

- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with the largest number of training samples at a node, the node error is $1 - p(j)$.

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.

- $P_{L_iL_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.
- $P_{R_iR_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Estimate the predictor importance for all variables in the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
imp = predictorImportance(ens)

imp =
    0.0001    0.0005    0.0384    0.0146
```

The first two predictors are not very important in `ens`.

Estimate the predictor importance for all variables in the Fisher iris data for an ensemble where the trees contain surrogate splits:

```
load fisheriris
surrtree = templateTree('Surrogate','on');
ens2 = fitensemble(meas,species,'AdaBoostM2',100,surrtree);
[imp2,ma] = predictorImportance(ens2)

imp2 =
    0.0224    0.0142    0.0525    0.0508

ma =
```

```
    1.0000         0    0.0001    0.0001
    0.0115    1.0000    0.0023    0.0054
    0.2810    0.1747    1.0000    0.5372
    0.0789    0.0463    0.2339    1.0000
```

The first two predictors show much more importance than in the previous example.

See Also

`predictorImportance` | `templateTree`

predictorImportance

Class: CompactClassificationTree

Estimates of predictor importance

Syntax

```
imp = predictorImportance(tree)
```

Description

`imp = predictorImportance(tree)` computes estimates of predictor importance for `tree` by summing changes in the risk due to splits on every predictor and dividing the sum by the number of branch nodes.

Input Arguments

`tree`

A classification tree created by `fitctree`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in tree`.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

Definitions

Predictor Importance

`predictorImportance` computes estimates of predictor importance for tree by summing changes in the *risk* due to splits on every predictor and dividing the sum by the number of branch nodes. If `tree` is grown without surrogate splits, this sum is taken over best splits found at each branch node. If `tree` is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. imp has one element for each input predictor in the data used to train tree. Predictor importance associated with this split is computed as the difference between the risk for the parent node and the total risk for the two children.

Estimates of predictor importance do not depend on the order of predictors if you use surrogate splits, but do depend on the order if you do not use surrogate splits.

If you use surrogate splits, `predictorImportance` computes estimates before the tree is reduced by pruning or merging leaves. If you do not use surrogate splits, `predictorImportance` computes estimates after the tree is reduced by pruning or merging leaves. Therefore, reducing the tree by pruning affects the predictor importance for a tree grown without surrogate splits, and does not affect the predictor importance for a tree grown with surrogate splits.

Impurity and Node Error

`ClassificationTree` splits nodes based on either *impurity* or *node error*.

Impurity means one of several things, depending on your choice of the `SplitCriterion` name-value pair argument:

- Gini's Diversity Index (`gdi`) — The Gini index of a node is

  $$1 - \sum_i p^2(i),$$

  where the sum is over the classes i at the node, and $p(i)$ is the observed fraction of classes with class i that reach the node. A node with just one class (a *pure* node) has Gini index `0`; otherwise the Gini index is positive. So the Gini index is a measure of node impurity.

- Deviance (`'deviance'`) — With $p(i)$ defined the same as for the Gini index, the deviance of a node is

  $$-\sum_i p(i)\log p(i).$$

  A pure node has deviance `0`; otherwise, the deviance is positive.
- Twoing rule (`'twoing'`) — Twoing is not a purity measure of a node, but is a different measure for deciding how to split a node. Let $L(i)$ denote the fraction of members of class i in the left child node after a split, and $R(i)$ denote the fraction of members of class i in the right child node after a split. Choose the split criterion to maximize

  $$P(L)P(R)\left(\sum_i |L(i)-R(i)|\right)^2,$$

  where $P(L)$ and $P(R)$ are the fractions of observations that split to the left and right respectively. If the expression is large, the split made each child node purer. Similarly, if the expression is small, the split made each child node similar to each other, and hence similar to the parent node, and so the split did not increase node purity.
- Node error — The node error is the fraction of misclassified classes at a node. If j is the class with the largest number of training samples at a node, the node error is $1 - p(j)$.

Examples

Estimate the predictor importance for all variables in the Fisher iris data:

```
load fisheriris
tree = fitctree(meas,species);
imp = predictorImportance(tree)

imp =
         0         0    0.0403    0.0303
```

The first two elements of `imp` are zero. Therefore, the first two predictors do not enter into `tree` calculations for classifying irises.

Estimate the predictor importance for all variables in the Fisher iris data for a tree grown with surrogate splits:

```
tree2 = fitctree(meas,species,...
    'Surrogate','on');
imp2 = predictorImportance(tree2)

imp2 =
    0.0287    0.0136    0.0560    0.0556
```

In this case, all predictors have some importance. As you expect by comparing to the first example, the first two predictors are less important than the final two.

Estimates of predictor importance do not depend on the order of predictors if you use surrogate splits, but do depend on the order if you do not use surrogate splits. For example, permute the order of the data columns in the previous example:

```
load fisheriris
meas3 = meas(:,[4 1 3 2]);
tree3 = fitctree(meas3,species);
imp3 = predictorImportance(tree2)

imp3 =
    0.0674         0    0.0033         0
```

The estimates of predictor importance are not a permutation of `imp` from the first example.

Estimate the predictor importance using surrogate splits.

```
tree4 = fitctree(meas3,species,...
    'Surrogate','on');
imp4 = predictorImportance(tree4)

imp4 =
    0.0556    0.0287    0.0560    0.0136
```

`imp4` is a permutation of `imp2`, demonstrating that estimates of predictor importance do not depend on the order of predictors with surrogate splits.

See Also

`predictorImportance` | `fitctree`

predictorImportance

Class: CompactRegressionEnsemble

Estimates of predictor importance

Syntax

```
imp = predictorImportance(ens)
[imp,ma] = predictorImportance(ens)
```

Description

`imp = predictorImportance(ens)` computes estimates of predictor importance for `ens` by summing these estimates over all weak learners in the ensemble. `imp` has one element for each input predictor in the data used to train this ensemble. A high value indicates that this predictor is important for `ens`.

`[imp,ma] = predictorImportance(ens)` returns a `P`-by-`P` matrix with predictive measures of association for `P` predictors.

Input Arguments

`ens`

A regression ensemble created by `fitensemble`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in `ens.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

`ma`

A `P`-by-`P` matrix of predictive measures of association for `P` predictors. Element `ma(I,J)` is the predictive measure of association averaged over surrogate splits on predictor `J` for which predictor `I` is the optimal split predictor. `predictorImportance` averages this predictive measure of association over all trees in the ensemble.

Definitions

Predictor Importance

`predictorImportance` computes estimates of predictor importance for tree by summing changes in the mean squared error (MSE) due to splits on every predictor and dividing the sum by the number of branch nodes. If the tree is grown without surrogate splits, this sum is taken over best splits found at each branch node. If the tree is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. imp has one element for each input predictor in the data used to train this tree. At each node, MSE is estimated as node error weighted by the node probability. Variable importance associated with this split is computed as the difference between MSE for the parent node and the total MSE for the two children.

Predictive Measure of Association

The predictive measure of association between the optimal split on variable i and a surrogate split on variable j is:

$$\lambda_{i,j} = \frac{\min(P_L, P_R) - \left(1 - P_{L_i L_j} - P_{R_i R_j}\right)}{\min(P_L, P_R)}.$$

Here

- P_L and P_R are the node probabilities for the optimal split of node i into Left and Right nodes respectively.
- $P_{L_i L_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Left.

- $P_{R_i R_j}$ is the probability that both (optimal) node i and (surrogate) node j send an observation to the Right.

Clearly, $\lambda_{i,j}$ lies from $-\infty$ to 1. Variable j is a worthwhile surrogate split for variable i if $\lambda_{i,j} > 0$.

Element `ma(i,j)` is the predictive measure of association averaged over surrogate splits on predictor `j` for which predictor `i` is the optimal split predictor. This average is computed by summing positive values of the predictive measure of association over optimal splits on predictor `i` and surrogate splits on predictor `j` and dividing by the total number of optimal splits on predictor `i`, including splits for which the predictive measure of association between predictors `i` and `j` is negative.

Examples

Estimate the predictor importance for all numeric variables in the `carsmall` data:

```
load carsmall
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
imp = predictorImportance(ens)

imp =
    0.0082         0    0.0049    0.0133    0.0142    0.1737
```

The weight (last predictor) has the most impact on mileage (MPG). The second predictor has importance 0; this means the number of cylinders has no impact on predictions made with `ens`.

Estimate the predictor importance for all variables in the `carsmall` data for an ensemble where the trees contain surrogate splits:

```
load carsmall
surrtree = templateTree('Surrogate','on');
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
ens2 = fitensemble(X,MPG,'LSBoost',100,surrtree);
[imp2,ma] = predictorImportance(ens2)

imp2 =
```

```
    0.0725    0.1342    0.1425    0.1397    0.1380    0.1855

ma =
    1.0000    0.0414    0.0607    0.0782    0.0102    0.0322
         0    1.0000         0         0         0         0
    0.0441    0.0704    1.0000    0.0883    0.0175    0.0913
    0.0944    0.1166    0.1400    1.0000    0.0390    0.1308
    0.0121    0.0139    0.0127    0.0127    1.0000    0.0113
    0.0818    0.1317    0.2072    0.1878    0.0340    1.0000
```

While weight (last predictor) still has the most impact on mileage (MPG), this estimate has the second predictor (number of cylinders) is essentially tied for third most important predictor.

See Also

`predictorImportance` | `templateTree`

predictorImportance

Class: CompactRegressionTree

Estimates of predictor importance

Syntax

```
imp = predictorImportance(tree)
```

Description

`imp = predictorImportance(tree)` computes estimates of predictor importance for `tree` by summing changes in the mean squared error due to splits on every predictor and dividing the sum by the number of branch nodes.

Input Arguments

`tree`

A regression tree created by `fitrtree`, or by the `compact` method.

Output Arguments

`imp`

A row vector with the same number of elements as the number of predictors (columns) in `tree.X`. The entries are the estimates of predictor importance, with `0` representing the smallest possible importance.

Definitions

Predictor Importance

`predictorImportance` computes estimates of predictor importance for tree by summing changes in the mean squared error (MSE) due to splits on every predictor and dividing the sum by the number of branch nodes. If the tree is grown without surrogate splits, this sum is taken over best splits found at each branch node. If the tree is grown with surrogate splits, this sum is taken over all splits at each branch node including surrogate splits. imp has one element for each input predictor in the data used to train this tree. At each node, MSE is estimated as node error weighted by the node probability. Variable importance associated with this split is computed as the difference between MSE for the parent node and the total MSE for the two children.

Estimates of predictor importance do not depend on the order of predictors if you use surrogate splits, but do depend on the order if you do not use surrogate splits.

If you use surrogate splits, `predictorImportance` computes estimates before the tree is reduced by pruning or merging leaves. If you do not use surrogate splits, `predictorImportance` computes estimates after the tree is reduced by pruning or merging leaves. Therefore, reducing the tree by pruning affects the predictor importance for a tree grown without surrogate splits, and does not affect the predictor importance for a tree grown with surrogate splits.

Examples

Find predictor importance for the `carsmall` data. Use just the numeric predictors:

```
load carsmall
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
tree = fitrtree(X,MPG);
imp = predictorImportance(tree)

imp =
    0.0315         0    0.1082    0.0686    0.1629    1.2924
```

The weight (last predictor) has the most impact on mileage (MPG). The second predictor has importance 0; this means the number of cylinders has no impact on predictions made with `tree`.

Estimate the predictor importance for all variables in the `carsmall` data for a tree grown with surrogate splits:

```
load carsmall
X = [Acceleration Cylinders Displacement ...
    Horsepower Model_Year Weight];
tree2 = fitrtree(X,MPG,...
    'Surrogate','on');
imp2 = predictorImportance(tree2)

imp2 =
    0.5287    1.1977    1.2400    0.7059    1.0677    1.4106
```

While weight (last predictor) still has the most impact on mileage (MPG), this estimate has the second predictor (number of cylinders) as the third most important predictor.

See Also

`predictorImportance` | `fitrtree`

princomp

Principal component analysis (PCA) on data

Compatibility

`princomp` will be removed in a future release. Use `pca` instead.

Syntax

```
[COEFF,SCORE] = princomp(X)
[COEFF,SCORE,latent] = princomp(X)
[COEFF,SCORE,latent,tsquare] = princomp(X)
[...] = princomp(X,'econ')
```

Description

`COEFF = princomp(X)` performs principal components analysis (PCA) on the *n*-by-*p* data matrix `X`, and returns the principal component coefficients, also known as loadings. Rows of `X` correspond to observations, columns to variables. `COEFF` is a *p*-by-*p* matrix, each column containing coefficients for one principal component. The columns are in order of decreasing component variance.

`princomp` centers `X` by subtracting off column means, but does not rescale the columns of `X`. To perform principal components analysis with standardized variables, that is, based on correlations, use `princomp(zscore(X))`. To perform principal components analysis directly on a covariance or correlation matrix, use `pcacov`.

`[COEFF,SCORE] = princomp(X)` returns `SCORE`, the principal component scores; that is, the representation of `X` in the principal component space. Rows of `SCORE` correspond to observations, columns to components.

`[COEFF,SCORE,latent] = princomp(X)` returns `latent`, a vector containing the eigenvalues of the covariance matrix of `X`.

`[COEFF,SCORE,latent,tsquare] = princomp(X)` returns `tsquare`, which contains Hotelling's T^2 statistic for each data point.

The scores are the data formed by transforming the original data into the space of the principal components. The values of the vector `latent` are the variance of the columns of `SCORE`. Hotelling's T^2 is a measure of the multivariate distance of each observation from the center of the data set.

When `n <= p`, `SCORE(:,n:p)` and `latent(n:p)` are necessarily zero, and the columns of `COEFF(:,n:p)` define directions that are orthogonal to `X`.

`[...] = princomp(X,'econ')` returns only the elements of `latent` that are not necessarily zero, and the corresponding columns of `COEFF` and `SCORE`, that is, when `n <= p`, only the first `n-1`. This can be significantly faster when `p` is much larger than `n`.

Examples

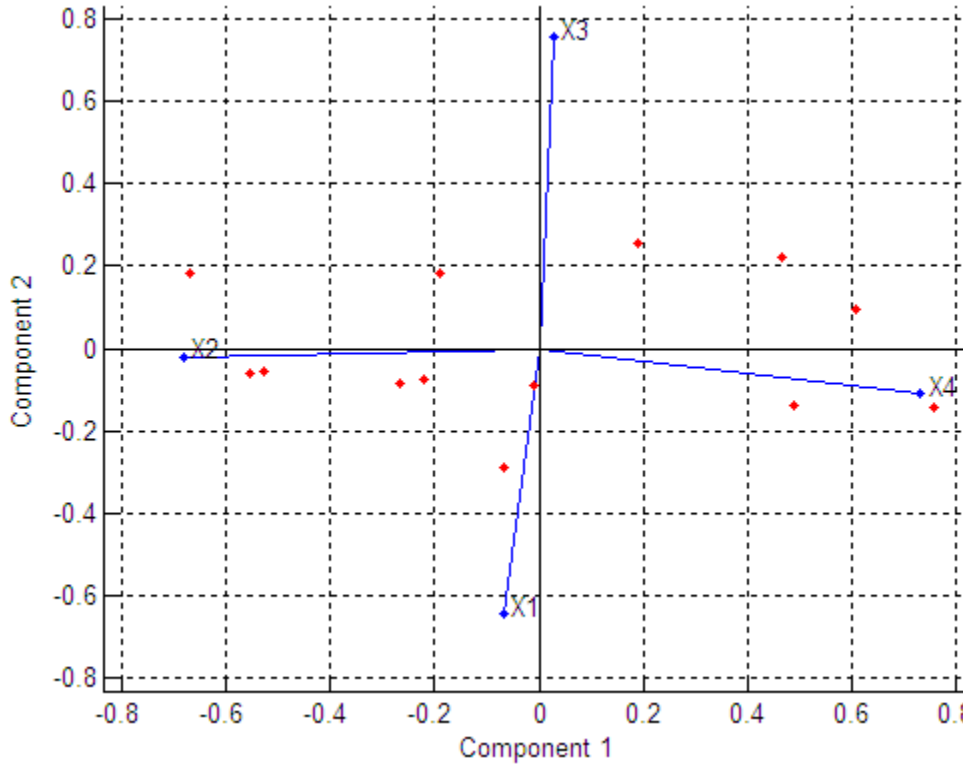
Compute principal components for the `ingredients` data in the Hald data set, and the variance accounted for by each component.

```
load hald;
[pc,score,latent,tsquare] = princomp(ingredients);
pc,latent

pc =

   -0.0678   -0.6460    0.5673    0.5062
   -0.6785   -0.0200   -0.5440    0.4933
    0.0290    0.7553    0.4036    0.5156
    0.7309   -0.1085   -0.4684    0.4844


latent =

  517.7969
   67.4964
   12.4054
    0.2372
```

The following command and plot show that two components account for 98% of the variance:

```
cumsum(latent)./sum(latent)
ans =
```

```
       0.86597
       0.97886
        0.9996
             1
biplot(pc(:,1:2),'Scores',score(:,1:2),'VarLabels',...
  {'X1' 'X2' 'X3' 'X4'})
```



For a more detailed example and explanation of this analysis method, see “Principal Component Analysis (PCA)” on page 13-75.

More About

- “Principal Component Analysis (PCA)” on page 13-75

References

[1] Jackson, J. E., *A User's Guide to Principal Components*, John Wiley and Sons, 1991, p. 592.

[2] Jolliffe, I. T., *Principal Component Analysis*, 2nd edition, Springer, 2002.

[3] Krzanowski, W. J. *Principles of Multivariate Analysis: A User's Perspective*. New York: Oxford University Press, 1988.

[4] Seber, G. A. F., *Multivariate Observations*, Wiley, 1984.

See Also

`barttest` | `biplot` | `canoncorr` | `factoran` | `pca` | `pcacov` | `pcares` | `rotatefactors`

Prior property

Class: TreeBagger

Prior class probabilities

Description

The `Prior` property is a vector with prior probabilities for classes. This property is empty for ensembles of regression trees.

See Also

`ClassificationTree` | `TreeBagger` | `fitctree`

ProbDist class

Object representing probability distribution

Compatibility

`ProbDist` will be removed in a future release. To create and fit probability distribution objects, use `makedist` and `fitdist` instead.

Description

`ProbDist` is an abstract class representing a probability distribution.

Construction

`ProbDist` is an abstract class. You cannot create instances of this class directly. You can construct an object in a subclass, such as `ProbDistUnivParam` or `ProbDistUnivKernel`, by calling the subclass constructors (`ProbDistUnivParam` or `ProbDistUnivKernel`).

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Properties

DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object
Support	Read-only structure containing information about support of ProbDist object

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

See Also

`ProbDistParametric` | `ProbDistUnivParam` | `ProbDistUnivKernel` | `ProbDistUnivParam` | `ProbDistKernel` | `ProbDistUnivKernel`

ProbDistKernel class

Superclasses: ProbDist

Object representing nonparametric probability distribution defined by kernel smoothing

Compatibility

`ProbDistKernel` will be removed in a future release. To create and fit probability distribution objects, use `makedist` and `fitdist` instead.

Description

`ProbDistKernel` is an abstract class defining the properties and methods of a nonparametric distribution defined by a kernel smoothing function.

Construction

`ProbDistKernel` is an abstract class. You cannot create instances of this class directly. You can construct an object in a subclass, `ProbDistUnivKernel` by calling the subclass constructor, `ProbDistUnivKernel`.

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Note: The above methods are inherited from the `ProbDist` class.

Properties

BandWidth

Read-only value specifying bandwidth of kernel smoothing function for ProbDistKernel object

DistName

Read-only string containing probability distribution name of ProbDist object

InputData

Read-only structure containing information about input data to ProbDist object

Kernel

Read-only string specifying name of kernel smoothing function for ProbDistKernel object

Support

Read-only structure containing information about support of ProbDist object

Note: Some of the above properties are inherited from the `ProbDist` class.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

See Also

`ProbDist` | `ProbDistUnivKernel` | `ProbDistUnivKernel`

ProbDistParametric class

Superclasses: ProbDist

Object representing parametric probability distribution

Compatibility

`ProbDistParametric` will be removed in a future release. To create and fit probability distribution objects, use `makedist` and `fitdist` instead.

Description

`ProbDistParametric` is an abstract class defining the properties and methods of a parametric probability distribution.

Construction

`ProbDistParametric` is an abstract class. You cannot create instances of this class directly. You can construct an object in its subclass, `ProbDistUnivParam`, by calling the subclass constructor, `ProbDistUnivParam`.

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Note: The above methods are inherited from the `ProbDist` class.

Properties

DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object
NLogL	Read-only value specifying negative log likelihood for input data to ProbDistParametric object
NumParams	Read-only value specifying number of parameters of ProbDistParametric object
ParamCov	Read-only covariance matrix of parameter estimates of ProbDistParametric object
ParamDescription	Read-only cell array specifying descriptions of parameters of ProbDistParametric object
ParamIsFixed	Read-only logical array specifying fixed parameters of ProbDistParametric object
ParamNames	Read-only cell array specifying names of parameters of ProbDistParametric object
Params	Read-only array specifying values of parameters of ProbDistParametric object
Support	Read-only structure containing information about support of ProbDist object

Note: Some of the above properties are inherited from the `ProbDist` class.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

See Also

`ProbDist` | `ProbDistUnivParam` | `ProbDistUnivParam`

ProbDistUnivKernel class

Superclasses: ProbDistKernel

Object representing univariate kernel probability distribution

Compatibility

`ProbDistUnivKernel` will be removed in a future release. To create and fit probability distribution objects, use `makedist` and `fitdist` instead.

Description

A `ProbDistUnivKernel` object represents a univariate nonparametric probability distribution defined by kernel smoothing. You create this object using the `ProbDistUnivKernel` function to fit the distribution to data.

Construction

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
icdf	Return inverse cumulative distribution function (ICDF) for ProbDistUnivKernel object
iqr	Return interquartile range (IQR) for ProbDistUnivKernel object
median	Return median of ProbDistUnivKernel object

pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object

Note: Some of the above methods are inherited from the `ProbDistKernel` class.

Properties

BandWidth	Read-only value specifying bandwidth of kernel smoothing function for ProbDistKernel object
DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object
Kernel	Read-only string specifying name of kernel smoothing function for ProbDistKernel object
NLogL	Read-only value specifying negative log likelihood for input data to ProbDistUnivKernel object
Support	Read-only structure containing information about support of ProbDist object

Note: Some of the above properties are inherited from the `ProbDistKernel` class.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

References

[1] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis*. New York: Oxford University Press, 1997.

See Also

`fitdist` | `ksdensity` | `ProbDist` | `ProbDistUnivKernel` | `ProbDistKernel`

ProbDistUnivKernel

Class: ProbDistUnivKernel

Construct ProbDistUnivKernel object

Syntax

```
PD = ProbDistUnivKernel(X)
PD = ProbDistUnivKernel(X, param1, val1, param2, val2, ...)
```

Description

`PD = ProbDistUnivKernel(X)` creates *PD*, a ProbDistUnivKernel object, which represents a nonparametric probability distribution, based on a normal kernel smoothing function.

`PD = ProbDistUnivKernel(X, param1, val1, param2, val2, ...)` specifies optional parameter name/value pairs, as described in the Parameter/Values table. Parameter and value names are case insensitive.

Compatibility

`ProbDistUnivKernel` will be removed in a future release. To create and fit probability distribution objects, use `makedist` and `fitdist` instead.

Input Arguments

X — A column vector of data.

Note: Any NaN values in *X* are ignored by the fitting calculations.

Parameter	Values
`'censoring'`	A Boolean vector the same size as *X*, containing `1`s when the corresponding elements in *X* are right-censored observations and `0`s

Parameter	Values
	when the corresponding elements are exact observations. Default is a vector of 0s. **Note:** Any NaN values in this censoring vector are ignored by the fitting calculations.
`'frequency'`	A vector the same size as *X*, containing nonnegative integers specifying the frequencies for the corresponding elements in *X*. Default is a vector of 1s. **Note:** Any NaN values in this frequency vector are ignored by the fitting calculations.
`'kernel'`	A string specifying the type of kernel smoother to use. Choices are: • `'normal'` (default) • `'box'` • `'triangle'` • `'epanechnikov'`
`'support'`	Any of the following to specify the support: • `'unbounded'` — Default. If the density can extend over the whole real line. • `'positive'` — To restrict it to positive values. • A two-element vector giving finite lower and upper limits for the support of the density.
`'width'`	A value specifying the bandwidth of the kernel smoothing window. The default is optimal for estimating normal densities, but you may want to choose a smaller value to reveal features such as multiple modes.

Output Arguments

PD — An object in the `ProbDistUnivKernel` class, which is derived from the `ProbDist` class. It represents a nonparametric probability distribution.

References

[1] Bowman, A. W., and A. Azzalini. *Applied Smoothing Techniques for Data Analysis*. New York: Oxford University Press, 1997.

See Also

`fitdist` | `ksdensity`

ProbDistUnivParam class

Superclasses: ProbDistParametric

Object representing univariate parametric probability distribution

Compatibility

`ProbDistUnivParam` will be removed in a future release. To create and fit probability distribution objects, use `makedist` and `fitdist` instead.

Description

A `ProbDistUnivParam` object represents a univariate parametric probability distribution. You create this object by using the constructor (`ProbDistUnivParam`) and supplying parameter values.

Construction

.ProbDistUnivParam	Construct ProbDistUnivParam object

Methods

cdf	Return cumulative distribution function (CDF) for ProbDist object
icdf	Return inverse cumulative distribution function (ICDF) for ProbDistUnivParam object
iqr	Return interquartile range (IQR) for ProbDistUnivParam object

mean	Return mean of ProbDistUnivParam object
median	Return median of ProbDistUnivParam object
paramci	Return parameter confidence intervals of ProbDistUnivParam object
pdf	Return probability density function (PDF) for ProbDist object
random	Generate random number drawn from ProbDist object
std	Return standard deviation of ProbDistUnivParam object
var	Return variance of ProbDistUnivParam object

Note: Some of the above methods are inherited from the `ProbDistParametric` class.

Properties

DistName	Read-only string containing probability distribution name of ProbDist object
InputData	Read-only structure containing information about input data to ProbDist object
NLogL	Read-only value specifying negative log likelihood for input data to ProbDistParametric object

NumParams	Read-only value specifying number of parameters of ProbDistParametric object
ParamCov	Read-only covariance matrix of parameter estimates of ProbDistParametric object
ParamDescription	Read-only cell array specifying descriptions of parameters of ProbDistParametric object
ParamIsFixed	Read-only logical array specifying fixed parameters of ProbDistParametric object
ParamNames	Read-only cell array specifying names of parameters of ProbDistParametric object
Params	Read-only array specifying values of parameters of ProbDistParametric object
Support	Read-only structure containing information about support of ProbDist object

Note: The above properties are inherited from the `ProbDistParametric` class.

Note: Parameter values are also properties. For example, if you create `PD`, a univariate parametric probability distribution object that represents a normal distribution, then `PD.mu` and `PD.sigma` are properties that give the values of the mu and sigma parameters.

Copy Semantics

Value. To learn how this affects your use of the class, see Copying Objects in the MATLAB Programming Fundamentals documentation.

References

[1] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 1, Hoboken, NJ: Wiley-Interscience, 1993.

[2] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 2, Hoboken, NJ: Wiley-Interscience, 1994.

See Also

`ProbDist` | `ProbDistUnivParam` | `ProbDistParametric`

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ProbDistUnivParam

Class: ProbDistUnivParam

Construct ProbDistUnivParam object

Syntax

```
PD = ProbDistUnivParam(DistName, Params)
```

Description

`PD = ProbDistUnivParam(DistName, Params)` creates *PD*, a ProbDistUnivParam object, which represents a probability distribution. This distribution is defined by the parametric distribution specified by *DistName*, with parameters specified by the numeric vector *Params*.

Compatibility

`ProbDistUnivParam` will be removed in a future release. To create and fit probability distribution objects, use `makedist` and `fitdist` instead.

Input Arguments

DistName — A string specifying a distribution. Choices are:

- `'beta'`
- `'binomial'`
- `'birnbaumsaunders'`
- `'exponential'`
- `'extreme value'` or `ev'`
- `'gamma'`
- `'generalized extreme value'` or `'gev'`

- `'generalized pareto'` or `'gp'`
- `'inversegaussian'`
- `'logistic'`
- `'loglogistic'`
- `'lognormal'`
- `'nakagami'`
- `'negative binomial'` or `'nbin'`
- `'normal'`
- `'poisson'`
- `'rayleigh'`
- `'rician'`
- `'tlocationscale'`
- `'weibull'` or `'wbl'`

For more information on these parametric distributions, see Appendix B.

Params — Numeric vector of distribution parameters. The number and type of parameters depends on the distribution you specify with *DistName*. For information on parameters for each distribution type, see Appendix B.

Output Arguments

PD — An object in the `ProbDistUnivParam` class, which is derived from the `ProbDist` class. It represents a parametric probability distribution.

Examples

1 Create an object representing a normal distribution with a mean of 100 and a standard deviation of 10.

```
pd = ProbDistUnivParam('normal',[100 10])
```

```
pd =

normal distribution

    mu = 100
    sigma = 10
```

2 Generate a 4-by-5 matrix of random values from this distribution.

```
random(pd,4,5)

ans =

  105.3767  103.1877  135.7840  107.2540   98.7586
  118.3389   86.9231  127.6944   99.3695  114.8970
   77.4115   95.6641   86.5011  107.1474  114.0903
  108.6217  103.4262  130.3492   97.9503  114.1719
```

References

[1] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 1, Hoboken, NJ: Wiley-Interscience, 1993.

[2] Johnson, N. L., S. Kotz, and N. Balakrishnan. *Continuous Univariate Distributions*. Vol. 2, Hoboken, NJ: Wiley-Interscience, 1994.

See Also

`fitdist`

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probplot

Probability plots

Syntax

```
probplot(Y)
probplot(distribution,Y)
probplot(Y,cens,freq)
probplot(ax,Y)
probplot(...,'noref')
probplot(ax,PD)
probplot(ax,fun,params)
h = probplot(...)
```

Description

`probplot(Y)` produces a normal probability plot comparing the distribution of the data `Y` to the normal distribution. `Y` can be a single vector, or a matrix with a separate sample in each column. The plot includes a reference line useful for judging whether the data follow a normal distribution.

`probplot` uses midpoint probability plotting positions. The i^{th} sorted value from a sample of size N is plotted against the midpoint in the jump of the empirical CDF on the y axis. With uncensored data, that midpoint is $(i–0.5)/N$. With censored data (see below), the y value is more complicated to compute.

`probplot(distribution,Y)` creates a probability plot for the distribution specified by *`distribution`*. Acceptable strings for *`distribution`* are:

- `'exponential'` — Exponential probability plot (nonnegative values)
- `'extreme value'` — Extreme value probability plot (all values)
- `'lognormal'` — Lognormal probability plot (positive values)
- `'normal'` — Normal probability plot (all values)
- `'rayleigh'` — Rayleigh probability plot (positive values)
- `'weibull'` — Weibull probability plot (positive values)

The *y* axis scale is based on the selected distribution. The *x* axis has a log scale for the Weibull and lognormal distributions, and a linear scale for the others.

Not all distributions are appropriate for all data sets, and `probplot` will error when asked to create a plot with a data set that is inappropriate for a specified distribution. Appropriate data ranges for each distribution are given parenthetically in the list above.

`probplot(Y,cens,freq)` or `probplot(distname,Y,cens,freq)` requires a vector `Y`. `cens` is a vector of the same size as `Y` and contains `1` for observations that are right-censored and `0` for observations that are observed exactly. `freq` is a vector of the same size as Y, containing integer frequencies for the corresponding elements in `Y`.

`probplot(ax,Y)` takes a handle `ax` to an existing probability plot, and adds additional lines for the samples in `Y`. `ax` is a handle for a set of axes.

`probplot(...,'noref')` omits the reference line.

`probplot(ax,PD)` takes a probability distribution object, `PD`, and adds a fitted line to the axes specified by `ax` to represent the probability distribution specified by `PD`. `PD` is a ProbDist object of the `ProbDistUnivParam` class or `ProbDistUnivKernel` class.

`probplot(ax,fun,params)` takes a function `fun` and a set of parameters, `params`, and adds fitted lines to the axes of an existing probability plot specified by `ax`. `fun` is a function handle to a cdf function, specified with `@` (for example, `@wblcdf`). `params` is the set of parameters required to evaluate `fun`, and is specified as a cell array or vector. The function must accept a vector of `X` values as its first argument, then the optional parameters, and must return a vector of cdf values evaluated at `X`.

`h = probplot(...)` returns handles to the plotted lines.

Examples

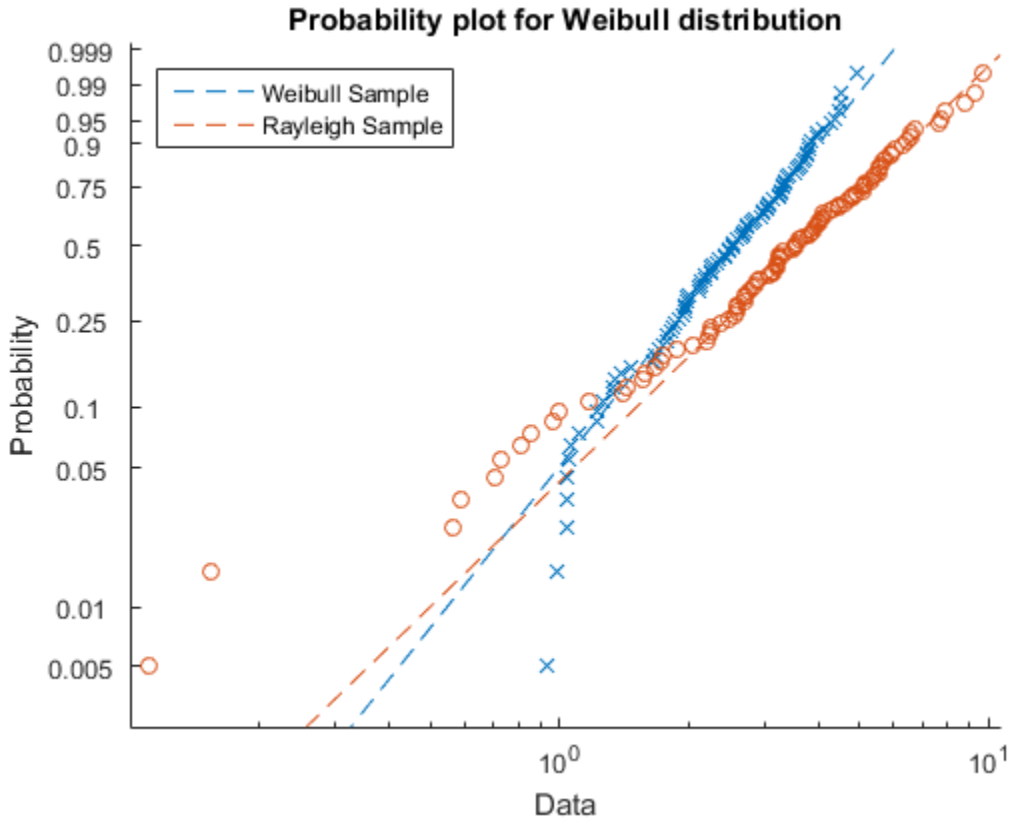
Test Data for Weibull Distribution Using `probplot`

Generate sample data. The sample `x1` contains 100 random numbers from a Weibull distribution with scale parameter `A = 3` and shape parameter `B = 3`. The sample `x2` contains 100 random numbers from a Rayleigh distribution with scale parameter `B = 3`.

```
rng('default');  % For reproducibility
x1 = wblrnd(3,3,100,1);
x2 = raylrnd(3,100,1);
```

Create a probability plot to assess whether the data in `x1` and `x2` comes from a Weibull distribution.

```
figure;
probplot('weibull',[x1 x2])
legend('Weibull Sample','Rayleigh Sample','Location','NW')
```



The probability plot shows that the data in `x1` comes from a Weibull distribution, while the data in `x2` does not.

Test Data for Normal Distribution Using `probplot`

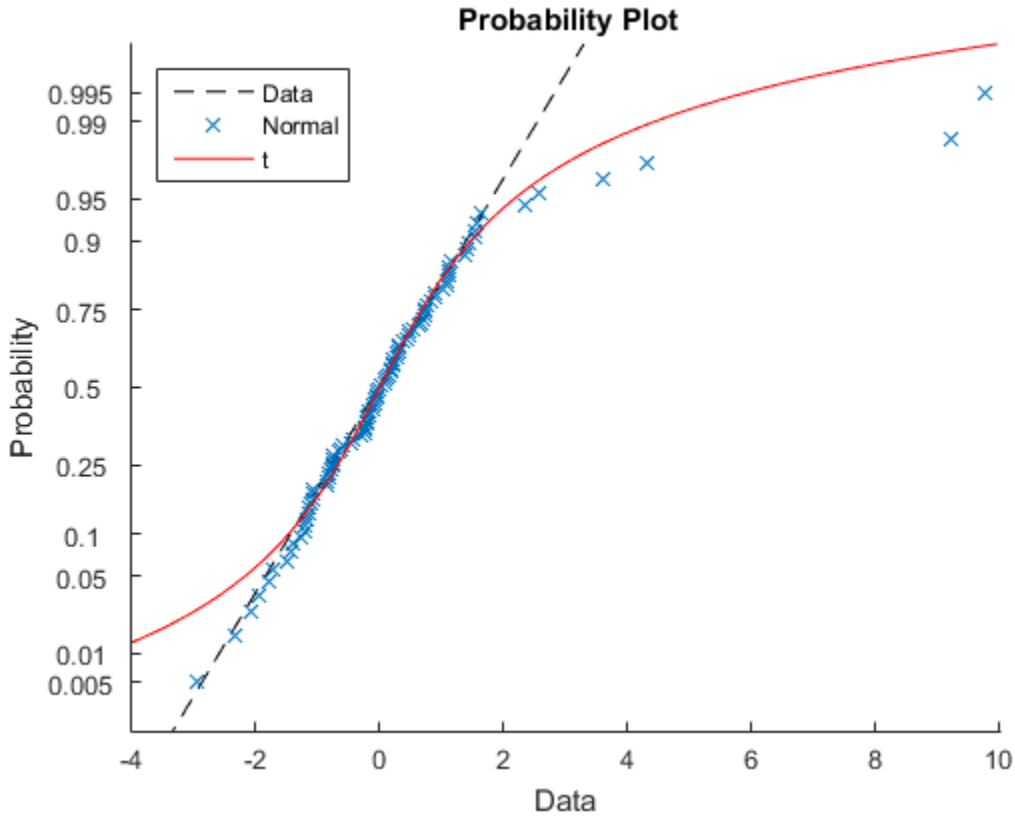
Generate sample data containing about 20% outliers in the tails. The left tail of the sample data contains 10 values randomly generated from an exponential distribution

with parameter `mu = 1`. The right tail contains 10 values randomly generated from an exponential distribution with parameter `mu = 5`. The center of the sample data contains 80 values randomly generated from a standard normal distribution.

```
rng default  % For reproducibility
left_tail = -exprnd(1,10,1);
right_tail = exprnd(5,10,1);
center = randn(80,1);
data = [left_tail;center;right_tail];
```

Create a probability plot to assess whether the data in `data` comes from a normal distribution. Plot a *t* location-scale curve on the same figure to compare with `data`.

```
figure;
probplot(data);
p = mle(data,'dist','tlo');
t = @(data,mu,sig,df)cdf('tlocationscale',data,mu,sig,df);
h = probplot(gca,t,p);
h.Color = 'r';
h.LineStyle = '-';
title('{\bf Probability Plot}')
legend('Data','Normal','t','Location','NW')
```



The plot shows that neither the normal line nor the *t* location-scale curve fit the tails very well because of the outliers.

See Also

`normplot` | `ecdf` | `wblplot`

procrustes

Procrustes analysis

Syntax

```
d = procrustes(X,Y)
[d,Z] = procrustes(X,Y)
[d,Z,transform] = procrustes(X,Y)
[...] = procrustes(...,'scaling',flag)
[...] = procrustes(...,'reflection',flag)
```

Description

`d = procrustes(X,Y)` determines a linear transformation (translation, reflection, orthogonal rotation, and scaling) of the points in matrix `Y` to best conform them to the points in matrix `X`. The goodness-of-fit criterion is the sum of squared errors. `procrustes` returns the minimized value of this dissimilarity measure in `d`. `d` is standardized by a measure of the scale of `X`, given by:

```
sum(sum((X-repmat(mean(X,1),size(X,1),1)).^2,1))
```

That is, the sum of squared elements of a centered version of `X`. However, if `X` comprises repetitions of the same point, the sum of squared errors is not standardized.

`X` and `Y` must have the same number of points (rows), and `procrustes` matches `Y(i)` to `X(i)`. Points in `Y` can have smaller dimension (number of columns) than those in `X`. In this case, `procrustes` adds columns of zeros to `Y` as necessary.

`[d,Z] = procrustes(X,Y)` also returns the transformed `Y` values.

`[d,Z,transform] = procrustes(X,Y)` also returns the transformation that maps `Y` to `Z`. `transform` is a structure array with fields:

- `c` — Translation component
- `T` — Orthogonal rotation and reflection component

- `b` — Scale component

That is:

```
c = transform.c;
T = transform.T;
b = transform.b;

Z = b*Y*T + c;
```

`[...] = procrustes(...,'scaling',flag)`, when *`flag`* is `false`, allows you to compute the transformation without a scale component (that is, with `b` equal to `1`). The default *`flag`* is `true`.

`[...] = procrustes(...,'reflection',flag)`, when *`flag`* is `false`, allows you to compute the transformation without a reflection component (that is, with `det(T)` equal to `1`). The default *`flag`* is `'best'`, which computes the best-fitting transformation, whether or not it includes a reflection component. A *`flag`* of `true` forces the transformation to be computed with a reflection component (that is, with `det(T)` equal to `-1`)

Examples

Procrustes Analysis

Generate the sample data in two dimensions.

```
rng('default')
n = 10;
X = normrnd(0,1,[n 2]);
```

Rotate, scale, translate, and add some noise to sample points.

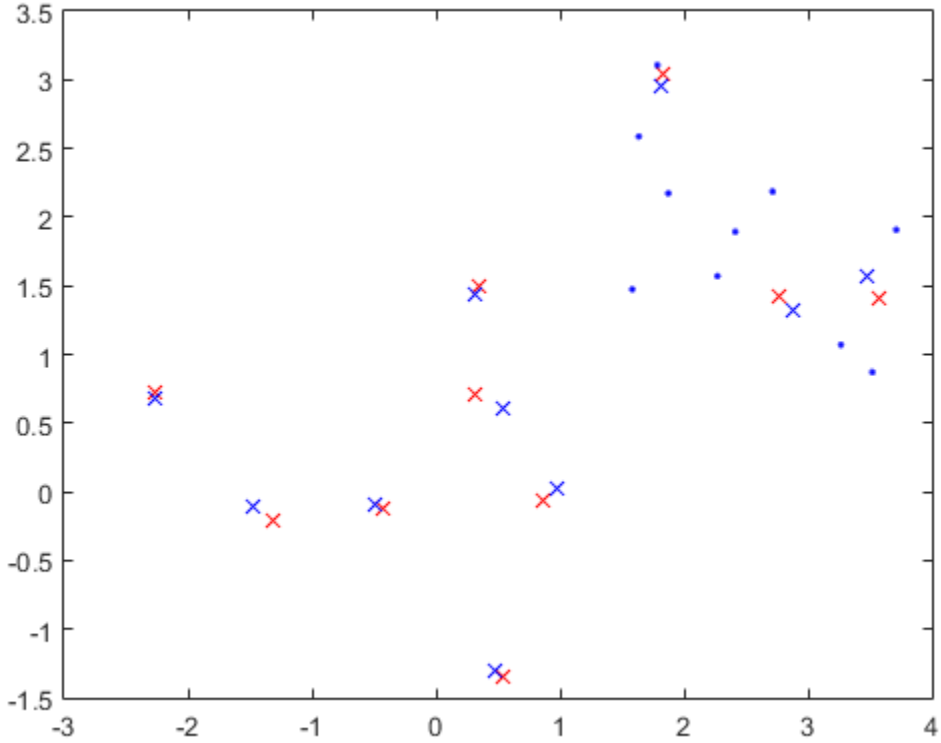
```
S = [0.5 -sqrt(3)/2; sqrt(3)/2 0.5];
Y = normrnd(0.5*X*S+2,0.05,n,2);
```

Conform `Y` to `X` using procrustes analysis.

```
[d,Z,tr] = procrustes(X,Y);
```

Plot the original `X` and `Y` with the transformed `Y` .

```
plot(X(:,1),X(:,2),'rx',Y(:,1),Y(:,2),'b.',Z(:,1),Z(:,2),'bx');
```



References

[1] Kendall, David G. “A Survey of the Statistical Theory of Shape.” *Statistical Science*. Vol. 4, No. 2, 1989, pp. 87–99.

[2] Bookstein, Fred L. *Morphometric Tools for Landmark Data*. Cambridge, UK: Cambridge University Press, 1991.

[3] Seber, G. A. F. *Multivariate Observations*. Hoboken, NJ: John Wiley & Sons, Inc., 1984.

See Also

`cmdscale` | `factoran`

proflik

Profile likelihood function for probability distribution

Syntax

```
[ll,param] = proflik(pd,pnum)
[ll,param] = proflik(pd,pnum,'Display',display)
[ll,param] = proflik(pd,pnum,setparam)
[ll,param] = proflik(pd,pnum,setparam,'Display',display)
[ll,param,other] = proflik( ___ )
```

Description

`[ll,param] = proflik(pd,pnum)` returns a vector ll of log likelihood values and a vector param of corresponding parameter values for the parameter in the position indicated by pnum.

`[ll,param] = proflik(pd,pnum,'Display',display)` returns the log likelihood values and corresponding parameter values, and plots the profile likelihood overlaid on an approximation of the log likelihood.

`[ll,param] = proflik(pd,pnum,setparam)` returns the log likelihood values and corresponding parameter values as specified by `setparam`.

`[ll,param] = proflik(pd,pnum,setparam,'Display',display)` returns the log likelihood values and corresponding parameter values as specified by setparam, and plots the profile likelihood overlaid on an approximation of the log likelihood.

`[ll,param,other] = proflik( ___ )` also returns a matrix other containing the values of the other parameters that maximize the likelihood, using any of the input arguments from the previous syntaxes.

Examples

Profile Likelihood of a Distribution Parameter

Load the sample data. Create a probability distribution object by fitting a Weibull distribution to the miles per gallon (MPG) data.

```
load carsmall;
pd = fitdist(MPG,'Weibull')
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 26.5079   [24.8333, 28.2954]
    B = 3.27193   [2.79441, 3.83104]
```

View the parameter names for the distribution.

```
pd.ParameterNames
```

```
ans =

    'A'    'B'
```

For the Weibull distribution, A is in position 1, and B is in position 2.

Compute the profile likelihood for B, which is in position `pnum = 2`.

```
[ll,param] = proflik(pd,2);
```

Display the loglikelihood values for the estimated values of B.

```
[ll',param']
```

```
ans =

 -329.9688    2.7132
 -329.4312    2.7748
 -328.9645    2.8365
 -328.5661    2.8981
 -328.2340    2.9597
 -327.9658    3.0213
```

```
-327.7596    3.0830
-327.6135    3.1446
-327.5256    3.2062
-327.4943    3.2678
-327.5178    3.3295
-327.5946    3.3911
-327.7233    3.4527
-327.9023    3.5143
-328.1303    3.5760
-328.4060    3.6376
-328.7281    3.6992
-329.0956    3.7608
-329.5071    3.8224
-329.9617    3.8841
-330.4583    3.9457
```

These results show that the profile log likelihood is maximized between the estimated B values of 3.2678 and 3.3295, which correspond to loglikelihood values -327.4943 and -327.5178. From the earlier fit, the MLE of B is 3.27193, which is in this interval as expected.

Profile Likelihood With Restricted Parameter Values

Load the sample data. Create a probability distribution object by fitting a generalized extreme value distribution to the miles per gallon (MPG) data.

```
load carsmall;
pd = fitdist(MPG,'GeneralizedExtremeValue')
```

```
pd =

  GeneralizedExtremeValueDistribution

  Generalized Extreme Value distribution
        k = -0.207765   [-0.381674, -0.0338564]
    sigma =   7.49674   [6.31755, 8.89603]
       mu =   20.6233   [18.8859, 22.3606]
```

View the parameter names for the distribution.

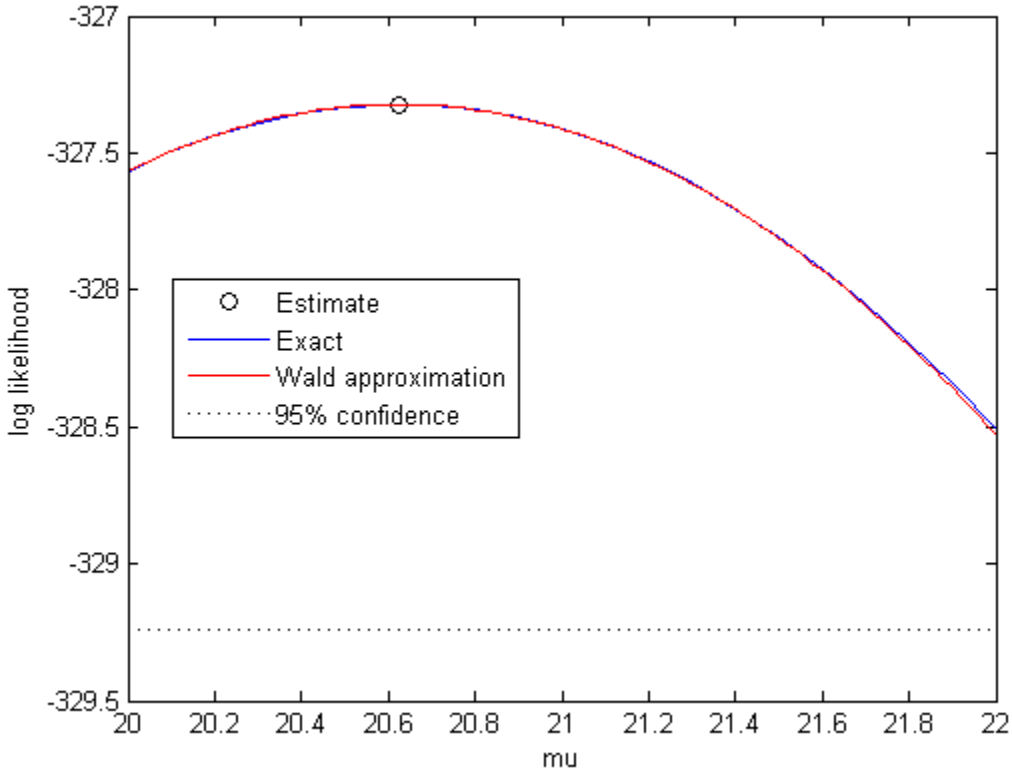
```
pd.ParameterNames
```

```
ans =

    'k'    'sigma'    'mu'
```

For the generalized extreme value distribution, `k` is in position 1, `sigma` is in position 2, and `mu` is in position 3.

Compute the profile likelihood for `mu`, which is in position `pnum = 3`. Restrict the computation to parameter values from 20 to 22, and display the plot.

```
[ll,param,other] = proflik(pd,3,20:.1:22,'display','on');
```



The plot shows the estimated value for the parameter `mu` that maximizes the loglikelihood.

Display the loglikelihood values for the estimated values of `mu`, and the values of the other distribution parameters that maximize the corresponding loglikelihood.

```
[ll',param',other]

ans =

 -327.5706   20.0000   -0.1803    7.4087
 -327.4971   20.1000   -0.1846    7.4218
 -327.4364   20.2000   -0.1890    7.4354
 -327.3887   20.3000   -0.1934    7.4493
 -327.3538   20.4000   -0.1978    7.4636
 -327.3317   20.5000   -0.2023    7.4783
 -327.3223   20.6000   -0.2067    7.4932
 -327.3257   20.7000   -0.2112    7.5084
 -327.3418   20.8000   -0.2156    7.5240
 -327.3706   20.9000   -0.2201    7.5399
 -327.4119   21.0000   -0.2245    7.5560
 -327.4659   21.1000   -0.2289    7.5723
 -327.5324   21.2000   -0.2333    7.5889
 -327.6113   21.3000   -0.2378    7.6057
 -327.7027   21.4000   -0.2422    7.6228
 -327.8065   21.5000   -0.2465    7.6400
 -327.9227   21.6000   -0.2509    7.6575
 -328.0511   21.7000   -0.2553    7.6751
 -328.1917   21.8000   -0.2596    7.6930
 -328.3446   21.9000   -0.2639    7.7111
 -328.5095   22.0000   -0.2682    7.7293
```

The first column contains the log likelihood value that corresponds to the estimate of `mu` in the second column. The log likelihood is maximized between the parameter values 20.6000 and 20.7000, corresponding to log likelihood values -327.3223 and -327.3257. The third column contains the value of `k` that maximizes the corresponding log likelihood for `mu`. The fourth column contains the value of `sigma` that maximizes the corresponding log likelihood for `mu`.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

pnum — Parameter number

positive integer value

Parameter number for which to compute the profile likelihood, specified as a positive integer value corresponding to the position of the desired parameter in the parameter name vector. For example, a Weibull distribution has a parameter name vector `{'A','B'}`, so specify `pnum` as `2` to compute the profile likelihood for `B`.

Data Types: `single` | `double`

setparam — Parameter value restriction

scalar value | vector of scalar values

Parameter value restriction, specified as a scalar value or a vector of such values. If you do not specify `setparam`, `proflik` chooses the values for output vector param based on the default confidence interval method for the probability distribution pd. If the parameter can take only restricted values, and if the confidence interval violates that restriction, you can use `setparam` to specify valid values.

Example: `[3,3.5,4]`

display — Display toggle

`'off'` (default) | `'on'`

Display toggle, specified as either `'on'` or `'off'`. Specify `'on'` to display a plot of the profile log likelihood overlaid on an approximation of the log likelihood. Specify `'off'` to omit the display. The approximation is based on a Taylor series expansion around the estimated parameter value, as a function of the parameter in position pnum or its logarithm. The intersection of the curves with the horizontal dotted line marks the endpoints of 95% confidence intervals.

Output Arguments

ll — Log likelihood values

vector

Log likelihood values, returned as a vector. The log likelihood is the value of the likelihood with the parameter in position pnum set to the values in param, maximized over the remaining parameters.

param — Parameter values

vector

Parameter values corresponding to the loglikelihood values in ll, returned as a vector. If you specify parameter values using setparam, then `param` is equal to `setparam`.

`other` — Other parameter values

matrix

Other parameter values that maximize the likelihood, returned as a matrix. Each row of other contains the values for all parameters except the parameter in position pnum.

See Also

`dfittool` | `fitdist` | `makedist`

proflik

Class: prob.ToolboxFittableParametricDistribution
Package: prob

Profile likelihood function for probability distribution object

Syntax

```
[ll,param] = proflik(pd,pnum)
[ll,param] = proflik(pd,pnum,'Display',display)
[ll,param] = proflik(pd,pnum,setparam)
[ll,param] = proflik(pd,pnum,setparam,'Display',display)
[ll,param,other] = proflik( ___ )
```

Description

`[ll,param] = proflik(pd,pnum)` returns a vector ll of loglikelihood values and a vector param of corresponding parameter values for the parameter in the position indicated by pnum.

`[ll,param] = proflik(pd,pnum,'Display',display)` returns the loglikelihood values and corresponding parameter values, and plots the profile likelihood overlaid on an approximation of the loglikelihood.

`[ll,param] = proflik(pd,pnum,setparam)` returns the loglikelihood values and corresponding parameter values as specified by `setparam`.

`[ll,param] = proflik(pd,pnum,setparam,'Display',display)` returns the loglikelihood values and corresponding parameter values as specified by setparam, and plots the profile likelihood overlaid on an approximation of the loglikelihood.

`[ll,param,other] = proflik( ___ )` also returns a matrix other containing the values of the other parameters that maximize the likelihood, using any of the input arguments from the previous syntaxes.

Input Arguments

`pd` — Probability distribution
probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

`pnum` — Parameter number
positive integer value

Parameter number for which to compute the profile likelihood, specified as a positive integer value corresponding to the position of the desired parameter in the parameter name vector. For example, a Weibull distribution has a parameter name vector `{'A','B'}`, so specify `pnum` as `2` to compute the profile likelihood for `B`.

Data Types: `single` | `double`

`setparam` — Parameter value restriction
scalar value | vector of scalar values

Parameter value restriction, specified as a scalar value or a vector of such values. If you do not specify `setparam`, `proflik` chooses the values for output vector param based on the default confidence interval method for the probability distribution pd. If the parameter can take only restricted values, and if the confidence interval violates that restriction, you can use `setparam` to specify valid values.

Example: `[3,3.5,4]`

`display` — Display toggle
`'off'` (default) | `'on'`

Display toggle, specified as either `'on'` or `'off'`. Specify `'on'` to display a plot of the profile loglikelihood overlaid on an approximation of the loglikelihood. Specify `'off'` to omit the display. The approximation is based on a Taylor series expansion around the estimated parameter value, as a function of the parameter in position pnum or its logarithm. The intersection of the curves with the horizontal dotted line marks the endpoints of 95% confidence intervals.

Output Arguments

`ll` — Loglikelihood values

vector

Loglikelihood values, returned as a vector. The loglikelihood is the value of the likelihood with the parameter in position pnum set to the values in param, maximized over the remaining parameters.

`param` — Parameter values

vector

Parameter values corresponding to the loglikelihood values in ll, returned as a vector. If you specify parameter values using setparam, then `param` is equal to `setparam`.

`other` — Other parameter values

matrix

Other parameter values that maximize the likelihood, returned as a matrix. Each row of other contains the values for all parameters except the parameter in position pnum.

Examples

Profile Likelihood of a Distribution Parameter

Load the sample data. Create a probability distribution object by fitting a Weibull distribution to the miles per gallon (`MPG`) data.

```
load carsmall;
pd = fitdist(MPG,'Weibull')
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 26.5079   [24.8333, 28.2954]
    B = 3.27193   [2.79441, 3.83104]
```

View the parameter names for the distribution.

```
pd.ParameterNames
```

```
ans =
```

```
    'A'    'B'
```

For the Weibull distribution, A is in position 1, and B is in position 2.

Compute the profile likelihood for B, which is in position `pnum = 2`.

```
[ll,param] = proflik(pd,2);
```

Display the loglikelihood values for the estimated values of B.

```
[ll',param']
```

```
ans =

 -329.9688    2.7132
 -329.4312    2.7748
 -328.9645    2.8365
 -328.5661    2.8981
 -328.2340    2.9597
 -327.9658    3.0213
 -327.7596    3.0830
 -327.6135    3.1446
 -327.5256    3.2062
 -327.4943    3.2678
 -327.5178    3.3295
 -327.5946    3.3911
 -327.7233    3.4527
 -327.9023    3.5143
 -328.1303    3.5760
 -328.4060    3.6376
 -328.7281    3.6992
 -329.0956    3.7608
 -329.5071    3.8224
 -329.9617    3.8841
 -330.4583    3.9457
```

These results show that the profile loglikelihood is maximized between the estimated B values of 3.2678 and 3.3295, which correspond to loglikelihood values -327.4943 and -327.5178. From the earlier fit, the MLE of B is 3.27193, which is in this interval as expected.

Profile Likelihood With Restricted Parameter Values

Load the sample data. Create a probability distribution object by fitting a generalized extreme value distribution to the miles per gallon (MPG) data.

```
load carsmall;
pd = fitdist(MPG,'GeneralizedExtremeValue')

pd =

  GeneralizedExtremeValueDistribution

  Generalized Extreme Value distribution
        k = -0.207765   [-0.381674, -0.0338564]
    sigma =   7.49674   [6.31755, 8.89603]
       mu =   20.6233   [18.8859, 22.3606]
```

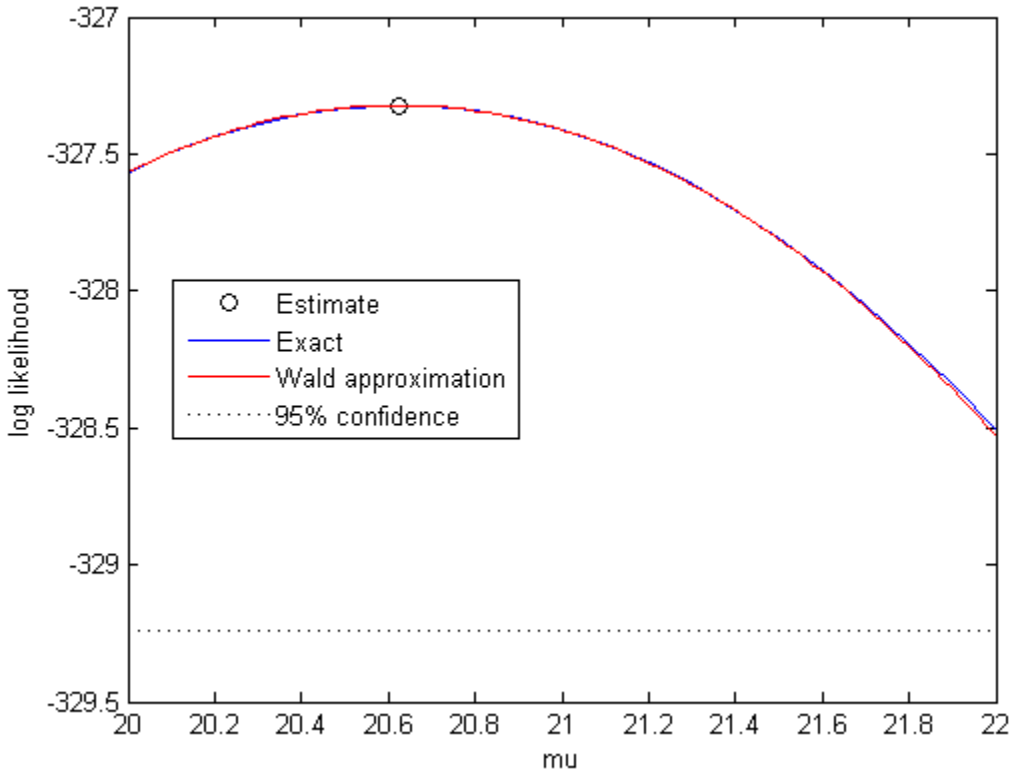
View the parameter names for the distribution.

```
pd.ParameterNames

ans =

    'k'    'sigma'    'mu'
```

For the generalized extreme value distribution, `k` is in position 1, `sigma` is in position 2, and `mu` is in position 3.

Compute the profile likelihood for `mu`, which is in position `pnum = 3`. Restrict the computation to parameter values from 20 to 22, and display the plot.

```
[ll,param,other] = proflik(pd,3,20:.1:22,'display','on');
```



The plot shows the estimated value for the parameter `mu` that maximizes the loglikelihood.

Display the loglikelihood values for the estimated values of `mu`, and the values of the other distribution parameters that maximize the corresponding loglikelihood.

```
[ll',param',other]

ans =

  -327.5706    20.0000    -0.1803     7.4087
  -327.4971    20.1000    -0.1846     7.4218
  -327.4364    20.2000    -0.1890     7.4354
  -327.3887    20.3000    -0.1934     7.4493
```

```
-327.3538   20.4000   -0.1978    7.4636
-327.3317   20.5000   -0.2023    7.4783
-327.3223   20.6000   -0.2067    7.4932
-327.3257   20.7000   -0.2112    7.5084
-327.3418   20.8000   -0.2156    7.5240
-327.3706   20.9000   -0.2201    7.5399
-327.4119   21.0000   -0.2245    7.5560
-327.4659   21.1000   -0.2289    7.5723
-327.5324   21.2000   -0.2333    7.5889
-327.6113   21.3000   -0.2378    7.6057
-327.7027   21.4000   -0.2422    7.6228
-327.8065   21.5000   -0.2465    7.6400
-327.9227   21.6000   -0.2509    7.6575
-328.0511   21.7000   -0.2553    7.6751
-328.1917   21.8000   -0.2596    7.6930
-328.3446   21.9000   -0.2639    7.7111
-328.5095   22.0000   -0.2682    7.7293
```

The first column contains the loglikelihood value that corresponds to the estimate of `mu` in the second column. The loglikelihood is maximized between the parameter values 20.6000 and 20.7000, corresponding to loglikelihood values -327.3223 and -327.3257. The third column contains the value of `k` that maximizes the corresponding loglikelihood for `mu`. The fourth column contains the value of `sigma` that maximizes the corresponding loglikelihood for `mu`.

See Also

`dfittool` | `fitdist` | `makedist`

proximity

Class: CompactTreeBagger

Proximity matrix for data

Syntax

```
prox = proximity(B,X)
```

Description

`prox = proximity(B,X)` computes a numeric matrix of size `Nobs`-by-`Nobs` of proximities for data `X`, where `Nobs` is the number of observations (rows) in `X`. Proximity between any two observations in the input data is defined as a fraction of trees in the ensemble `B` for which these two observations land on the same leaf. This is a symmetric matrix with ones on the diagonal and off-diagonal elements ranging from 0 to 1.

Proximity property

Class: TreeBagger

Proximity matrix for observations

Description

The `Proximity` property is a numeric matrix of size `Nobs`-by-`Nobs`, where `Nobs` is the number of observations in the training data, containing measures of the proximity between observations. For any two observations, their proximity is defined as the fraction of trees for which these observations land on the same leaf. This is a symmetric matrix with 1s on the diagonal and off-diagonal elements ranging from 0 to 1.

See Also

`ClassificationTree` | `proximity` | `fitctree` | `fitrtree` | `RegressionTree` | `TreeBagger`

prune

Class: ClassificationTree

Produce sequence of subtrees by pruning

Syntax

```
tree1 = prune(tree)
tree1 = prune(tree,Name,Value)
```

Description

`tree1 = prune(tree)` creates a copy of the classification tree `tree` with its optimal pruning sequence filled in.

`tree1 = prune(tree,Name,Value)` creates a pruned tree with additional options specified by one Name,Value pair argument. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Tips

- `tree1 = prune(tree)` returns the decision tree `tree1` that is the full, unpruned `tree`, but with optimal pruning information added. This is useful only if you created `tree` by pruning another tree, or by using the `fitctree` function with pruning set `'off'`. If you plan to prune a tree multiple times along the optimal pruning sequence, it is more efficient to create the optimal pruning sequence first.

Input Arguments

`tree`

A classification tree created with `fitctree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'`

A numeric scalar. `prune` prunes `tree` to the specified value of the pruning cost.

`'Level'`

A numeric scalar from `0` (no pruning) to the largest pruning level of this tree `max(tree.PruneList)`. `prune` returns the tree pruned to this level.

`'Nodes'`

A numeric vector with elements from `1` to `tree.NumNodes`. Any tree branch nodes listed in `nodes` become leaf nodes in tree1, unless their parent nodes are also pruned.

Output Arguments

`tree1`

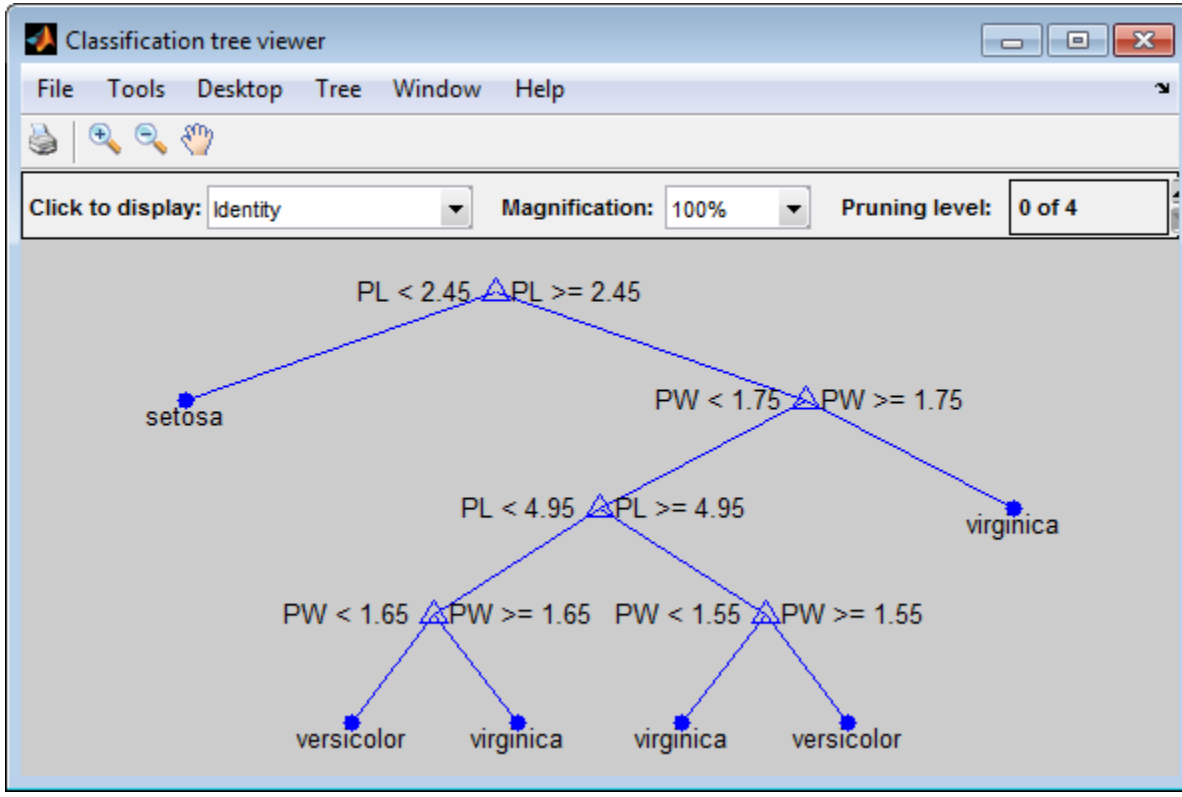
A classification tree.

Examples

Prune and Display a Classification Tree

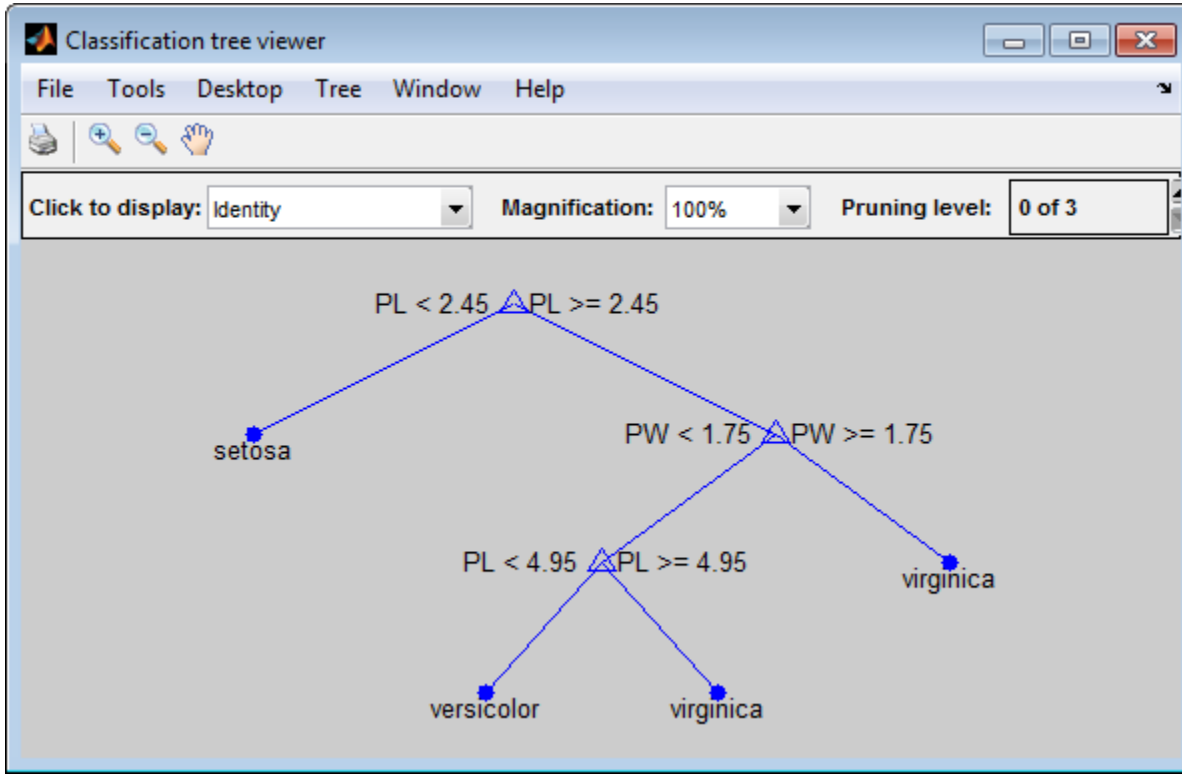
Construct and display a full classification tree for Fisher's iris data.

```
load fisheriris;
varnames = {'SL' 'SW' 'PL' 'PW'};
t1 = fitctree(meas,species,...
    'minparent',5,'predictornames',varnames);
view(t1,'mode','graph');
```



Construct and display the next largest tree from the optimal pruning sequence.

```
t2 = prune(t1,'level',1);
view(t2,'mode','graph');
```



See Also

`fitctree`

prune

Class: classregtree

Prune tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
t2 = prune(t1,'level',level)
t2 = prune(t1,'nodes',nodes)
t2 = prune(t1)
```

Description

`t2 = prune(t1,'level',level)` takes a decision tree `t1` and a pruning level `level`, and returns the decision tree `t2` pruned to that level. If `level` is 0, there is no pruning. Trees are pruned based on an optimal pruning scheme that first prunes branches giving less improvement in error cost.

`t2 = prune(t1,'nodes',nodes)` prunes the nodes listed in the `nodes` vector from the tree. Any `t1` branch nodes listed in `nodes` become leaf nodes in `t2`, unless their parent nodes are also pruned. Use `view` to display the node numbers for any node you select.

`t2 = prune(t1)` returns the decision tree `t2` that is the full, unpruned `t1`, but with optimal pruning information added. This is useful only if `t1` is created by pruning another tree, or by using the `classregtree` function with the `'prune'` parameter set to `'off'`. If you plan to prune a tree multiple times along the optimal pruning sequence, it is more efficient to create the optimal pruning sequence first.

Pruning is the process of reducing a tree by turning some branch nodes into leaf nodes and removing the leaf nodes under the original branch.

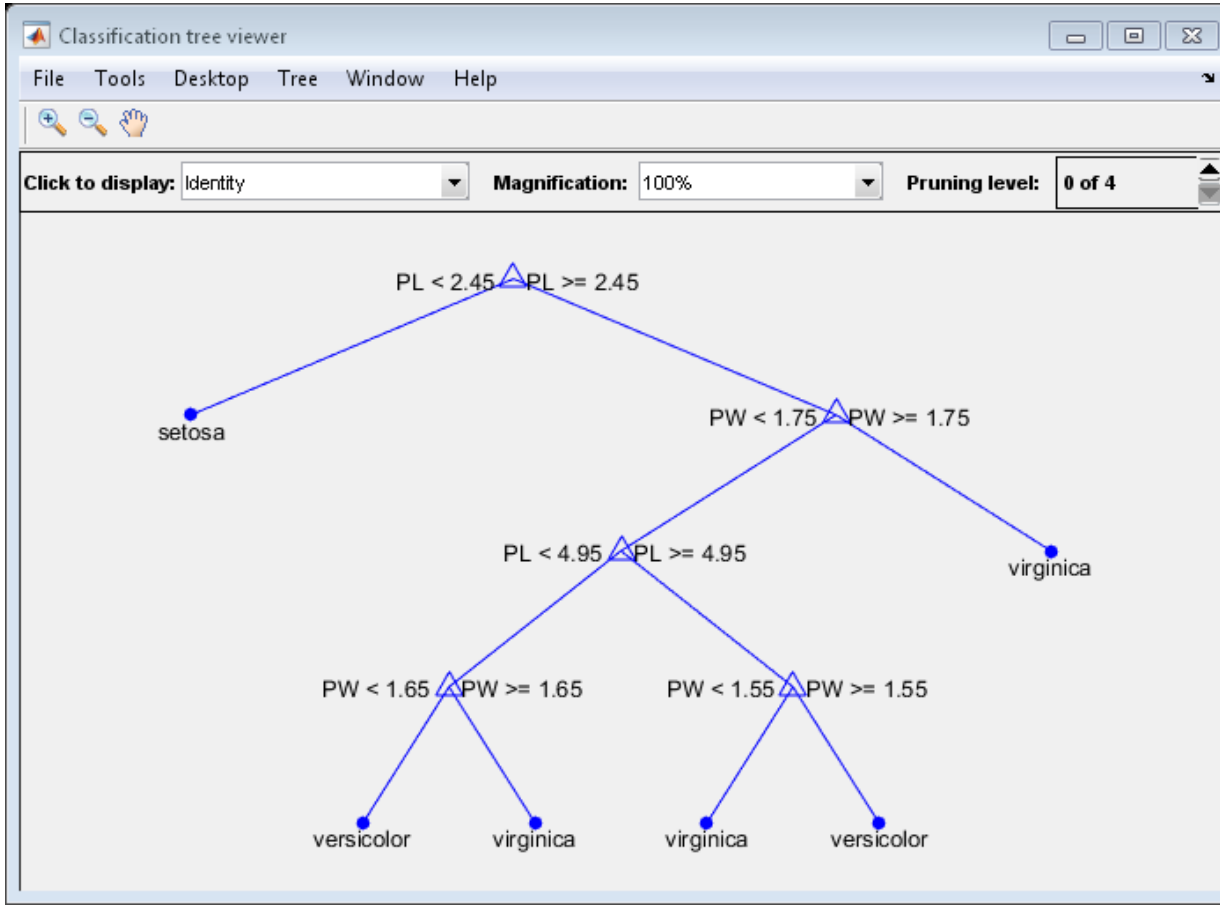
Examples

Prune a Decision Tree

Display the full tree for Fisher's iris data:

```
load fisheriris;
t1 = classregtree(meas,species,...
                  'names',{'SL' 'SW' 'PL' 'PW'},...
                  'minparent',5)
view(t1)
```

```
t1 =

Decision tree for classification
 1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
 2  class = setosa
 3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
 4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
 5  class = virginica
 6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
 7  if PW<1.55 then node 10 elseif PW>=1.55 then node 11 else virginica
 8  class = versicolor
 9  class = virginica
10  class = virginica
11  class = versicolor
```

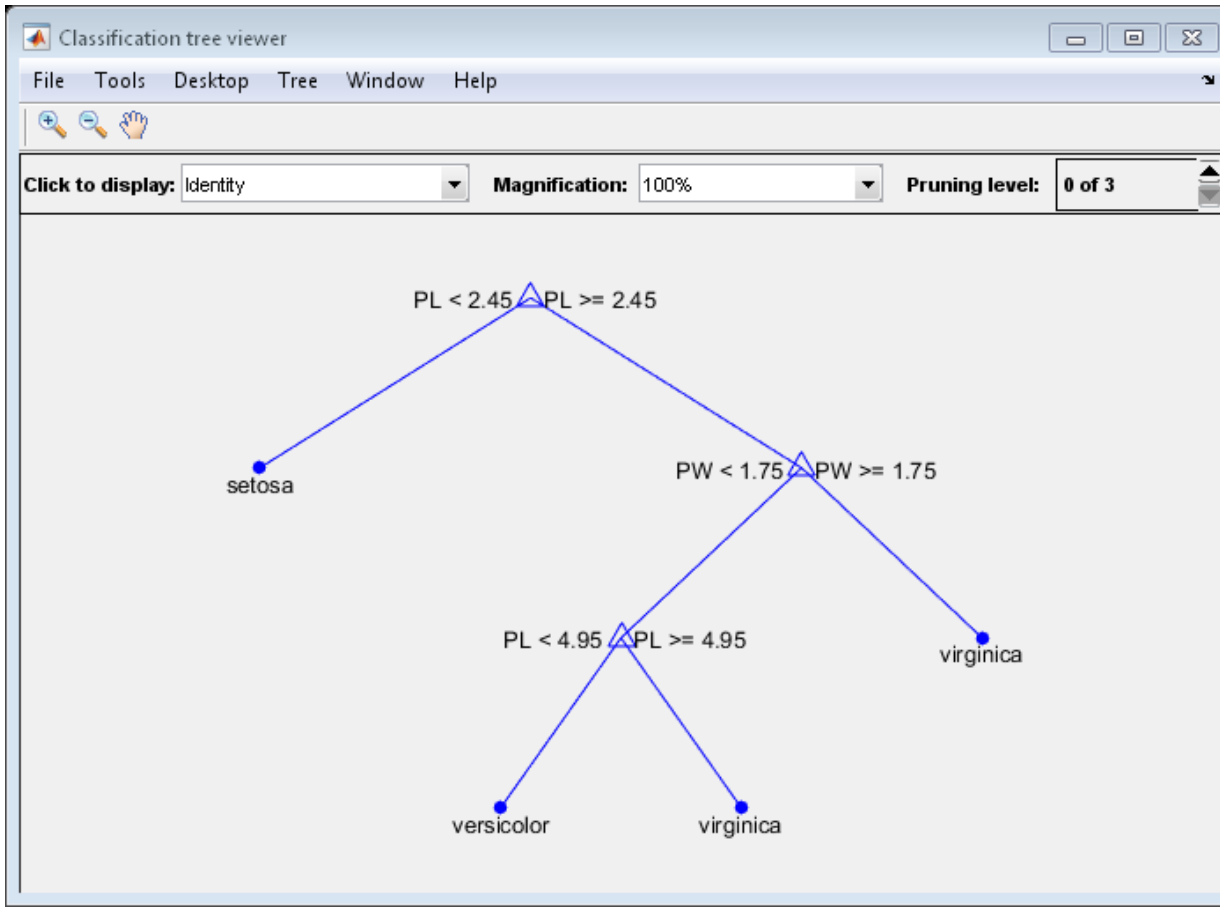


Display the next largest tree from the optimal pruning sequence:

```
t2 = prune(t1,'level',1)
view(t2)
```

```
t2 =

Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
```

```
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  class = versicolor
7  class = virginica
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `view` | `test`

prune

Class: RegressionTree

Produce sequence of subtrees by pruning

Syntax

```
tree1 = prune(tree)
tree1 = prune(tree,Name,Value)
```

Description

`tree1 = prune(tree)` creates a copy of the regression tree `tree` with its optimal pruning sequence filled in.

`tree1 = prune(tree,Name,Value)` creates a pruned tree with additional options specified by one Name,Value pair argument. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Tips

- `tree1 = prune(tree)` returns the decision tree `tree1` that is the full, unpruned `tree`, but with optimal pruning information added. This is useful only if you created `tree` by pruning another tree, or by using `fitrtree` with pruning set `'off'`. If you plan to prune a tree multiple times along the optimal pruning sequence, it is more efficient to create the optimal pruning sequence first.

Input Arguments

`tree`

A regression tree created with `fitrtree`.

Name-Value Pair Arguments

Optional comma-separated pair of Name,Value arguments, where `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify only one name-value pair argument.

`'Alpha'`

A numeric scalar from `0` (no pruning) to `1` (prune to one node). Prunes to minimize the sum of (`Alpha` times the number of leaf nodes) and a cost (mean squared error).

`'Level'`

A numeric scalar from `0` (no pruning) to the largest pruning level of this tree `max(tree.PruneList)`. `prune` returns the tree pruned to this level.

`'Nodes'`

A numeric vector with elements from `1` to `tree.NumNodes`. Any tree branch nodes listed in `Nodes` become leaf nodes in tree1, unless their parent nodes are also pruned.

Output Arguments

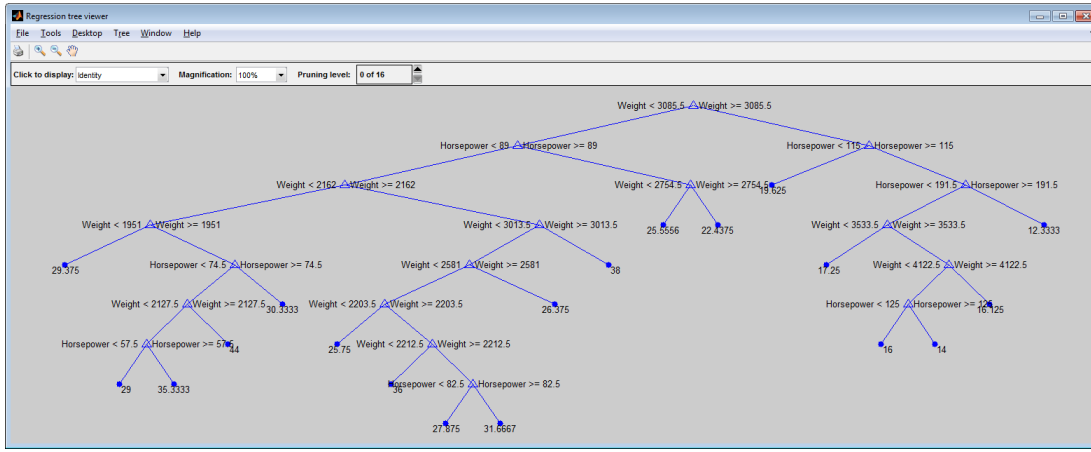
`tree1`

A regression tree.

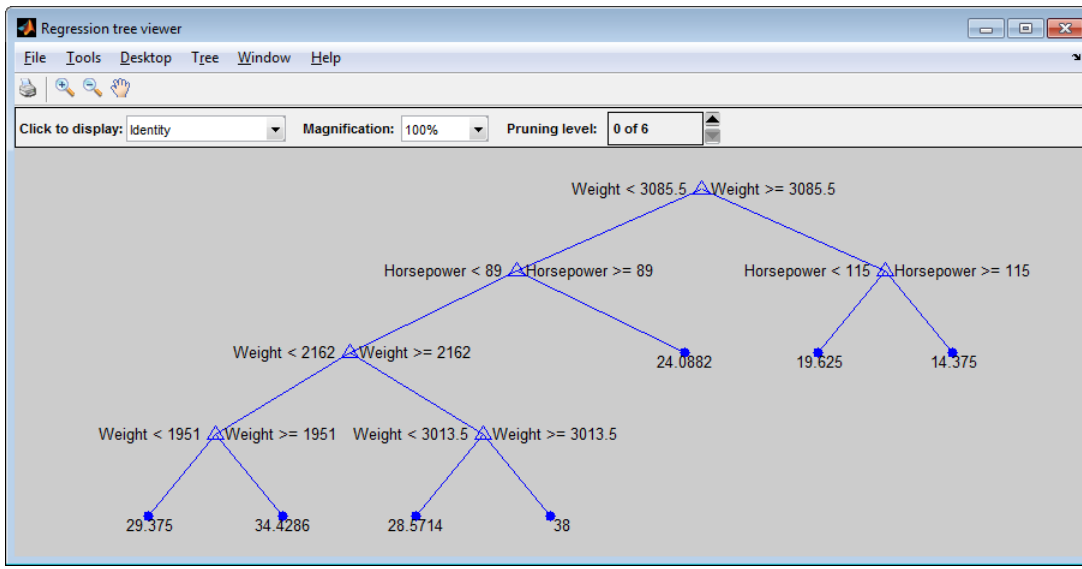
Examples

Display a full tree for the `carsmall` data, as well as the tree pruned to level `10`:

```
load carsmall;
varnames = {'Weight' 'Horsepower'};
t1 = fitrtree([Weight Horsepower],MPG,...
    'predictornames',varnames)
view(t1,'Mode','graph');
```




```
t2 = prune(t1,'Level',10);
view(t2,'Mode','graph');
```



See Also

`fitrtree`

Prune property

Class: TreeBagger

Flag to prune trees

Description

The `Prune` property is true if decision trees are pruned and false if they are not. Pruning decision trees is not recommended for ensembles. The default value is false.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

prunelist

Class: classregtree

Pruning levels for decision tree nodes

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
P = prunelist(T)
P = prunelist(T,J)
```

Description

`P = prunelist(T)` returns an *n*-element numeric vector with the pruning levels in each node of the tree `T`, where *n* is the number of nodes. When you call `prune(T,'level',level)`, nodes with the pruning levels below *`level`* are pruned, and nodes with the pruning levels greater or equal to *`level`* are not pruned.

`P = prunelist(T,J)` takes an array `J` of node numbers and returns the pruning levels for the specified nodes.

See Also

`classregtree` | `numnodes`

qrand

Class: qrandstream

Generate quasi-random points from stream

Syntax

```
x = qrand(q)
X = qrand(q,n)
```

Description

`x = qrand(q)` returns the next value `x` in the quasi-random number stream `q` of the `qrandstream` class. `x` is a 1-by-*d* vector, where *d* is the dimension of the stream. The command sets `q.State` to the index in the underlying point set of the next value to be returned.

`X = qrand(q,n)` returns the next `n` values `X` in an `n`-by-*d* matrix.

Objects `q` of the `qrandstream` class encapsulate properties of a specified quasi-random number stream. Values of the stream are not generated and stored in memory until `q` is accessed using `qrand`.

Examples

Use `qrandstream` to construct a 3-D Halton stream, based on a point set that skips the first 1000 values and then retains every 101st point:

```
q = qrandstream('halton',3,'Skip',1e3,'Leap',1e2)
q =
   Halton quasi-random stream in 3 dimensions
   Point set properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

```
nextIdx = q.State
nextIdx =
     1
```

Use `qrand` to generate two samples of size four:

```
X1 = qrand(q,4)
X1 =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
nextIdx = q.State
nextIdx =
     5

X2 = qrand(q,4)
X2 =
    0.2446    0.0238    0.8102
    0.5298    0.7540    0.0438
    0.3843    0.5112    0.2758
    0.8335    0.2245    0.4694
nextIdx = q.State
nextIdx =
     9
```

Use `reset` to reset the stream, then generate another sample:

```
reset(q)
nextIdx = q.State
nextIdx =
     1

X = qrand(q,4)
X =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
```

See Also

`qrandstream` | `reset`

qrandset class

Quasi-random point sets

Description

`qrandset` is a base class that encapsulates a sequence of multi- dimensional quasi-random numbers. This base class is abstract and cannot be instantiated directly. Concrete subclasses include `sobolset` and `haltonset`.

Construction

.qrandset	Abstract quasi-random point set class

Methods

disp	Display qrandset object
end	Last index in indexing expression for point set
length	Length of point set
ndims	Number of dimensions in matrix
net	Generate quasi-random point set
scramble	Scramble quasi-random point set
size	Number of dimensions in matrix

subsref	Subscripted reference for qrandset

Properties

Dimensions	Number of dimensions
Leap	Interval between points
ScrambleMethod	Settings that control scrambling
Skip	Number of initial points to omit from sequence
Type	Name of sequence on which point set P is based

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

See Also

`haltonset` | `sobolset`

How To

- “Quasi-Random Point Sets” on page 6-17

qrandset

Class: qrandset

Abstract quasi-random point set class

Description

`qrandset` is an abstract class, and you cannot create instances of it directly. You must use `haltonset` or `sobolset` to create a `qrandset` object.

See Also

`haltonset` | `sobolset`

qrandstream class

Quasi-random number streams

Construction

.qrandstream	Construct quasi-random number stream

Methods

addlistener	Add listener for event
delete	Delete handle object
disp	Display `qrandstream` object
eq	Test handle equality
findobj	Find objects matching specified conditions
findprop	Find property of MATLAB handle object
ge	Greater than or equal relation for handles
gt	Greater than relation for handles
isvalid	Test handle validity
le	Less than or equal relation for handles
lt	Less than relation for handles

ne	Not equal relation for handles
notify	Notify listeners of event
qrand	Generate quasi-random points from stream
rand	Generate quasi-random points from stream
reset	Reset state

Properties

PointSet	Point set from which stream is drawn
State	Current state of the stream

Copy Semantics

Handle. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

qrandstream

Class: qrandstream

Construct quasi-random number stream

Syntax

```
q = qrandstream(type,d)
q = qrandstream(type,d,prop1,val1,prop2,val2,...)
q = qrandstream(p)
```

Description

`q = qrandstream(type,d)` constructs a `d`-dimensional quasi-random number stream `q` of the `qrandstream` class, of type specified by the string *`type`*. *`type`* is either `'halton'` or `'sobol'`, and `q` is based on a point set from either the `haltonset` class or `sobolset` class, respectively, with default property settings.

`q = qrandstream(type,d,prop1,val1,prop2,val2,...)` specifies property name/value pairs for the point set on which the stream is based. Applicable properties depend on *`type`*.

`q = qrandstream(p)` constructs a stream based on the specified point set `p`. `p` must be a point set from either the `haltonset` class or `sobolset` class.

Examples

Construct a 3-D Halton stream, based on a point set that skips the first 1000 values and then retains every 101st point:

```
q = qrandstream('halton',3,'Skip',1e3,'Leap',1e2)
q =
   Halton quasi-random stream in 3 dimensions
   Point set properties:
              Skip : 1000
              Leap : 100
```

```
    ScrambleMethod : none

nextIdx = q.State
nextIdx =
     1
```

Use `qrand` to generate two samples of size four:

```
X1 = qrand(q,4)
X1 =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
nextIdx = q.State
nextIdx =
     5

X2 = qrand(q,4)
X2 =
    0.2446    0.0238    0.8102
    0.5298    0.7540    0.0438
    0.3843    0.5112    0.2758
    0.8335    0.2245    0.4694
nextIdx = q.State
nextIdx =
     9
```

Use `reset` to reset the stream, and then generate another sample:

```
reset(q)
nextIdx = q.State
nextIdx =
     1

X = qrand(q,4)
X =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
```

See Also

`haltonset` | `reset` | `sobolset` | `qrand`

qqplot

Quantile-quantile plot

Syntax

```
qqplot(X)
qqplot(X,Y)
qqplot(X,PD)
qqplot(X,Y,pvec)
h = qqplot(X,Y,pvec)
```

Description

`qqplot(X)` displays a quantile-quantile plot of the sample quantiles of `X` versus theoretical quantiles from a normal distribution. If the distribution of `X` is normal, the plot will be close to linear.

`qqplot(X,Y)` displays a quantile-quantile plot of two samples. If the samples do come from the same distribution, the plot will be linear.

`qqplot(X,PD)` makes an empirical quantile-quantile plot of the quantiles of the data in the vector `X` versus the quantiles of the distribution specified by `PD`, a `ProbDist` object of the `ProbDistUnivParam` class or `ProbDistUnivKernel` class.

For matrix `X` and `Y`, `qqplot` displays a separate line for each pair of columns. The plotted quantiles are the quantiles of the smaller data set.

The plot has the sample data displayed with the plot symbol `'+'`. Superimposed on the plot is a line joining the first and third quartiles of each distribution (this is a robust linear fit of the order statistics of the two samples). This line is extrapolated out to the ends of the sample to help evaluate the linearity of the data.

Use `qqplot(X,Y,pvec)` to specify the quantiles in the vector `pvec`.

`h = qqplot(X,Y,pvec)` returns handles to the lines in `h`.

Examples

Quantile-Quantile Plot With Two Samples

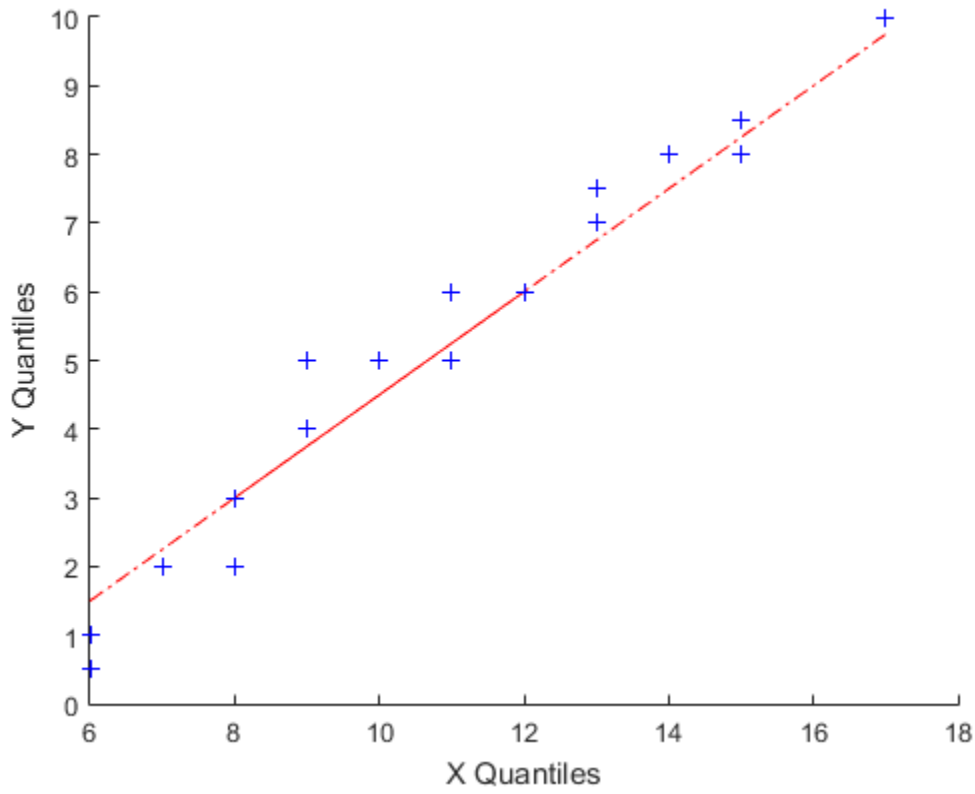
This example shows how to create a quantile-quantile plot using two sets of sample data.

Generate random numbers from two Poisson distributions. The vector `x` contains 50 random numbers from a Poisson distribution with `lambda = 10`. The vector `y` contains 100 random numbers from a Poisson distribution with `lambda = 5`.

```
rng default;  % For reproducibility
x = poissrnd(10,50,1);
y = poissrnd(5,100,1);
```

Create a quantile-quantile plot using the two sets of sample data.

```
qqplot(x,y);
```



The solid line in the plot joins the first and third quartiles. The dashed line extrapolates the solid line.

More About

- `normplot`

quantile

Quantiles of a data set

Syntax

```
Y = quantile(X,p)
Y = quantile(X,p,dim)

Y = quantile(X,N)
Y = quantile(X,N,dim)
```

Description

`Y = quantile(X,p)` returns quantiles of the values in data vector or matrix `X` for the cumulative probability or probabilities `p` in the interval [0,1].

- If `X` is a vector, then `Y` is a scalar or a vector having the same length as `p`.
- If `X` is a matrix, then `Y` is a row vector or a matrix where the number of rows of `Y` is equal to the length of `p`.
- For multidimensional arrays, `quantile` operates along the first nonsingleton dimension of `X`.

`Y = quantile(X,p,dim)` returns quantiles along dimension `dim`.

`Y = quantile(X,N)` returns quantiles for `N` evenly spaced cumulative probabilities (1/(`N` + 1), 2/(`N` + 1), ..., `N`/(`N` + 1)) for integer `N`>1.

- If `X` is a vector, then `Y` is a scalar or a vector with length `N`.
- If `X` is a matrix, then `Y` is a matrix where the number of rows of `Y` is equal to `N`.
- For multidimensional arrays, `quantile` operates along the first nonsingleton dimension of `X`.

`Y = quantile(X,N,dim)` returns quantiles at the `N` evenly-spaced cumulative probabilities (1/(`N`+1), 2/(`N`+1), ..., `N`/(`N`+1)) for integer `N`>1 along dimension `dim`.

Examples

Quantiles for Given Probabilities

Calculate the quantiles of a data set for specified probabilities.

Generate a data set of size 10.

```
rng('default'); % for reproducibility
x = normrnd(0,1,1,10)
```

```
x =
    0.5377    1.8339   -2.2588    0.8622    0.3188   -1.3077   -0.4336    0.3426    3.5
```

Calculate the 0.3 quantile.

```
y = quantile(x,0.30)
```

```
y =
   -0.0574
```

Calculate the quantiles for the cumulative probabilities 0.025, 0.25, 0.5, 0.75, and 0.975.

```
y = quantile(x,[0.025 0.25 0.50 0.75 0.975])
```

```
y =
   -2.2588   -0.4336    0.4401    1.8339    3.5784
```

Quantiles of a Matrix for Given Probabilities

Calculate the quantiles along the columns and rows of a data matrix for specified probabilities.

Generate a 4-by-6 data matrix.

```
rng('default'); % for reproducibility
X = normrnd(0,1,4,6)
```

```
X =
    0.5377    0.3188    3.5784    0.7254   -0.1241    0.6715
    1.8339   -1.3077    2.7694   -0.0631    1.4897   -1.2075
   -2.2588   -0.4336   -1.3499    0.7147    1.4090    0.7172
    0.8622    0.3426    3.0349   -0.2050    1.4172    1.6302
```

Calculate the 0.3 quantile for each column of `X` (`dim` = 1).

```
y = quantile(x,0.3,1)
```

```
y =
   -0.3013   -0.6958    1.5336   -0.1056    0.9491    0.1078
```

`quantile` returns a row vector `y` when calculating one quantile for each column of a matrix. For example, `-0.3013` is the 0.3 quantile of the first column of `X` with elements (0.5377, 1.8339, -2.2588, 0.8622). `y = quantile(X,0.3)` returns the same answer because the default value of `dim` is 1.

Calculate the 0.3 quantile for each row of `X` (`dim` = 2).

```
y = quantile(x,0.3,2)
```

```
y =
    0.3844
   -0.8642
   -1.0750
    0.4985
```

`quantile` returns a column vector `y` when calculating one quantile for each row of a matrix. For example `0.3844` is the 0.3 quantile of the first row of `X` with elements (0.5377, 0.3188, 3.5784, 0.7254, -0.1241, 0.6715).

Quantiles for *N* Evenly Spaced Cumulative Probabilities

Calculate the quantiles of a data set for a given number of quantiles.

Generate a data set of size 10.

```
rng('default'); % for reproducibility
x = normrnd(0,1,1,10)
```

```
x =
    0.5377    1.8339   -2.2588    0.8622    0.3188   -1.3077   -0.4336    0.3426    3.5
```

Calculate four evenly spaced quantiles.

```
y = quantile(x,4)
```

```
y =
   -0.8706    0.3307    0.6999    2.3017
```

Using `y = quantile(x,[0.2,0.4,0.6,0.8])` is another way to return the four evenly spaced quantiles.

Quantiles of a Matrix for Given Number of Quantiles

Calculate the *N* evenly spaced quantiles along the columns and rows of a data matrix.

Generate a 6-by-10 data matrix.

```
rng('default');  % for reproducibility
X = unidrnd(10,6,7)
```

```
X =

     9     3    10     8     7     8     7
    10     6     5    10     8     1     4
     2    10     9     7     8     3    10
    10    10     2     1     4     1     1
     7     2     5     9     7     1     5
     1    10    10    10     2     9     4
```

Calculate three evenly spaced quantiles for each column of `X` (`dim` = 1).

```
y = quantile(X,3,1)
```

```
y =

    2.0000    3.0000    5.0000    7.0000    4.0000    1.0000    4.0000
    8.0000    8.0000    7.0000    8.5000    7.0000    2.0000    4.5000
   10.0000   10.0000   10.0000   10.0000    8.0000    8.0000    7.0000
```

Each column of matrix `y` corresponds to the three evenly spaced quantiles of each column of matrix `X`. For example, the first column of `y` with elements (2, 8, 10) has the quantiles for the first column of `X` with elements (9, 10, 2, 10, 7, 1). `y = quantile(X,3)` returns the same answer because the default value of `dim` is 1.

Calculate three evenly spaced quantiles for each row of `X` (`dim` = 2).

```
y = quantile(X,3,2)
```

```
y =

    7.0000    8.0000    8.7500
    4.2500    6.0000    9.5000
    4.0000    8.0000    9.7500
```

```
    1.0000    2.0000    8.5000
    2.7500    5.0000    7.0000
    2.5000    9.0000   10.0000
```

Each row of matrix `y` corresponds to the three evenly spaced quantiles of each row of matrix `X`. For example, the first row of `y` with elements (7, 8, 8.75) has the quantiles for the first column of `X` with elements (9, 3, 10, 8, 7, 8, 7).

Median and Quartiles for Even Number of Data Elements

Find median and quartiles of a vector, `x`, with even number of elements.

Enter the data.

```
x = [2 5 6 10 11 13]
```

```
x =
     2     5     6    10    11    13
```

Calculate the median of `x`.

```
y = quantile(x,0.50)
```

```
y =
     8
```

Calculate the quartiles of `x`.

```
y = quantile(x,[0.25, 0.5, 0.75])
```

```
y =
     5     8    11
```

Using `y = quantile(x,3)` is another way to compute the quartiles of `x`.

These results might be different than the textbook definitions because `quantile` uses linear interpolation to find the median and quartiles.

Median and Quartiles for Odd Number of Data Elements

Find median and quartiles of a vector, `x`, with odd number of elements.

Enter the data.

```
x = [2 4 6 8 10 12 14]
```

```
x =

     2     4     6     8    10    12    14
```

Find the median of `x`.

```
y = quantile(x,0.50)
```

```
y =
     8
```

Find the quartiles of `x`.

```
y = quantile(x,[0.25, 0.5, 0.75])
```

```
y =
    4.5000    8.0000   11.5000
```

Using `y = quantile(x,3)` is another way to compute the quartiles of `x`.

These results might be different than the textbook definitions because `quantile` uses linear interpolation to find the median and quartiles.

Input Arguments

`X` — Input data

vector | array

Input data, specified as a vector or array.

Data Types: `double` | `single`

`p` — Cumulative probabilities

scalar | vector

Cumulative probabilities, for which to compute the quantiles, specified as a scalar or vector of scalars from 0 to 1.

Example: 0.3

Example: [0.25, 0.5, 0.75]

Example: (0:0.25:1)

Data Types: `double` | `single`

N — Number of quantiles

positive integer

Number of quantiles to compute, specified as a positive integer. `quantile` returns `N` quantiles that divide the data set into evenly distributed `N`+1 segments.

Data Types: `double` | `single`

dim — Dimension

1 (default) | positive integer

Dimension along which the quantiles of a matrix `X` are required, specified as a positive integer. For example, for a matrix `X`, when `dim` = 1, `quantile` returns the quantile(s) of the columns of `X` and when `dim` = 2, quantile returns the quantile(s) of the rows of `X`. For a multidimensional array `X`, the length of the `dim`th dimension of `Y` is same as length of `p`.

Output Arguments

Y — Quantiles

scalar | array

Quantiles of a data vector or matrix, returned as a scalar or array for one or multiple values of cumulative probabilities.

- If `X` is a vector, then `Y` is a scalar or a vector with the same length as the number of quantiles required (`N` or `length(p)`). `Y(i)` contains the `p(i)` quantile.
- If `X` is a matrix, then `Y` is a vector or a matrix with the length of `dim`th dimension equal to the number of quantiles required (`N` or `length(p)`). When `dim` = 1, for example, the `i`th row of `Y` contains the `p(i)` quantiles of columns of `X`.
- If `X` is an array of dimension *d*, then `Y` is an array with the length of `dim`th dimension equal to the number of quantiles required (`N` or `length(p)`).

More About

Multidimensional Array

A *multidimensional array* is an array with more than two dimensions. For example, if `X` is a 1-by-3-by-4 array, then `X` is a 3-D array.

First Nonsingleton Dimension

A *first nonsingleton dimension* is the first dimension of an array whose size is not equal to 1. For example, if `X` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `X`.

Linear Interpolation

Linear interpolation uses linear polynomials to find $y_i = f(x_i)$, the values of the underlying function $Y = f(X)$ at the points in the vector or array x. Given the data points (x_1, y_1) and (x_2, y_2), where $y_1 = f(x_1)$ and $y_2 = f(x_2)$, linear interpolation finds $y = f(x)$ for a given x between x_1 and x_2 as follows:

$$y = f(x) = y_1 + \frac{(x - x_1)}{(x_2 - x_1)}(y_2 - y_1).$$

Similarly, if the $1.5/n$ quantile is $y_{1.5/n}$ and the $2.5/n$ quantile is $y_{2.5/n}$, then linear interpolation finds the $2.3/n$ quantile $y_{2.3/n}$ as

$$y_{\frac{2.3}{n}} = y_{\frac{1.5}{n}} + \frac{\left(\frac{2.3}{n} - \frac{1.5}{n}\right)}{\left(\frac{2.5}{n} - \frac{1.5}{n}\right)}\left(y_{\frac{2.5}{n}} - y_{\frac{1.5}{n}}\right).$$

Algorithms

For an n-element vector `X`, `quantile` computes quantiles as follows:

1. The sorted values in `X` are taken as the $(0.5/n)$, $(1.5/n)$, ..., $([n - 0.5]/n)$ quantiles. For example:
   - For a data vector of five elements such as {6, 3, 2, 10, 1}, the sorted elements {1, 2, 3, 6, 10} respectively correspond to the 0.1, 0.3, 0.5, 0.7, 0.9 quantiles.
   - For a data vector of six elements such as {6, 3, 2, 10, 8, 1}, the sorted elements {1, 2, 3, 6, 8, 10} respectively correspond to the (0.5/6), (1.5/6), (2.5/6), (3.5/6), (4.5/6), (5.5/6) quantiles.
2. `quantile` uses Linear interpolation to compute quantiles for probabilities between $(0.5/n)$ and $([n - 0.5]/n)$.

3 For the quantiles corresponding to the probabilities outside that range, `quantile` assigns the minimum or maximum values in `X`.

`quantile` treats `NaN`s as missing values and removes them.

- "Quantiles and Percentiles" on page 3-7

See Also

`iqr` | `median` | `prctile`

rand

Class: qrandstream

Generate quasi-random points from stream

Syntax

```
rand
rand(q,n)
rand(q)
rand(q,m,n)
rand(q,[m,n])
rand(q,m,n,p,...)
rand(q,[m,n,p,...])
```

Description

`rand` returns a matrix of quasi-random values and is intended to allow objects of the `qrandstream` class to be used in code that contains calls to the `rand` method of the MATLAB pseudo-random `randstream` class. Due to the multidimensional nature of quasi-random numbers, only some syntaxes of `rand` are supported by the `qrandstream` class.

`rand(q,n)` returns an `n`-by-`n` matrix only when `n` is equal to the number of dimensions. Any other value of `n` produces an error.

`rand(q)` returns a scalar only when the stream is in one dimension. Having more than one dimension in `q` produces an error.

`rand(q,m,n)` or `rand(q,[m,n])` returns an `m`-by-`n` matrix only when `n` is equal to the number of dimensions in the stream. Any other value of `n` produces an error.

`rand(q,m,n,p,...)` or `rand(q,[m,n,p,...])` produces an error unless `p` and all following dimensions sizes are equal to one.

Examples

Generate the first 256 points from a 5-D Sobol sequence:

```
q = qrandstream('sobol',5);
X = rand(q,256,5);
```

See Also

`qrandstream` | `qrand` | `rand`

randg

Gamma random numbers with unit scale

Syntax

```
Y = randg
Y = randg(A)
Y = randg(A,m)
Y = randg(A,m,n,p,...)
Y = randg(A,[m,n,p,...])
```

Description

`Y = randg` returns a scalar random value chosen from a gamma distribution with unit scale and shape.

`Y = randg(A)` returns a matrix of random values chosen from gamma distributions with unit scale. `Y` is the same size as `A`, and `randg` generates each element of `Y` using a shape parameter equal to the corresponding element of `A`.

`Y = randg(A,m)` returns an `m`-by-`m` matrix of random values chosen from gamma distributions with shape parameters `A`. `A` is either an `m`-by-`m` matrix or a scalar. If `A` is a scalar, `randg` uses that single shape parameter value to generate all elements of `Y`.

`Y = randg(A,m,n,p,...)` or `Y = randg(A,[m,n,p,...])` returns an `m`-by-`n`-by-`p`-by-`...` array of random values chosen from gamma distributions with shape parameters `A`. `A` is either an `m`-by-`n`-by-`p`-by-`...` array or a scalar.

`randg` produces pseudo-random numbers using the MATLAB functions `rand` and `randn`. The sequence of numbers generated is determined by the settings of the uniform random number generator that underlies `rand` and `randn`. Control that shared random number generator using `rng`. See the `rng` documentation for more information.

Note: To generate gamma random numbers and specify both the scale and shape parameters, you should call `gamrnd`.

Examples

Example 1

Generate a 100-by-1 array of values drawn from a gamma distribution with shape parameter 3.

```
r = randg(3,100,1);
```

Example 2

Generate a 100-by-2 array of values drawn from gamma distributions with shape parameters 3 and 2.

```
A = [ones(100,1)*3,ones(100,1)*2];
r = randg(A,[100,2]);
```

Example 3

To create reproducible output from `randg`, reset the random number generator used by `rand` and `randn` to its default startup settings. This way `randg` produces the same random numbers as if you restarted MATLAB.

```
rng('default')
randg(3,1,5)

ans =

    6.9223    4.3369    1.0505    3.2662   11.3269
```

Example 4

Save the settings for the random number generator used by `rand` and `randn`, generate 5 values from `randg`, restore the settings, and repeat those values.

```
s = rng; % Obtain the current state of the random stream
r1 = randg(10,1,5)

r1 =
```

```
    9.4719    9.0433   15.0774   14.7763    6.3775

rng(s); % Reset the stream to the previous state
r2 = randg(10,1,5)

r2 =

    9.4719    9.0433   15.0774   14.7763    6.3775
```

`r2` contains exactly the same values as `r1`.

Example 5

Reinitialize the random number generator used by `rand` and `randn` with a seed based on the current time. `randg` returns different values each time you do this. Note that it is usually not necessary to do this more than once per MATLAB session.

```
rng('shuffle');
randg(2,1,5);
```

References

[1] Marsaglia, G., and W. W. Tsang. "A Simple Method for Generating Gamma Variables." *ACM Transactions on Mathematical Software*. Vol. 26, 2000, pp. 363–372.

See Also

`gamrnd`

random

Random numbers

Syntax

```
Y = random(pd)
Y = random(pd,m,n,...)
Y = random(pd,[m,n,...])
Y = random(name,A)
Y = random(name,A,B)
Y = random(name,A,B,C)
Y = random(name,A,m,n,...)
Y = random(name,A,[m,n,...])
Y = random(name,A,B,m,n,...)
Y = random(name,A,B,[m,n,...])
Y = random(name,A,B,C,m,n,...)
Y = random(name,A,B,C,[m,n,...])
```

Description

`Y = random(pd)` returns a random number `Y` from the distribution specified by the probability distribution object `pd`. You can create a probability distribution object with specified parameter values using `makedist`, or fit a probability distribution object to sample data using `fitdist`.

`Y = random(pd,m,n,...)` or `Y = random(pd,[m,n,...])` returns an `m`-by-`n`-by... matrix of random numbers from the probability distribution specified by `pd`.

`Y = random(name,A)` where `name` is the name of a distribution that takes a single parameter, returns random numbers `Y` from the one-parameter family of distributions specified by `name`. Parameter values for the distribution are given in `A`.

`Y` is the same size as `A`.

`Y = random(name,A,B)` returns random numbers `Y` from a two-parameter family of distributions. Parameter values for the distribution are given in `A` and `B`.

If A and B are arrays, they must be the same size. If either A or B are scalars, they are expanded to constant matrices of the same size.

`Y = random(name,A,B,C)` returns random numbers Y from a three-parameter family of distributions. Parameter values for the distribution are given in A, B, and C.

If A, B, and C are arrays, they must be the same size. If any of A, B, or C are scalars, they are expanded to constant matrices of the same size.

`Y = random(name,A,m,n,...)` or `Y = random(name,A,[m,n,...])` returns an m-by-n-by... matrix of random numbers.

Similarly, `Y = random(name,A,B,m,n,...)` or `Y = random(name,A,B,[m,n,...])` returns an m-by-n-by... matrix of random numbers for distributions that require two parameters. `Y = random(name,A,B,C,m,n,...)` or `Y = random(name,A,B,C,[m,n,...])` returns an m-by-n-by... matrix of random numbers for distributions that require three parameters.

If any of A, B, or C are arrays, then the specified dimensions must match the common dimensions of A, B, and C after any necessary scalar expansion.

The following table denotes the acceptable strings for name, as well as the parameters for that distribution:

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
'beta' or 'Beta'	"Beta Distribution" on page B-4	a	b	—
'bino' or 'Binomial'	"Binomial Distribution" on page B-9	n: number of trials	p: probability of success for each trial	—
'birnbaumsaunder	"Birnbaum-Saunders Distribution" on page B-13	β	γ	—
'burr' or 'Burr'	"Burr Type XII Distribution" on page B-15	α: scale parameter	c: shape parameter	k: shape parameter
'chi2' or 'Chisquare'	"Chi-Square Distribution" on page B-29	ν: degrees of freedom	—	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
`'exp'` or `'Exponential'`	"Exponential Distribution" on page B-35	μ: mean	—	—
`'ev'` or `'Extreme Value'`	"Extreme Value Distribution" on page B-39	μ: location parameter	σ: scale parameter	—
`'f'` or `'F'`	"F Distribution" on page B-45	$\nu 1$: numerator degrees of freedom	$\nu 2$: denominator degrees of freedom	—
`'gam'` or `'Gamma'`	"Gamma Distribution" on page B-48	`a`: shape parameter	`b`: scale parameter	—
`'gev'` or `'Generalized Extreme Value'`	"Generalized Extreme Value Distribution" on page B-54	`k`: shape parameter	σ: scale parameter	μ: location parameter
`'gp'` or `'Generalized Pareto'`	"Generalized Pareto Distribution" on page B-60	`k`: tail index (shape) parameter	σ: scale parameter	μ: threshold (location) parameter
`'geo'` or `'Geometric'`	"Geometric Distribution" on page B-65	`p`: probability parameter	—	—
`'hyge'` or `'Hypergeometric'`	"Hypergeometric Distribution" on page B-74	`M`: size of the population	`K`: number of items with the desired characteristic in the population	`n`: number of samples drawn
`'inversegaussian'`	"Inverse Gaussian Distribution" on page B-77	μ	λ	—
`'logistic'`	"Logistic Distribution" on page B-91	μ	σ	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
`'loglogistic'`	"Loglogistic Distribution" on page B-93	μ	σ	—
`'logn'` or `'Lognormal'`	"Lognormal Distribution" on page B-95	μ	σ	—
`'nakagami'`	"Nakagami Distribution" on page B-113	μ	ω	—
`'nbin'` or `'Negative Binomial'`	"Negative Binomial Distribution" on page B-115	`r`: number of successes	`p`: probability of success in a single trial	—
`'ncf'` or `'Noncentral F'`	"Noncentral F Distribution" on page B-123	ν`1`: numerator degrees of freedom	ν`2`: denominator degrees of freedom	δ: noncentrality parameter
`'nct'` or `'Noncentral t'`	"Noncentral t Distribution" on page B-126	ν: degrees of freedom	δ: noncentrality parameter	—
`'ncx2'` or `'Noncentral Chi-square'`	"Noncentral Chi-Square Distribution" on page B-120	ν: degrees of freedom	δ: noncentrality parameter	—
`'norm'` or `'Normal'`	"Normal Distribution" on page B-130	μ: mean	σ: standard deviation	—
`'poiss'` or `'Poisson'`	"Poisson Distribution" on page B-138	λ: mean	—	—
`'rayl'` or `'Rayleigh'`	"Rayleigh Distribution" on page B-141	`b`: scale parameter	—	—
`'rician'`	"Rician Distribution" on page B-144	`s`: noncentrality parameter	σ: scale parameter	—

name	Distribution	Input Parameter A	Input Parameter B	Input Parameter C
't' or 'T'	"Student's t Distribution" on page B-146	ν: degrees of freedom	—	—
'tlocationscale'	"t Location-Scale Distribution" on page B-154	μ: location parameter	σ: scale parameter	ν: shape parameter
'unif' or 'Uniform'	"Uniform Distribution (Continuous)" on page B-163	a: lower endpoint (minimum)	b: upper endpoint (maximum)	—
'unid' or 'Discrete Uniform'	"Uniform Distribution (Discrete)" on page B-169	N: maximum observable value	—	—
'wbl' or 'Weibull'	"Weibull Distribution" on page B-172	a: scale parameter	b: shape parameter	—

Examples

Generate a 2-by-4 array of random values from the normal distribution with mean 0 and standard deviation 1:

```
x1 = random('Normal',0,1,2,4)
```

```
x1 =
  1.1650   0.0751   -0.6965   0.0591
  0.6268   0.3516   1.6961   1.7971
```

The order of the parameters is the same as for normrnd.

Generate a single random value from Poisson distributions with rate parameters 1, 2, ..., 6, respectively:

```
x2 = random('Poisson',1:6,1,6)
```

```
x2 = random('Poisson',1:6,1,6)
x2 =
```

```
    0    0    1    2    5    7
```

See Also

`cdf` | `pdf` | `icdf` | `mle` | `makedist` | `fitdist`

random

Class: GeneralizedLinearModel

Simulate responses for generalized linear regression model

Syntax

```
ysim = random(mdl,Xnew)
ysim = random(mdl,Xnew,Name,Value)
```

Description

`ysim = random(mdl,Xnew)` simulates responses from the `mdl` generalized linear model to the data in `Xnew`.

`ysim = random(mdl,Xnew,Name,Value)` simulates responses with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`Xnew`

Points at which `mdl` predicts responses.

- If `Xnew` is a table or dataset array, it must contain the predictor names in `mdl`.
- If `Xnew` is a numeric matrix, it must have the same number of variables (columns) as was used to create `mdl`. Furthermore, all variables used in creating `mdl` must be numeric.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinomialSize'`

The value of the binomial n parameter for each row in the training data. `BinomialSize` can be a vector the same length as `Xnew`, or a scalar that applies to each row. The default value `1` produces `ysim` values that are predicted proportions. Use `BinomialSize` only if `mdl` is fit to a binomial distribution.

Default: `1`

`'Offset'`

Value of the offset for each row in `Xnew`. `Offset` can be a vector the same length as `Xnew`, or a scalar that applies to each row. The offset is used as an additional predictor with a coefficient value fixed at `1`. In other words, if `b` is the fitted coefficient vector, and `link` is the link function,
`link(ysim) = Offset + Xnew * b`.

Default: `zeros(size(Xnew,1))`

Output Arguments

`ysim`

Vector of simulated values at `Xnew`.

`random` generates `ysim` using random values with mean given by the fitted model, and with the distribution used in `mdl`. The values in `ysim` are independent conditional on the predictors. For binomial and Poisson fits, `random` generates `ysim` with the specified distribution with no adjustment for any estimated dispersion.

Examples

Generalized Linear Model Simulation

Create a generalized linear model, and simulate its response to new data.

Generate artificial data for the model, Poisson random numbers with one underlying predictors X.

```
rng('default') % reproducible
X = rand(20,1);
mu = exp(1 + 2*X);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data.

```
mdl = fitglm(X,y,'y ~ x1','distr','poisson');
```

Create points for prediction.

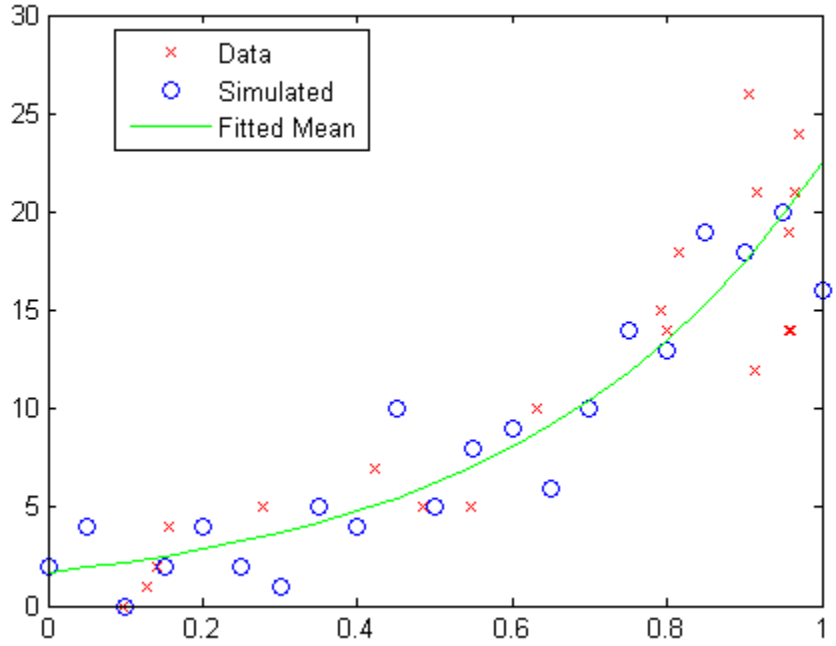
```
Xnew = (0:.05:1)';
```

Simulate responses at the new points.

```
ysim = random(mdl,Xnew);
```

Plot the simulated values along with the original values.

```
plot(X,y,'rx',Xnew,ysim,'bo',...
    Xnew,feval(mdl,Xnew),'g-')
legend('Data','Simulated','Fitted Mean',...
    'Location','best')
```



- “random” on page 10-37

Alternatives

For predictions without random noise, use `predict` or `feval`.

See Also

`GeneralizedLinearModel` | `predict`

More About

- “Generalized Linear Models” on page 10-12

random

Class: GeneralizedLinearMixedModel

Generate random responses from fitted generalized linear mixed-effects model

Syntax

```
ysim = random(glme)
ysim = random(glme,tblnew)
ysim = random( ___ ,Name,Value)
```

Description

`ysim = random(glme)` returns simulated responses, ysim, from the fitted generalized linear mixed-effects model glme, at the original design points.

`ysim = random(glme,tblnew)` returns simulated responses using new input values specified in the table or dataset array, tblnew.

`ysim = random( ___ ,Name,Value)` returns simulated responses using additional options specified by one or more `Name,Value` pair arguments, using any of the previous syntaxes. For example, you can specify observation weights, binomial sizes, or offsets for the model.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

`tblnew` — New input data

table | dataset array

New input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or dataset array. The predictor variables can be continuous or grouping variables. tblnew must contain the same variables as the original table or dataset array, `tbl`, used to fit the generalized linear mixed-effects model glme.

Data Types: `single` | `double` | `logical` | `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinomialSize'` — Number of trials for binomial distribution

`ones(m,1)` (default) | *m*-by-1 vector of positive integer values

Number of trials for binomial distribution, specified as the comma-separated pair consisting of 'BinomialSize' and an *m*-by-1 vector of positive integer values, where *m* is the number of rows in tblnew. The 'BinomialSize' name-value pair applies only to the binomial distribution. The value specifies the number of binomial trials when generating the random response values.

Data Types: `single` | `double`

`'Offset'` — Model offset

`zeros(m,1)` (default) | vector of scalar values

Model offset, specified as a vector of scalar values of length *m*, where *m* is the number of rows in tblnew. The offset is used as an additional predictor and has a coefficient value fixed at `1`.

`'Weights'` — Observation weights

m-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and an *m*-by-1 vector of nonnegative scalar values, where *m* is the number of rows in tblnew. If the response distribution is binomial or Poisson, then 'Weights' must be a vector of positive integers.

Data Types: `single` | `double`

Output Arguments

`ysim` — Simulated response values

m-by-1 vector

Simulated response values, returned as an *m*-by-1 vector, where *m* is the number of rows in tblnew. `random` creates ysim by first generating the random-effects vector based on its fitted prior distribution. `random` then generates ysim from its fitted conditional distribution given the random effects. `random` takes into account the effect of observation weights specified when fitting the model using `fitglme`, if any.

Definitions

Conditional Distribution Method

`random` generates random data from the fitted generalized linear mixed-effects model as follows:

- Sample $b_{sim} \sim P\left(b \mid \theta, \sigma^2\right)$, where $P\left(b \mid \theta, \sigma^2\right)$ is the estimated prior distribution of random effects, and $\hat{\theta}$ is a vector of estimated covariance parameters, and $\hat{\sigma}^2$ is the estimated dispersion parameter.
- Given b_{sim}, for $i = 1$ to m, sample $y_{sim\_i} \sim P\left(y_{new\_i} \mid b_{sim}, \beta, \theta, \sigma^2\right)$, where $P\left(y_{new\_i} \mid b_{sim}, \beta, \theta, \sigma^2\right)$ is the conditional distribution of the ith new response y_{new_i} given b_{sim} and the model parameters.

Examples

Simulate Random Responses From a GLME Model

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

```
load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Use `random` to simulate a new response vector from the fitted model.

```
rng(0,'twister');  % For reproducibility
ynew = random(glme);
```

Display the first 10 rows of the simulated response vector.

```
ynew(1:10)
```

```
ans =

     3
     3
     1
     7
     5
     8
     7
     9
     5
     9
```

Simulate a new response vector using new input values. Create a new table by copying the first 10 rows of `mfr` into `tblnew`.

```
tblnew = mfr(1:10,:);
```

The first 10 rows of `mfr` include data collected from trials 1 through 5 for factories 1 and 2. Both factories used the old process for all of their trials during the experiment, so `newprocess = 0` for all 10 observations.

Change the value of `newprocess` to `1` for the observations in `tblnew`.

```
tblnew.newprocess = ones(height(tblnew),1);
```

Simulate new responses using the new input values in `tblnew`.

```
ynew2 = random(glme,tblnew)
```

```
ynew2 =

     2
     3
     5
     4
     2
     2
     2
     1
     2
     0
```

See Also

`GeneralizedLinearMixedModel` | `fitglme` | `fitted` | `predict`

random

Class: gmdistribution

Random numbers from Gaussian mixture distribution

Syntax

```
y = random(obj)
Y = random(obj,n)
[Y,idx] = random(obj,n)
```

Description

`y = random(obj)` generates a 1-by-*d* vector `y` drawn at random from the *d*-dimensional Gaussian mixture distribution defined by `obj`. `obj` is an object created by `gmdistribution` or `fitgmdist`.

`Y = random(obj,n)` generates an `n`-by-*d* matrix `Y` of `n` *d*-dimensional random samples.

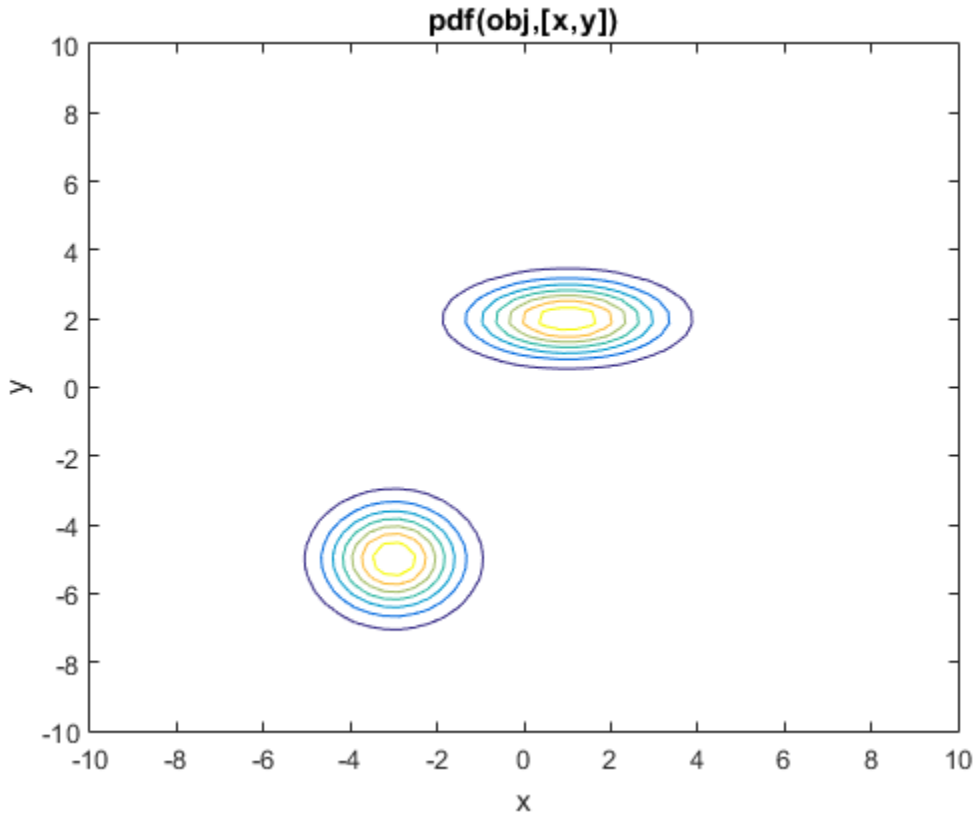
`[Y,idx] = random(obj,n)` also returns an `n`-by-1 vector `idx`, where `idx(I)` is the index of the component used to generate `Y(I,:)`.

Examples

Generate Gaussian Mixture Variates

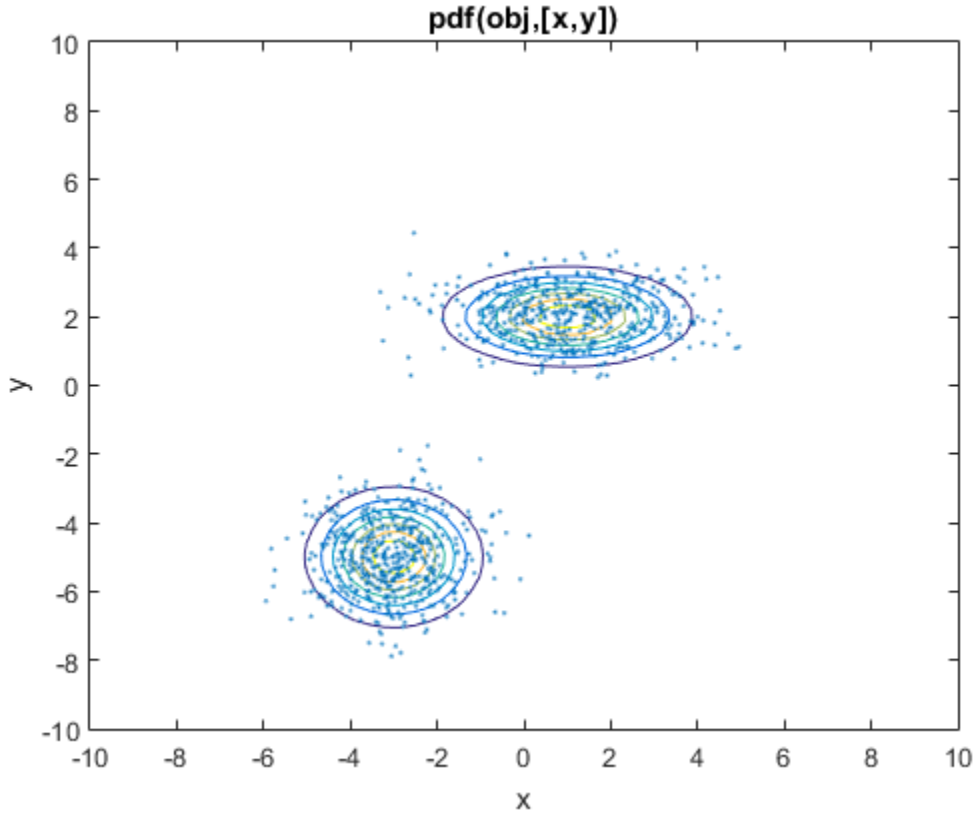
Create a `gmdistribution` object defining a two-component mixture of bivariate Gaussian distributions.

```
MU = [1 2;-3 -5];
SIGMA = cat(3,[2 0;0 .5],[1 0;0 1]);
p = ones(1,2)/2;
obj = gmdistribution(MU,SIGMA,p);

ezcontour(@(x,y)pdf(obj,[x y]),[-10 10],[-10 10])
hold on
```



Generate 1000 random values.

```
rng(1); % For reproducibility
Y = random(obj,1000);

scatter(Y(:,1),Y(:,2),10,'.')
```



See Also

`gmdistribution` | `mvnrnd` | `fitgmdist`

random

Class: LinearModel

Simulate responses for linear regression model

Syntax

```
ysim = random(mdl)
ysim = random(mdl,Xnew)
```

Description

`ysim = random(mdl)` simulates responses from the fitted linear model `mdl` at the original design points.

`ysim = random(mdl,Xnew)` simulates responses from the `mdl` linear model to the data in `Xnew`, adding random noise.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`Xnew`

Points at which `mdl` predicts responses.

- If `Xnew` is a table or dataset array, it must contain the predictor names in `mdl`.
- If `Xnew` is a numeric matrix, it must have the same number of variables (columns) as was used to create `mdl`. Furthermore, all variables used in creating `mdl` must be numeric.

Output Arguments

`ysim`

Vector of predicted mean values at `Xnew`, perturbed by random noise. The noise is independent, normally distributed, with mean zero, and variance equal to the estimated error variance of the model.

Examples

Simulate Response Data

Create a model of car mileage as a function of weight, and simulate the response.

Create a quadratic model of car mileage as a function of weight from the `carsmall` data.

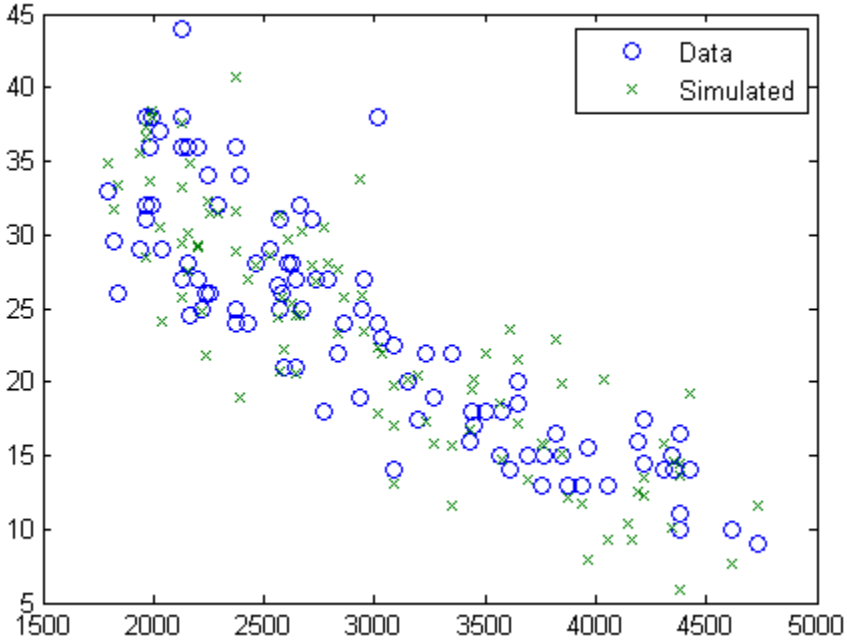
```
load carsmall
X = Weight;
y = MPG;
mdl = fitlm(X,y,'quadratic');
```

Create simulated responses to the data.

```
Xnew = X;
ysim = random(mdl,Xnew);
```

Plot the original responses and the simulated responses to see how they differ.

```
plot(X,y,'o',X,ysim,'x')
legend('Data','Simulated')
```



- “random” on page 9-39

Alternatives

For predictions without random noise, use `predict` or `feval`.

See Also

`predict` | `feval` | `LinearModel`

How To

- “Linear Regression” on page 9-11

random

Class: LinearMixedModel

Generate random responses from fitted linear mixed-effects model

Syntax

```
ysim = random(lme)
ysim = random(lme,tblnew)
ysim = random(lme,Xnew,Znew)
ysim = random(lme,Xnew,Znew,Gnew)
```

Description

`ysim = random(lme)` returns a vector of simulated responses ysim from the fitted linear mixed-effects model lme at the original fixed- and random-effects design points, used to fit lme.

`random` simulates new random-effects vector and new observation errors. So, the simulated response is

$$y_{sim} = X\hat{\beta} + Z\hat{b} + \varepsilon,$$

where $\hat{\beta}$ is the estimated fixed-effects coefficients, $\hat{b}$ is the new random effects, and ε is the new observation error.

`random` also accounts for the effect of observation weights, if you use any when fitting the model.

`ysim = random(lme,tblnew)` returns a vector of simulated responses ysim from the fitted linear mixed-effects model lme at the values in the new table or dataset array `tblnew`. Use a table or dataset array for `random` if you use a table or dataset array for fitting the model lme.

`ysim = random(lme,Xnew,Znew)` returns a vector of simulated responses ysim from the fitted linear mixed-effects model lme at the values in the new fixed- and random-

effects design matrices, `Xnew` and `Znew`, respectively. `Znew` can also be a cell array of matrices. Use the matrix format for `random` if you use design matrices for fitting the model `lme`.

`ysim = random(lme,Xnew,Znew,Gnew)` returns a vector of simulated responses `ysim` from the fitted linear mixed-effects model `lme` at the values in the new fixed- and random-effects design matrices, `Xnew` and `Znew`, respectively, and the grouping variable `Gnew`.

`Znew` and `Gnew` can also be cell arrays of matrices and grouping variables, respectively.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

`tblnew` — New input data

table | `dataset` array

New input data, which includes the response variable, predictor variables, and grouping variables, specified as a table or dataset array. The predictor variables can be continuous or grouping variables. `tblnew` must have the same variables as in the original table or dataset array used to fit the linear mixed-effects model `lme`.

Data Types: `single` | `double` | `logical` | `char`

`Xnew` — New fixed-effects design matrix

n-by-p matrix

New fixed-effects design matrix, specified as an n-by-p matrix, where n is the number of observations and p is the number of fixed predictor variables. Each row of `X` corresponds to one observation and each column of `X` corresponds to one variable.

Data Types: `single` | `double`

`Znew` — New random-effects design

n-by-q matrix | cell array of length R

New random-effects design, specified as an n-by-q matrix or a cell array of R design matrices `Z{r}`, where $r = 1, 2, ..., R$. If `Znew` is a cell array, then each `Z{r}` is an n-by-$q(r)$ matrix, where n is the number of observations, and $q(r)$ is the number of random predictor variables.

Data Types: `single` | `double` | `logical` | `char` | `cell`

`Gnew` — New grouping variable or variables

vector | cell array of grouping variables of length R

New grouping variable or variables, specified as a vector or a cell array, of length R, of grouping variables used to fit the linear mixed-effects model, lme.

`random` treats all levels of each grouping variable as new levels. It draws an independent random effects vector for each level of each grouping variable.

Data Types: `single` | `double` | `logical` | `char` | `cell`

Output Arguments

`ysim` — Simulated response values

n-by-1 vector

Simulated response values, returned as an n-by-1 vector, where n is the number of observations.

Examples

Generate Random Responses at the Original Design Values

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into

five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Generate random response values at the original design points. Display the first five values.

```
rng(123,'twister') % For reproducibility
ysim = random(lme);
ysim(1:5)
```

```
ans =

  114.8785
  134.2018
  154.2818
  169.7554
   84.6089
```

Plot Randomly Generated vs. Observed Response Values

Load the sample data.

```
load carsmall
```

Fit a linear mixed-effects model, with a fixed-effects for `Weight`, and a random intercept grouped by `Model_Year`. First, store the data in a table.

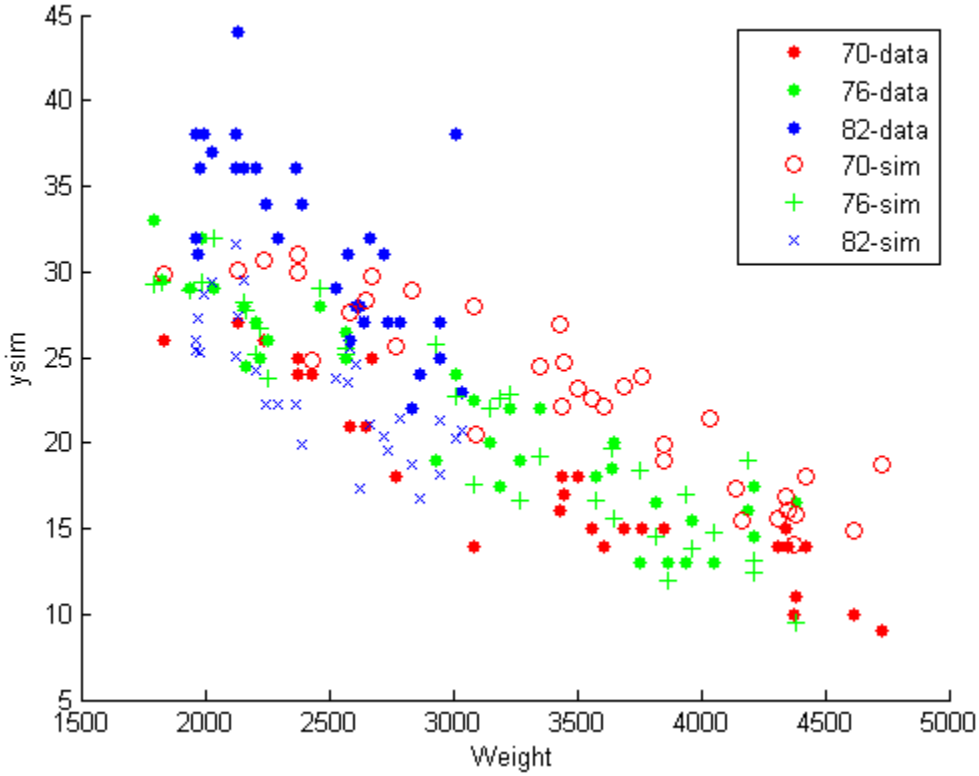
```
tbl = table(MPG,Weight,Model_Year);
lme = fitlme(tbl,'MPG ~ Weight + (1|Model_Year)');
```

Randomly generate responses using the original data.

```
rng(123,'twister') % For reproducibility
ysim = random(lme,tbl);
```

Plot the original and the randomly generated responses to see how they differ. Group them by model year.

```
figure()
gscatter(Weight,MPG,Model_Year)
hold on
gscatter(Weight,ysim,Model_Year,[],'o+x')
legend('70-data','76-data','82-data','70-sim','76-sim','82-sim')
hold off
```



Note that the simulated random response values for year 82 are lower than the original data for that year. This might be due to a lower simulated random effect for year 82 than the estimated random effect in the original data.

Generate Responses Using a New Dataset Array

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Create a new dataset array with design values. The new dataset array must have the same variables as the original dataset array you use for fitting the model `lme`.

```
dsnew = dataset();
dsnew.Soil = nominal({'Sandy';'Silty';'Silty'});
dsnew.Tomato = nominal({'Cherry';'Vine';'Plum'});
dsnew.Fertilizer = nominal([2;2;4]);
```

Generate random responses at the new points.

```
rng(123,'twister') % For reproducibility
ysim = random(lme,dsnew)
```

```
ysim =

   99.6006
  101.9911
  161.4026
```

Generate Random Responses Using New Design Matrices

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower, and cylinders, and potentially correlated random effect for intercept and acceleration grouped by model year.

First, prepare the design matrices for fitting the linear mixed-effects model.

```
X = [ones(406,1) Acceleration Horsepower];
Z = [ones(406,1) Acceleration];
Model_Year = nominal(Model_Year);
G = Model_Year;
```

Now, fit the model using `fitlmematrix` with the defined design matrices and grouping variables.

```
lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept','Acceleration'}},'RandomEffectGroups',{'Model_Year'});
```

Create the design matrices that contain the data at which to predict the response values. `Xnew` must have three columns as in `X`. The first column must be a column of 1s. And the values in the last two columns must correspond to `Acceleration` and `Horsepower`, respectively. The first column of `Znew` must be a column of 1s, and the second column must contain the same `Acceleration` values as in `Xnew`. The original grouping variable in `G` is the model year. So, `Gnew` must contain values for the model year. Note that `Gnew` must contain nominal values.

```
Xnew = [1,13.5,185; 1,17,205; 1,21.2,193];
Znew = [1,13.5; 1,17; 1,21.2];
```

```
Gnew = nominal([73 77 82]);
```

Generate random responses for the data in the new design matrices.

```
rng(123,'twister') % For reproducibility
ysim = random(lme,Xnew,Znew,Gnew)
```

```
ysim =

   15.7416
   10.6085
    6.8796
```

Now, repeat the same for a linear mixed-effects model with uncorrelated random-effects terms for intercept and acceleration. First, change the original random effects design and the random effects grouping variables. Then, fit the model.

```
Z = {ones(406,1),Acceleration};
G = {Model_Year,Model_Year};

lme = fitlmematrix(X,MPG,Z,G,'FixedEffectPredictors',....
{'Intercept','Acceleration','Horsepower'},'RandomEffectPredictors',...
{{'Intercept'},{'Acceleration'}},'RandomEffectGroups',{'Model_Year','Model_Year'});
```

Now, recreate the new random effects design, `Znew`, and the grouping variable design, `Gnew`, using which to predict the response values.

```
Znew = {[1;1;1],[13.5;17;21.2]};
MY = nominal([73 77 82]);
Gnew = {MY,MY};
```

Generate random responses using the new design matrices.

```
rng(123,'twister') % For reproducibility
ysim = random(lme,Xnew,Znew,Gnew)
```

```
ysim =

   16.8280
   10.4375
    4.1027
```

See Also

`fitlme` | `fitlmematrix` | `LinearMixedModel` | `predict`

random

Class: NonLinearModel

Simulate responses for nonlinear regression model

Syntax

```
ysim = random(mdl)
ysim = random(mdl,Xnew)
ysim = random(mdl,Xnew,'Weights',W)
```

Description

`ysim = random(mdl)` simulates responses from the fitted nonlinear model `mdl` at the original design points.

`ysim = random(mdl,Xnew)` simulates responses from the fitted nonlinear model `mdl` to the data in `Xnew`, adding random noise.

`ysim = random(mdl,Xnew,'Weights',W)` simulates responses using the observation weights, `W`.

Input Arguments

`mdl`

Nonlinear regression model, constructed by `fitnlm`.

`Xnew`

Points at which `mdl` predicts responses.

- If `Xnew` is a table or dataset array, it must contain the predictor names in `mdl`.
- If `Xnew` is a numeric matrix, it must have the same number of variables (columns) as was used to create `mdl`. Furthermore, all variables used in creating `mdl` must be numeric.

`W`

Vector of real, positive value weights or a function handle.

- If you specify a vector, then it must have the same number of elements as the number of observations (or rows) in `Xnew`.
- If you specify a function handle, the function must accept a vector of predicted response values as input, and returns a vector of real positive weights as output.

Given weights, `W`, `random` estimates the error variance at observation `i` by `MSE*(1/W(i))`, where MSE is the mean squared error.

Default: No weights

Output Arguments

`ysim`

Vector of predicted mean values at `Xnew`, perturbed by random noise. The noise is independent, normally distributed, with mean zero, and variance equal to the estimated error variance of the model.

Examples

Simulate Responses

Create a nonlinear model of car mileage as a function of weight, and simulate the response.

Create an exponential model of car mileage as a function of weight from the `carsmall` data. Scale the weight by a factor of 1000 so all the variables are roughly equal in size.

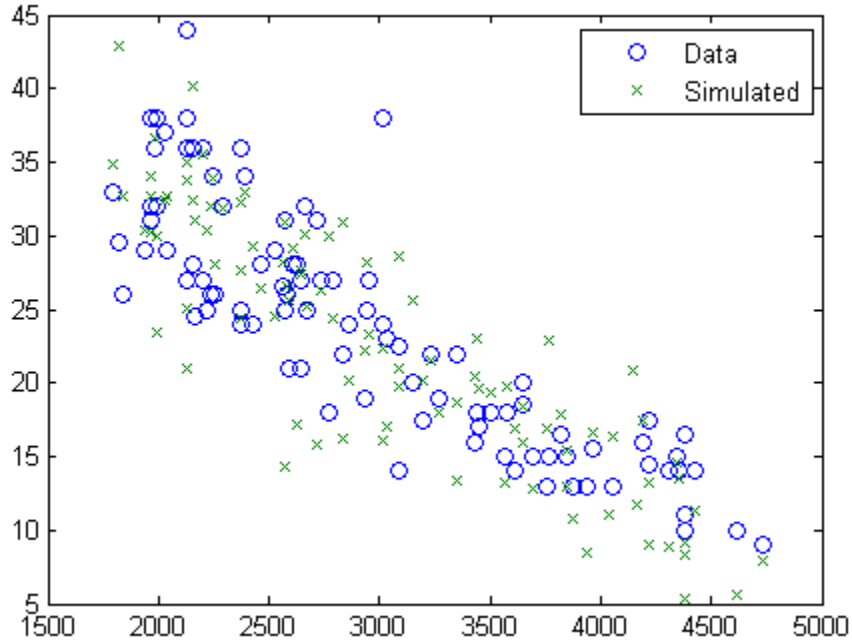
```
load carsmall
X = Weight;
y = MPG;
modelfun = 'y ~ b1 + b2*exp(-b3*x/1000)';
beta0 = [1 1 1];
mdl = fitnlm(X,y,modelfun,beta0);
```

Create simulated responses to the data.

```
Xnew = X;
ysim = random(mdl,Xnew);
```

Plot the original responses and the simulated responses to see how they differ.

```
plot(X,y,'o',X,ysim,'x')
legend('Data','Simulated')
```



- “Predict or Simulate Responses Using a Nonlinear Model” on page 11-10

Alternatives

For predictions without added noise, use `predict`.

See Also

`feval` | `NonLinearModel` | `predict`

More About

- “Nonlinear Regression” on page 11-2

random

Class: piecewisedistribution

Random numbers from piecewise distribution

Syntax

```
r = random(obj)
R = random(obj,n)
R = random(obj,m,n)
R = random(obj,[m,n])
R = random(obj,m,n,p,...)
R = random(obj,[m,n,p,...])
```

Description

`r = random(obj)` generates a pseudo-random number `r` drawn from the piecewise distribution object `obj`.

`R = random(obj,n)` generates an *n*-by-*n* matrix of pseudo-random numbers `R`.

`R = random(obj,m,n)` or `R = random(obj,[m,n])` generates an *m*-by-*n* matrix of pseudo-random numbers `R`.

`R = random(obj,m,n,p,...)` or `R = random(obj,[m,n,p,...])` generates an *m*-by-*n*-by-*p*-by-... array of pseudo-random numbers `R`.

Examples

Fit Pareto tails to a *t* distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

r = random(obj)
r =
```

```
    0.8285
```

See Also

`paretotails` | `icdf` | `cdf`

random

Class: ProbDist

Generate random number drawn from ProbDist object

Syntax

```
Y = random(PD)
Y = random(PD, N)
Y = random(PD, N, M, ...)
```

Description

`Y = random(PD)` generates a random number drawn from the distribution specified by *PD*, a ProbDist object.

`Y = random(PD, N)` generates an *N*-by-*N* array of random numbers drawn from the distribution specified by *PD*, a ProbDist object.

`Y = random(PD, N, M, ...)` generates an *N*-by-*M*-by`...` array of random numbers drawn from the distribution specified by *PD*, a ProbDist object.

Input Arguments

PD	An object of the class `ProbDistUnivParam` or `ProbDistUnivKernel`.
N	A positive integer.
M	A positive integer.

Output Arguments

Y	A random number drawn from the distribution specified by *PD*.

See Also

`random`

random

Class: RepeatedMeasuresModel

Generate new random response values given predictor values

Syntax

```
ysim = random(rm,tnew)
```

Description

`ysim = random(rm,tnew)` generates random response values from the repeated measures model rm using the predictor variables from table tnew.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`tnew` — New data

table used to create `rm` (default) | table

New data including the values of the response variables and the between-subject factors used as predictors in the repeated measures model, rm, specified as a table. `tnew` must contain all of the between-subject factors used to create rm.

Output Arguments

`ysim` — Random response values

n-by-*r* matrix

Random response values random generates, returned as an n-by-r matrix, where n is the number of rows in tnew, and r is the number of repeated measures in rm.

Examples

Randomly Generate New Response Values

Load the sample data.

```
load fisheriris
```

The column vector `species`consists of iris flowers of three different species: setosa, versicolor, and virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the `species` is the predictor variable.

```
  rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Randomly generate new response values.

```
ysim = random(rm);
```

`random` uses the predictor values in the original sample data you use to fit the repeated measures model `rm` in table `t`.

Randomly Generate Response Values Using New Data

Load the sample data.

```
load repeatedmeas
```

The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ through $y8$ as responses. The table `within` includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ through $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Define a table with new values for the predictor variables.

```
tnew = table(16,93,{'B'},{'Male'},'VariableNames',{'Age','IQ','Group','Gender'})
```

```
tnew =

    Age    IQ    Group    Gender
    ___    __    _____    ______

    16     93    'B'      'Male'
```

Randomly generate new response values using the values in the new table `tnew`.

```
ysim = random(rm,tnew)
```

```
ysim =

  159.0920  114.8927   -6.5618   46.9944   38.6707   -5.6725   70.8690   11.7813
```

Algorithms

`random` computes `ysim` by creating predicted values and adding random noise values. For each row, the noise has a multivariate normal distribution with covariance the same as `rm.Covariance`.

See Also

`fitrm` | `predict`

random

Class: prob.TruncatableDistribution
Package: prob

Generate random numbers from probability distribution object

Syntax

```
r = random(pd)
r = random(pd,sz1,...,szN)
r = random(pd,[sz1,...,szN])
```

Description

`r = random(pd)` generates a random number r from the probability distribution pd.

`r = random(pd,sz1,...,szN)` generates a sz1-by-...-by-szN array of random numbers from the probability distribution pd.

`r = random(pd,[sz1,...,szN])` generates a sz1-by-...-by-szN array of random numbers from the probability distribution pd.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

`sz1,...,szN` — Size of each dimension

two or more integer values | vector of integer values

Size of each dimension, specified as two or more integer values, or a vector of such values. For example, specifying `5,3,2` or `[5,3,2]` generates a 5-by-3-by-2 array of random numbers from the probability distribution pd.

Data Types: `single` | `double`

Output Arguments

`r` — Random number

scalar value | array of values

Random number generated from the probability distribution, returned as a scalar value or an array of scalar values with the dimensions specified by sz1,...,szN.

Examples

Generate One Random Number

Create a standard normal probability distribution object.

```
pd = makedist('Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Generate one random number from the distribution.

```
r = random(pd)
```

```
r =

    0.5377
```

Generate Multiple Random Numbers

Create a Weibull probability distribution object using the default parameter values.

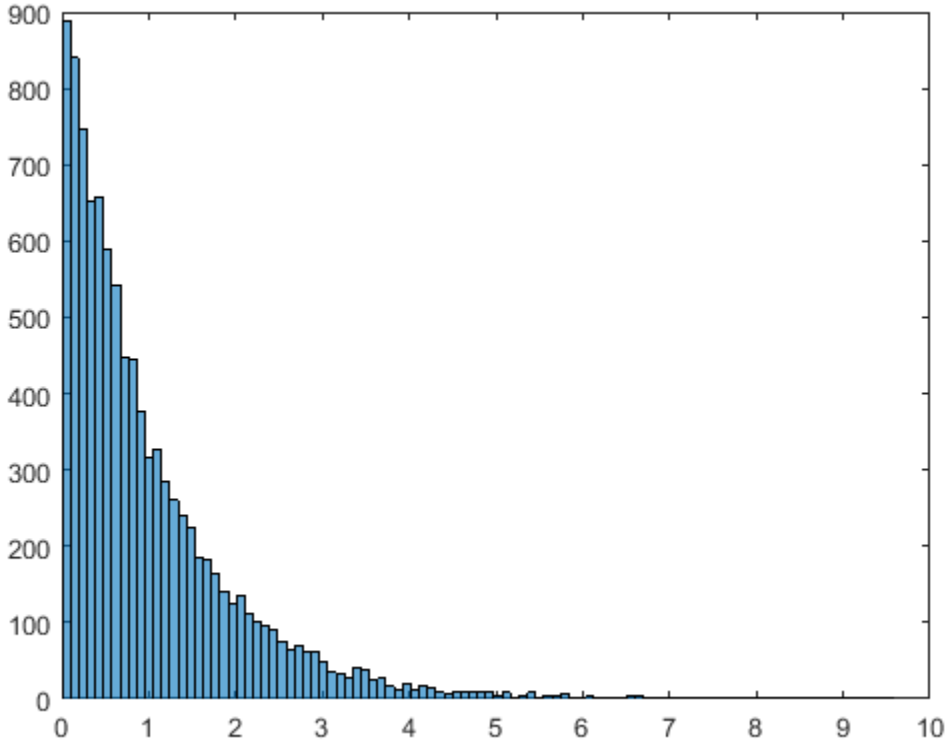
```
pd = makedist('Weibull')
```

```
pd =

  WeibullDistribution
```

```
  Weibull distribution
    A = 1
    B = 1
```

Generate random numbers from distribution and visualize with a histogram.

```
rng default  % For reproducibility
r = random(pd,10000,1);
histogram(r,100)
```



Generate a Multidimensional Array of Random Numbers

Create a standard normal probability distribution object.

```
pd = makedist('Normal')

pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Generate a 2-by-3-by-2 array of random numbers from the distribution.

```
r = random(pd,[2,3,2])

random_make_array(:,:,1) =

   -1.0689   -2.9443    0.3252
   -0.8095    1.4384   -0.7549


random_make_array(:,:,2) =

    1.3703   -0.1022    0.3192
   -1.7115   -0.2414    0.3129
```

See Also

dfittool | fitdist | makedist

randomEffects

Class: GeneralizedLinearMixedModel

Estimates of random effects and related statistics

Syntax

```
B = randomEffects(glme)
[B,BNames] = randomEffects(glme)
[B,BNames,stats] = randomEffects(glme)
[B,BNames,stats] = randomEffects(glme,Name,Value)
```

Description

`B = randomEffects(glme)` returns the estimates of the empirical Bayes predictors (EPBs) of random effects in the generalized linear mixed-effects model glme conditional on the estimated covariance parameters and the observed response.

`[B,BNames] = randomEffects(glme)` also returns the names of the coefficients, BNames. Each name corresponds to a coefficient in B.

`[B,BNames,stats] = randomEffects(glme)` also returns related statistics, stats, for the estimated EBPs of random effects in glme.

`[B,BNames,stats] = randomEffects(glme,Name,Value)` returns any of the above output arguments using additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the confidence interval level, or the method for computing the approximate degrees of freedom.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range [0,1]

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range [0,1]. For a value α, the confidence level is $100 \times (1 - \alpha)\%$.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single | double`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'residual'` (default) | `'none'`

Method for computing approximate degrees of freedom, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'residual'`	The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'none'`	All degrees of freedom are set to infinity.

Example: `'DFMethod','none'`

Output Arguments

`B` — Estimated empirical Bayes predictors for the random effects

column vector

Estimated empirical Bayes predictors (EBPs) for the random effects in the generalized linear mixed-effects model glme, returned as a column vector. The EBPs in B are

approximated by the mode of the empirical posterior distribution of the random effects given the estimated covariance parameters and the observed response.

Suppose glme has R grouping variables g_1, g_2, ..., g_R, with levels m_1, m_2, ..., m_R, respectively. Also suppose q_1, q_2, ..., q_R are the lengths of the random-effects vectors that are associated with g_1, g_2, ..., g_R, respectively. Then, `B` is a column vector of length $q_1*m_1 + q_2*m_2 + ... + q_R*m_R$.

`randomEffects` creates `B` by concatenating the empirical Bayes predictors of random-effects vectors corresponding to each level of each grouping variable as `[`g_1`level`$_1$`; `g_1`level`$_2$`; ...; `g_1`level`$_{m_1}$`; `g_2`level`$_1$`; `g_2`level`$_2$`; ...; `g_2`level`$_{m_2}$`; ...; `g_R`level`$_1$`; `g_R`level`$_2$`; ...; `g_R`level`$_{m_R}$`]'`.

`BNames` — Names of random-effects coefficients

table

Names of random-effects coefficients in B, returned as a table.

`stats` — Estimated empirical Bayes predictors and related statistics

table

Estimated empirical Bayes predictors (EBPs) and related statistics for the random effects in the generalized linear mixed-effects model glme, returned as a table. stats has one row for each of the random effects, and one column for each of the following statistics.

`Group`	Grouping variable associated with the random effect
`Level`	Level within the grouping variable corresponding to the random effect
`Name`	Name of the random-effect coefficient
`Estimate`	Empirical Bayes predictor (EBP) of random effect
`SEPred`	Square root of the conditional mean squared error of prediction (CMSEP) given covariance parameters and response
`tStat`	t-statistic for a test that the random-effects coefficient is equal to 0
`DF`	Estimated degrees of freedom for the t-statistic

`pValue`	*p*-value for the *t*-statistic
`Lower`	Lower limit of a 95% confidence interval for the random-effects coefficient
`Upper`	Upper limit of a 95% confidence interval for the random-effects coefficient

`randomEffects` computes the confidence intervals using the conditional mean squared error of prediction (CMSEP) approach conditional on the estimated covariance parameters and the observed response. An alternative interpretation of the confidence intervals is that they are approximate Bayesian credible intervals conditional on the estimated covariance parameters and the observed response.

When fitting a GLME model using `fitglme` and one of the pseudo likelihood fit methods (`'MPL'` or `'REMPL'`), `randomEffects` computes confidence intervals and related statistics based on the fitted linear mixed-effects model from the final pseudo likelihood iteration.

Examples

Compute and Plot Estimated Random Effects

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)

- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where $i = 1, 2, ..., 20$) during batch j (where $j = 1, 2, ..., 5$).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.

- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Compute and display the names and estimated values of the empirical Bayes predictors (EBPs) for the random effects.

```
[B,BNames] = randomEffects(glme)
```

```
B =

    0.2913
    0.1542
   -0.2633
   -0.4257
    0.5453
   -0.1069
    0.3040
   -0.1653
   -0.1458
   -0.0816
    0.0145
    0.1771
    0.2487
    0.2115
    0.2777
   -0.2518
   -0.1351
   -0.1627
   -0.3208
    0.0584


Bnames =

      Group       Level        Name
    _________    _____    _____________

    'factory'    '1'      '(Intercept)'
    'factory'    '2'      '(Intercept)'
    'factory'    '3'      '(Intercept)'
    'factory'    '4'      '(Intercept)'
    'factory'    '5'      '(Intercept)'
    'factory'    '6'      '(Intercept)'
```

```
'factory'    '7'      '(Intercept)'
'factory'    '8'      '(Intercept)'
'factory'    '9'      '(Intercept)'
'factory'    '10'     '(Intercept)'
'factory'    '11'     '(Intercept)'
'factory'    '12'     '(Intercept)'
'factory'    '13'     '(Intercept)'
'factory'    '14'     '(Intercept)'
'factory'    '15'     '(Intercept)'
'factory'    '16'     '(Intercept)'
'factory'    '17'     '(Intercept)'
'factory'    '18'     '(Intercept)'
'factory'    '19'     '(Intercept)'
'factory'    '20'     '(Intercept)'
```

Each row of `B` contains the estimated EPB for the random-effects coefficient named in the corresponding row of `Bnames`. For example, the value –0.2633 in row 3 of `B` is the estimated EPB for `'(Intercept)'` for level `'3'` of `factory`.

Compute 99% Confidence Intervals for Random Effects

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)

- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Compute and display the 99% confidence intervals for the random-effects coefficients.

```
[B,BNames,stats] = randomEffects(glme,'Alpha',0.01);
stats
```

```
stats =


    Random effect coefficients: DFMethod = 'residual', Alpha = 0.01

    Group            Level       Name                Estimate
    'factory'        '1'         '(Intercept)'         0.29131
    'factory'        '2'         '(Intercept)'         0.15423
    'factory'        '3'         '(Intercept)'        -0.26325
    'factory'        '4'         '(Intercept)'        -0.42568
    'factory'        '5'         '(Intercept)'          0.5453
    'factory'        '6'         '(Intercept)'        -0.10692
    'factory'        '7'         '(Intercept)'         0.30404
    'factory'        '8'         '(Intercept)'        -0.16527
    'factory'        '9'         '(Intercept)'        -0.14577
    'factory'        '10'        '(Intercept)'       -0.081632
    'factory'        '11'        '(Intercept)'        0.014529
    'factory'        '12'        '(Intercept)'         0.17706
    'factory'        '13'        '(Intercept)'         0.24872
    'factory'        '14'        '(Intercept)'         0.21145
    'factory'        '15'        '(Intercept)'          0.2777
    'factory'        '16'        '(Intercept)'        -0.25175
    'factory'        '17'        '(Intercept)'        -0.13507
    'factory'        '18'        '(Intercept)'         -0.1627
    'factory'        '19'        '(Intercept)'        -0.32083
    'factory'        '20'        '(Intercept)'        0.058418


    SEPred     tStat       DF    pValue       Lower       Upper
    0.19163      1.5202    94      0.13182    -0.21251    0.79514
    0.19216     0.80259    94      0.42423      -0.351    0.65946
    0.21249     -1.2389    94      0.21846    -0.82191    0.29541
    0.21667     -1.9646    94     0.052408    -0.99534    0.14398
    0.17963      3.0356    94    0.0031051    0.073019     1.0176
    0.20133    -0.53105    94      0.59664    -0.63625    0.42241
    0.18397      1.6527    94      0.10173    -0.17964    0.78771
    0.20505    -0.80597    94      0.42229    -0.70438    0.37385
      0.203    -0.71806    94       0.4745    -0.67949    0.38795
    0.20256      -0.403    94      0.68786    -0.61419    0.45093
    0.21421    0.067826    94      0.94607    -0.54866    0.57772
```

```
    0.20721      0.85446     94       0.39502     -0.36774     0.72185
    0.20522        1.212     94       0.22857     -0.29083     0.78827
    0.20678       1.0226     94       0.30913     -0.33221     0.75511
    0.20345        1.365     94       0.17552     -0.25719     0.81259
    0.22568      -1.1156     94       0.26746     -0.84509     0.34158
    0.22301     -0.60568     94       0.54619      -0.7214     0.45125
    0.22269     -0.73061     94       0.46684     -0.74817     0.42278
    0.23294      -1.3773     94       0.17168     -0.93325     0.29159
    0.21481      0.27195     94       0.78626     -0.50635     0.62319
```

The first three columns of `stats` contain the group name, level, and random-effects coefficient name. Column 4 contains the estimated EBP of the random-effects coefficient. The last two columns of `stats`, `Lower` and `Upper`, contain the lower and upper bounds of the 99% confidence interval, respectively. For example, for the coefficient for `'(Intercept)'` for level `3` of `factory`, the estimated EBP is –0.26325, and the 99% confidence interval is [-0.82191,0.29541].

References

[1] Booth, J.G., and J.P. Hobert. “Standard Errors of Prediction in Generalized Linear Mixed Models.” *Journal of the American Statistical Association*, Vol. 93, 1998, pp. 262–272.

See Also

`GeneralizedLinearMixedModel` | `coefCI` | `coefTest` | `fixedEffects`

randomEffects

Class: LinearMixedModel

Estimates of random effects and related statistics

Syntax

```
B = randomEffects(lme)
[B,Bnames] = randomEffects(lme)
[B,Bnames,stats] = randomEffects(lme)
[B,Bnames,stats] = randomEffects(lme,Name,Value)
```

Description

`B = randomEffects(lme)` returns the estimates of the best linear unbiased predictors (BLUPs) of random effects in the linear mixed-effects model `lme`.

`[B,Bnames] = randomEffects(lme)` also returns the names of the coefficients in `Bnames`. Each name corresponds to a coefficient in `B`.

`[B,Bnames,stats] = randomEffects(lme)` also returns the estimated BLUPs of random effects in the linear mixed-effects model `lme` and related statistics.

`[B,Bnames,stats] = randomEffects(lme,Name,Value)` also returns the BLUPs of random effects in the linear mixed-effects model `lme` and related statistics with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Alpha'` — Confidence level

0.05 (default) | scalar value in the range 0 to 1

Confidence level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range 0 to 1. For a value α, the confidence level is 100*(1–α)%.

For example, for 99% confidence intervals, you can specify the confidence level as follows.

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'DFMethod'` — Method for computing approximate degrees of freedom

`'Residual'` (default) | `'Satterthwaite'` | `'None'`

Method for computing approximate degrees of freedom for the *t*-statistics that test the random-effects coefficients against 0, specified as the comma-separated pair consisting of `'DFMethod'` and one of the following.

`'Residual'`	Default. The degrees of freedom are assumed to be constant and equal to $n - p$, where n is the number of observations and p is the number of fixed effects.
`'Satterthwaite'`	Satterthwaite approximation.
`'None'`	All degrees of freedom are set to infinity.

For example, you can specify the Satterthwaite approximation as follows.

Example: `'DFMethod','Satterthwaite'`

Output Arguments

`B` — Estimated best linear unbiased predictors of random effects

column vector

Estimated best linear unbiased predictors of random effects of linear mixed-effects model `lme`, returned as a column vector.

Suppose `lme` has R grouping variables g_1, g_2, ..., g_R, with levels m_1, m_2, ..., m_R, respectively. Also suppose q_1, q_2, ..., q_R are the lengths of the random-effects vectors that are associated with g_1, g_2, ..., g_R, respectively. Then, `B` is a column vector of length $q_1*m_1 + q_2*m_2 + ... + q_R*m_R$.

`randomEffects` creates `B` by concatenating the best linear unbiased predictors of random-effects vectors corresponding to each level of each grouping variable as $[g_1level_1; g_1level_2; ...; g_1level_{m_1}; g_2level_1; g_2level_2; ...; g_2level_{m_2}; ...; g_Rlevel_1; g_Rlevel_2; ...; g_Rlevel_{m_R}]'$.

`Bnames` — Names of random-effects coefficients

table

Names of random-effects coefficients in B, returned as a table.

`stats` — Estimates of random effects BLUPs and related statistics

dataset array

Estimates of random effects BLUPs and related statistics, returned as a dataset array that has one row for each of the fixed effects and one column for each of the following statistics.

`Group`	Grouping variable associated with the random effect
`Level`	Level within the grouping variable corresponding to the random effect
`Name`	Name of the random-effect coefficient
`Estimate`	Best linear unbiased predictor (BLUP) of random effect
`SEPred`	Standard error of the estimate (BLUP minus random effect)
`tStat`	t-statistic for a test that the random effect is zero
`DF`	Estimated degrees of freedom for the t-statistic

`pValue`	p-value for the t-statistic
`Lower`	Lower limit of a 95% confidence interval for the random effect
`Upper`	Upper limit of a 95% confidence interval for the random effect

Examples

Display Random-Effects Estimates and Coefficient Names

Load the sample data.

```
load carbig
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration and horsepower, and potentially correlated random effects for intercept and acceleration, grouped by the model year. First, store the data in a table.

```
tbl = table(Acceleration,Horsepower,Model_Year,MPG);
```

Fit the model.

```
lme = fitlme(tbl, 'MPG ~ Acceleration + Horsepower + (Acceleration|Model_Year)');
```

Compute the BLUPs of the random-effects coefficients and display the names of the corresponding random effects.

```
[B,Bnames] = randomEffects(lme)
```

```
B =

    3.1270
   -0.2426
   -1.6532
   -0.0086
    1.2075
   -0.2179
    4.4107
   -0.4887
   -1.3103
   -0.0208
    2.8029
   -0.3790
```

```
    0.0865
   -0.1280
    0.4216
   -0.0259
   -2.3889
    0.1634
    0.9618
    0.0117
   -2.2345
    0.5020
   -2.1332
    0.3254
   -3.2979
    0.5090


Bnames =

    Group              Level      Name
    'Model_Year'       '70'       '(Intercept)'
    'Model_Year'       '70'       'Acceleration'
    'Model_Year'       '71'       '(Intercept)'
    'Model_Year'       '71'       'Acceleration'
    'Model_Year'       '72'       '(Intercept)'
    'Model_Year'       '72'       'Acceleration'
    'Model_Year'       '73'       '(Intercept)'
    'Model_Year'       '73'       'Acceleration'
    'Model_Year'       '74'       '(Intercept)'
    'Model_Year'       '74'       'Acceleration'
    'Model_Year'       '75'       '(Intercept)'
    'Model_Year'       '75'       'Acceleration'
    'Model_Year'       '76'       '(Intercept)'
    'Model_Year'       '76'       'Acceleration'
    'Model_Year'       '77'       '(Intercept)'
    'Model_Year'       '77'       'Acceleration'
    'Model_Year'       '78'       '(Intercept)'
    'Model_Year'       '78'       'Acceleration'
    'Model_Year'       '79'       '(Intercept)'
    'Model_Year'       '79'       'Acceleration'
    'Model_Year'       '80'       '(Intercept)'
    'Model_Year'       '80'       'Acceleration'
    'Model_Year'       '81'       '(Intercept)'
    'Model_Year'       '81'       'Acceleration'
    'Model_Year'       '82'       '(Intercept)'
```

```
    'Model_Year'        '82'        'Acceleration'
```

Since intercept and acceleration have potentially correlated random effects, grouped by model year of the cars, `randomEffects` creates a separate row for intercept and acceleration at each level of the grouping variable.

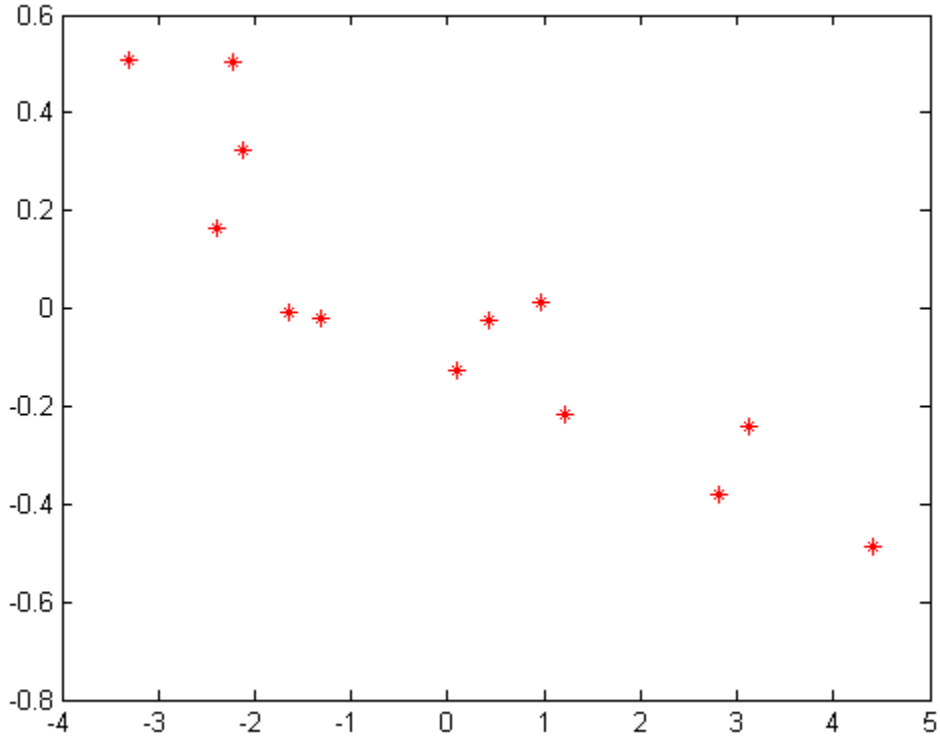
Compute the covariance parameters of the random effects.

```
[~,~,stats] = covarianceParameters(lme)
stats{1}
```

```
ans =


    Covariance Type: FullCholesky

    Group         Name1               Name2               Type          Estimate
    Model_Year    '(Intercept)'       '(Intercept)'       'std'            6.6672
    Model_Year    'Weight'            '(Intercept)'       'corr'               -1
    Model_Year    'Weight'            'Weight'            'std'         0.0014668
```

The correlation value suggests that random effects seem negatively correlated. Plot the random effects for intercept versus acceleration to confirm this.

```
plot(B(1:2:end),B(2:2:end),'r*')
```



Compute Random-Effects Estimates and Related Statistics

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load fertilizer
```

The dataset array includes data from a split-plot experiment, where soil is divided into three blocks based on the soil type: sandy, silty, and loamy. Each block is divided into five plots, where five different types of tomato plants (cherry, heirloom, grape, vine, and

plum) are randomly assigned to these plots. The tomato plants in the plots are then divided into subplots, where each subplot is treated by one of four fertilizers. This is simulated data.

Store the data in a dataset array called `ds`, for practical purposes, and define `Tomato`, `Soil`, and `Fertilizer` as categorical variables.

```
ds = fertilizer;
ds.Tomato = nominal(ds.Tomato);
ds.Soil = nominal(ds.Soil);
ds.Fertilizer = nominal(ds.Fertilizer);
```

Fit a linear mixed-effects model, where `Fertilizer` and `Tomato` are the fixed-effects variables, and the mean yield varies by the block (soil type), and the plots within blocks (tomato types within soil types) independently.

```
lme = fitlme(ds,'Yield ~ Fertilizer * Tomato + (1|Soil) + (1|Soil:Tomato)');
```

Compute the BLUPs and related statistics for random effects.

```
[~,~,stats] = randomEffects(lme)
```

```
stats =


    Random effect coefficients: DFMethod = 'Residual', Alpha = 0.05

    Group               Level                Name                Estimate    SEPre
    'Soil'              'Loamy'              '(Intercept)'        1.0061     2.337
    'Soil'              'Sandy'              '(Intercept)'       -1.5236     2.337
    'Soil'              'Silty'              '(Intercept)'       0.51744     2.337
    'Soil:Tomato'       'Loamy Cherry'       '(Intercept)'         12.46     7.176
    'Soil:Tomato'       'Loamy Grape'        '(Intercept)'       -2.6429     7.176
    'Soil:Tomato'       'Loamy Heirloom'     '(Intercept)'        16.681     7.176
    'Soil:Tomato'       'Loamy Plum'         '(Intercept)'       -5.0172     7.176
    'Soil:Tomato'       'Loamy Vine'         '(Intercept)'       -4.6874     7.176
    'Soil:Tomato'       'Sandy Cherry'       '(Intercept)'       -17.393     7.176
    'Soil:Tomato'       'Sandy Grape'        '(Intercept)'       -7.3679     7.176
    'Soil:Tomato'       'Sandy Heirloom'     '(Intercept)'        -8.621     7.176
    'Soil:Tomato'       'Sandy Plum'         '(Intercept)'         7.669     7.176
    'Soil:Tomato'       'Sandy Vine'         '(Intercept)'       0.28246     7.176
    'Soil:Tomato'       'Silty Cherry'       '(Intercept)'        4.9326     7.176
    'Soil:Tomato'       'Silty Grape'        '(Intercept)'         10.011    7.176
    'Soil:Tomato'       'Silty Heirloom'     '(Intercept)'       -8.0599     7.176
```

```
    'Soil:Tomato'        'Silty Plum'            '(Intercept)'        -2.6519     7.176
    'Soil:Tomato'        'Silty Vine'            '(Intercept)'          4.405     7.176
```

The first three rows contain the random-effects estimates and the statistics for the three levels, `Loamy`, `Sandy`, and `Silty` of the grouping variable `Soil`. The corresponding *p*-values 0.66918, 0.51825, and 0.82593 indicate that these random-effects are not significantly different from 0. The following 15 rows include the BLUPS of random-effects estimates for the intercept, grouped by the variable Tomato nested in Soil, i.e. interaction of `Tomato` and `Soil`.

Compute Confidence Intervals with Specified Options

Load the sample data.

```
load carsmall
```

`Shift` and `Operator` are nominal variables.

```
shift.Shift = nominal(shift.Shift);
shift.Operator = nominal(shift.Operator);
```

Fit a linear mixed-effects model with a random intercept grouped by operator, to assess if there is a significant difference in the performance according to the time of the shift. Use the restricted maximum likelihood method.

```
lme = fitlme(shift,'QCDev ~ Shift + (1|Operator)');
```

Compute the 99% confidence intervals for random effects using the residuals option to compute the degrees of freedom. This is the default method.

```
[~,~,stats] = randomEffects(lme,'alpha',0.01)
```

```
stats =


    Random effect coefficients: DFMethod = 'Residual', Alpha = 0.01

    Group            Level      Name                Estimate    SEPred     tStat
    'Operator'       '1'        '(Intercept)'       0.57753     0.90378    0.63902
    'Operator'       '2'        '(Intercept)'        1.1757     0.90378     1.3009
    'Operator'       '3'        '(Intercept)'       -2.1715     0.90378    -2.4027
    'Operator'       '4'        '(Intercept)'        2.3655     0.90378     2.6174
    'Operator'       '5'        '(Intercept)'       -1.9472     0.90378    -2.1546
```

Compute the 99% confidence intervals for random effects using the Satterthwaite approximation to compute the degrees of freedom.

```
[~,~,stats] = randomEffects(lme,'DFMethod','Satterthwaite','alpha',0.01)
```

```
stats =


    Random effect coefficients: DFMethod = 'Satterthwaite', Alpha = 0.01

    Group             Level      Name                Estimate    SEPred     tStat
    'Operator'        '1'        '(Intercept)'        0.57753    0.90378    0.63902
    'Operator'        '2'        '(Intercept)'         1.1757    0.90378     1.3009
    'Operator'        '3'        '(Intercept)'        -2.1715    0.90378    -2.4027
    'Operator'        '4'        '(Intercept)'         2.3655    0.90378     2.6174
    'Operator'        '5'        '(Intercept)'        -1.9472    0.90378    -2.1546
```

The Satterhwaite method usually produces smaller values for the degrees of freedom (`DF`), which results in larger *p*-values (`pValue`) and larger confidence intervals (`Lower` and `Upper`) for the random-effects estimates.

See Also

`coefCI` | `coefTest` | `fitlme` | `fixedEffects` | `LinearMixedModel`

randsample

Random sample

Syntax

```
y = randsample(n,k)
y = randsample(population,k)
y = randsample(n,k,replacement)
y = randsample(population,k,replacement)
y = randsample(n,k,true,w)
y = randsample(population,k,true,w)
y = randsample(s,...)
```

Description

`y = randsample(n,k)` returns a `k`-by-`1` vector `y` of values sampled uniformly at random, without replacement, from the integers 1 to `n`.

`y = randsample(population,k)` returns a vector of `k` values sampled uniformly at random, without replacement, from the values in the vector `population`. The orientation of `y` (row or column) is the same as `population`.

`y = randsample(n,k,replacement)` or `y = randsample(population,k,replacement)` returns a sample taken with replacement if `replacement` is `true`, or without replacement if `replacement` is `false`. The default is `false`.

`y = randsample(n,k,true,w)` or `y = randsample(population,k,true,w)` returns a weighted sample taken with replacement, using a vector of positive weights `w`, whose length is `n`. The probability that the integer `i` is selected for an entry of `y` is `w(i)/sum(w)`. Usually, `w` is a vector of probabilities. `randsample` does not support weighted sampling without replacement.

`y = randsample(s,...)` uses the stream `s` for random number generation. `s` is a member of the `RandStream` class. Default is the MATLAB default random number stream.

Examples

Draw a single value from the integers `1` through `10`:

```
n = 10;
x = randsample(n,1);
```

Draw a single value from the population `1` through `n`, where `n > 1`:

```
y = randsample(1:n,1);
```

Note: If `population` is a numeric vector containing only nonnegative integer values, and `population` can have length `1`, use

```
y = population(randsample(length(population),k))
```

instead of `y = randsample(population,k)`.

Generate a random sequence of the characters `A`, `C`, `G`, and `T`, with replacement, according to the specified probabilities.

```
R = randsample('ACGT',48,true,[0.15 0.35 0.35 0.15])
```

More About

Tips

- To randomly sample data, with or without replacement, use `datasample`.

See Also

`rand` | `randperm` | `datasample` | `RandStream`

randtool

Interactive random number generation

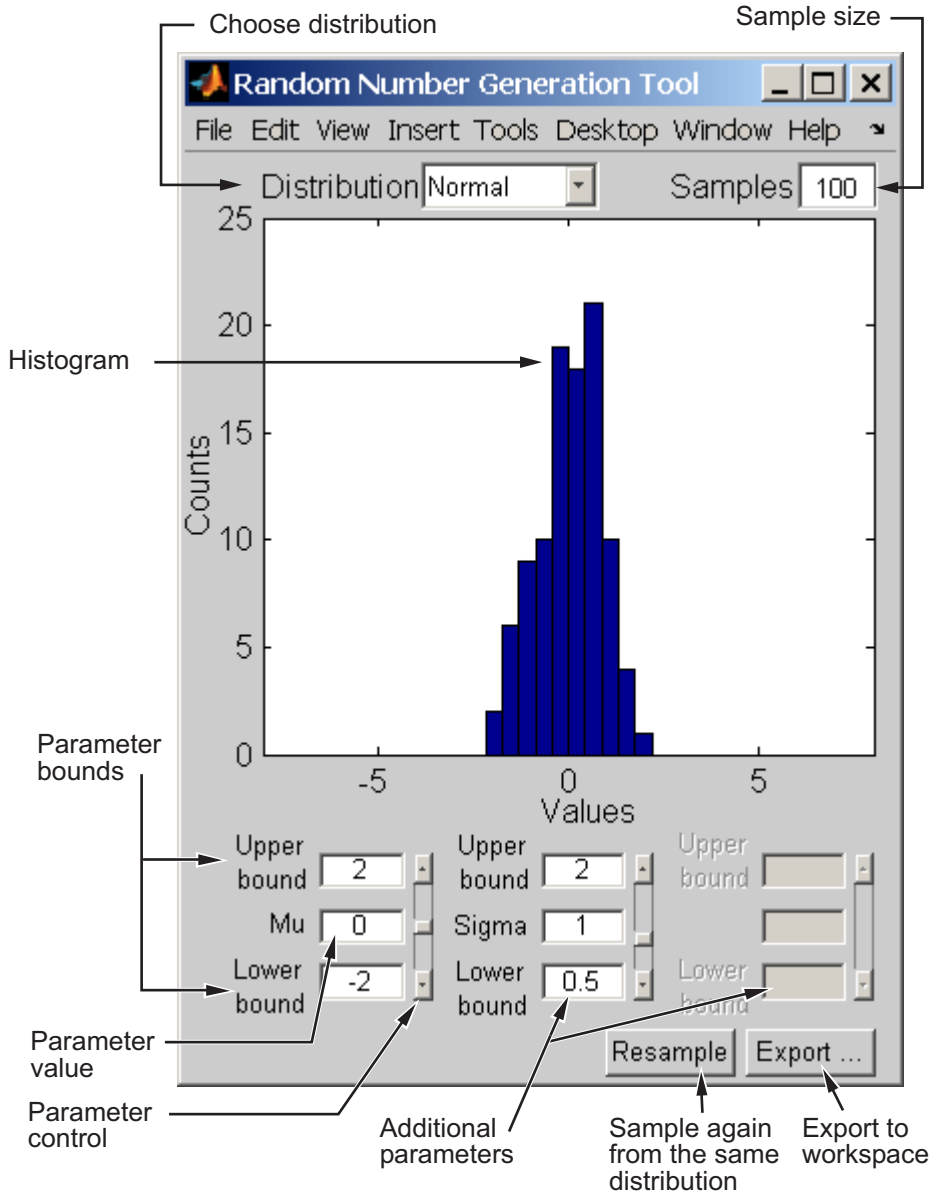
Syntax

```
randtool
```

Description

`randtool` opens the Random Number Generation Tool.

The Random Number Generation Tool is a graphical user interface that generates random samples from specified probability distributions and displays the samples as histograms. Use the tool to explore the effects of changing parameters and sample size on the distributions.



Start by selecting a distribution, then enter the desired sample size.

You can also

- Use the controls at the bottom of the window to set parameter values for the distribution and to change their upper and lower bounds.
- Draw another sample from the same distribution, with the same size and parameters.
- Export the current sample to your workspace. A dialog box enables you to provide a name for the sample.

See Also

`disttool` | `dfittool`

range

Range of values

Syntax

```
range(X)
y = range(X,dim)
```

Description

`range(X)` returns the difference between the maximum and the minimum of a sample. For vectors, `range(x)` is the range of the elements. For matrices, `range(X)` is a row vector containing the range of each column of X. For N-dimensional arrays, `range` operates along the first nonsingleton dimension of `X`.

`y = range(X,dim)` operates along the dimension `dim` of `X`.

`range` treats `NaN`s as missing values and ignores them.

The range is an easily-calculated estimate of the spread of a sample. Outliers have an undue influence on this statistic, which makes it an unreliable estimator.

Examples

The range of a large sample of standard normal random numbers is approximately six. This is the motivation for the process capability indices C_p and C_{pk} in statistical quality control applications.

```
rv = normrnd(0,1,1000,5);
near6 = range(rv)
near6 =
  6.1451  6.4986  6.2909  5.8894  7.0002
```

See Also

`std` | `iqr` | `mad`

rangesearch

Find all neighbors within specified distance using exhaustive search or *K*d-tree

Syntax

```
Idx = rangesearch(Mdl,Y,r)
Idx = rangesearch(Mdl,Y,r,Name,Value)
[Idx,D] = rangesearch( ___ )
```

Description

`Idx = rangesearch(Mdl,Y,r)` searches for all neighbors (i.e., points, rows, or observations) in `Mdl.X` within radius `r` of each point (i.e., row or observation) in the query data `Y` using an exhaustive search or a *K*d-tree. `rangesearch` returns `Idx`, which is a column vector of the indices of `Mdl.X` within `r` units.

`Idx = rangesearch(Mdl,Y,r,Name,Value)` returns the indices of the observation in `Mdl.X` within radius `r` of each observation in `Y` with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify to use a different distance metric than is stored in `Mdl.Distance` or a different distance metric parameter than is stored in `Mdl.DistParameter`.

`[Idx,D] = rangesearch( ___ )` additionally returns the matrix `D` using any of the input arguments in the previous syntaxes. `D` contains the distances between the observations in `Mdl.X` within radius `r` of each observation in `Y`. The function arranges the columns of `D` in ascending order by closeness, with respect to the distance metric.

Examples

Search for Neighbors Within A Radius Using a *K* d-tree and Exhaustive Search

`rangesearch` accepts `ExhaustiveSearcher` or `KDTreeSearcher` model objects to search the training data for the nearest neighbors to the query data. An

`ExhaustiveSearcher` model invokes the exhaustive searcher algorithm, and a `KDTreeSearcher` model defines a K d-tree, which `rangesearch` uses to search for nearest neighbors.

Load Fisher's iris data set. Randomly reserve five observations from the data for query data. Focus on the petal dimensions.

```
load fisheriris
rng(1); % For reproducibility
n = size(meas,1);
idx = randsample(n,5);
X = meas(~ismember(1:n,idx),3:4); % Training data
Y = meas(idx,3:4);                % Query data
```

Grow a default two-dimensional K d-tree.

```
MdlKDT = KDTreeSearcher(X)
```

```
MdlKDT =

  KDTreeSearcher with properties:

      BucketSize: 50
        Distance: 'euclidean'
    DistParameter: []
                X: [145x2 double]
```

`MdlKDT` is a `KDTreeSearcher` model object. You can alter its writable properties using dot notation.

Prepare an exhaustive nearest neighbors searcher.

```
MdlES = ExhaustiveSearcher(X)
```

```
MdlES =

  ExhaustiveSearcher with properties:

        Distance: 'euclidean'
    DistParameter: []
                X: [145x2 double]
```

`MdlKDT` is an `ExhaustiveSearcher` model object. It contains the options, such as the distance metric, to use to find nearest neighbors.

Alternatively, you can grow a K d-tree or prepare an exhaustive nearest neighbors searcher using `createns`.

Search training data for the nearest neighbor indices that correspond to each query observation that are within a 0.5 cm radius. Conduct both types of searches and use the default settings.

```
r = 0.15; % Search radius
IdxKDT = rangesearch(MdlKDT,Y,r);
IdxES = rangesearch(MdlES,Y,r);
[IdxKDT IdxES]
```

```
ans =

    [1x27 double]    [1x27 double]
    [         13]    [         13]
    [1x27 double]    [1x27 double]
    [1x2  double]    [1x2  double]
    [1x0  double]    [1x0  double]
```

`IdxKDT` and `IdxES` are cell arrays of vectors corresponding to the indices of `X` that are within 0.15 cm of the observations in `Y`. Each row of the index matrices corresponds to a query observation.

Compare the results between the methods.

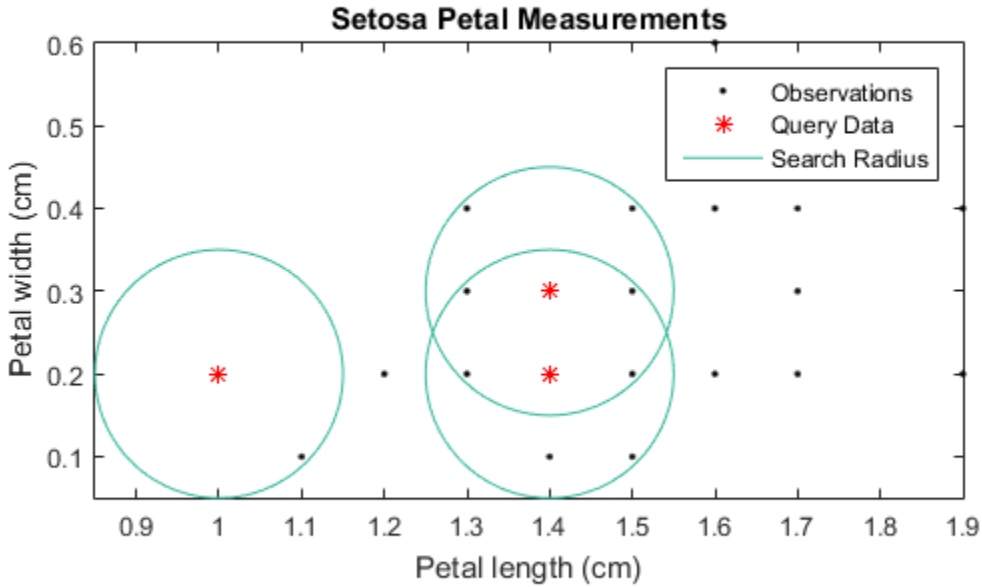
```
cellfun(@isequal,IdxKDT,IdxES)
```

```
ans =

     1
     1
     1
     1
     1
```

In this case, the results are the same.

Plot the results for the setosa irises.

```
setosaIdx = strcmp(species(~ismember(1:n,idx)),'setosa');
XSetosa = X(setosaIdx,:);
ySetosaIdx = strcmp(species(idx),'setosa');
YSetosa = Y(ySetosaIdx,:);

figure;
plot(XSetosa(:,1),XSetosa(:,2),'.k');
hold on;
plot(YSetosa(:,1),YSetosa(:,2),'*r');
for j = 1:sum(ySetosaIdx);
    c = YSetosa(j,:);
    circleFun = @(x1,x2)r^2 - (x1 - c(1)).^2 - (x2 - c(2)).^2;
    ezplot(circleFun,[c(1) + [-1 1]*r, c(2) + [-1 1]*r])
end
xlabel 'Petal length (cm)';
ylabel 'Petal width (cm)';
title 'Setosa Petal Measurements';
legend('Observations','Query Data','Search Radius');
axis equal
hold off
```



Search for Neighbors Within a Radius Using the Mahalanobis Distance

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(1);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
X = meas(~ismember(1:n,qIdx),:);
Y = meas(qIdx,:);
```

Prepare a default exhaustive nearest neighbors searcher.

```
Mdl = ExhaustiveSearcher(X)
```

```
Mdl =

  ExhaustiveSearcher with properties:

         Distance: 'euclidean'
    DistParameter: []
                X: [145x4 double]
```

`Mdl` is an `ExhaustiveSearcher` model.

Find the indices of the training data (`X`) that are within 0.15 cm of each point in the query data (`Y`). Specify that the distances are with respect to the Mahalanobis metric.

```
r = 1;
Idx = rangesearch(Mdl,Y,r,'Distance','mahalanobis')
Idx{3}
```

```
Idx =

    [1x15 double]
    [1x5  double]
    [1x6  double]
    [         84]
    [         69]


ans =

     1    34    33    22    24     2
```

Each cell of `Idx` corresponds to a query data observation and contains in `X` a vector of indices of the neighbors within 0.15cm of the query data. `rangesearch` arranges the indices in ascending order by distance. For example, using thre Mahalanobis distance, the second nearest neighbor of `Y(3,:)` is `X(34,:)`.

Compute Distances of Neighbors Within a Radius

Load Fisher's iris data set.

```
load fisheriris
```

Remove five irises randomly from the predictor data to use as a query set.

```
rng(4);                      % For reproducibility
n = size(meas,1);            % Sample size
qIdx = randsample(n,5);      % Indices of query data
X = meas(~ismember(1:n,qIdx),:);
Y = meas(qIdx,:);
```

Grow a four-dimensional K d-tree using the training data. Specify to use the Minkowski distance for finding nearest neighbors later.

```
Mdl = KDTreeSearcher(X);
```

`Mdl` is a `KDTreeSearcher` model. By default, the distance metric for finding nearest neighbors is the Euclidean metric.

Find the indices of the training data (`X`) that are within 0.5 cm from each point in the query data (`Y`).

```
r = 0.5;
[Idx,D] = rangesearch(Mdl,Y,r);
```

`Idx` and `D` are five-element cell arrays of vectors. The vector values in `Idx` are the indices in `X`. The `X` indices represent the observations that are within 0.5 cm of the query data, `Y`. `D` contains the distances that correspond to the observations.

Display the results for query observation 3.

```
Idx{3}
D{3}
```

```
ans =

   127   122


ans =

    0.2646    0.4359
```

The closest observation to `Y(3,:)` is `X(127,:)`, which is `0.2646` cm away. The next closest is `X(122,:)`, which is `0.4359` cm away. All other observations are greater than `0.5` cm away from `Y(5,:)`.

Input Arguments

`Mdl` — Nearest neighbors searcher

`ExhaustiveSearcher` model object | `KDTreeSearcher` model object

Nearest neighbors searcher, specified as an `ExhaustiveSearcher` or `KDTreeSearcher` model object, respectively. To create `Mdl`, with the appropriate mode creator. You can also use `createns`.

If `Mdl` is an `ExhaustiveSearcher` model, then `rangesearch` searches for nearest neighbors using an exhaustive search. Otherwise, `rangesearch` uses the grown *K*d-tree to search for nearest neighbors.

`Y` — Query data

numeric matrix

Query data, specified as a numeric matrix.

`Y` is an *m*-by-*K* matrix. Rows of `Y` correspond to observations (i.e., examples), and columns correspond to predictors (i.e., variables or features). `Y` must have the same number of columns as the training data stored in `Mdl.X`.

`r` — Search radius

nonnegative scalar

Search radius around each point in the query data, specified as a nonnegative scalar.

`rangesearch` finds all observations in Mdl.`X` that are within distance `r` of each observation in Y. The property `Mdl.Distance` stores the distance.

Data Types: `double` | `single`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Distance','minkowski','P',3` specifies to find all observations in `Mdl.X` within distance `r` of each observation in `Y`, using the Minkowski distance metric with exponent 3.

For Both Nearest Neighbor Searchers

`'Distance'` — Distance metric
`Mdl.Distance` (default) | `'cityblock'` | `'euclidean'` | `'mahalanobis'` | `'minkowski'` | `'seuclidean'` | function handle | ...

Distance metric used to find neighbors of the training data to the query observations, specified as the comma-separated pair consisting of `'Distance'` and a string or function handle.

For both types of nearest neighbor searchers, `Mdl` supports these distance metrics.

Value	Description
`'chebychev'`	Chebychev distance (maximum coordinate difference)
`'cityblock'`	City block distance
`'euclidean'`	Euclidean distance
`'minkowski'`	Minkowski distance

If Mdl is an `ExhaustiveSearcher` model object, then `rangesearch` supports these distance metrics.

Value	Description
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values)
`'cosine'`	One minus the cosine of the included angle between observations (row vectors)

Value	Description
`'hamming'`	Hamming distance, which is the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, which is the percentage of nonzero coordinates that differ
`'mahalanobis'`	Mahalanobis distance
`'seuclidean'`	Standardized Euclidean distance
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values)

If `Mdl` is an `ExhaustiveSearcher` model object, then you can also specify a function handle for a custom distance metric using `@` (for example, `@distfun`). The custom distance function must:

- Have the form `function D2 = distfun(ZI, ZJ)`
- Take as arguments:
  - A 1-by-*K* vector `ZI` containing a single row from `X` or from the query points `Y`
  - An *m*-by-*K* matrix `ZJ` containing multiple rows of `X` or `Y`
- Return an *m*-by-1 vector of distances `D2`, whose *j*th element is the distance between the observations `ZI` and `ZJ(`*j*`,:)`

For more details, see “Distance Metrics”.

Example: `'Distance','minkowski'`

Data Types: `char | function_handle`

`'P'` — Exponent for Minkowski distance metric

`2` (default) | positive scalar

Exponent for the Minkowski distance metric, specified as the comma-separated pair consisting of `'P'` and a positive scalar. If you specify `P` and do not specify `'Distance','minkowski'`, then the software throws an error.

Example: `'P',3`

Data Types: `double | single`

For Exhaustive, Nearest Neighbor Searchers

`'Cov'` — Covariance matrix for Mahalanobis distance metric
`nancov(X)` (default) | positive definite matrix

Covariance matrix for the Mahalanobis distance metric, specified as the comma-separated pair consisting of `'Cov'` and a positive definite matrix. `Cov` is a K-by-K matrix, where K is the number of columns of X. If you specify `Cov` and do not specify `'Distance','mahalanobis'`, then `rangesearch` throws an error.

Example: `'Cov',eye(3)`

Data Types: `double | single`

`'Scale'` — Scale parameter value for standard Euclidean distance metric
`nanstd(X)` (default) | nonnegative numeric vector

Scale parameter value for the standard Euclidean distance metric, specified as the comma-separated pair consisting of `'Scale'` and a nonnegative numeric vector. `Scale` has length K, where K is the number of columns of X.

The software scales each difference between the training and query data using the corresponding element of `Scale`. If you specify `Scale` and do not specify `'Distance','seuclidean'`, then `rangesearch` throws an error.

Example: `'Scale',quantile(X,0.75) - quantile(X,0.25)`

Data Types: `double | single`

Note: If you specify `'Distance'`, `'Cov'`, `'P'`, or `'Scale'`, then `Mdl.Distance` and `Mdl.DistParameter` do not change value.

Output Arguments

`Idx` — Training data indices of nearest neighbors
cell array of numeric vectors

Training data indices of nearest neighbors, returned as a cell array of numeric vectors.

Idx is an m-by-1 cell array such that cell `j` (`Idx{j}`) contains an m_j-dimensional vector of indices of the observations in `Mdl.X` that are within r units to the query observation

`Y(j,:)`. `rangesearch` arranges the elements of the vectors in ascending order by distance.

`D` — Distances of nearest neighbors to the query data

cell array of numeric vectors

Distances of the neighbors to the query data, returned as a numeric matrix or cell array of numeric vectors.

D is an m-by-`1` cell array such that cell `j` (`D{j}`) contains an m_j-dimensional vector of the distances that the observations in `Mdl.X` are from the query observation `Y(j,:)`. All elements of the vector are less than `r`. The function arranges the elements of the vectors in ascending order.

Alternatives

`rangesearch` is an object function of that requires an `ExhaustiveSearcher` or a `KDTreeSearcher` model object, query data, and a distance. Under equivalent conditions, `rangesearch` returns the same results as `rangesearch` when you specify the name-value pair argument `'NSMethod','exhaustive'` or `'NSMethod','kdtree'`, respectively.

More About

Algorithms

For positive integer `K`, `knnsearch` finds the `K` points in `Mdl.X` that are nearest each `Y` point. In contrast, for positive scalar `r`, `rangesearch` finds all the points in `Mdl.X` that are within a distance `r` of each `Y` point.

- Using ExhaustiveSearcher Objects
- Using KDTreeSearcher Objects
- “*k*-Nearest Neighbor Search and Radius Search” on page 16-11
- “Distance Metrics”

See Also

`createns` | `ExhaustiveSearcher` | `KDTreeSearcher` | `knnsearch` | `rangesearch`

Introduced in R2011b

rangesearch

Find all neighbors within specified distance

Syntax

```
idx = rangesearch(X,Y,r)
[idx,D]= rangesearch(X,Y,r)
[idx,D]= rangesearch(X,Y,r,Name,Value)
```

Description

`idx = rangesearch(X,Y,r)` finds all the `X` points that are within distance `r` of the `Y` points. Rows of `X` and `Y` correspond to observations, and columns correspond to variables.

`[idx,D]= rangesearch(X,Y,r)` returns the distances between each row of `Y` and the rows of `X` that are `r` or less distant.

`[idx,D]= rangesearch(X,Y,r,Name,Value)` finds nearby points with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`X`

mx-by-*n* numeric matrix, where each row represents one *n*-dimensional point. The number of columns *n* must equal as the number of columns in Y.

`Y`

my-by-*n* numeric matrix, where each row represents one *n*-dimensional point. The number of columns *n* must equal as the number of columns in X.

`r`

Search radius, a scalar. `rangesearch` finds all X points (rows) that are within distance `r` of each Y point. The meaning of distance depends on the `Distance` name-value pair.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BucketSize'`

Maximum number of data points in the leaf node of the *k*d-tree. This argument is only meaningful when *k*d-tree is used for finding nearest neighbors.

Default: `50`

`'Cov'`

Positive definite matrix indicating the covariance matrix when computing the Mahalanobis distance. This argument is only valid when the `Distance` name-value pair argument is `'mahalanobis'`.

Default: `nancov(X)`

`'Distance'`

String or function handle specifying the distance metric.

Value	Description
`'euclidean'`	Euclidean distance.
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between X and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from `X`, `S = nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair argument.
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of `X`, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair argument.
`'cityblock'`	City block distance.

Value	Description
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'P'` name-value pair argument.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'cosine'`	One minus the cosine of the included angle between observations (treated as vectors).
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values).
`'hamming'`	Hamming distance, the percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@`*`distfun`*	Distance function handle. *`distfun`* has the form
	`function D2 = DISTFUN(ZI,ZJ)`
	`...`
	where
	• `ZI` is a `1`-by-`N` vector containing one row of X or Y.
	• `ZJ` is an `M2`-by-`N` matrix containing multiple rows of X or Y.
	• `D2` is an `M2`-by-`1` vector of distances, and `D2(k)` is the distance between the observations `ZI` and `ZJ(J,:)`.

For definitions, see “Distance Metrics”.

Default: `NS.Distance`

`'NSMethod'`

Nearest neighbors search method.

Value	Meaning
`'kdtree'`	Creates and uses a *k*d-tree to find nearest neighbors. `'kdtree'` is only valid when the distance metric is one of:

Value	Meaning
	• 'chebychev' • 'cityblock' • 'euclidean' • 'minkowski'
'exhaustive'	Uses the exhaustive search algorithm. The distances from all X points to each Y point are computed to find nearest neighbors.

Default: 'kdtree' when the number of columns of X is not greater than 10, X is not sparse, and the distance metric is one of the valid 'kdtree' metrics. Otherwise, the default is 'exhaustive'.

'P'

Positive scalar indicating the exponent of Minkowski distance. This argument is only valid when the Distance name-value pair argument is 'minkowski'.

Default: 2

'Scale'

Vector S containing nonnegative values, with length equal to the number of columns in X. Each coordinate difference between X and a query point is scaled by the corresponding element of S. This argument is only valid when the Distance name-value pair argument is 'seuclidean'.

Default: nanstd(X)

Output Arguments

idx

my-by-1 cell array, where *my* is the number of rows in Y. idx{I} contains the indices of points (rows) in X whose distances to Y(I,:) are not greater than r. The entries in idx{I} are in ascending order of distance.

D

my-by-1 cell array, where *my* is the number of rows in Y. `D{I}` contains the distance values between `Y(I,:)` and the corresponding points in `idx{I}`.

Examples

Find the `X` points that are within a Euclidean distance `1.5` of each `Y` point. Both `X` and `Y` are samples of 5-D normally distributed variables.

```
rng('default') % for reproducibility
X = randn(100,5);
Y = randn(10,5);
[idx, dist] = rangesearch(X,Y,1.5)

idx =
    [1x7  double]
    [1x2  double]
    [1x11 double]
    [1x2  double]
    [1x12 double]
    [1x9  double]
    [         89]
    [1x0  double]
    [1x0  double]
    [1x0  double]

dist =
    [1x7  double]
    [1x2  double]
    [1x11 double]
    [1x2  double]
    [1x12 double]
    [1x9  double]
    [     1.1739]
    [1x0  double]
    [1x0  double]
    [1x0  double]
```

In this case, the last three `Y` points are more than `1.5` distant from any `X` point. `X(89,:)` is `1.1739` distant from `Y(7,:)`, and there is no other `X` point that is within distance `1.5` of `Y(7,:)`. There are `12` points in `X` within distance `1.5` of `Y(5,:)`.

Alternatives

`rangesearch` is the `ExhaustiveSearcher` function for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'exhaustive'`.

`rangesearch` is the `KDTreeSearcher` function for distance search. It is equivalent to the `rangesearch` function with the `NSMethod` name-value pair set to `'kdtree'`.

More About

Distance Metrics

For definitions, see "Distance Metrics".

Tips

- For a fixed positive integer `K`, `knnsearch` finds `K` points in `X` that are nearest each `Y` point. In contrast, for a fixed positive real value `r`, `rangesearch` finds all the `X` points that are within a distance `r` of each `Y` point.

Algorithms

For an overview of the *k*d-tree algorithm, see "*k*-Nearest Neighbor Search Using a *K*d-Tree" on page 16-13.

The exhaustive search algorithm finds the distance of each point in X to each point in Y.

- "*k*-Nearest Neighbor Search and Radius Search" on page 16-11

See Also

`createns` | `ExhaustiveSearcher` | `KDTreeSearcher` | `knnsearch` | `pdist2`

ranksum

Wilcoxon rank sum test

Syntax

```
p = ranksum(x,y)
[p,h] = ranksum(x,y)
[p,h,stats] = ranksum(x,y)
[___] = ranksum(x,y,Name,Value)
```

Description

`p = ranksum(x,y)` returns the *p*-value of a two-sided Wilcoxon rank sum test. `ranksum` tests the null hypothesis that data in `x` and `y` are samples from continuous distributions with equal medians, against the alternative that they are not. The test assumes that the two samples are independent. `x` and `y` can have different lengths.

This test is equivalent to a Mann-Whitney U-test.

`[p,h] = ranksum(x,y)` also returns a logical value indicating the test decision. The result `h = 1` indicates a rejection of the null hypothesis, and `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level.

`[p,h,stats] = ranksum(x,y)` also returns the structure `stats` with information about the test statistic.

`[___] = ranksum(x,y,Name,Value)` returns any of the output arguments in the previous syntaxes, for a rank sum test with additional options specified by one or more `Name,Value` pair arguments.

Examples

Test for Equal Median of Two Populations

Test the hypothesis of equal medians for two independent unequal-sized samples.

Generate sample data.

```
rng('default') % for reproducibility
x = unifrnd(0,1,10,1);
y = unifrnd(0.25,1.25,15,1);
```

These samples come from populations with identical distributions except for a shift of 0.25 in the location.

Test the equality of medians of `x` and `y`.

```
p = ranksum(x,y)
```

```
p =
  0.0375
```

The *p*-value of 0.0375 indicates that `ranksum` rejects the null hypothesis of equal medians at the default 5% significance level.

Statistics of the Test for Two Population Medians

Obtain the statistics of the test for the equality of two population medians.

Load the sample data.

```
load mileage
```

Test if the mileage per gallon is the same for the first and second type of cars.

```
[p,h,stats] = ranksum(mileage(:,1),mileage(:,2))
```

```
p =
    0.0043

h =
     1

stats =
    ranksum: 21.5000
```

Both the *p*-value, 0.043, and `h = 1` indicate the rejection of the null hypothesis of equal medians at the default 5% significance level. Because the sample sizes are small (six each), `ranksum` calculates the *p*-value using the exact method. The structure `stats` includes only the value of the rank sum test statistic.

Increase in the Median

Test the hypothesis of an increase in the population median.

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weather
```

The weather data shows the daily high temperatures taken in the same month in two consecutive years.

Perform a left-sided test to assess the increase in the median at the 1% significance level.

```
[p,h,stats] = ranksum(year1,year2,'alpha',0.01,...
'tail','left')
```

```
p =

    0.1271


h =

     0


stats =

       zval: -1.1403
    ranksum: 837.5000
```

Both the *p*-value of 0.1271 and `h = 0` indicate that there is not enough evidence to reject the null hypothesis and conclude that there is a positive shift in the median of observed high temperatures in the same month from year 1 to year 2 at the 1% significance level. Notice that `ranksum` uses the approximate method to calculate the *p*-value due to the large sample sizes.

Use the exact method to calculate the *p*-value.

```
[p,h,stats] = ranksum(year1,year2,'alpha',0.01,...
'tail','left','method','exact')
```

```
p =
```

```
    0.1273

h =

     0

stats =

    ranksum: 837.5000
```

The results of the approximate and exact methods are consistent with each other.

Input Arguments

x — Sample data

vector

Sample data, specified as a vector.

Data Types: `single` | `double`

y — Sample data

vector

Sample data, specified as a vector. The length of `y` does not have to be the same as the length of `x`.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'alpha',0.01,'method','approximate','tail','right'` specifies a right-tailed rank sum test with 1% significance level, which returns the approximate p-value.

'alpha' — Significance level

0.05 (default) | scalar value in the range 0 to 1

Significance level of the decision of a hypothesis test, specified as the comma-separated pair consisting of 'alpha' and a scalar value in the range 0 to 1. The significance level of h is 100 * alpha%.

Example: 'alpha', 0.01

Data Types: double | single

'method' — Computation method of the *p*-value

'exact' | 'approximate'

Computation method of the *p*-value, p, specified as the comma-separated pair consisting of 'method' and one of the following:

'exact'	Exact computation of the *p*-value, p.
'approximate'	Normal approximation while computing the *p*-value, p.

When 'method' is unspecified, the default is:

- 'exact' if $\min(n_x,n_y) < 10$ and $n_x + n_y < 20$
- 'approximate' otherwise

n_x and n_y are the sizes of the samples in x and y, respectively.

Example: 'method','exact'

Data Types: char

'tail' — Type of test

'both' (default) | 'right' | 'left'

Type of test, specified as the comma-separated pair consisting of 'tail' and one of the following:

'both'	Two-sided hypothesis test, where the alternative hypothesis states that x and y have different medians. Default test type if 'tail' is not specified.
'right'	Right-tailed hypothesis test, where the alternative hypothesis states that the median of x is greater than the median of y.
'left'	Left-tailed hypothesis test, where the alternative hypothesis states that the median of x is less than the median of y.

Example: `'tail','left'`

Data Types: `char`

Output Arguments

p — *p*-value of the test

nonnegative scalar

p-value of the test, returned as a positive scalar from 0 to 1. `p` is the probability of observing a test statistic as or more extreme than the observed value under the null hypothesis. `ranksum` computes the two-sided *p*-value by doubling the most significant one-sided value.

h — Result of the hypothesis test

1 | 0

Result of the hypothesis test, returned as a logical value.

- If `h` = 1, this indicates rejection of the null hypothesis at the 100 * `alpha`% significance level.
- If `h` = 0, this indicates a failure to reject the null hypothesis at the 100 * `alpha`% significance level.

stats — Test statistics

structure

Test statistics, returned as a structure. The test statistics stored in `stats` are:

- `ranksum` : Value of the rank sum test statistic
- `zval`: Value of the z-statistic (computed when `'method'` is `'approximate'`)

More About

Wilcoxon Rank Sum Test

The Wilcoxon rank sum test is a nonparametric test for two populations when samples are independent. If `X` and `Y` are independent samples with different sample sizes, the test statistic which `ranksum` returns is the rank sum of the first sample.

The Wilcoxon rank sum test is equivalent to the Mann-Whitney U-test. The Mann-Whitney U-test is a nonparametric test for equality of population medians of two independent samples `X` and `Y`.

The Mann-Whitney U-test statistic, U, is the number of times a y precedes an x in an ordered arrangement of the elements in the two independent samples `X` and `Y`. It is related to the Wilcoxon rank sum statistic in the following way: If `X` is a sample of size n_X, then

$$U = W - \frac{n_X(n_X+1)}{2}.$$

z-Statistic

For large samples, `ranksum` uses a z-statistic to compute the approximate p-value of the test.

If `X` and `Y` are two independent samples of size n_X and n_Y, where $n_X < n_Y$ the z-statistic is

$$z = \frac{W - E(W)}{\sqrt{V(W)}} = \frac{W - \left[\frac{n_X n_Y + n_X(n_X+1)}{2}\right] - 0.5 * sign(W - E(W))}{\sqrt{\frac{n_X n_Y (n_X + n_Y + 1) - tiescor}{12}}},$$

with continuity correction and tie adjustment. Here *tiescor* is given by

$$tiescor = \frac{2 * tieadj}{(n_X + n_Y)(n_X + n_Y - 1)},$$

where `ranksum` uses `[ranks,tieadj] = tiedrank(x,y)` to obtain tie adjustments. The standard normal distribution gives the p-value for this z-statistic.

Algorithms

`ranksum` treats `NaN`s in `x` and `y` as missing values and ignores them.

For a two-sided test of medians with unequal sample sizes, the test statistic that `ranksum` returns is the rank sum of the first sample.

References

[1] Gibbons, J. D., and S. Chakraborti. *Nonparametric Statistical Inference*, 5th Ed., Boca Raton, FL: Chapman & Hall/CRC Press, Taylor & Francis Group, 2011.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`kruskalwallis` | `signrank` | `signtest` | `ttest2`

ranova

Class: RepeatedMeasuresModel

Repeated measures analysis of variance

Syntax

```
ranovatbl = ranova(rm)
ranovatbl = ranova(rm,'WithinModel',WM)
[ranovatbl,A,C,D] = ranova(___)
```

Description

`ranovatbl = ranova(rm)` returns the results of repeated measures analysis of variance for a repeated measures model rm in table ranovatbl.

`ranovatbl = ranova(rm,'WithinModel',WM)` returns the results of repeated measures analysis of variance using the responses specified by the within-subject model WM.

`[ranovatbl,A,C,D] = ranova(___)` also returns arrays A, C, and D for the hypotheses tests of the form `A*B*C = D`, where `D` is zero.

Input Arguments

`rm` — Repeated measures model

`RepeatedMeasuresModel` object

Repeated measures model, returned as a `RepeatedMeasuresModel` object.

For properties and methods of this object, see `RepeatedMeasuresModel`.

`WM` — Model specifying responses

`'separatemeans'` (default) | *r*-by-*nc* contrast matrix | string that defines a model specification

Model specifying the responses, specified as one of the following:

- `'separatemeans'` — Compute a separate mean for each group.
- `C` — *r*-by-*nc* contrast matrix specifying the *nc* contrasts among the *r* repeated measures. If *Y* represents a matrix of repeated measures, `ranova` tests the hypothesis that the means of *Y***C* are zero.
- A string that defines a model specification in the within-subject factors. You can define the model based on the rules for the `terms` in the modelspec argument of `fitrm`. Also see "Model Specification for Repeated Measures Models" on page 8-77.

For example, if there are three within-subject factors `w1`, `w2`, and `w3`, then you can specify a model for the within-subject factors as follows.

Example: `'WithinModel','w1+w2+w2*w3'`

Data Types: `single | double`

Output Arguments

`ranovatbl` — Results of repeated measures anova

table

Results of repeated measures anova, returned as a `table`.

`ranovatbl` includes a term represents all differences across the within-subjects factors. This term has either the name of the within-subjects factor if specified while fitting the model, or the name `Time` if the name of the within-subjects factor is not specified while fitting the model or there are more than one within-subjects factors. `ranovatbl` also includes all interactions between the terms in the within-subject model and all between-subject model terms. It contains the following columns.

Column Name	Definition
`SumSq`	Sum of squares.
`DF`	Degrees of freedom.
`MeanSq`	Mean squared error.
`F`	*F*-statistic.
`pValue`	*p*-value for the corresponding *F*-statistic. A small *p*-value indicates significant term effect.

Column Name	Definition
`pValueGG`	*p*-value with Greenhouse-Geisser adjustment.
`pValueHF`	*p*-value with Huynh-Feldt adjustment.
`pValueLB`	*p*-value with Lower bound adjustment.

The last three *p*-values are the adjusted *p*-values for use when the compound symmetry assumption is not satisfied. For details, see "Compound Symmetry Assumption and Epsilon Corrections" on page 8-79. The `mauchy` method tests for sphericity (hence, compound symmetry) and `epsilon` method returns the epsilon adjustment values.

`A` — Specification based on between-subjects model

matrix | cell array

Specification based on the between-subjects model, returned as a matrix or a cell array. It permits the hypothesis on the elements within given columns of `B` (within time hypothesis). If ranovatbl contains multiple hypothesis tests, A might be a cell array.

Data Types: `single` | `double` | `cell`

`C` — Specification based on within-subjects model

matrix | cell array

Specification based on the within-subjects model, returned as a matrix or a cell array. It permits the hypotheses on the elements within given rows of `B` (between time hypotheses). If ranovatbl contains multiple hypothesis tests, C might be a cell array.

Data Types: `single` | `double` | `cell`

`D` — Hypothesis value

0

Hypothesis value, returned as 0.

Examples

Repeated Measures Analysis of Variance

Load the sample data.

```
load fisheriris
```

The column vector `species`consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = dataset([1 2 3 4]','VarNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas);
```

Perform repeated measures analysis of variance.

```
ranovatbl = ranova(rm)
```

```
ans =

                                SumSq      DF      MeanSq        F          pValue
                                ______     ___     ________     ______     ___________

    (Intercept):Measurements    1656.3      3      552.09      6873.3              0
    species:Measurements        282.47      6      47.078       586.1    1.4271e-206
    Error(Measurements)         35.423    441    0.080324
```

There are four measurements, three types of species, and 150 observations. So, degrees of freedom for measurements is (4–1) = 3, for species-measurements interaction it is (4–1)*(3–1) = 6, and for error it is (150–4)*(3–1) = 441. `ranova` computes the last three *p*-values using Greenhouse-Geisser, Huynh-Feldt, and Lower bound corrections, respectively. You can check the compound symmetry (sphericity) assumption using the `mauchly` method, and display the epsilon corrections using the `epsilon` method.

Longitudinal Data

Navigate to the folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load('longitudinalData')
```

The matrix Y contains response data for 16 individuals. The response is the blood level of a drug measured at five time points (time = 0, 2, 4, 6, and 8). Each row of Y corresponds to an individual, and each column corresponds to a time point. The first eight subjects are female, and the second eight subjects are male. This is simulated data.

Define a variable that stores gender information.

```
Gender = ['F' 'F' 'F' 'F' 'F' 'F' 'F' 'F' 'M' 'M' 'M' 'M' 'M' 'M' 'M' 'M']';
```

Store the data in a proper table array format to do repeated measures analysis.

```
t = table(Gender,Y(:,1),Y(:,2),Y(:,3),Y(:,4),Y(:,5),...
'VariableNames',{'Gender','t0','t2','t4','t6','t8'});
```

Define the within-subjects variable.

```
Time = [0 2 4 6 8]';
```

Fit a repeated measures model, where the blood levels are the responses and gender is the predictor variable.

```
rm = fitrm(t,'t0-t8 ~ Gender','WithinDesign',Time);
```

Perform repeated measures analysis of variance.

```
ranovatbl = ranova(rm)
```

```
ranovatbl =

                      SumSq     DF    MeanSq       F         pValue       pValueGG
                      ______    __    ______    _______    __________    __________

    (Intercept):Time   881.7     4    220.43     37.539    3.0348e-15    4.7325e-09
    Gender:Time        17.65     4    4.4125    0.75146      0.56126        0.4877
    Error(Time)        328.83    56    5.872
```

There are 5 time points, 2 genders, and 16 observations. So, the degrees of freedom for time is (5–1) = 4, for gender-time interaction it is (5–1)*(2–1) = 4, and for error it is (16–2)*(5–1) = 56. The small p-value of 2.6198e–05 indicates that there is a significant effect of time on blood pressure. The p -value of 0.40063 indicates that there is no significant gender-time interaction.

Specify the Within-Subjects Model

Load the sample data.

```
load repeatedmeas
```

The table `between` includes the between-subject variables age, IQ, group, gender, and eight repeated measures $y1$ through $y8$ as responses. The table within includes the within-subject variables $w1$ and $w2$. This is simulated data.

Fit a repeated measures model, where the repeated measures $y1$ through $y8$ are the responses, and age, IQ, group, gender, and the group-gender interaction are the predictor variables. Also specify the within-subject design matrix.

```
rm = fitrm(between,'y1-y8 ~ Group*Gender + Age + IQ','WithinDesign',within);
```

Perform repeated measures analysis of variance.

```
ranovatbl = ranova(rm)
```

```
ranovatbl =
```

	SumSq	DF	MeanSq	F	pValue	pValueGG
(Intercept):Time	6645.2	7	949.31	2.2689	0.031674	0.071235
Age:Time	5824.3	7	832.05	1.9887	0.059978	0.10651
IQ:Time	5188.3	7	741.18	1.7715	0.096749	0.14492
Group:Time	15800	14	1128.6	2.6975	0.0014425	0.011884
Gender:Time	4455.8	7	636.55	1.5214	0.16381	0.20533
Group:Gender:Time	4247.3	14	303.38	0.72511	0.74677	0.663
Error(Time)	64433	154	418.39			

Specify the model for the within-subject factors. Also display the matrices used in the hypothesis test.

```
[ranovatbl,A,C,D] = ranova(rm,'WithinModel','w1+w2')
```

```
ranovatbl =
```

	SumSq	DF	MeanSq	F	pValue	pValueGG
(Intercept)	3141.7	1	3141.7	2.5034	0.12787	0.12787
Age	537.48	1	537.48	0.42828	0.51962	0.51962
IQ	2975.9	1	2975.9	2.3712	0.13785	0.13785
Group	20836	2	10418	8.3012	0.0020601	0.0020601
Gender	3036.3	1	3036.3	2.4194	0.13411	0.13411
Group:Gender	211.8	2	105.9	0.084385	0.91937	0.91937

```
    Error                27609    22      1255
    (Intercept):w1       146.75     1    146.75     0.23326      0.63389      0.63389
    Age:w1               942.02     1    942.02      1.4974      0.23402      0.23402
    IQ:w1                11.563     1    11.563     0.01838      0.89339      0.89339
    Group:w1             4481.9     2    2240.9       3.562     0.045697     0.045697
    Gender:w1            270.65     1    270.65      0.4302      0.51869      0.51869
    Group:Gender:w1      240.37     2    120.19     0.19104      0.82746      0.82746
    Error(w1)             13841    22    629.12
    (Intercept):w2       3663.8     3    1221.3      3.8381     0.013513     0.020339
    Age:w2               1199.9     3    399.95      1.2569       0.2964      0.29645
    IQ:w2                3650.1     3    1216.7      3.8237     0.013744     0.020636
    Group:w2             5963.8     6    993.96      3.1237    0.0093493     0.015434
    Gender:w2            2173.1     3    724.38      2.2765     0.087813      0.10134
    Group:Gender:w2      3339.6     6     556.6      1.7492      0.12345         0.14
    Error(w2)             21001    66     318.2


A =

    [1x8 double]
    [1x8 double]
    [1x8 double]
    [2x8 double]
    [1x8 double]
    [2x8 double]


C =

    [8x1 double]    [8x1 double]    [8x3 double]


D =

     0
```

Display the contents of A.

```
[A{1};A{2};A{3};A{4};A{5};A{6}]

ans =

     1     0     0     0     0     0     0     0
     0     1     0     0     0     0     0     0
     0     0     1     0     0     0     0     0
```

```
     0     0     0     1     0     0     0     0
     0     0     0     0     1     0     0     0
     0     0     0     0     0     1     0     0
     0     0     0     0     0     0     1     0
     0     0     0     0     0     0     0     1
```

Display the contents of `C`.

```
[C{1} C{2} C{3}]
```

```
ans =

     1     1     1     0     0
     1     1     0     1     0
     1     1     0     0     1
     1     1    -1    -1    -1
     1    -1     1     0     0
     1    -1     0     1     0
     1    -1     0     0     1
     1    -1    -1    -1    -1
```

Algorithms

`ranova` computes the regular p-value (in the `pValue` column of the `rmanova` table) using the F-statistic cumulative distribution function:
p-value = 1 – fcdf(F,v_1,v_2).

When the compound symmetry assumption is not satisfied, `ranova` uses a correction factor epsilon, ε, to compute the corrected p-values as follows:
p-value_corrected = 1 – fcdf(F,ε*v_1,ε*v_2).

The `mauchly` method tests for sphericity (hence, compound symmetry) and `epsilon` method returns the epsilon adjustment values.

See Also

`anova` | `epsilon` | `fitrm` | `manova` | `mauchly`

More About

- “Model Specification for Repeated Measures Models” on page 8-77
- “Compound Symmetry Assumption and Epsilon Corrections” on page 8-79

- “Mauchly’s Test of Sphericity” on page 8-81

raylcdf

Rayleigh cumulative distribution function

Syntax

```
p = raylcdf(x,b)
p = raylcdf(x,b,'upper')
```

Description

`p = raylcdf(x,b)` returns the Rayleigh cdf at each value in `x` using the corresponding scale parameter, `b`. `x` and `b` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `x` or `b` is expanded to a constant array with the same dimensions as the other input.

`p = raylcdf(x,b,'upper')` returns the complement of the Rayleigh cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The Rayleigh cdf is

$$y = F(x \mid b) = \int_0^x \frac{t}{b^2} e^{\left(\frac{-t^2}{2b^2}\right)} dt$$

Examples

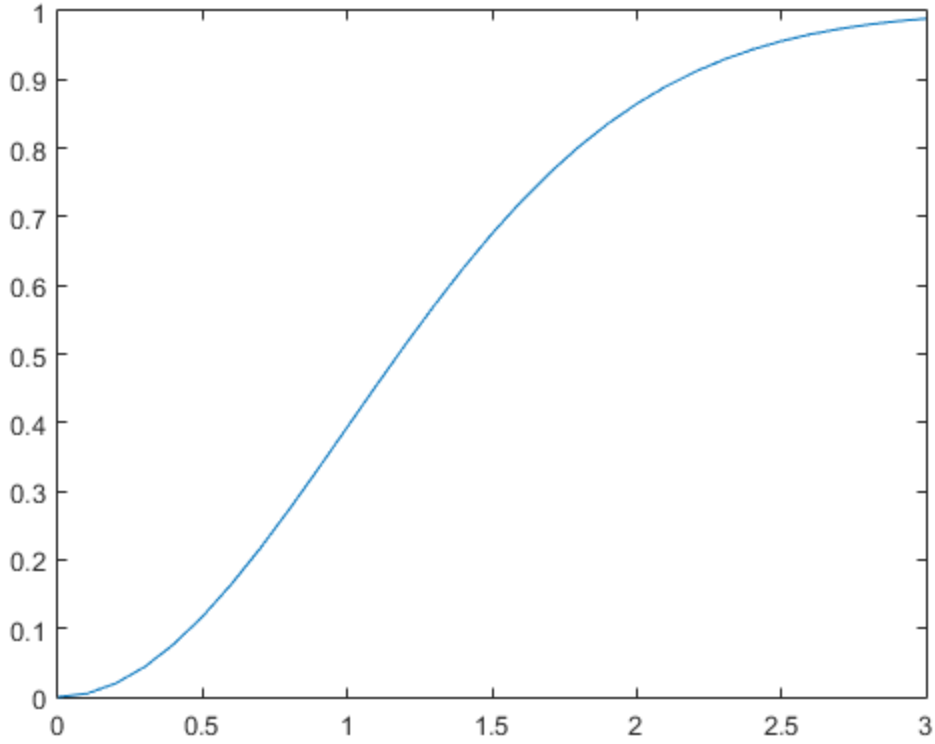
Compute and Plot Rayleigh Distribution cdf

Compute the cdf of a Rayleigh distribution with parameter `B = 1`.

```
x = 0:0.1:3;
p = raylcdf(x,1);
```

Plot the cdf.

```
figure;
plot(x,p)
```



More About

- “Rayleigh Distribution” on page B-141

References

[1] Evans, M., N. Hastings, and B. Peacock. *Statistical Distributions*. Hoboken, NJ: Wiley-Interscience, 2000. pp. 134–136.

See Also

`cdf` | `raylpdf` | `raylinv` | `raylstat` | `raylfit` | `raylrnd`

prob.RayleighDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Rayleigh probability distribution object

Description

`prob.RayleighDistribution` is an object consisting of parameters, a model description, and sample data for a normal probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Rayleigh')` creates a Rayleigh probability distribution object using the default parameter values.

`pd = makedist('Rayleigh','b',b)` creates a Rayleigh probability distribution object using the specified parameter value.

Input Arguments

b — Defining parameter

1 (default) | positive scalar value

Defining parameter for the Rayleigh distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

b — Defining parameter

positive scalar value

Defining parameter for the Rayleigh distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between

the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters

proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Rayleigh Distribution

The Rayleigh distribution is a special case of the Weibull distribution. It is often used in communication theory to model scattered signals that reach a receiver by multiple paths.

The Rayleigh distribution uses the following parameter.

Parameter	Description	Support
b	Defining parameter	$b > 0$

The probability density function (pdf) is

$$f(x \mid b) = \frac{x}{b^2} \exp\left\{\frac{-x^2}{2b^2}\right\} \quad ; \quad x \geq 0 .$$

Examples

Create a Rayleigh Distribution Object Using Default Parameters

Create a Rayleigh distribution object using the default parameter values.

```
pd = makedist('Rayleigh')
```

```
pd =
```

```
  RayleighDistribution

  Rayleigh distribution
    B = 1
```

Create a Rayleigh Distribution Object Using Specified Parameters

Create a Rayleigh distribution object by specifying the parameter values.

```
pd = makedist('Rayleigh','b',3)
```

```
pd =

  RayleighDistribution

  Rayleigh distribution
    B = 3
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    3.7599
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Rayleigh Distribution"
- Class Attributes
- Property Attributes

raylfit

Rayleigh parameter estimates

Syntax

```
raylfit(data,alpha)
[phat,pci] = raylfit(data,alpha)
```

Description

`raylfit(data,alpha)` returns the maximum likelihood estimates of the parameter of the Rayleigh distribution given the data in the vector `data`.

`[phat,pci] = raylfit(data,alpha)` returns the maximum likelihood estimate and 100(1 - `alpha`)% confidence interval given the data. The default value of the optional parameter `alpha` is 0.05, corresponding to 95% confidence intervals.

More About

- “Rayleigh Distribution” on page B-141

See Also

`mle` | `raylpdf` | `raylcdf` | `raylinv` | `raylstat` | `raylrnd`

raylinv

Rayleigh inverse cumulative distribution function

Syntax

```
X = raylinv(P,B)
```

Description

`X = raylinv(P,B)` returns the inverse of the Rayleigh cumulative distribution function using the corresponding scale parameter, `B` at the corresponding probabilities in `P`. `P` and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input for `P` or `B` is expanded to a constant array with the same dimensions as the other input.

Examples

```
x = raylinv(0.9,1)
x =
  2.1460
```

More About

- “Rayleigh Distribution” on page B-141

See Also

`raylcdf` | `raylpdf` | `raylrnd` | `raylstat`

raylpdf

Rayleigh probability density function

Syntax

```
Y = raylpdf(X,B)
```

Description

`Y = raylpdf(X,B)` computes the Rayleigh pdf at each of the values in `X` using the corresponding scale parameter, `B`. `X` and `B` can be vectors, matrices, or multidimensional arrays that all have the same size, which is also the size of `Y`. A scalar input for `X` or `B` is expanded to a constant array with the same dimensions as the other input.

The Rayleigh pdf is

$$y = f(x \mid b) = \frac{x}{b^2} e^{\left(\frac{-x^2}{2b^2}\right)}$$

Examples

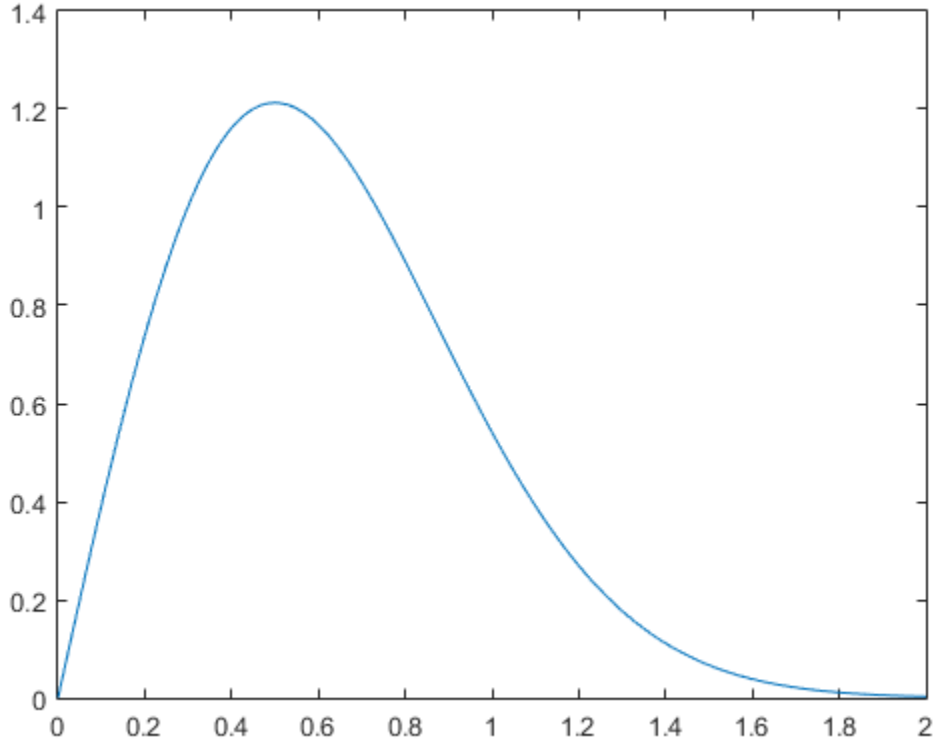
Compute and Plot Rayleigh Distribution pdf

Compute the pdf of a Rayleigh distribution with parameter `B = 0.5`.

```
x = [0:0.01:2];
p = raylpdf(x,0.5);
```

Plot the pdf.

```
figure;
plot(x,p)
```



More About

- "Rayleigh Distribution" on page B-141

See Also

`pdf` | `raylcdf` | `raylinv` | `raylstat` | `raylfit` | `raylrnd`

raylrnd

Rayleigh random numbers

Syntax

```
R = raylrnd(B)
R = raylrnd(B,v)
R = raylrnd(B,m,n)
```

Description

`R = raylrnd(B)` returns a matrix of random numbers chosen from the Rayleigh distribution with scale parameter, `B`. `B` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `B`.

`R = raylrnd(B,v)` returns a matrix of random numbers chosen from the Rayleigh distribution with parameter `B`, where `v` is a row vector. If `v` is a 1-by-2 vector, `R` is a matrix with `v(1)` rows and `v(2)` columns. If `v` is 1-by-n, `R` is an n-dimensional array.

`R = raylrnd(B,m,n)` returns a matrix of random numbers chosen from the Rayleigh distribution with parameter `B`, where scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
r = raylrnd(1:5)
r =
  1.7986  0.8795  3.3473  8.9159  3.5182
```

More About

- “Rayleigh Distribution” on page B-141

See Also

`random` | `raylpdf` | `raylcdf` | `raylinv` | `raylstat` | `raylfit`

raylstat

Rayleigh mean and variance

Syntax

```
[M,V] = raylstat(B)
```

Description

`[M,V] = raylstat(B)` returns the mean of and variance for the Rayleigh distribution with scale parameter `B`.

The mean of the Rayleigh distribution with parameter b is $b\sqrt{\pi / 2}$ and the variance is

$$\frac{4-\pi}{2}b^2$$

Examples

```
[mn,v] = raylstat(1)
mn =
  1.2533
v =
  0.4292
```

More About

- “Rayleigh Distribution” on page B-141

See Also

`raylpdf` | `raylcdf` | `raylinv` | `raylfit` | `raylrnd`

rcoplot

Residual case order plot

Syntax

```
rcoplot(r,rint)
```

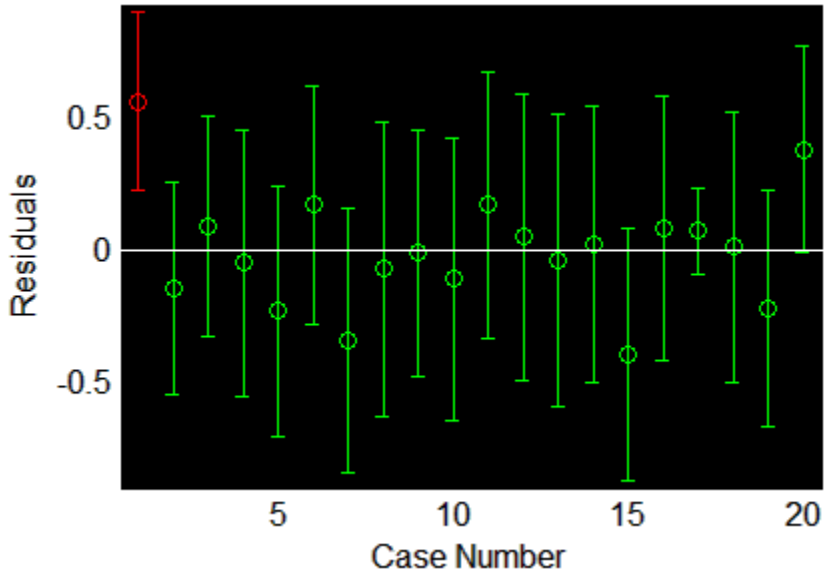
Description

`rcoplot(r,rint)` displays an errorbar plot of the confidence intervals on the residuals from a regression. The residuals appear in the plot in case order. Inputs `r` and `rint` are outputs from the `regress` function.

Examples

The following plots residuals and prediction intervals from a regression of a linearly additive model to the data in `moore.mat`:

```
load moore
X = [ones(size(moore,1),1) moore(:,1:5)];
y = moore(:,6);
alpha = 0.05;
[betahat,Ibeta,res,Ires,stats] = regress(y,X,alpha);
rcoplot(res,Ires)
```



The interval around the first residual, shown in red, does not contain zero. This indicates that the residual is larger than expected in 95% of new observations, and suggests the data point is an outlier.

See Also

`regress`

refcurve

Add reference curve to plot

Syntax

```
refcurve(p)
refcurve
hcurve = refcurve(...)
```

Description

`refcurve(p)` adds a polynomial reference curve with coefficients `p` to the current axes. If `p` is a vector with `n+1` elements, the curve is:

```
y = p(1)*x^n + p(2)*x^(n-1) + ... + p(n)*x + p(n+1)
```

`refcurve` with no input arguments adds a line along the *x* axis.

`hcurve = refcurve(...)` returns the handle `hcurve` to the curve.

Examples

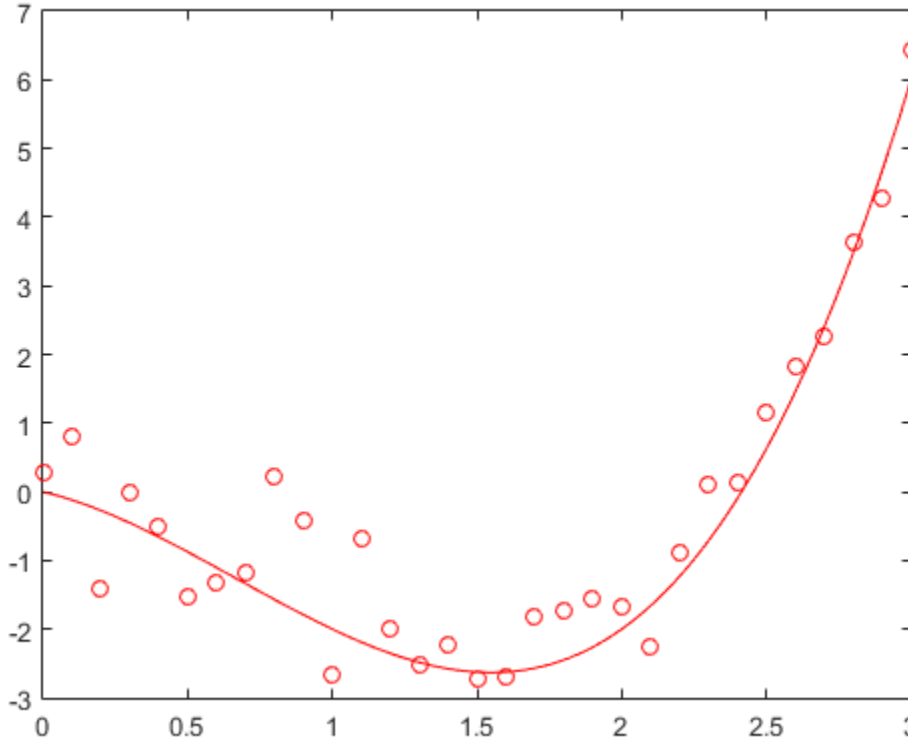
Add Population and Fitted Mean Functions

Generate data with a polynomial trend.

```
p = [1 -2 -1 0];
t = 0:0.1:3;
rng default  % For reproducibility
y = polyval(p,t) + 0.5*randn(size(t));
```

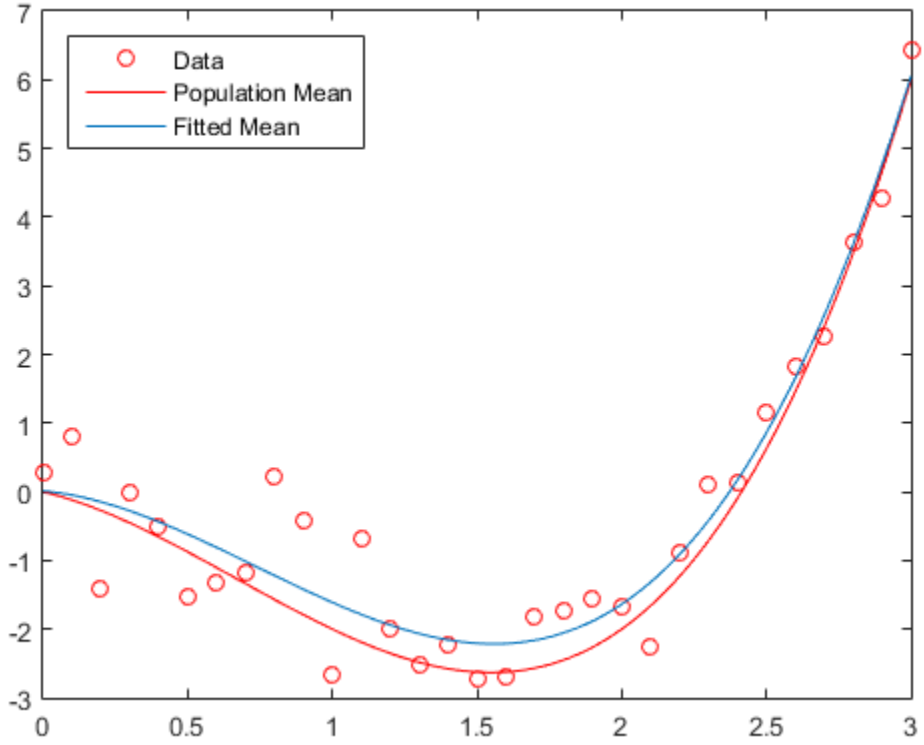
Plot data and add the population mean function using `refcurve` .

```
plot(t,y,'ro')
h = refcurve(p);
h.Color = 'r';
```



Also add the fitted mean function.

```
q = polyfit(t,y,3);
refcurve(q)
legend('Data','Population Mean','Fitted Mean',...
  'Location','NW')
```



Plot Trajectories of a Batted Baseball Using refcurve

Introduce the relevant physical constants.

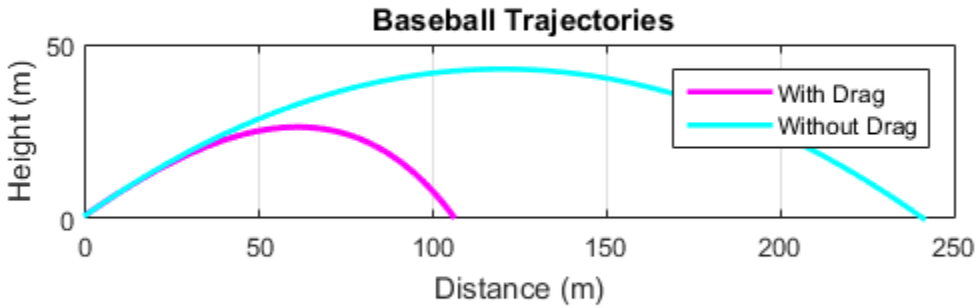
```
M = 0.145;       % Mass (kg)
R = 0.0366;      % Radius (m)
A = pi*R^2;      % Area (m^2)
rho = 1.2;       % Density of air (kg/m^3)
C = 0.5;         % Drag coefficient
D = rho*C*A/2;   % Drag proportional to the square of the speed
g = 9.8;         % Acceleration due to gravity (m/s^2)
```

Simulate the trajectory with drag proportional to the square of the speed, assuming constant acceleration in each time interval.

```
dt = 1e-2;      % Simulation time interval (s)
r0 = [0 1];     % Initial position (m)
s0 = 50;        % Initial speed (m/s)
alpha0 = 35;    % Initial angle (deg)
v0 = s0*[cosd(alpha0) sind(alpha0)]; % Initial velocity (m/s)

r = r0;
v = v0;
trajectory = r0;
while r(2) > 0
    a = [0 -g] - (D/M)*norm(v)*v;
    v = v + a*dt;
    r = r + v*dt + (1/2)*a*(dt^2);
    trajectory = [trajectory;r];
end
```

Plot trajectory and use refcurve to add the drag-free parabolic trajectory (found analytically) to the plot of trajectory.

```
figure
plot(trajectory(:,1),trajectory(:,2),'m','LineWidth',2)
xlim([0,250])
h = refcurve([-g/(2*v0(1)^2),...
    (g*r0(1)/v0(1)^2) + (v0(2)/v0(1)),...
    (-g*r0(1)^2/(2*v0(1)^2)) - (v0(2)*r0(1)/v0(1)) + r0(2)]);
h.Color = 'c';
h.LineWidth = 2;
axis equal
ylim([0,50])
grid on
xlabel('Distance (m)')
ylabel('Height (m)')
title('{\bf Baseball Trajectories}')
legend('With Drag','Without Drag')
```



See Also

`refline` | `lsline` | `gline` | `polyfit`

refit

Class: GeneralizedLinearMixedModel

Refit generalized linear mixed-effects model

Syntax

```
glmenew = refit(glme,ynew)
```

Description

`glmenew = refit(glme,ynew)` returns a refitted generalized linear mixed-effects model, glmenew, based on the input model glme, using a new response vector, ynew.

Tips

- You can use `refit` and `random` to conduct a simulated likelihood ratio test or parametric bootstrap.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

`ynew` — New response vector

n-by-1 vector of scalar values

New response vector, specified as an n-by-1 vector of scalar values, where n is the number of observations used to fit glme.

For an observation i with prior weights w_i^p and binomial size n_i (when applicable), the response values y_i contained in ynew can have the following values.

Distribution	Permitted Values	Notes
`Binomial`	$\left\{0,\frac{1}{w_i^p n_i},\frac{2}{w_i^p n_i},\ldots,1\right\}$	w_i^p and n_i are integer values > 0
`Poisson`	$\left\{0,\frac{1}{w_i^p},\frac{2}{w_i^p},\cdots,1\right\}$	w_i^p is an integer value > 0
`Gamma`	$(0,\infty)$	$w_i^p \geq 0$
`InverseGaussian`	$(0,\infty)$	$w_i^p \geq 0$
`Normal`	$(-\infty,\infty)$	$w_i^p \geq 0$

You can access the prior weights property w_i^p using dot notation.

```
glme.ObservationInfo.Weights
```

Data Types: `single` | `double`

Output Arguments

`glmenew` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, returned as a `GeneralizedLinearMixedModel` object. glmenew is an updated version of the generalized linear mixed-effects model glme, refit to the values in the response vector ynew.

For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Examples

Refit Model to New Response Vector

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
```

```
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.
- μ_{ij} is the mean number of defects corresponding to factory i (where $i = 1, 2, ..., 20$) during batch j (where $j = 1, 2, ..., 5$).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Use `random` to simulate a new response vector from the fitted model.

```
rng(0,'twister');  % For reproducibility
ynew = random(glme);
```

Refit the model using the new response vector.

```
glme = refit(glme,ynew)
```

```
glme =


Generalized linear mixed-effects model fit by ML

Model information:
    Number of observations             100
    Fixed effects coefficients           6
    Random effects coefficients         20
    Covariance parameters                1
    Distribution                   Poisson
    Link                           Log
    FitMethod                      Laplace

Formula:
    defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1 | factory)
```

```
Model fit statistics:
    AIC       BIC       LogLikelihood    Deviance
    469.24    487.48    -227.62          455.24

Fixed effects coefficients (95% CIs):
    Name                Estimate    SE          tStat       DF    pValue
    '(Intercept)'         1.5738     0.18674      8.4276    94    4.0158e-13
    'newprocess'         -0.21089     0.2306    -0.91455    94       0.36277
    'time_dev'           -0.13769    0.77477    -0.17772    94       0.85933
    'temp_dev'            0.24339    0.84657      0.2875    94       0.77436
    'supplier_C'         -0.12102    0.07323     -1.6526    94       0.10175
    'supplier_B'         0.098254   0.066943      1.4677    94       0.14551


    Lower        Upper
        1.203      1.9445
     -0.66875     0.24696
       -1.676      1.4006
      -1.4375      1.9243
     -0.26642    0.024381
    -0.034662     0.23117

Random effects covariance parameters:
Group: factory (20 Levels)
    Name1               Name2               Type         Estimate
    '(Intercept)'       '(Intercept)'       'std'        0.46587

Group: Error
    Name                    Estimate
    'sqrt(Dispersion)'      1
```

See Also

`GeneralizedLinearMixedModel` | `designMatrix` | `fitted` | `residuals`

refline

Add reference line to plot

Syntax

```
refline(m,b)
refline(coeffs)
refline
refline(ax, ___ )
hline = refline( ___ )
```

Description

`refline(m,b)` adds a reference line with slope `m` and intercept `b` to the current axes.

`refline(coeffs)`, where `coeffs` is a two-element coefficient vector, adds the line

```
y = coeffs(1)*x + coeffs(2)
```

to the figure.

`refline` with no input arguments is equivalent to `lsline`.

`refline(ax, ___ )` adds a reference line to the plot in the axis specified by `ax`, using any of the previous syntaxes.

`hline = refline( ___ )` returns the handle `hline` to the line.

Examples

Add a Reference Line at the Mean

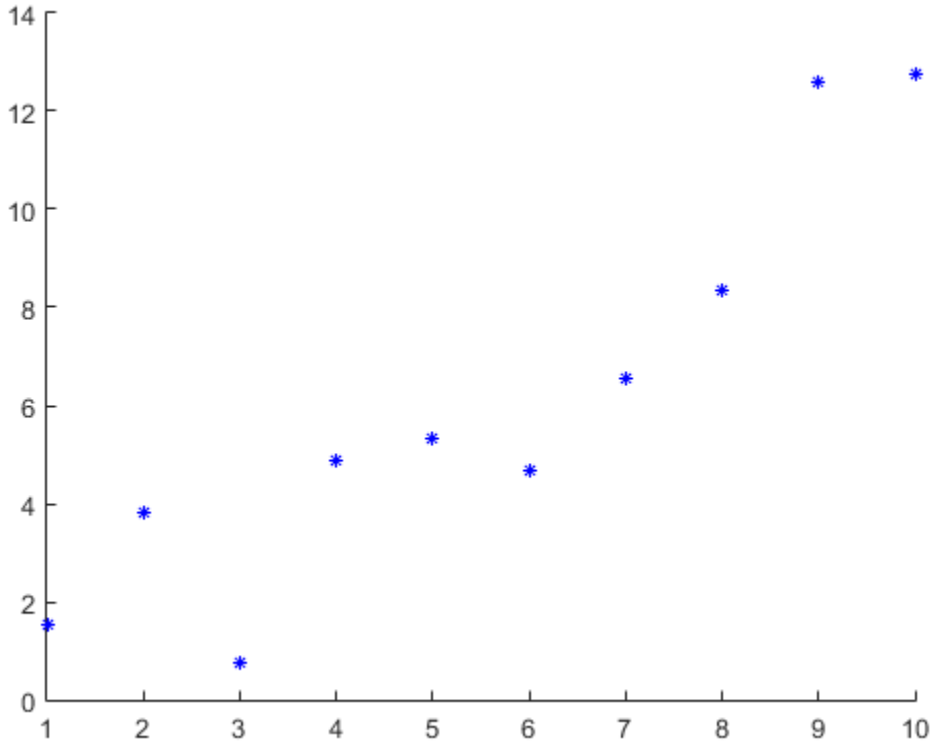
Generate sample data for independent variable `x` and a dependent variable `y` .

```
x = 1:10;
```

```
y = x + randn(1,10);
```

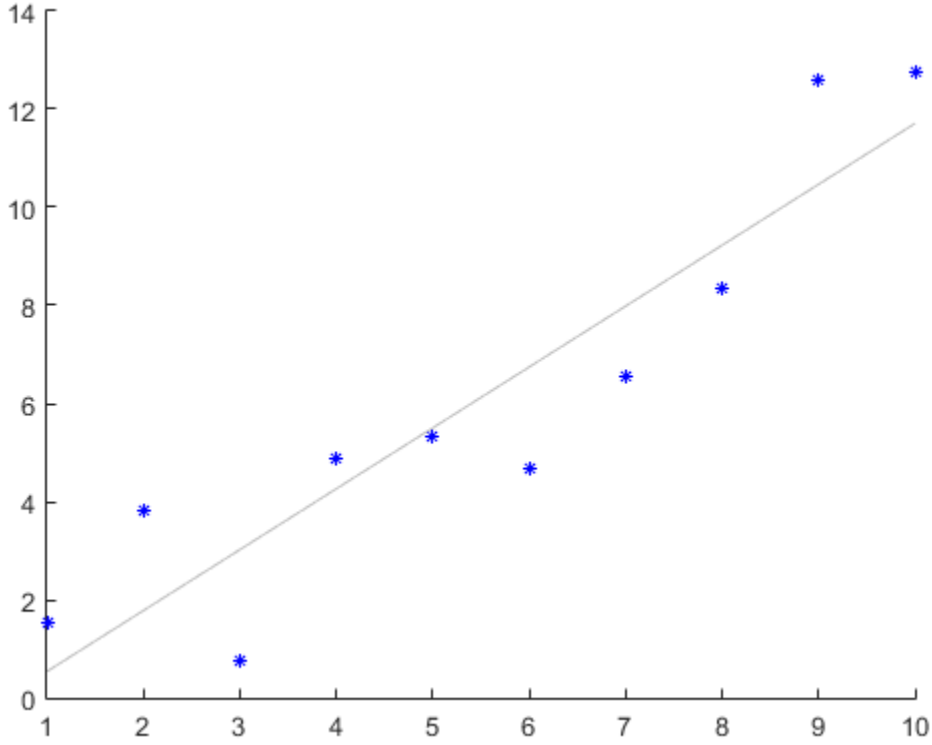
Create a scatter plot of `x` and `y` .

```
scatter(x,y,25,'b','*')
```



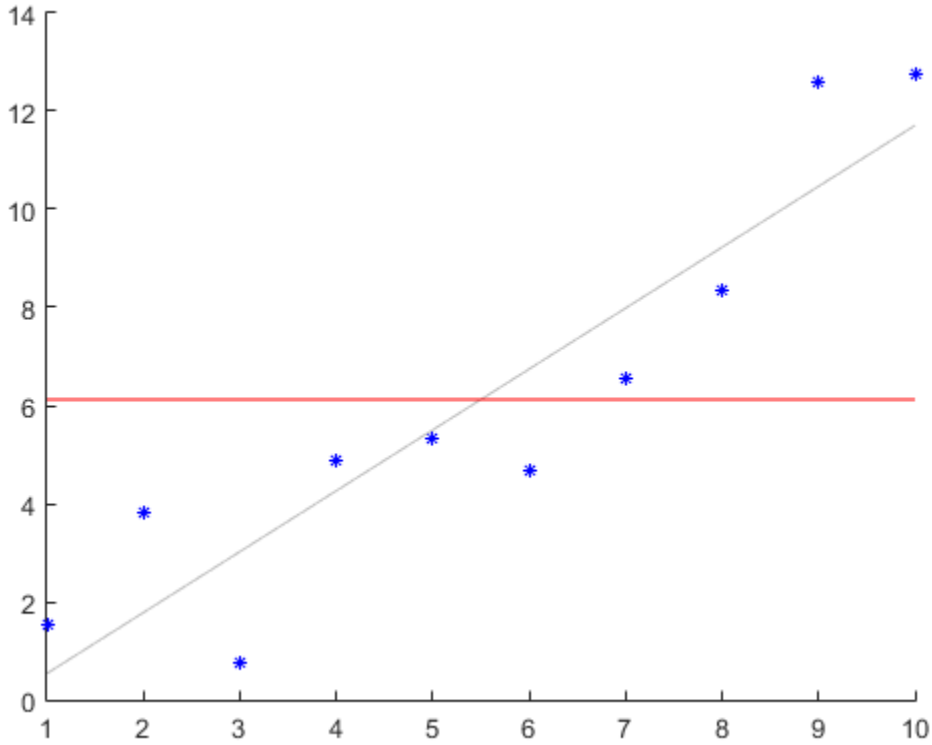
Superimpose a least-squares line on the scatter plot.

```
lsline
```



Add a reference line at the mean of the scatter and its least-squares line.

```
mu = mean(y);
hline = refline([0 mu]);
hline.Color = 'r';
```



The red line shows the reference line at the mean of data.

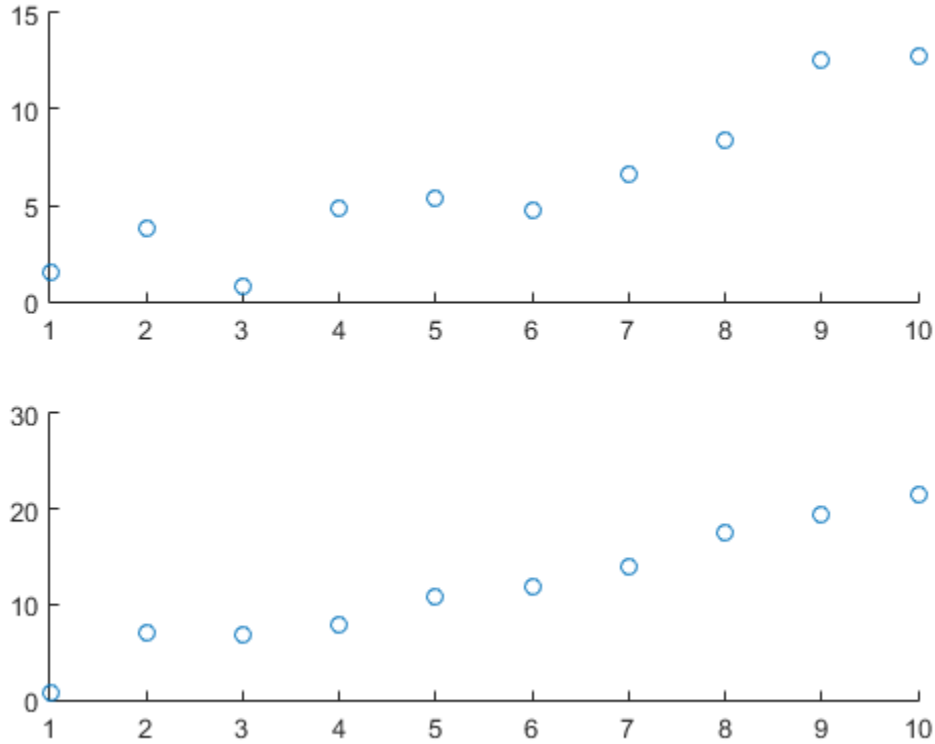
Specify Axes for Least-Squares and Reference Lines

Define the x-variable and two different y-variables to use for the plots.

```
rng default  % For reproducibility
x = 1:10;
y1 = x + randn(1,10);
y2 = 2*x + randn(1,10);
```

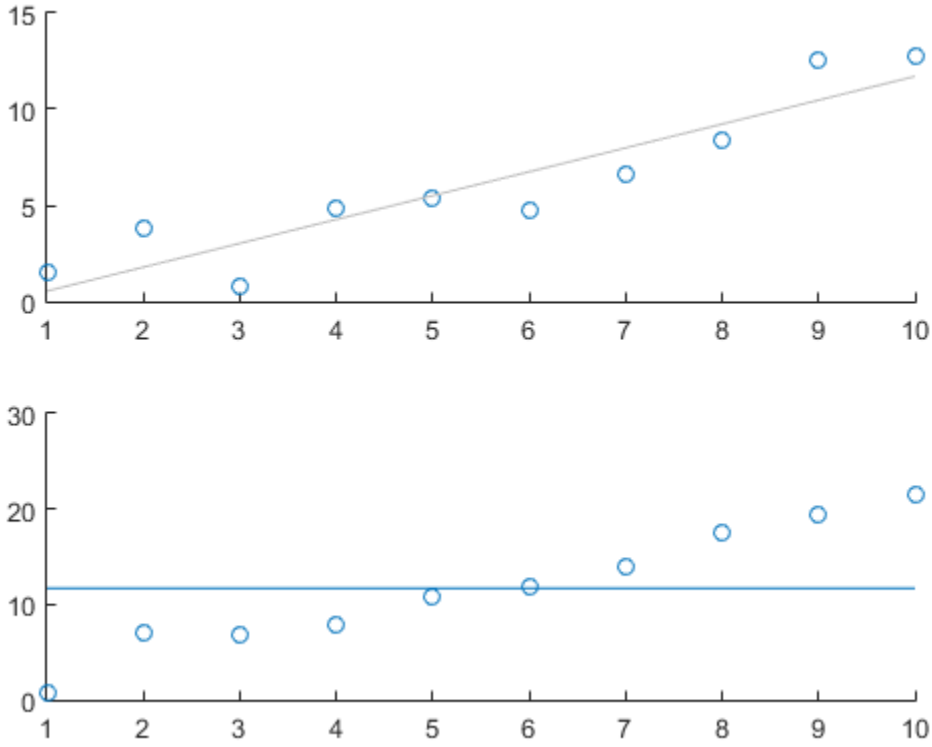
Define `ax1` as the top half of the figure, and `ax2` as the bottom half of the figure. Create the first scatter plot on the top axis using `y1`, and the second scatter plot on the bottom axis using `y2`.

```
figure
ax1 = subplot(2,1,1);
ax2 = subplot(2,1,2);

scatter(ax1,x,y1)
scatter(ax2,x,y2)
```



Superimpose a least-squares line on the top plot, and a reference line at the mean of the `y2` values in the bottom plot.

```
lsline(ax1)

mu = mean(y2);
refline(ax2,[0 mu])
```



See Also

`refcurve` | `lsline` | `gline`

regress

Multiple linear regression

Syntax

```
b = regress(y,X)
[b,bint] = regress(y,X)
[b,bint,r] = regress(y,X)
[b,bint,r,rint] = regress(y,X)
[b,bint,r,rint,stats] = regress(y,X)
[...] = regress(y,X,alpha)
```

Description

`b = regress(y,X)` returns a p-by-1 vector `b` of coefficient estimates for a multilinear regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses.

`regress` treats `NaN`s in `X` or `y` as missing values, and ignores them.

If the columns of `X` are linearly dependent, `regress` obtains a basic solution by setting the maximum number of elements of `b` to zero.

`[b,bint] = regress(y,X)` returns a p-by-2 matrix `bint` of 95% confidence intervals for the coefficient estimates. The first column of `bint` contains lower confidence bounds for each of the p coefficient estimates; the second column contains upper confidence bounds.

If the columns of `X` are linearly dependent, `regress` returns zeros in elements of `bint` corresponding to the zero elements of `b`.

`[b,bint,r] = regress(y,X)` returns an n-by-1 vector `r` of residuals.

`[b,bint,r,rint] = regress(y,X)` returns an n-by-2 matrix `rint` of intervals that can be used to diagnose outliers. If the interval `rint(i,:)` for observation `i` does

not contain zero, the corresponding residual is larger than expected in 95% of new observations, suggesting an outlier.

In a linear model, observed values of `y` are random variables, and so are their residuals. Residuals have normal distributions with zero mean but with different variances at different values of the predictors. To put residuals on a comparable scale, they are "Studentized," that is, they are divided by an estimate of their standard deviation that is independent of their value. Studentized residuals have t distributions with known degrees of freedom. The intervals returned in `rint` are shifts of the 95% confidence intervals of these t distributions, centered at the residuals.

`[b,bint,r,rint,stats] = regress(y,X)` returns a 1-by-4 vector `stats` that contains, in order, the R^2 statistic, the F statistic and its p value, and an estimate of the error variance.

Note: When computing statistics, `X` should include a column of 1s so that the model contains a constant term. The F statistic and its p value are computed under this assumption, and they are not correct for models without a constant.

The F statistic is the test statistic of the F-test on the regression model, for a significant linear regression relationship between the response variable and the predictor variables.

The R^2 statistic can be negative for models without a constant, indicating that the model is not appropriate for the data.

`[...] = regress(y,X,alpha)` uses a `100*(1-alpha)`% confidence level to compute `bint` and `rint`.

Examples

Estimate Multiple Linear Regression Coefficients

This example shows how to estimate the coefficients of a multiple linear regression.

Load the sample data. Identify weight and horsepower as predictors, and mileage as the response.

```
load carsmall
```

```
x1 = Weight;
x2 = Horsepower;    % Contains NaN data
y = MPG;
```

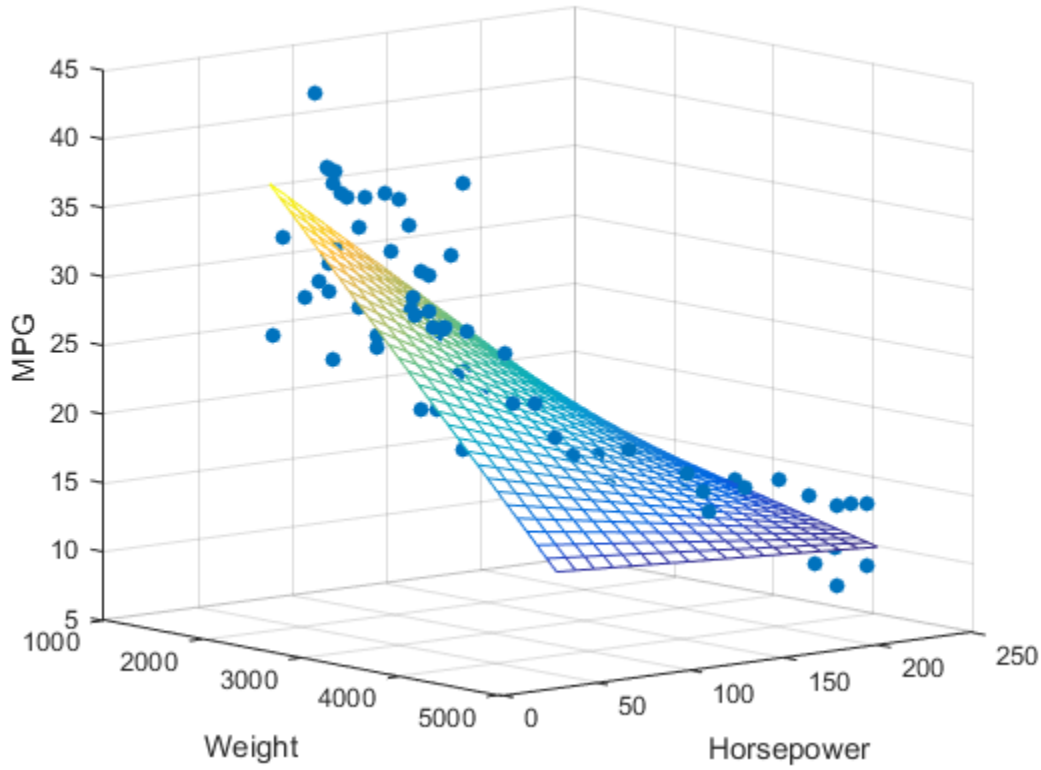
Compute the regression coefficients for a linear model with an interaction term.

```
X = [ones(size(x1)) x1 x2 x1.*x2];
b = regress(y,X)    % Removes NaN data
```

```
b =

   60.7104
   -0.0102
   -0.1882
    0.0000
```

Plot the data and the model.

```
scatter3(x1,x2,y,'filled')
hold on
x1fit = min(x1):100:max(x1);
x2fit = min(x2):10:max(x2);
[X1FIT,X2FIT] = meshgrid(x1fit,x2fit);
YFIT = b(1) + b(2)*X1FIT + b(3)*X2FIT + b(4)*X1FIT.*X2FIT;
mesh(X1FIT,X2FIT,YFIT)
xlabel('Weight')
ylabel('Horsepower')
zlabel('MPG')
view(50,10)
```



- "Interpret Linear Regression Results" on page 9-63
- "Linear Regression Workflow" on page 9-41

References

[1] Chatterjee, S., and A. S. Hadi. "Influential Observations, High Leverage Points, and Outliers in Linear Regression." *Statistical Science*. Vol. 1, 1986, pp. 379–416.

See Also

`fitlm` | `LinearModel` | `mvregress` | `rcoplot` | `stepwiselm`

RegressionBaggedEnsemble class

Superclasses: RegressionEnsemble

Regression ensemble grown by resampling

Description

`RegressionBaggedEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners.

Construction

`ens = fitensemble(X,Y,'bag',nlearn,learners,'type','regression')` creates a bagged regression ensemble. For more information on the syntax, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

A string describing how the ensemble combines learner predictions.

`FitInfo`

A numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

FResample

A numeric scalar between `0` and `1`. `FResample` is the fraction of training data `fitensemble` resampled at random for every weak learner when constructing the ensemble.

LearnerNames

Cell array of strings with names of the weak learners in the ensemble. The name of each learner appears just once. For example, if you have an ensemble of 100 trees, `LearnerNames` is `{'Tree'}`.

Method

A string with the name of the algorithm `fitensemble` used for training the ensemble.

ModelParameters

Parameters used in training ens.

NumObservations

Numeric scalar containing the number of observations in the training data.

NumTrained

Number of trained learners in the ensemble, a positive scalar.

PredictorNames

A cell array of names for the predictor variables, in the order in which they appear in `X`.

ReasonForTermination

A string describing the reason `fitensemble` stopped adding weak learners to the ensemble.

Regularization

A structure containing the result of the `regularize` method. Use `Regularization` with `shrink` to lower resubstitution error and shrink the ensemble.

Replace

Boolean flag indicating if training data for weak learners in this ensemble were sampled with replacement. `Replace` is `true` for sampling with replacement, `false` otherwise.

ResponseName

A string with the name of the response variable `Y`.

ResponseTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function using dot notation:

```
ens.ResponseTransform = @function
```

Trained

The trained learners, a cell array of compact regression models.

TrainedWeights

A numeric vector of weights the ensemble assigns to its learners. The ensemble computes predicted response by aggregating weighted predictions from its learners.

UseObsForLearner

A logical matrix of size `N`-by-`NumTrained`, where `N` is the number of rows (observations) in the training data `X`, and `NumTrained` is the number of trained weak learners. `UseObsForLearner(I,J)` is `true` if observation `I` was used for training learner `J`, and is `false` otherwise.

W

The scaled weights, a vector with length `n`, the number of rows in X. The sum of the elements of `W` is `1`.

X

The matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

Y

The numeric column vector with the same number of rows as X that trained the ensemble. Each entry in Y is the response to the data in the corresponding row of X.

Methods

oobLoss	Out-of-bag regression error
oobPredict	Predict out-of-bag response of ensemble

Inherited Methods

compact	Create compact regression ensemble
crossval	Cross validate ensemble
cvshrink	Cross validate shrinking (pruning) ensemble
regularize	Find weights to minimize resubstitution error plus penalty term
resubLoss	Regression error by resubstitution
resubPredict	Predict response of ensemble by resubstitution
resume	Resume training ensemble
shrink	Prune ensemble
loss	Regression error

predict	Predict response of ensemble
predictorImportance	Estimates of predictor importance
removeLearners	Remove members of compact regression ensemble

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Create a bagged regression ensemble to predict the mileage of cars in the `carsmall` data set based on their engine displacement, horsepower, and weight:

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'bag',100,'Tree',...
    'type','regression')

ens =

classreg.learning.regr.RegressionBaggedEnsemble:
           PredictorNames: {'x1'  'x2'  'x3'}
    CategoricalPredictors: []
             ResponseName: 'Y'
        ResponseTransform: 'none'
            NumObservations: 94
                 NumTrained: 100
                   Method: 'Bag'
             LearnerNames: {'Tree'}
     ReasonForTermination: [1x77 char]
                  FitInfo: []
       FitInfoDescription: 'None'
           Regularization: []
                FResample: 1
```

```
                Replace: 1
        UseObsForLearner: [94x100 logical]
```

Predict the mileage of a car whose characteristics are the average of those of the first 10 cars:

```
car10 = mean(X(1:10,:));
predict(ens,car10)

ans =
   14.6569
```

See Also

`RegressionEnsemble` | `fitensemble`

RegressionEnsemble class

Superclasses: CompactRegressionEnsemble

Ensemble regression

Description

`RegressionEnsemble` combines a set of trained weak learner models and data on which these learners were trained. It can predict ensemble response for new data by aggregating predictions from its weak learners.

Construction

`ens = fitensemble(X,Y,method,nlearn,learners)` returns an ensemble model that can predict responses to data. The ensemble consists of models listed in learners. For more information on the syntax, see the `fitensemble` function reference page.

`ens = fitensemble(X,Y,method,nlearn,learners,Name,Value)` returns an ensemble model with additional options specified by one or more Name,Value pair arguments. For more information on the syntax, see the `fitensemble` function reference page.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CombineWeights`

A string describing how the ensemble combines learner predictions.

`FitInfo`

A numeric array of fit information. The `FitInfoDescription` property describes the content of this array.

`FitInfoDescription`

String describing the meaning of the `FitInfo` array.

`LearnerNames`

Cell array of strings with names of the weak learners in the ensemble. The name of each learner appears just once. For example, if you have an ensemble of 100 trees, `LearnerNames` is `{'Tree'}`.

`Method`

A string with the name of the algorithm `fitensemble` used for training the ensemble.

`ModelParameters`

Parameters used in training ens.

`NumObservations`

Numeric scalar containing the number of observations in the training data.

`NumTrained`

Number of trained learners in the ensemble, a positive scalar.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`ReasonForTermination`

A string describing the reason `fitensemble` stopped adding weak learners to the ensemble.

`Regularization`

A structure containing the result of the `regularize` method. Use `Regularization` with `shrink` to lower resubstitution error and shrink the ensemble.

`ResponseName`

A string with the name of the response variable `Y`.

`ResponseTransform`

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function using dot notation:

```
ens.ResponseTransform = @function
```

`Trained`

The trained learners, a cell array of compact regression models.

`TrainedWeights`

A numeric vector of weights the ensemble assigns to its learners. The ensemble computes predicted response by aggregating weighted predictions from its learners.

`W`

The scaled weights, a vector with length `n`, the number of rows in X. The sum of the elements of `W` is `1`.

`X`

The matrix of predictor values that trained the ensemble. Each column of `X` represents one variable, and each row represents one observation.

`Y`

The numeric column vector with the same number of rows as `X` that trained the ensemble. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

compact	Create compact regression ensemble
crossval	Cross validate ensemble
cvshrink	Cross validate shrinking (pruning) ensemble

regularize	Find weights to minimize resubstitution error plus penalty term
resubLoss	Regression error by resubstitution
resubPredict	Predict response of ensemble by resubstitution
resume	Resume training ensemble
shrink	Prune ensemble

Inherited Methods

loss	Regression error
predict	Predict response of ensemble
predictorImportance	Estimates of predictor importance
removeLearners	Remove members of compact regression ensemble

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Create a boosted regression ensemble to predict the mileage of cars in the `carsmall` data set based on their weights and numbers of cylinders:

```
load carsmall
learner = templateTree('MinParent',20);
ens = fitensemble([Weight, Cylinders],MPG,...
    'LSBoost',100,learner,'PredictorNames',{'W','C'},...
    'categoricalpredictors',2)

ens =
classreg.learning.regr.RegressionEnsemble:
           PredictorNames: {'W'  'C'}
    CategoricalPredictors: 2
             ResponseName: 'Response'
        ResponseTransform: 'none'
            NumObservations: 94
                 NumTrained: 100
                   Method: 'LSBoost'
            LearnerNames: {'Tree'}
     ReasonForTermination: [1x77 char]
                  FitInfo: [100x1 double]
       FitInfoDescription: [2x83 char]
           Regularization: []
```

Predict the mileage of 4,000-pound cars with 4, 6, and 8 cylinders:

```
mileage4K = predict(ens,[4000 4; 4000 6; 4000 8])

mileage4K =
   20.0294
   19.4206
   15.5000
```

See Also

`CompactRegressionEnsemble` | `ClassificationEnsemble` | `fitensemble` | `templateTree`

RegressionPartitionedEnsemble class

Superclasses: RegressionPartitionedModel

Cross-validated regression ensemble

Description

`RegressionPartitionedEnsemble` is a set of regression ensembles trained on cross-validated folds. Estimate the quality of classification by cross validation using one or more "kfold" methods: `kfoldfun`, `kfoldLoss`, or `kfoldPredict`. Every "kfold" method uses models trained on in-fold observations to predict response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, every training fold contains roughly 4/5 of the data and every test fold contains roughly 1/5 of the data. The first model stored in `Trained{1}` was trained on `X` and `Y` with the first 1/5 excluded, the second model stored in `Trained{2}` was trained on `X` and `Y` with the second 1/5 excluded, and so on. When you call `kfoldPredict`, it computes predictions for the first 1/5 of the data using the first model, for the second 1/5 of data using the second model and so on. In short, response for every observation is computed by `kfoldPredict` using the model trained without this observation.

Construction

`cvens = crossval(ens)` creates a cross-validated ensemble from `ens`, a regression ensemble. For syntax details, see the `crossval` method reference page.

`cvens = fitensemble(X,Y,method,nlearn,learners,name,value)` creates a cross-validated ensemble when `name` is one of `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`. For syntax details, see the `fitensemble` function reference page.

Input Arguments

ens

A regression ensemble constructed with `fitensemble`.

Properties

CategoricalPredictors

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

CrossValidatedModel

Name of the cross-validated model, a string.

Kfold

Number of folds used in a cross-validated tree, a positive integer.

ModelParameters

Object holding parameters of tree.

NumObservations

Numeric scalar containing the number of observations in the training data.

NTrainedPerFold

Vector of `Kfold` elements. Each entry contains the number of trained learners in this cross-validation fold.

Partition

The partition of class `cvpartition` used in creating the cross-validated ensemble.

PredictorNames

A cell array of names for the predictor variables, in the order in which they appear in `X`.

ResponseName

Name of the response variable Y, a string.

ResponseTransform

Function handle for transforming scores, or string representing a built-in transformation function. `'none'` means no transformation; equivalently, `'none'` means `@(x)x`.

Add or change a `ResponseTransform` function using dot notation:

```
ens.ResponseTransform = @function
```

`Trainable`

Cell array of ensembles trained on cross-validation folds. Every ensemble is full, meaning it contains its training data and weights.

`Trained`

Cell array of compact ensembles trained on cross-validation folds.

`W`

The scaled weights, a vector with length `n`, the number of rows in X.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

kfoldLoss	Cross-validation loss of partitioned regression ensemble
resume	Resume training ensemble

Inherited Methods

kfoldfun	Cross validate function

kfoldLoss	Cross-validation loss of partitioned regression model
kfoldPredict	Predict response for observations not used for training.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a partitioned regression ensemble, and examine the cross-validation losses for the folds:

```
load carsmall
XX = [Cylinders Displacement Horsepower Weight];
YY = MPG;
rens = fitensemble(XX,YY,'LSBoost',100,'Tree');
cvrens = crossval(rens);
L = kfoldLoss(cvrens,'mode','individual')

L =
   42.4468
   12.3158
   65.9432
   39.0019
   30.5908
   16.6225
   17.3071
   46.1769
    8.0561
   12.9689
```

See Also

`ClassificationPartitionedEnsemble` | `RegressionEnsemble` | `RegressionPartitionedModel`

RegressionPartitionedModel class

Cross-validated regression model

Description

`RegressionPartitionedModel` is a set of regression models trained on cross-validated folds. Estimate the quality of regression by cross validation using one or more "kfold" methods: `kfoldPredict`, `kfoldLoss`, and `kfoldfun`. Every "kfold" method uses models trained on in-fold observations to predict response for out-of-fold observations. For example, suppose you cross validate using five folds. In this case, every training fold contains roughly 4/5 of the data and every test fold contains roughly 1/5 of the data. The first model stored in `Trained{1}` was trained on `X` and `Y` with the first 1/5 excluded, the second model stored in `Trained{2}` was trained on `X` and `Y` with the second 1/5 excluded, and so on. When you call `kfoldPredict`, it computes predictions for the first 1/5 of the data using the first model, for the second 1/5 of data using the second model and so on. In short, response for every observation is computed by `kfoldPredict` using the model trained without this observation.

Construction

`cvmodel = crossval(tree)` creates a cross-validated classification model from a regression tree. For syntax details, see the `crossval` method reference page.

`cvmodel = fitrtree(X,Y,Name,Value)` creates a cross-validated model when `name` is one of `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`. For syntax details, see the `fitrtree` function reference page.

Input Arguments

`tree`

A regression tree constructed with `fitrtree`.

Properties

`CategoricalPredictors`

List of categorical predictors. `CategoricalPredictors` is a numeric vector with indices from `1` to `p`, where `p` is the number of columns of `X`.

`CrossValidatedModel`

Name of the cross-validated model, a string.

`Kfold`

Number of folds used in a cross-validated tree, a positive integer.

`ModelParameters`

Object holding parameters of tree.

`Partition`

The partition of class `cvpartition` used in the cross-validated model.

`PredictorNames`

A cell array of names for the predictor variables, in the order in which they appear in `X`.

`ResponseName`

Name of the response variable Y, a string.

`ResponseTransform`

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function using dot notation:

```
ctree.ResponseTransform = @function
```

`Trained`

The trained learners, a cell array of compact regression models.

W

The scaled weights, a vector with length `n`, the number of rows in X.

X

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

Y

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

kfoldfun	Cross validate function
kfoldLoss	Cross-validation loss of partitioned regression model
kfoldPredict	Predict response for observations not used for training.

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Evaluate Cross-Validation Error

Load the sample data. Create a variable `X` containing the `Horsepower` and `Weight` data.

```
load carsmall
```

```
X = [Horsepower Weight];
```

Construct a regression tree using the sample data.

```
tree = fitrtree(X,MPG);
```

Evaluate the cross-validation error of the `carsmall` data using `Horsepower` and `Weight` as predictor variables for mileage (`MPG`).

```
L = kfoldLoss(cvtree)
```

```
L =

   26.4414
```

See Also

`RegressionPartitionedEnsemble` | `ClassificationPartitionedModel`

RegressionTree class

Superclasses: CompactRegressionTree

Regression tree

Description

A decision tree with binary splits for regression. An object of class `RegressionTree` can predict responses for new data with the `predict` method. The object contains the data used for training, so can compute resubstitution predictions.

Construction

`tree = fitrtree(x,y)` returns a regression tree based on the input variables (also known as predictors, features, or attributes) x and output (response) y. tree is a binary tree where each branching node is split based on the values of a column of x.

`tree = fitrtree(x,y,Name,Value)` fits a tree with additional options specified by one or more Name,Value pair arguments.

Input Arguments

x

A matrix of predictor values. Each column of x represents one variable, and each row represents one observation.

`fitrtree` considers `NaN` values in x as missing values. `fitrtree` does not use observations with all missing values for x the fit. `fitrtree` uses observations with some missing values for x to find splits on variables for which these observations have valid values.

y

A numeric column vector with the same number of rows as x. Each entry in y is the response to the data in the corresponding row of x.

`fitrtree` considers `NaN` values in y to be missing values. `fitrtree` does not use observations with missing values for y in the fit.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CategoricalPredictors'` — Categorical predictors list

numeric or logical vector | cell array of strings | character matrix | `'all'`

Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following.

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of x.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of x is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in the `PredictorNames` property.
- A character matrix, where each row of the matrix is a name of a predictor variable. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

Data Types: `single` | `double` | `logical` | `char` | `cell`

`'CrossVal'` — Cross-validation flag

`'off'` (default) | `'on'`

Cross-validation flag, specified as the comma-separated pair consisting of `'CrossVal'` and either `'on'` or `'off'`.

If `'on'`, `fitrtree` grows a cross-validated decision tree with 10 folds. You can override this cross-validation setting using one of the `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` name-value pair arguments. Note that you can only use one of these four options (`'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'`) at a time when creating a cross-validated tree.

Alternatively, cross-validate tree later using the `crossval` method.

Example: `'CrossVal','on'`

`'CVPartition'` — Partition for cross-validation tree
`cvpartition` object

Partition for cross-validated tree, specified as the comma-separated pair consisting of `'CVPartition'` and an object created using `cvpartition`.

Note that if you use `'CVPartition'`, you cannot use any of the `'KFold'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

`'Holdout'` — Fraction of data for holdout validation
`0` (default) | scalar value in the range `[0,1]`

Fraction of data used for holdout validation, specified as the comma-separated pair consisting of `'Holdout'` and a scalar value in the range `[0,1]`. Holdout validation tests the specified fraction of the data, and uses the rest of the data for training.

Note that if you use `'Holdout'`, you cannot use any of the `'CVPartition'`, `'KFold'`, or `'Leaveout'` name-value pair arguments.

Example: `'Holdout',0.1`

Data Types: `single` | `double`

`'KFold'` — Number of folds
`10` (default) | positive integer value

Number of folds to use in a cross-validated tree, specified as the comma-separated pair consisting of `'KFold'` and a positive integer value.

Note that if you use `'KFold'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'Leaveout'` name-value pair arguments.

Example: `'KFold',8`

Data Types: `single` | `double`

`'Leaveout'` — Leave-one-out cross-validation flag
`'off'` (default) | `'on'`

Leave-one-out cross-validation flag, specified as the comma-separated pair consisting of `'Leaveout'` and either `'on'` or `'off`. Use leave-one-out cross validation by setting to `'on'`.

Note that if you use `'Leaveout'`, you cannot use any of the `'CVPartition'`, `'Holdout'`, or `'KFold'` name-value pair arguments.

Example: `'Leaveout','on'`

`'MergeLeaves'` — Leaf merge flag

`'on'` (default) | `'off'`

Leaf merge flag, specified as the comma-separated pair consisting of `'MergeLeaves'` and `'on'` or `'off'`.

If `MergeLeaves` is `'on'`, then `RegressionTree`:

- Merges leaves that originate from the same parent node, and that yields a sum of risk values greater or equal to the risk associated with the parent node
- Estimates the optimal sequence of pruned subtrees, but does not prune the regression tree

Otherwise, `RegressionTree` does not merge leaves.

Example: `'MergeLeaves','off'`

`'MinLeafSize'` — Minimum number of leaf node observations

1 (default) | positive integer value

Minimum number of leaf node observations, specified as the comma-separated pair consisting of `'MinLeafSize'` and a positive integer value. Each leaf has at least `MinLeafSize` observations per tree leaf. If you supply both `MinParentSize` and `MinLeafSize`, `fitrtree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinLeafSize',3`

Data Types: `single` | `double`

`'MinParentSize'` — Minimum number of branch node observations

10 (default) | positive integer value

Minimum number of branch node observations, specified as the comma-separated pair consisting of `'MinParentSize'` and a positive integer value. Each branch node in the tree has at least `MinParentSize` observations. If you supply both `MinParentSize` and `MinLeafSize`, `fitrtree` uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

Example: `'MinParentSize',8`

Data Types: `single` | `double`

`'NumVariablesToSample'` — Number of predictors for split
`'all'` (default) | positive integer value

Number of predictors to select at random for each split, specified as the comma-separated pair consisting of `'NumVariablesToSample'` and a positive integer value. You can also specify `'all'` to use all available predictors.

Example: `'NumVariablesToSample',3`

Data Types: `single` | `double`

`'PredictorNames'` — Predictor variable names
`{'x1','x2',...}` (default) | cell array of strings

Predictor variable names, specified as the comma-separated pair consisting of `'PredictorNames'` and a cell array of strings containing the names for the predictor variables, in the order in which they appear in x.

Data Types: `cell`

`'Prune'` — Flag to estimate optimal sequence of pruned subtrees
`'on'` (default) | `'off'`

Flag to estimate the optimal sequence of pruned subtrees, specified as the comma-separated pair consisting of `'Prune'` and `'on'` or `'off'`.

If `Prune` is `'on'`, then `RegressionTree` grows the regression tree and estimates the optimal sequence of pruned subtrees, but does not prune the regression tree. Otherwise, `RegressionTree` grows the regression tree without estimating the optimal sequence of pruned subtrees.

To prune a trained regression tree, pass the regression tree to `prune`.

Example: `'Prune','off'`

`'PruneCriterion'` — Pruning criterion
`'error'` (default)

Pruning criterion, specified as the comma-separated pair consisting of `'PruneCriterion'` and `'error'`.

Example: `'PruneCriterion','error'`

`'QuadraticErrorTolerance'` — Quadratic error tolerance

`1e-6` (default) | positive scalar value

Quadratic error tolerance per node, specified as the comma-separated pair consisting of `'QuadraticErrorTolerance'` and a positive scalar value. Splitting nodes stops when quadratic error per node drops below `QuadraticErrorTolerance*QED`, where `QED` is the quadratic error for the entire data computed before the decision tree is grown.

Example: `'QuadraticErrorTolerance',1e-4`

`'ResponseName'` — Response variable name

`'Y'` (default) | string

Response variable name, specified as the comma-separated pair consisting of `'ResponseName'` and a string containing the name of the response variable in y.

Example: `'ResponseName','Response'`

Data Types: `char`

`'ResponseTransform'` — Response transform function

`'none'` (default) | function handle

Response transform function for transforming the raw response values, specified as the comma-separated pair consisting of `'ResponseTransform'` and either a function handle or `'none'`. The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function using dot notation:

```
tree.ResponseTransform = @function
```

Data Types: `function_handle`

`'SplitCriterion'` — Split criterion

`'MSE'` (default)

Split criterion, specified as the comma-separated pair consisting of `'SplitCriterion'` and `'MSE'`, meaning mean squared error.

Example: `'SplitCriterion','MSE'`

'Surrogate' — Surrogate decision splits flag

'off' | 'on' | 'all' | positive integer value

Surrogate decision splits flag, specified as the comma-separated pair consisting of 'Surrogate' and 'on', 'off', 'all', or a positive integer value.

- When 'on', fitrtree finds at most 10 surrogate splits at each branch node.
- When set to a positive integer value, fitrtree finds at most the specified number of surrogate splits at each branch node.
- When set to 'all', fitrtree finds all surrogate splits at each branch node. The 'all' setting can use much time and memory.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also enables you to compute measures of predictive association between predictors.

Example: 'Surrogate','on'

Data Types: single | double

'Weights' — Observation weights

ones(size(X,1),1) (default) | vector of scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and a vector of scalar values. The length of Weights is the number of rows in x.

Data Types: single | double

Properties

CategoricalPredictors

List of categorical predictors, a numeric vector with indices from 1 to p, where p is the number of columns of X.

CategoricalSplits

An *n*-by-2 cell array, where n is the number of categorical splits in tree. Each row in CategoricalSplits gives left and right values for a categorical split. For each branch node with categorical split j based on a categorical predictor variable z, the left child is chosen if z is in CategoricalSplits(j,1) and the right child is chosen if z is in

`CategoricalSplits(j,2)`. The splits are in the same order as nodes of the tree. Nodes for these splits can be found by running `cuttype` and selecting `'categorical'` cuts from top to bottom.

Children

An *n*-by-2 array containing the numbers of the child nodes for each node in tree, where *n* is the number of nodes. Leaf nodes have child node `0`.

CutCategories

An *n*-by-2 cell array of the categories used at branches in tree, where *n* is the number of nodes. For each branch node `i` based on a categorical predictor variable `x`, the left child is chosen if `x` is among the categories listed in `CutCategories{i,1}`, and the right child is chosen if `x` is among those listed in `CutCategories{i,2}`. Both columns of `CutCategories` are empty for branch nodes based on continuous predictors and for leaf nodes.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

CutPoint

An *n*-element vector of the values used as cut points in tree, where *n* is the number of nodes. For each branch node `i` based on a continuous predictor variable `x`, the left child is chosen if `x<CutPoint(i)` and the right child is chosen if `x>=CutPoint(i)`. `CutPoint` is `NaN` for branch nodes based on categorical predictors and for leaf nodes.

CutType

An *n*-element cell array indicating the type of cut at each node in tree, where *n* is the number of nodes. For each node `i`, `CutType{i}` is:

- `'continuous'` — If the cut is defined in the form `x < v` for a variable `x` and cut point `v`.
- `'categorical'` — If the cut is defined by whether a variable `x` takes a value in a set of categories.
- `''` — If `i` is a leaf node.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

CutPredictor

An *n*-element cell array of the names of the variables used for branching in each node in tree, where *n* is the number of nodes. These variables are sometimes known as *cut variables*. For leaf nodes, `CutPredictor` contains an empty string.

`CutPoint` contains the cut points for `'continuous'` cuts, and `CutCategories` contains the set of categories.

IsBranchNode

An *n*-element logical vector `ib` that is `true` for each branch node and `false` for each leaf node of tree.

ModelParameters

Object holding parameters of tree.

NumObservations

Number of observations in the training data, a numeric scalar. `NumObservations` can be less than the number of rows of input data X when there are missing values in X or response Y.

NodeError

An *n*-element vector `e` of the errors of the nodes in tree, where *n* is the number of nodes. `e(i)` is the misclassification probability for node `i`.

NodeMean

An *n*-element numeric array with mean values in each node of tree, where *n* is the number of nodes in the tree. Every element in `NodeMean` is the average of the true `Y` values over all observations in the node.

NodeProbability

An *n*-element vector `p` of the probabilities of the nodes in tree, where *n* is the number of nodes. The probability of a node is computed as the proportion of observations from the original data that satisfy the conditions for the node. This proportion is adjusted for any prior probabilities assigned to each class.

NodeRisk

An n-element vector of the risk of the nodes in the tree, where n is the number of nodes. The risk for each node is the node error weighted by the node probability.

NodeSize

An n-element vector `sizes` of the sizes of the nodes in tree, where n is the number of nodes. The size of a node is defined as the number of observations from the data used to create the tree that satisfy the conditions for the node.

NumNodes

The number of nodes `n` in tree.

Parent

An n-element vector `p` containing the number of the parent node for each node in tree, where n is the number of nodes. The parent of the root node is `0`.

PredictorNames

A cell array of names for the predictor variables, in the order in which they appear in `X`.

PruneAlpha

Numeric vector with one element per pruning level. If the pruning level ranges from 0 to M, then `PruneAlpha` has $M + 1$ elements sorted in ascending order. `PruneAlpha(1)` is for pruning level 0 (no pruning), `PruneAlpha(2)` is for pruning level 1, and so on.

PruneList

An n-element numeric vector with the pruning levels in each node of tree, where n is the number of nodes. The pruning levels range from 0 (no pruning) to M, where M is the distance between the deepest leaf and the root node.

ResponseName

Name of the response variable Y, a string.

ResponseTransform

Function handle for transforming the raw response values (mean squared error). The function handle should accept a matrix of response values and return a matrix of the same size. The default string `'none'` means `@(x)x`, or no transformation.

Add or change a `ResponseTransform` function using dot notation:

```
tree.ResponseTransform = @function
```

SurrogateCutCategories

An n-element cell array of the categories used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutCategories{k}` is a cell array. The length of `SurrogateCutCategories{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutCategories{k}` is either an empty string for a continuous surrogate predictor, or is a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split, and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutCategories` contains an empty cell.

SurrogateCutFlip

An n-element cell array of the numeric cut assignments used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutFlip{k}` is a numeric vector. The length of `SurrogateCutFlip{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutFlip{k}` is either zero for a categorical surrogate predictor, or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either –1 or +1. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z < C$ and the cut assignment for this surrogate split is +1, or if $Z \geq C$ and the cut assignment for this surrogate split is –1. Similarly, the right child is chosen if $Z \geq C$ and the cut assignment for this surrogate split is +1, or if $Z < C$ and the cut assignment for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogateCutFlip` contains an empty array.

SurrogateCutPoint

An n-element cell array of the numeric values used for surrogate splits in tree, where n is the number of nodes in tree. For each node `k`, `SurrogateCutPoint{k}` is a numeric vector. The length of `SurrogateCutPoint{k}` is equal to the number of surrogate predictors found at this node. Every element of `SurrogateCutPoint{k}` is either

NaN for a categorical surrogate predictor, or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and SurrogateCutFlip for this surrogate split is +1, or if $Z\geq C$ and SurrogateCutFlip for this surrogate split is –1. Similarly, the right child is chosen if $Z \geq C$ and SurrogateCutFlip for this surrogate split is +1, or if $Z < C$ and SurrogateCutFlip for this surrogate split is –1. The order of the surrogate split variables at each node is matched to the order of variables returned by SurrCutPredictor. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, SurrogateCutPoint contains an empty cell.

SurrogateCutType

An n-element cell array indicating types of surrogate splits at each node in tree, where n is the number of nodes in tree. For each node k, SurrogateCutType{k} is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables in SurrogateCutPredictor. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, SurrogateCutType contains an empty cell. A surrogate split type can be either 'continuous' if the cut is defined in the form Z < V for a variable Z and cut point V or 'categorical' if the cut is defined by whether Z takes a value in a set of categories.

SurrogateCutPredictor

An n-element cell array of the names of the variables used for surrogate splits in each node in tree, where n is the number of nodes in tree. Every element of SurrogateCutPredictor is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, SurrogateCutPredictor contains an empty cell.

SurrogatePredictorAssociation

An n-element cell array of the predictive measures of association for surrogate splits in tree, where n is the number of nodes in tree. For each node k, SurrogatePredictorAssociation{k} is a numeric vector. The length of SurrogatePredictorAssociation{k} is equal to the number of surrogate predictors found at this node. Every element of SurrogatePredictorAssociation{k} gives

the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is the order of variables in `SurrogateCutPredictor`. The optimal-split variable at this node does not appear. For nonbranch (leaf) nodes, `SurrogatePredictorAssociation` contains an empty cell.

`W`

The scaled weights, a vector with length `n`, the number of rows in X.

`X`

A matrix of predictor values. Each column of `X` represents one variable, and each row represents one observation.

`Y`

A numeric column vector with the same number of rows as `X`. Each entry in `Y` is the response to the data in the corresponding row of `X`.

Methods

compact	Compact regression tree
crossval	Cross-validated decision tree
cvloss	Regression error by cross validation
prune	Produce sequence of subtrees by pruning
resubLoss	Regression error by resubstitution
resubPredict	Predict resubstitution response of tree

Inherited Methods

loss	Regression error

surrogateAssociation	Mean predictive measure of association for surrogate splits in decision tree
predict	Predict response of regression tree
predictorImportance	Estimates of predictor importance
view	View tree

Copy Semantics

Value. To learn how value classes affect copy operations, see Copying Objects in the MATLAB documentation.

Examples

Construct a Regression Tree

Load the sample data.

```
load carsmall;
```

Construct a regression tree using the sample data.

```
tree = fitrtree([Weight, Cylinders],MPG,...
                'categoricalpredictors',2,'MinParentSize',20,...
                'PredictorNames',{'W','C'})
```

```
tree =

  RegressionTree
           PredictorNames: {'W'  'C'}
             ResponseName: 'Y'
        ResponseTransform: 'none'
    CategoricalPredictors: 2
          NumObservations: 94
```

Predict the mileage of 4,000-pound cars with 4, 6, and 8 cylinders.

```
mileage4K = predict(tree,[4000 4; 4000 6; 4000 8])
```

```
mileage4K =

   19.2778
   19.2778
   14.3889
```

- "Classification Trees and Regression Trees" on page 16-33

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`RegressionEnsemble` | `predict` | `ClassificationTree` | `fitrtree` | `CompactRegressionTree`

regstats

Regression diagnostics

Syntax

```
regstats(y,X,model)
stats = regstats(...)
stats = regstats(y,X,model,whichstats)
```

Description

`regstats(y,X,model)` performs a multilinear regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses.

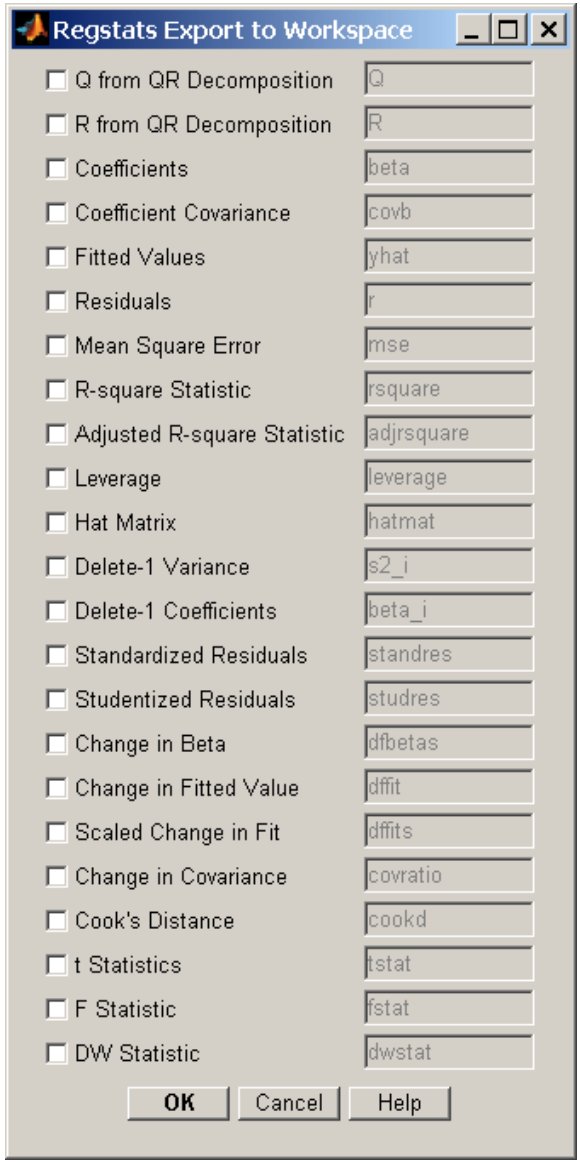
Note: By default, `regstats` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`.

The optional input *`model`* controls the regression model. By default, `regstats` uses a linear additive model with a constant term. *`model`* can be any one of the following strings:

- `'linear'` — Constant and linear terms (the default)
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

Alternatively, `model` can be a matrix of model terms accepted by the `x2fx` function. See `x2fx` for a description of this matrix and for a description of the order in which terms appear. You can use this matrix to specify other models including ones without a constant term.

With this syntax, the function displays a graphical user interface (GUI) with a list of diagnostic statistics, as shown in the following figure.



When you select check boxes corresponding to the statistics you want to compute and click **OK**, `regstats` returns the selected statistics to the MATLAB workspace. The names of the workspace variables are displayed on the right-hand side of the interface.

You can change the name of the workspace variable to any valid MATLAB variable name.

`stats = regstats(...)` creates the structure `stats`, whose fields contain all of the diagnostic statistics for the regression. This syntax does not open the GUI. The fields of `stats` are listed in the following table.

Field	Description
`Q`	Q from the QR decomposition of the design matrix
`R`	R from the QR decomposition of the design matrix
`beta`	Regression coefficients
`covb`	Covariance of regression coefficients
`yhat`	Fitted values of the response data
`r`	Residuals
`mse`	Mean squared error
`rsquare`	R^2 statistic
`adjrsquare`	Adjusted R^2 statistic
`leverage`	Leverage
`hatmat`	Hat matrix
`s2_i`	Delete-1 variance
`beta_i`	Delete-1 coefficients
`standres`	Standardized residuals
`studres`	Studentized residuals
`dfbetas`	Scaled change in regression coefficients
`dffit`	Change in fitted values
`dffits`	Scaled change in fitted values
`covratio`	Change in covariance
`cookd`	Cook's distance
`tstat`	t statistics and p-values for coefficients
`fstat`	F statistic and p-value
`dwstat`	Durbin-Watson statistic and p-value

Note that the fields names of `stats` correspond to the names of the variables returned to the MATLAB workspace when you use the GUI. For example, `stats.beta` corresponds to the variable `beta` that is returned when you select **Coefficients** in the GUI and click **OK**.

`stats = regstats(y,X,model,whichstats)` returns only the statistics that you specify in *`whichstats`*. *`whichstats`* can be a single string such as `'leverage'` or a cell array of strings such as `{'leverage' 'standres' 'studres'}`. Set *`whichstats`* to `'all'` to return all of the statistics.

Note: The F statistic is computed under the assumption that the model contains a constant term. It is not correct for models without a constant. The R^2 statistic can be negative for models without a constant, which indicates that the model is not appropriate for the data.

Examples

Open the `regstats` GUI using data from `hald.mat`:

```
load hald
regstats(heat,ingredients,'linear');
```

Select **Fitted Values** and **Residuals** in the GUI:

Click **OK** to export the fitted values and residuals to the MATLAB workspace in variables named `yhat` and `r`, respectively.

You can create the same variables using the `stats` output, without opening the GUI:

```
whichstats = {'yhat','r'};
stats = regstats(heat,ingredients,'linear',whichstats);
yhat = stats.yhat;
r = stats.r;
```

References

[1] Belsley, D. A., E. Kuh, and R. E. Welsch. *Regression Diagnostics*. Hoboken, NJ: John Wiley & Sons, Inc., 1980.

[2] Chatterjee, S., and A. S. Hadi. "Influential Observations, High Leverage Points, and Outliers in Linear Regression." *Statistical Science*. Vol. 1, 1986, pp. 379–416.

[3] Cook, R. D., and S. Weisberg. *Residuals and Influence in Regression*. New York: Chapman & Hall/CRC Press, 1983.

[4] Goodall, C. R. "Computation Using the QR Decomposition." *Handbook in Statistics*. Vol. 9, Amsterdam: Elsevier/North-Holland, 1993.

See Also

`fitlm` | `LinearModel` | `stepwiselm`

regularize

Class: RegressionEnsemble

Find weights to minimize resubstitution error plus penalty term

Syntax

```
ens1 = regularize(ens)
ens1 = regularize(ens,Name,Value)
```

Description

`ens1 = regularize(ens)` finds optimal weights for learners in `ens` by lasso regularization. `regularize` returns a regression ensemble identical to `ens`, but with a populated `Regularization` property.

`ens1 = regularize(ens,Name,Value)` computes optimal weights with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble, created by `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'lambda'`

Vector of nonnegative regularization parameter values for lasso. For the default setting of `lambda`, `regularize` calculates the smallest value `lambda_max` for which all optimal

weights for learners are `0`. The default value of `lambda` is a vector including `0` and nine exponentially-spaced numbers from `lambda_max/1000` to `lambda_max`.

Default: `[0 logspace(log10(lambda_max/1000),log10(lambda_max),9)]`

`'npass'`

Maximal number of passes for lasso optimization, a positive integer.

Default: `10`

`'reltol'`

Relative tolerance on the regularized loss for lasso, a numeric positive scalar.

Default: `1e-3`

`'verbose'`

Verbosity level, either `0` or `1`. When set to `1`, `regularize` displays more information as it runs.

Default: `0`

Output Arguments

`ens1`

A regression ensemble. Usually you set `ens1` to the same name as ens.

Definitions

Lasso

The lasso algorithm finds an optimal set of learner weights α_t that minimize

$$\sum_{n=1}^{N} w_n g\left(\left(\sum_{t=1}^{T}\alpha_t h_t(x_n)\right), y_n\right) + \lambda\sum_{t=1}^{T}|\alpha_t|.$$

Here

- $\lambda \geq 0$ is a parameter you provide, called the lasso parameter.
- h_t is a weak learner in the ensemble trained on N observations with predictors x_n, responses y_n, and weights w_n.
- $g(f,y) = (f - y)^2$ is the squared error.

Examples

Regularize an ensemble of bagged trees:

```
X = rand(2000,20);
Y = repmat(-1,2000,1);
Y(sum(X(:,1:5),2)>2.5) = 1;
bag = fitensemble(X,Y,'Bag',300,'Tree',...
    'type','regression');
bag = regularize(bag,'lambda',[0.001 0.1],'verbose',1);
```

`regularize` reports on its progress.

To see the resulting regularization structure:

```
bag.Regularization
ans =
            Method: 'Lasso'
    TrainedWeights: [300x2 double]
            Lambda: [1.0000e-003 0.1000]
 ResubstitutionMSE: [0.0616 0.0812]
    CombineWeights: @classreg.learning.combiner.WeightedSum
```

See how many learners in the regularized ensemble have positive weights (so would be included in a shrunken ensemble):

```
sum(bag.Regularization.TrainedWeights > 0)

ans =
   116    91
```

To shrink the ensemble using the weights from `Lambda = 0.1`:

```
cmp = shrink(bag,'weightcolumn',2)
```

```
cmp =

classreg.learning.regr.CompactRegressionEnsemble:
           PredictorNames: {1x20 cell}
    CategoricalPredictors: []
             ResponseName: 'Y'
        ResponseTransform: 'none'
                NumTrained: 91
```

There are 91 members in the regularized ensemble, which is less than 1/3 of the original 300.

See Also

shrink | cvshrink | lasso

RegularizationValue property

Class: gmdistribution

Value of `'Regularize'` parameter

Description

The value of the parameter `'Regularize'`.

Note: This property applies only to `gmdistribution` objects constructed with `fitgmdist`.

---

relieff

Importance of attributes (predictors) using ReliefF algorithm

Syntax

```
[RANKED,WEIGHT] = relieff(X,Y,K)
[RANKED,WEIGHT] = relieff(X,Y,K,'PARAM1',val1,'PARAM2',val2,...)
```

Description

`[RANKED,WEIGHT] = relieff(X,Y,K)` computes ranks and weights of attributes (predictors) for input data matrix `X` and response vector `Y` using the ReliefF algorithm for classification or RReliefF for regression with `K` nearest neighbors. For classification, `relieff` uses `K` nearest neighbors per class. `RANKED` are indices of columns in `X` ordered by attribute importance, meaning `RANKED(1)` is the index of the most important predictor. `WEIGHT` are attribute weights ranging from `-1` to `1` with large positive weights assigned to important attributes.

If `Y` is numeric, `relieff` by default performs RReliefF analysis for regression. If `Y` is categorical, logical, a character array, or a cell array of strings, `relieff` by default performs ReliefF analysis for classification.

Attribute ranks and weights computed by `relieff` usually depend on `K`. If you set `K` to 1, the estimates computed by `relieff` can be unreliable for noisy data. If you set `K` to a value comparable with the number of observations (rows) in `X`, `relieff` can fail to find important attributes. You can start with `K = 10` and investigate the stability and reliability of `relieff` ranks and weights for various values of `K`.

`[RANKED,WEIGHT] = relieff(X,Y,K,'PARAM1',val1,'PARAM2',val2,...)` specifies optional parameter name/value pairs.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'method'`

Either `'regression'` (default if `Y` is numeric) or `'classification'` (default if `Y` is not numeric).

`'prior'`

Prior probabilities for each class, specified as a string (`'empirical'` or `'uniform'`) or as a vector (one value for each distinct group name) or as a structure `S` with two fields:

- `S.group` containing the group names as a categorical variable, character array, or cell array of strings
- `S.prob` containing a vector of corresponding probabilities

If the input value is `'empirical'` (default), class probabilities are determined from class frequencies in `Y`. If the input value is `'uniform'`, all class probabilities are set equal.

`'updates'`

Number of observations to select at random for computing the weight of every attribute. By default all observations are used.

`'categoricalx'`

`'on'` or `'off'`, `'off'` by default. If `'on'`, treat all predictors in `X` as categorical. If `'off'`, treat all predictors in `X` as numerical. You cannot mix numerical and categorical predictors.

`'sigma'`

Distance scaling factor. For observation *i*, influence on the attribute weight from its nearest neighbor *j* is multiplied by exp((-`rank`(*i*,*j*)/`sigma`)^2), where `rank`(*i*,*j*) is the position of *j* in the list of nearest neighbors of *i* sorted by distance in the ascending order. Default is `Inf` (all nearest neighbors have the same influence) for classification and 50 for regression.

Examples

Rank Predictors by Importance

Load the sample data.

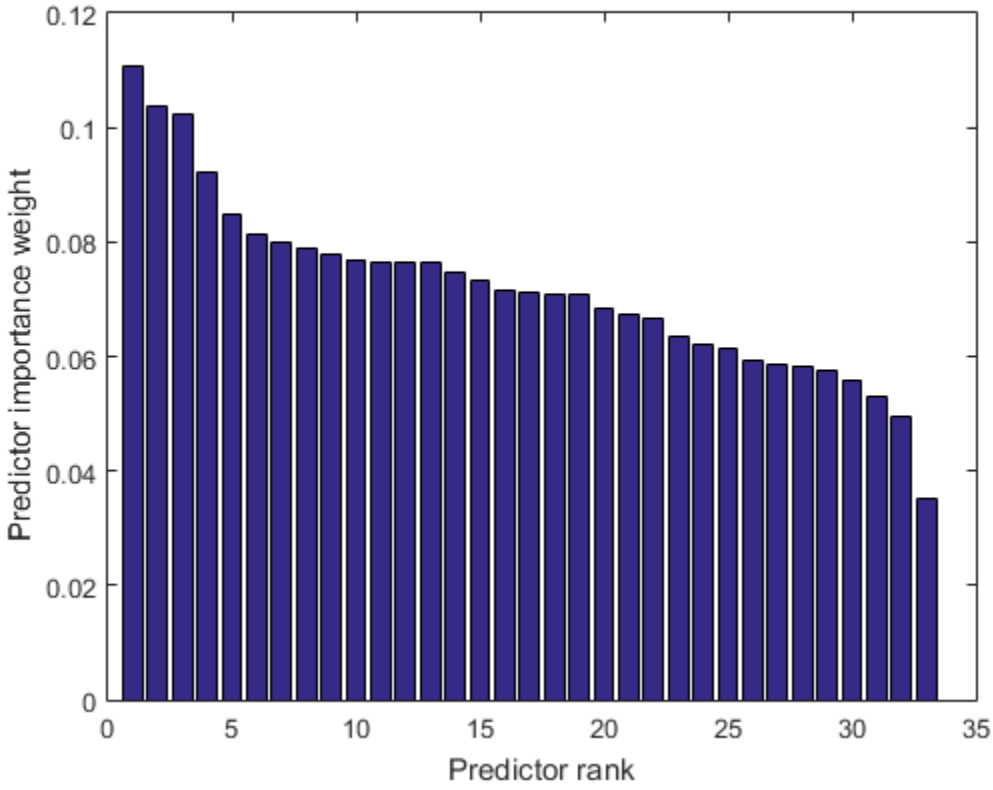
```
load ionosphere;
```

Rank the predictors based on importance.

```
[ranked,weights] = relieff(X,Y,10);
```

Create a bar plot of predictor importance weights.

```
bar(weights(ranked));
xlabel('Predictor rank');
ylabel('Predictor importance weight');
```



Determine the Important Predictors

Load the sample data.

```
load fisheriris
```

Find the important predictors.

```
[ranked,weight] = relieff(meas,species,10)
```

```
ranked =

     4     3     1     2
```

```
weight =

    0.1399    0.1226    0.3590    0.3754
```

The fourth predictor is the most important, and the second predictor is the least important.

References

[1] Kononenko, I., Simec, E., & Robnik-Sikonja, M. (1997). *Overcoming the myopia of inductive learning algorithms with RELIEFF*. Retrieved from CiteSeerX: http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.56.4740

[2] Robnik-Sikonja, M., & Kononenko, I. (1997). *An adaptation of Relief for attribute estimation in regression*. Retrieved from CiteSeerX: http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.34.8381

[3] Robnik-Sikonja, M., & Kononenko, I. (2003). *Theoretical and empirical analysis of ReliefF and RReliefF*. Machine Learning , 53, 23–69.

See Also

`knnsearch` | `pdist2`

removeLearners

Class: CompactClassificationEnsemble

Remove members of compact classification ensemble

Syntax

```
cens1 = removeLearners(cens,idx)
```

Description

`cens1 = removeLearners(cens,idx)` creates a compact classification ensemble identical to `cens` only without the ensemble members in the `idx` vector.

Tips

- Typically, set `cens1` equal to `cens` to retain just one ensemble.
- Removing learners reduces the memory used by the ensemble and speeds up its predictions.

Input Arguments

`cens`

Compact classification ensemble, constructed with `compact`.

`idx`

Vector of positive integers with entries from `1` to `cens.NumTrained`, where `cens.NumTrained` is the number of members in `cens`. `cens1` contains all members of `cens` except those with indices in `idx`.

Typically, you set `idx = j:cens.NumTrained` for some positive integer `j`.

Output Arguments

`cens1`

Compact classification ensemble, identical to `cens` except `cens1` does not contain those members of `cens` with indices in `idx`.

Examples

Remove Learners from an Ensemble

Create a compact classification ensemble. Compact it further by removing members of the ensemble.

Create a compact classification ensemble for the `ionosphere` data.

```
load ionosphere
ens = fitensemble(X,Y,'AdaBoostM1',100,'Tree');
cens = compact(ens);
```

Remove the last 50 members of the ensemble.

```
idx = cens.NumTrained-49:cens.NumTrained;
cens1 = removeLearners(cens,idx);
```

- “Classification with Imbalanced Data” on page 16-84

See Also

`CompactClassificationEnsemble`

removeLearners

Class: CompactRegressionEnsemble

Remove members of compact regression ensemble

Syntax

```
cens1 = removeLearners(cens,idx)
```

Description

`cens1 = removeLearners(cens,idx)` creates a compact regression ensemble identical to `cens` only without the ensemble members in the `idx` vector.

Tips

- Typically, set `cens1` equal to `cens` to retain just one ensemble.
- Removing learners reduces the memory used by the ensemble and speeds up its predictions.

Input Arguments

`cens`

Compact regression ensemble, constructed with `compact`.

`idx`

Vector of positive integers with entries from `1` to `cens.NumTrained`, where `cens.NumTrained` is the number of members in `cens`. `cens1` contains the members of `cens` except those with indices in `idx`.

Typically, you set `idx = j:cens.NumTrained` for some positive integer `j`.

Output Arguments

`cens1`

Compact regression ensemble, identical to `cens` except `cens1` does not contain members of `cens` with indices in `idx`.

Examples

Remove Learners from an Ensemble

Create a compact regression ensemble. Compact it further by removing members of the ensemble.

Create a compact regression ensemble for the `carsmall` data.

```
load carsmall
X = [Weight Cylinders];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree','categorical',2);
cens = compact(ens);
```

Remove the last 50 members of the ensemble.

```
idx = cens.NumTrained-49:cens.NumTrained;
cens1 = removeLearners(cens,idx);
```

See Also

`CompactRegressionEnsemble`

removeTerms

Class: GeneralizedLinearModel

Remove terms from generalized linear model

Syntax

```
mdl1 = removeTerms(mdl,terms)
```

Description

`mdl1 = removeTerms(mdl,terms)` returns a linear model the same as `mdl` but with fewer terms.

Input Arguments

`mdl`

Generalized linear model, as constructed by `fitglm` or `stepwiseglm`.

`terms`

Terms to remove from the `mdl` regression model. Specify as either a:

- Text string representing one or more terms to remove. For details, see "Wilkinson Notation" on page 22-4081.
- Row or rows in the terms matrix (see `modelspec` in `fitglm`). For example, if there are three variables `A`, `B`, and `C`:

```
[0 0 0] represents a constant term or intercept
[0 1 0] represents B; equivalently, A^0 * B^1 * C^0
[1 0 1] represents A*C
[2 0 0] represents A^2
[0 1 2] represents B*(C^2)
```

Output Arguments

`mdl1`

Generalized linear model, the same as `mdl` but without the terms given in `terms`. You can set `mdl1` equal to `mdl` to overwrite `mdl`.

Definitions

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

For details, see Wilkinson and Rogers [1].

Examples

Remove a Term from a Generalized Linear Regression Model

This example makes a model using two predictors, then removes one.

Generate artificial data for the model, Poisson random numbers with two underlying predictors `X(1)` and `X(2)`.

```
rng('default') % for reproducibility
rndvars = randn(100,2);
X = [2+rndvars(:,1),rndvars(:,2)];
mu = exp(1 + X*[1;2]);
y = poissrnd(mu);
```

Create a generalized linear regression model of Poisson data.

```
mdl = fitglm(X,y,'y ~ x1 + x2','distr','poisson')
```

```
mdl =


Generalized Linear regression model:
    log(y) ~ 1 + x1 + x2
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE           tStat     pValue
    (Intercept)    1.0405       0.022122    47.034    0
    x1             0.9968       0.003362    296.49    0
    x2              1.987      0.0063433    313.24    0


100 observations, 97 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 2.95e+05, p-value = 0
```

Remove the second predictor from the model.

```
mdl1 = removeTerms(mdl,'x2')
```

```
mdl1 =
```

```
Generalized Linear regression model:
    log(y) ~ 1 + x1
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE           tStat     pValue
    (Intercept)    2.7784       0.014043    197.85    0
    x1             1.1732      0.0033653     348.6    0


100 observations, 98 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 1.25e+05, p-value = 0
```

- "Plots to Understand Predictor Effects and How to Modify a Model" on page 10-30
- "Generalized Linear Model Workflow" on page 10-39

References

[1] Wilkinson, G. N., and C. E. Rogers. *Symbolic description of factorial models for analysis of variance.* J. Royal Statistics Society 22, pp. 392–399, 1973.

Alternatives

`step` adds or removes terms from a model using a greedy one-step algorithm.

See Also

`addTerms` | `GeneralizedLinearModel` | `step` | `stepwiseglm`

More About

- "Generalized Linear Models" on page 10-12

removeTerms

Class: LinearModel

Remove terms from linear model

Syntax

```
mdl1 = removeTerms(mdl,terms)
```

Description

`mdl1 = removeTerms(mdl,terms)` returns a linear model the same as `mdl` but with terms removed.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

`terms`

Terms to remove from the `mdl` regression model. Specify as either a:

- Text string representing one or more terms to remove. For details, see "Wilkinson Notation" on page 22-4085.
- Row or rows in the terms matrix (see `modelspec` in `fitlm`). For example, if there are three variables `A`, `B`, and `C`:

```
[0 0 0] represents a constant term or intercept
[0 1 0] represents B; equivalently, A^0 * B^1 * C^0
[1 0 1] represents A*C
[2 0 0] represents A^2
[0 1 2] represents B*(C^2)
```

Output Arguments

`mdl1`

Linear model, the same as `mdl` but with `terms` removed. You can set `mdl1` equal to `mdl` to overwrite `mdl`.

Definitions

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

For details, see Wilkinson and Rogers [1].

Examples

Remove Terms from Model

Construct a default linear model of the Hald data. Remove terms with high p-values.

Load the data.

```
load hald
X = ingredients; % predictor variables
y = heat; % response
```

Fit a default linear model to the data.

```
mdl = fitlm(X,y)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1 + x2 + x3 + x4

Estimated Coefficients:
                   Estimate    SE         tStat       pValue
    (Intercept)      62.405     70.071      0.8906     0.39913
    x1               1.5511    0.74477      2.0827    0.070822
    x2              0.51017    0.72379     0.70486      0.5009
    x3              0.10191    0.75471     0.13503     0.89592
    x4             -0.14406    0.70905    -0.20317     0.84407

Number of observations: 13, Error degrees of freedom: 8
Root Mean Squared Error: 2.45
R-squared: 0.982,  Adjusted R-Squared 0.974
F-statistic vs. constant model: 111, p-value = 4.76e-07
```

Remove the `x3` and `x4` terms because their p-values are so high.

```
terms = 'x3 + x4'; % terms to remove
mdl1 = removeTerms(mdl, terms)
```

```
mdl1 =


Linear regression model:
    y ~ 1 + x1 + x2
```

```
Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)     52.577       2.2862    22.998    5.4566e-10
    x1               1.4683      0.1213    12.105    2.6922e-07
    x2              0.66225     0.045855    14.442     5.029e-08


Number of observations: 13, Error degrees of freedom: 10
Root Mean Squared Error: 2.41
R-squared: 0.979,  Adjusted R-Squared 0.974
F-statistic vs. constant model: 230, p-value = 4.41e-09
```

The new model has the same adjusted R-Squared value (0.974) as the previous model, meaning it is about as good a fit. All the terms in the new model have extremely low *p*-values.

- "Change Models" on page 9-35

References

[1] Wilkinson, G. N., and C. E. Rogers. *Symbolic description of factorial models for analysis of variance.* J. Royal Statistics Society 22, pp. 392–399, 1973.

Alternatives

Use `stepwiselm` to select a model from a starting model, continuing until no single step is beneficial.

Use `addTerms` to add particular terms.

Use `step` to optimally improve the model by adding or removing terms.

See Also

`addTerms` | `LinearModel` | `step` | `stepwiselm`

How To

- "Linear Regression" on page 9-11

reorderlevels

Reorder levels of nominal or ordinal arrays

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
B = reorderlevels(A,newlevels)
```

Description

`B = reorderlevels(A,newlevels)` returns a `nominal` or `ordinal` array object the same as A but with levels in the new order specified by newlevels.

For ordinal arrays, the order of the levels has significance for relational operators, minimum and maximum, and for sorting.

Examples

- “Reorder Category Levels” on page 2-11
- “Sort Ordinal Arrays” on page 2-40

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

`newlevels` — New order of levels

cell array of strings | 2-D character matrix

New order of levels, specified as a cell array of strings or 2-D character matrix. newlevels must be a reordering of the labels returned by `getlabels`.

Data Types: `char` | `cell`

Output Arguments

`B` — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, returned as a `nominal` or `ordinal` array object.

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`addlevels` | `droplevels` | `getlabels` | `nominal` | `ordinal` | `reorderlevels`

repartition

Class: cvpartition

Repartition data for cross-validation

Syntax

```
cnew = repartition(c)
```

Description

`cnew = repartition(c)` constructs an object `cnew` of the `cvpartition` class defining a random partition of the same type as `c`, where `c` is also an object of the `cvpartition` class.

Repartitioning is useful for Monte-Carlo repetitions of cross-validation analyses. `repartition` is called by `crossval` when the `'mcreps'` parameter is specified.

Examples

Partition and repartition 100 observations for 3-fold cross-validation:

```
c = cvpartition(100,'kfold',3)
c =
K-fold cross validation partition
             N: 100
   NumTestSets: 3
     TrainSize: 67  66  67
      TestSize: 33  34  33

cnew = repartition(c)
cnew =
K-fold cross validation partition
             N: 100
   NumTestSets: 3
     TrainSize: 67  66  67
      TestSize: 33  34  33
```

Check for equality of the test data in the first fold:

```
isequal(test(c,1),test(cnew,1))
ans =
     0
```

See Also

`cvpartition`

RepeatedMeasuresModel class

Repeated measures model class

Description

A `RepeatedMeasuresModel` object represents a model fitted to data with multiple measurements per subject. The object comprises data, fitted coefficients, covariance parameters, design matrix, error degrees of freedom, and between- and within-subjects factor names for a repeated measures model. You can predict model responses using the `predict` method and generate random data at new design points using the `random` method.

Construction

You can fit a repeated measures model using `fitrm(t,modelspec)`.

Input Arguments

`t` — Input data

table

Input data, which includes the values of the response variables and the between-subject factors to use as predictors in the repeated measures model, specified as a table.

Data Types: `table`

`modelspec` — Formula for model specification

string of the form `'y1-yk ~ terms'`

Formula for model specification, specified as a string of the form `'y1-yk ~ terms'`. Specify the terms using Wilkinson notation. `fitrm` treats the variables used in model terms as categorical if they are categorical (nominal or ordinal), logical, char arrays, or a cell array of strings.

Example: `'y1-y4 ~ x1 + x2 * x3'`

Properties

`BetweenDesign` — Design for between-subject factors
table

Design for between-subject factors and values of repeated measures, stored as a table.

Data Types: `table`

`BetweenModel` — Model for between-subjects factors
string

Model for between-subjects factors, stored as a string. This string is the text representation to the right of the tilde in the model specification you provide when fitting the repeated measures model using `fitrm`.

Data Types: `char`

`BetweenFactorNames` — Names of variables used as between-subject factors
cell array of strings

Names of variables used as between-subject factors in the repeated measures model, rm, stored as a cell array of strings.

Data Types: `cell`

`ResponseNames` — Names of variables used as response variables
cell array of strings

Names of variables used as response variables in the repeated measures model, rm, stored as a cell array of strings.

Data Types: `cell`

`WithinDesign` — Values of within-subject factors
table

Values of the within-subject factors, stored as a table.

Data Types: `table`

`WithinModel` — Model for within-subjects factors
string

Model for within-subjects factors, stored as a string.

Data Types: `char`

`WithinFactorNames` — Names of within-subject factors

cell array of strings

Names of the within-subject factors, stored as a cell array of strings.

Data Types: `cell`

`Coefficients` — Values of estimated coefficients

table

Values of the estimated coefficients for fitting the repeated measures as a function of the terms in the between-subjects model, stored as a table.

`fitrm'` defines the coefficients for a categorical term using 'effects' coding, which means coefficients sum to 0. There is one coefficient for each level except the first. The implied coefficient for the first level is the sum of the other coefficients for the term.

You can display the coefficient values as a matrix rather than a table using `coef = r.Coefficients{:,:}`.

You can display marginal means for all levels using the `margmean` method.

Data Types: `table`

`Covariance` — Estimated response covariances

table

Estimated response covariances, that is, covariance of the repeated measures, stored as a table. `fitrm` computes the covariances around the mean returned by the fitted repeated measures model rm.

You can display the covariance values as a matrix rather than a table using `coef = r.Covariance{:,:}`.

Data Types: `table`

`DFE` — Error degrees of freedom

scalar value

Error degrees of freedom, stored as a scalar value. `DFE` is the number of observations minus the number of estimated coefficients in the between-subjects model.

Data Types: `double`

Methods

anova	Analysis of variance for between-subject effects
epsilon	Epsilon adjustment for repeated measures anova
grpstats	Compute descriptive statistics of repeated measures data by group
manova	Multivariate analysis of variance
margmean	Estimate marginal means
mauchly	Mauchly's test for sphericity
multcompare	Multiple comparison of estimated marginal means
plot	Plot data with optional grouping
plotprofile	Plot expected marginal means with optional grouping
predict	Compute predicted values given predictor values
random	Generate new random response values given predictor values
ranova	Repeated measures analysis of variance

Definitions

Wilkinson Notation

Wilkinson notation describes the factors present in models. It does not describe the multipliers (coefficients) of those factors.

Use these rules to specify the responses in modelspec.

Wilkinson Notation	Description
`Y1,Y2,Y3`	Specific list of variables
`Y1-Y5`	All table variables from `Y1` through `Y5`

Use these rules to specify terms in modelspec.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`X^k`, where `k` is a positive integer	`X`, X^2, ..., X^k
`X1 + X2`	`X1`, `X2`
`X1*X2`	`X1`, `X2`, `X1*X2`
`X1:X2`	`X1*X2` only
`-X2`	Do not include `X2`
`X1*X2 + X3`	`X1`, `X2`, `X3`, `X1*X2`
`X1 + X2 + X3 + X1:X2`	`X1`, `X2`, `X3`, `X1*X2`
`X1*X2*X3 - X1:X2:X3`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`, `X2*X3`
`X1*(X2 + X3)`	`X1`, `X2`, `X3`, `X1*X2`, `X1*X3`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Examples

Fit a Repeated Measures Model

Load the sample data.

```
load fisheriris
```

The column vector, `species`, consists of iris flowers of three different species: setosa, versicolor, virginica. The double matrix `meas` consists of four types of measurements on the flowers: the length and width of sepals and petals in centimeters, respectively.

Store the data in a table array.

```
t = table(species,meas(:,1),meas(:,2),meas(:,3),meas(:,4),...
'VariableNames',{'species','meas1','meas2','meas3','meas4'});
Meas = table([1 2 3 4]','VariableNames',{'Measurements'});
```

Fit a repeated measures model, where the measurements are the responses and the species is the predictor variable.

```
rm = fitrm(t,'meas1-meas4~species','WithinDesign',Meas)
```

```
rm =

  RepeatedMeasuresModel with properties:

   Between Subjects:
         BetweenDesign: [150x5 table]
         ResponseNames: {'meas1'  'meas2'  'meas3'  'meas4'}
    BetweenFactorNames: {'species'}
          BetweenModel: '1 + species'

   Within Subjects:
         WithinDesign: [4x1 table]
    WithinFactorNames: {'Measurements'}
          WithinModel: 'separatemeans'

   Estimates:
    Coefficients: [3x4 table]
      Covariance: [4x4 table]
```

Display the coefficients.

```
rm.Coefficients
```

```
ans =

                          meas1       meas2       meas3       meas4
                        ________    ________    ________    ________
```

```
(Intercept)             5.8433      3.0573     3.758      1.1993
species_setosa         -0.83733     0.37067    -2.296     -0.95333
species_versicolor     0.092667    -0.28733     0.502     0.12667
```

`fitrm` uses the `'effects'` contrasts, which means that the coefficients sum to 0. The `rm.DesignMatrix` has one column of 1s for the intercept, and two other columns `species_setosa` and `species_versicolor`, which are as follows:

$$\text{species\_setosa} = \begin{cases} 1, & \textit{if setosa} \\ 0, & \textit{if versicolor} \\ -1, & \textit{if virginica} \end{cases} \quad \text{and} \quad \text{species\_versicolor} = \begin{cases} 0, & \textit{if setosa} \\ 1, & \textit{if versicolor} \\ -1, & \textit{if virginica} \end{cases}$$

Display the covariance matrix.

```
rm.Covariance
```

```
ans =

              meas1        meas2        meas3        meas4
            ________    _________    _________    _________

    meas1     0.26501     0.092721     0.16751     0.038401
    meas2    0.092721      0.11539    0.055244      0.03271
    meas3     0.16751     0.055244     0.18519     0.042665
    meas4    0.038401      0.03271    0.042665     0.041882
```

Display the error degrees of freedom.

```
rm.DFE
```

```
ans =

   147
```

The error degrees of freedom is the number of observations minus the number of estimated coefficients in the between-subjects model, e.g. 150 – 3 = 147.

See Also

`fitrm`

More About

- Class Attributes

- Property Attributes

replacedata

Class: dataset

Replace dataset variables

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
B = replacedata(A,X)
B = replacedata(A,X,vars)
B = replacedata(A,fun)
B = replacedata(A,fun,vars)
```

Description

`B = replacedata(A,X)` creates a dataset array `B` with the same variables as the dataset array `A`, but with the data for those variables replaced by the data in the array `X`. `replacedata` creates each variable in `B` using one or more columns from `X`, in order. `X` must have as many columns as the total number of columns in all of the variables in `A`, and as many rows as `A` has observations.

`B = replacedata(A,X,vars)` creates a dataset array `B` with the same variables as the dataset array `A`, but with the data for the variables specified in `vars` replaced by the data in the array `X`. The remaining variables in `B` are copies of the corresponding variables in `A`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. Each variable in `B` has as many columns as the corresponding variable in `A`. `X` must have as many columns as the total number of columns in all the variables specified in `vars`.

`B = replacedata(A,fun)` or `B = replacedata(A,fun,vars)` creates a dataset array `B` by applying the function `fun` to the values in `A`'s variables. `replacedata` first

horizontally concatenates A's variables into a single array, then applies the function `fun`. The specified variables in A must have types and sizes compatible with the concatenation. `fun` is a function handle that accepts a single input array and returns an array with the same number of rows and columns as the input.

Examples

```
data = dataset({rand(3,3),'Var1','Var2','Var3'})

% Use ZSCORE to normalize each variable in a dataset array
% separately, by explicitly extracting and transforming the
% data, and then replacing it.
X = double(data);
X = zscore(X);
data = replacedata(data,X)

% Equivalently, provide a handle to ZSCORE.
data = replacedata(data,@zscore)

% Use ZSCORE to normalize each observation in a dataset
% array separately by creating an anonymous function.
data = replacedata(data,@(x) zscore(x,[],2))
```

See Also

dataset

replaceWithMissing

Class: dataset

Insert missing data indicators into a dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds2 = replaceWithMissing(ds,Name,Value)
```

Description

`ds2 = replaceWithMissing(ds,Name,Value)` replaces specified values in a dataset array with standard missing data indicators using options specified by one or more Name,Value pair arguments. Use `replaceWithMissing` to specify:

- Which numeric missing value indicators to replace with `NaN`.
- Which string missing value indicators to replace with an empty string.
- Which categorical levels to replace with `<undefined>`.

Input Arguments

`ds`

`dataset` array.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'NumericValues'`

Vector of numeric values that `replaceWithMissing` replaces with `NaN`.

`'CategoricalLevels'`

String or cell array of strings naming the categorical levels that `replaceWithMissing` replaces with `<undefined>`.

`'Strings'`

String or cell array of strings containing the strings that `replaceWithMissing` replaces with the empty string, `''`.

`'DataVars'`

Specified set of variables in ds for which `replaceWithMissing` replaces values. You can specify a positive integer or vector of positive integers indicating the variable column numbers, a variable name or a cell array of variables names, or a logical vector indicating which variables to replace missing values in.

Default: All variables in ds.

Output Arguments

`ds2`

`dataset` array that has the specified missing value indicators, in the specified variables of ds, replaced with standard missing value indicators.

Examples

Replace Nonstandard Missing Value Indicators

Replace nonstandard missing value indicators with standard missing value indicators.

Replace numeric missing values coded `99` with `NaN`, and string missing values coded `'.'` with the empty string.

```
ds = replaceWithMissing(ds,'NumericValues',99,'Strings','.');
```

- “Clean Messy and Missing Data” on page 2-113

See Also

`dataset | ismissing`

More About

- “Dataset Arrays” on page 2-132

reset

Class: qrandstream

Reset state

Syntax

```
reset(q)
```

Description

`reset(q)` resets the state of the quasi-random number stream `q` of the `qrandstream` class back to its initial state, `1`. Subsequent points drawn from the stream will be the same as those drawn from a new stream. The command is equivalent to `q.State = 1`.

Examples

Use `qrandstream` to construct a 3-D Halton stream, based on a point set that skips the first 1000 values and then retains every 101st point:

```
q = qrandstream('halton',3,'Skip',1e3,'Leap',1e2)
q =
   Halton quasi-random stream in 3 dimensions
   Point set properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none

nextIdx = q.State
nextIdx =
     1
```

Use `qrand` to generate two samples of size four:

```
X1 = qrand(q,4)
X1 =
    0.0928    0.3475    0.0051
```

```
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
nextIdx = q.State
nextIdx =
     5

X2 = qrand(q,4)
X2 =
    0.2446    0.0238    0.8102
    0.5298    0.7540    0.0438
    0.3843    0.5112    0.2758
    0.8335    0.2245    0.4694
nextIdx = q.State
nextIdx =
     9
```

Use `reset` to reset the stream, then generate another sample:

```
reset(q)
nextIdx = q.State
nextIdx =
     1

X = qrand(q,4)
X =
    0.0928    0.3475    0.0051
    0.6958    0.2035    0.2371
    0.3013    0.8496    0.4307
    0.9087    0.5629    0.6166
```

See Also

`qrandstream` | `qrand`

residuals

Class: GeneralizedLinearMixedModel

Residuals of fitted generalized linear mixed-effects model

Syntax

```
r = residuals(glme)
r = residuals(glme,Name,Value)
```

Description

`r = residuals(glme)` returns the raw conditional residuals from a fitted generalized linear mixed-effects model glme.

`r = residuals(glme,Name,Value)` returns the residuals using additional options specified by one or more Name,Value pair arguments. For example, you can specify to return Pearson residuals for the model.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

'Conditional' — Indicator for conditional residuals

`true` (default) | `false`

Indicator for conditional residuals, specified as the comma-separated pair consisting of `'Conditional'` and one of the following.

`true`	Contributions from both fixed effects and random effects (conditional)
`false`	Contribution from only fixed effects (marginal)

Conditional residuals include contributions from both fixed- and random-effects predictors. Marginal residuals include contribution from only fixed effects. To obtain marginal residual values, `residuals` computes the conditional mean of the response with the empirical Bayes predictor vector of random effects, b, set to 0.

Example: `'Conditional',false`

'ResidualType' — Residual type

`'raw'` (default) | `'Pearson'`

Residual type, specified as the comma-separated pair consisting of `'ResidualType'` and one of the following.

Residual Type	Conditional	Marginal
`'raw'`	$r_{ci} = y_i - g^{-1}\left(x_i^T\hat{\beta} + z_i^T\hat{b}\right)$	$r_{mi} = y_i - g^{-1}\left(x_i^T\hat{\beta} + \delta_i\right)$
`'Pearson'`	$r_{ci}^{pearson} = \frac{r_{ci}}{\sqrt{\frac{\widehat{\sigma^2}}{w_i}v_i\left(\mu_i\left(\hat{\beta},\hat{b}\right)\right)}}$	$r_{mi}^{pearson} = \frac{r_{mi}}{\sqrt{\frac{\widehat{\sigma^2}}{w_i}v_i\left(\mu_i\left(\hat{\beta},0\right)\right)}}$

In each of these equations:

- y_i is the ith element of the n-by-1 response vector, y, where $i = 1, ..., n$.
- g^{-1} is the inverse link function for the model.
- x_i^T is the ith row of the fixed-effects design matrix X.

- z_i^T is the ith row of the random-effects design matrix Z.
- δ_i is the ith offset value.
- σ^2 is the dispersion parameter.
- w_i is the ith observation weight.
- v_i is the variance term for the ith observation.
- μ_i is the mean of the response for the ith observation.
- $\hat{\beta}$ and $\hat{b}$ are estimated values of β and b.

Raw residuals from a generalized linear mixed-effects model have nonconstant variance. Pearson residuals are expected to have an approximately constant variance, and are generally used for analysis.

Example: `'ResidualType','Pearson'`

Output Arguments

r — Residuals

n-by-1 vector

Residuals of the fitted generalized linear mixed-effects model glme returned as an n-by-1 vector, where n is the number of observations.

Examples

Plot Residuals Versus Fitted Values

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The

company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).

- μ_{ij} is the mean number of defects corresponding to factory i during batch j.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Generate the conditional Pearson residuals and the conditional fitted values from the model.

```
r = residuals(glme,'ResidualType','Pearson');
mufit = fitted(glme);
```

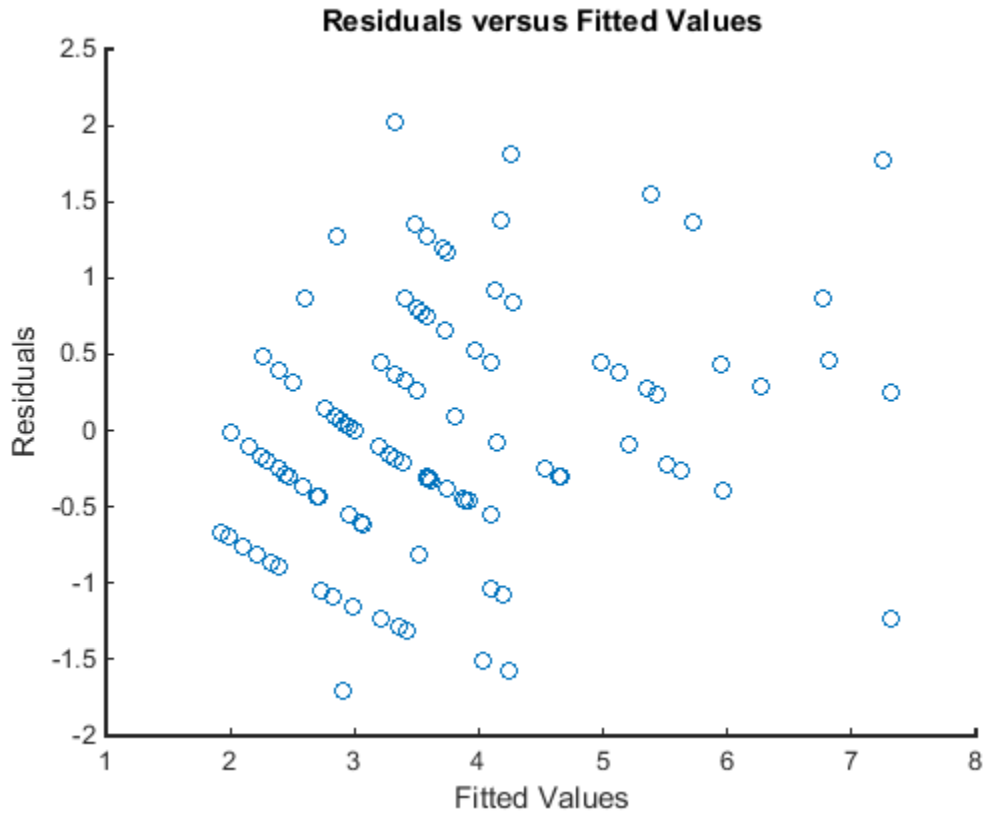
Display the first ten rows of the Pearson residuals.

```
r(1:10)
```

```
ans =

    0.4530
    0.4339
    0.3833
   -0.2653
    0.2811
   -0.0935
   -0.2984
   -0.2509
    1.5547
   -0.3027
```

Plot the Pearson residuals versus the fitted values, to check for signs of nonconstant variance among the residuals (heteroscedasticity).

```
figure
scatter(mufit,r)
title('Residuals versus Fitted Values')
xlabel('Fitted Values')
ylabel('Residuals')
```



The plot does not show a systematic dependence on the fitted values, so there are no signs of nonconstant variance among the residuals.

See Also

`GeneralizedLinearMixedModel` | `designMatrix` | `fitted` | `response`

residuals

Class: LinearMixedModel

Residuals of fitted linear mixed-effects model

Syntax

```
R = residuals(lme)
R = residuals(lme,Name,Value)
```

Description

`R = residuals(lme)` returns the raw conditional residuals from a fitted linear mixed-effects model `lme`.

`R = residuals(lme,Name,Value)` returns the residuals from the linear mixed-effects model `lme` with additional options specified by one or more Name,Value pair arguments.

For example, you can specify Pearson or standardized residuals, or residuals with contributions from only fixed effects.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Conditional'` — Indicator for conditional residuals

`True` (default) | `False`

Indicator for conditional residuals, specified as the comma-separated pair consisting of `'Conditional'` and one of the following.

`True`	Contribution from both fixed effects and random effects (conditional)
`False`	Contribution from only fixed effects (marginal)

Example: `'Conditional','False'`

`'ResidualType'` — Residual type

`'Raw'` (default) | `'Pearson'` | `'Standardized'`

Residual type, specified by the comma-separated pair consisting of `ResidualType` and one of the following.

Residual Type	Conditional	Marginal
`'Raw'`	$r_i^C = \left[y - X\hat{\beta} - Z\hat{b} \right]_i$	$r_i^M = \left[y - X\hat{\beta} \right]_i$
`'Pearson'`	$pr_i^C = \frac{r_i^C}{\sqrt{\left[\widehat{Var}_{y,b}\left(y - X\beta\right.\right.}}$	$pr_i^M = \frac{r_i^M}{\sqrt{\left[\widehat{Var}_y \left(y - X\beta\right) \right]_{ii}}}$
`'Standardized'`	$st_i^C = \frac{r_i^C}{\sqrt{\left[\widehat{Var}_y \left(r^C\right) \right]_{ii}}}$	$st_i^M = \frac{r_i^M}{\sqrt{\left[\widehat{Var}_y \left(r^M\right) \right]_{ii}}}$

For more information on the conditional and marginal residuals and residual variances, see `Definitions` at the end of this page.

Example: `'ResidualType','Standardized'`

Output Arguments

R — Residuals

n-by-1 vector

Residuals of the fitted linear mixed-effects model lmereturned as an *n*-by-1 vector, where *n* is the number of observations.

Examples

Plot Residuals vs. Fitted Values

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over six 2-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

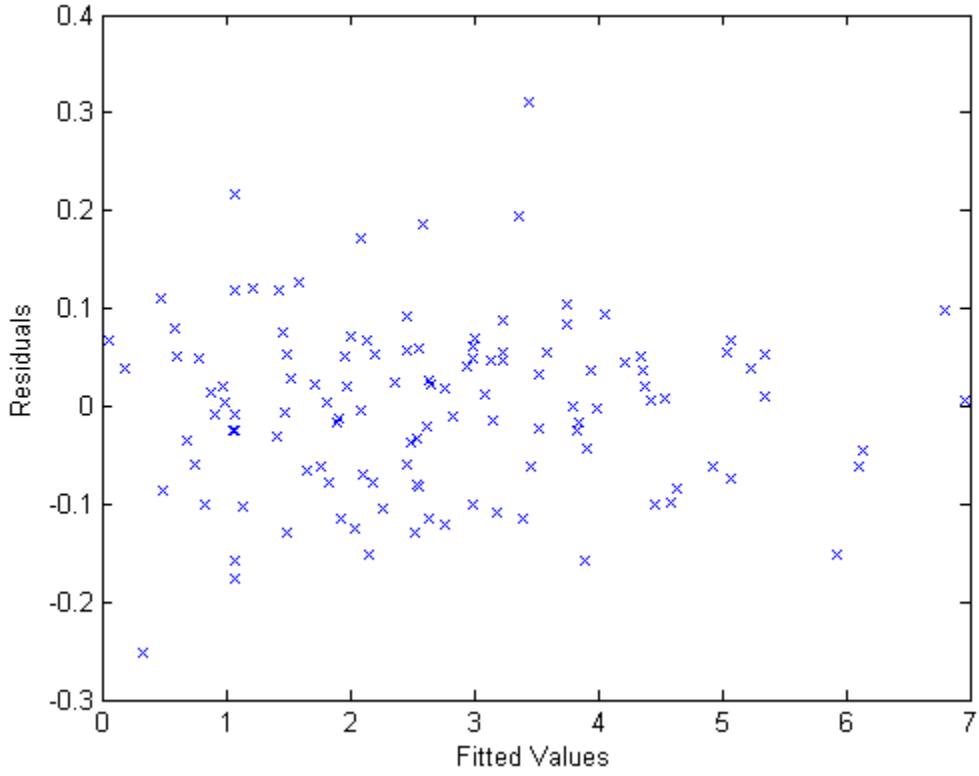
```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)');
```

Compute the fitted values and raw residuals.

```
F = fitted(lme);
R = residuals(lme);
```

Plot the residuals versus the fitted values.

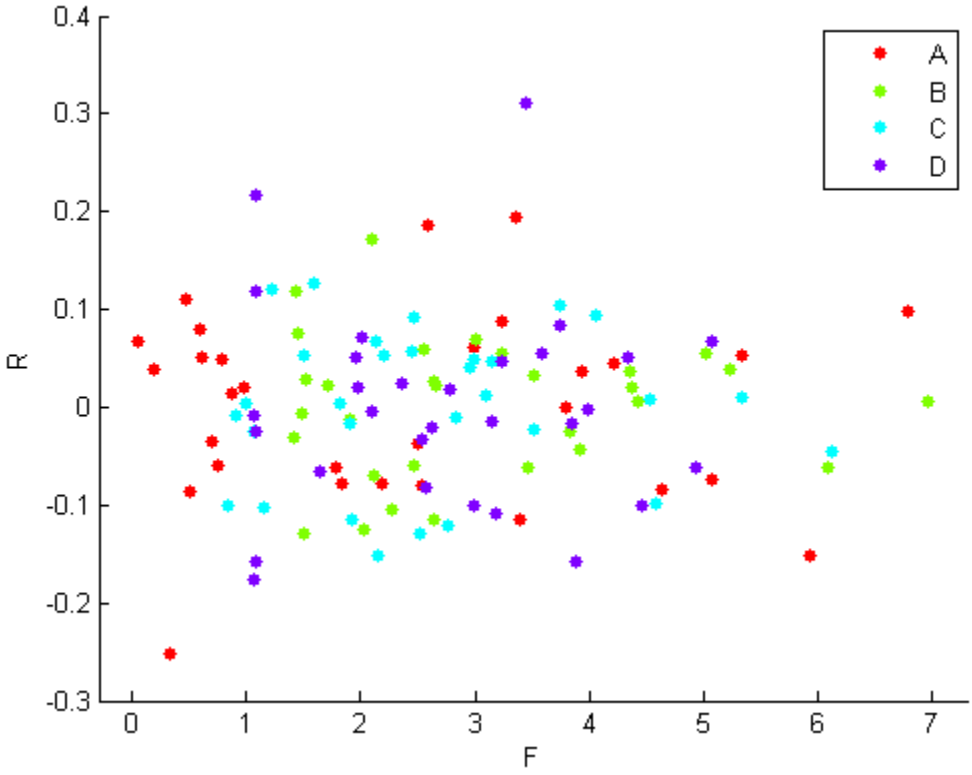
```
plot(F,R,'bx')
xlabel('Fitted Values')
ylabel('Residuals')
```



Now, plot the residuals versus the fitted values, grouped by program.

```
figure();
```

```
gscatter(F,R,Program)
```



The residuals seem to behave similarly across levels of the program as expected.

Compute Conditional and Marginal Pearson Residuals

Load the sample data.

```
load carbig
```

Store the variables for miles per gallon (MPG), acceleration, horsepower, cylinders, and model year in a table.

```
tbl = table(MPG,Acceleration,Horsepower,Cylinders,Model_Year);
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower, and the cylinders, and potentially correlated random effects for intercept and acceleration grouped by model year.

```
lme = fitlme(tbl,'MPG ~ Acceleration + Horsepower + Cylinders + (Acceleration|Model_Yea
```

Compute the conditional Pearson residuals and display the first five residuals.

```
PR = residuals(lme,'ResidualType','Pearson');
PR(1:5)
```

```
ans =

   -0.0533
    0.0652
    0.3655
   -0.0106
   -0.3340
```

Compute the marginal Pearson residuals and display the first five residuals.

```
PRM = residuals(lme,'ResidualType','Pearson','Conditional',false);
PRM(1:5)
```

```
ans =

   -0.1250
    0.0130
    0.3242
   -0.0861
   -0.3006
```

Examine Residuals

Load the sample data.

```
load carbig
```

Store the variables for miles per gallon (MPG), acceleration, horsepower, cylinders, and model year in a table.

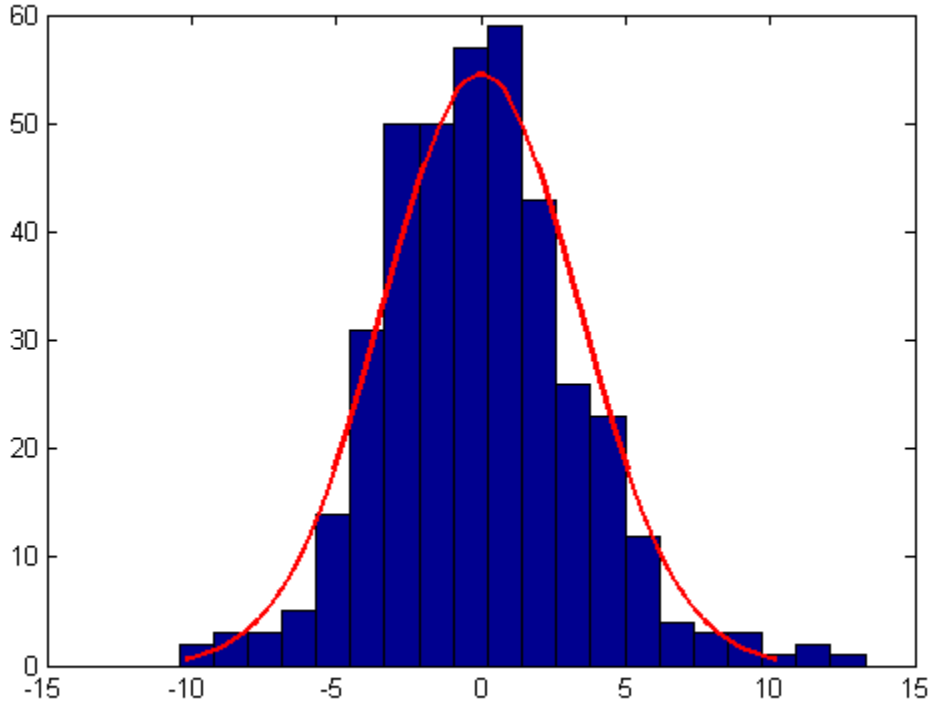
```
tbl = table(MPG,Acceleration,Horsepower,Cylinders,Model_Year);
```

Fit a linear mixed-effects model for miles per gallon (MPG), with fixed effects for acceleration, horsepower, and the cylinders, and potentially correlated random effects for intercept and acceleration grouped by model year.

```
lme = fitlme(tbl,'MPG ~ Acceleration + Horsepower + Cylinders + (Acceleration|Model_Yea
```

Draw a histogram of the raw residuals with a normal fit.

```
r = residuals(lme);
histfit(r)
```

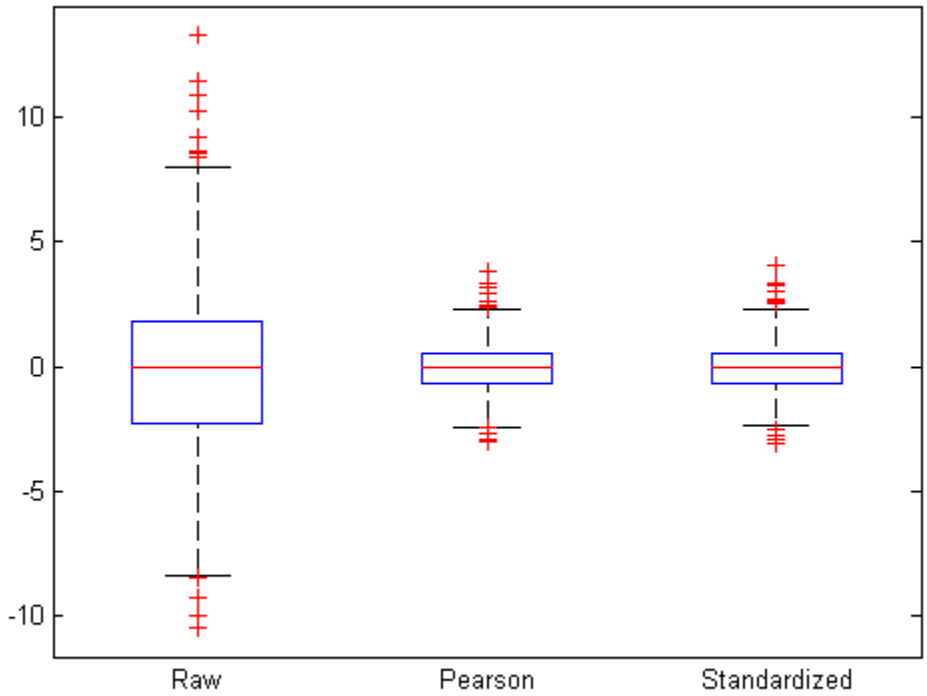


Normal distribution seems to be a good fit for the residuals.

Compute the conditional Pearson and standardized residuals and create box plots of all three types of residuals.

```
pr = residuals(lme,'ResidualType','Pearson');
st = residuals(lme,'ResidualType','Standardized');
```

```
X = [r pr st];
figure();
boxplot(X)
```



Red plus signs show the observations with residuals above or below $q3 + 1.5(q3 - q1)$ and $q1 - 1.5(q3 - q1)$, where $q1$ and $q3$ are the 25th and 75th percentiles, respectively.

Find the observations with residuals that are 2.5 standard deviations above and below the mean.

```
find(r > nanmean(r) + 2.5*nanstd(r))
```

```
ans =
```

```
    62
   252
   255
   330
   337
   341
   396

find(r < nanmean(r) - 2.5*nanstd(r))

ans =

   119
   324
   375
```

Definitions

Conditional and Marginal Residuals

Conditional residuals include contributions from both fixed and random effects, whereas marginal residuals include contribution from only fixed effects.

Suppose the linear mixed-effects model `lme`has an n-by-p fixed-effects design matrix X and an n-by-q random-effects design matrix Z. Also, suppose the p-by-1 estimated fixed-effects vector is $\hat{\beta}$, and the q-by-1 estimated best linear unbiased predictor (BLUP) vector of random effects is $\hat{b}$. The fitted conditional response is

$$\hat{y}_{Cond} = X\hat{\beta} + Z\hat{b},$$

and the fitted marginal response is

$$\hat{y}_{Mar} = X\hat{\beta},$$

`residuals` can return three types of residuals: raw, Pearson, and standardized. For any type, you can compute the conditional or the marginal residuals. For example, the conditional raw residual is

$$r_{Cond} = y - X\hat{\beta} - Z\hat{b},$$

and the marginal raw residual is

$$r_{Mar} = y - X\hat{\beta}.$$

For more information on other types of residuals, see the ResidualType name-value pair argument.

See Also

`fitted` | `LinearMixedModel` | `plotResiduals` | `response`

response

Class: GeneralizedLinearMixedModel

Response vector of generalized linear mixed-effects model

Syntax

```
y = response(glme)
[y,binomialsize] = response(glme)
```

Description

`y = response(glme)` returns the response vector y used to fit the generalized linear mixed effects model glme.

`[y,binomialsize] = response(glme)` also returns the binomial size associated with each element of y if the conditional distribution of response given the random effects is binomial.

Input Arguments

`glme` — Generalized linear mixed-effects model

`GeneralizedLinearMixedModel` object

Generalized linear mixed-effects model, specified as a `GeneralizedLinearMixedModel` object. For properties and methods of this object, see `GeneralizedLinearMixedModel`.

Output Arguments

y — Response values

n-by-1 vector

Response values, specified as an n-by-1 vector, where n is the number of observations.

For an observation i with prior weights w_i^p and binomial size n_i (when applicable), the response values y_i can have the following values.

Distribution	Permitted Values	Notes
`Binomial`	$\left\{0,\frac{1}{w_i^p n_i},\frac{2}{w_i^p n_i},\ldots,1\right\}$	w_i^p and n_i are integer values > 0
`Poisson`	$\left\{0,\frac{1}{w_i^p},\frac{2}{w_i^p},\ldots\right\}$	w_i^p is an integer value > 0
`Gamma`	$(0,\infty)$	$w_i^p \geq 0$
`InverseGaussian`	$(0,\infty)$	$w_i^p \geq 0$
`normal`	$(-\infty,\infty)$	$w_i^p \geq 0$

You can access the prior weights property w_i^p using dot notation. For example, to access the prior weights property for a model `glme`:

```
glme.ObservationInfo.Weights
```

`binomialsize` — Binomial size

vector

Binomial size associated with each element of y, returned as an n-by-1 vector, where n is the number of observations. `response` only returns binomialsize if the conditional distribution of response given the random effects is binomial. binomialsize is empty for other distributions.

Examples

Plot Response Versus Fitted Values

Navigate to the folder containing the sample data. Load the sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

load mfr
```

This simulated data is from a manufacturing company that operates 50 factories across the world, with each factory running a batch process to create a finished product. The

company wants to decrease the number of defects in each batch, so it developed a new manufacturing process. To test the effectiveness of the new process, the company selected 20 of its factories at random to participate in an experiment: Ten factories implemented the new process, while the other ten continued to run the old process. In each of the 20 factories, the company ran five batches (for a total of 100 batches) and recorded the following data:

- Flag to indicate whether the batch used the new process (`newprocess`)
- Processing time for each batch, in hours (`time`)
- Temperature of the batch, in degrees Celsius (`temp`)
- Categorical variable indicating the supplier (`A`, `B`, or `C`) of the chemical used in the batch (`supplier`)
- Number of defects in the batch (`defects`)

The data also includes `time_dev` and `temp_dev`, which represent the absolute deviation of time and temperature, respectively, from the process standard of 3 hours at 20 degrees Celsius.

Fit a generalized linear mixed-effects model using `newprocess`, `time_dev`, `temp_dev`, and `supplier` as fixed-effects predictors. Include a random-effects term for intercept grouped by `factory`, to account for quality differences that might exist due to factory-specific variations. The response variable `defects` has a Poisson distribution, and the appropriate link function for this model is log. Use the Laplace fit method to estimate the coefficients. Specify the dummy variable encoding as `'effects'`, so the dummy variable coefficients sum to 0.

The number of defects can be modeled using a Poisson distribution

$$defects_{ij} \sim Poisson\left(\mu_{ij}\right)$$

This corresponds to the generalized linear mixed-effects model

$$\log\left(\mu_{ij}\right) = \beta_0 + \beta_1 newprocess_{ij} + \beta_2 time\_dev_{ij} + \beta_3 temp\_dev_{ij} + \beta_4 supplier\_C_{ij} + \beta_5 supplier\_B_{ij} +$$

where

- $defects_{ij}$ is the number of defects observed in the batch produced by factory i during batch j.

- μ_{ij} is the mean number of defects corresponding to factory i (where i = 1, 2, ..., 20) during batch j (where j = 1, 2, ..., 5).
- $newprocess_{ij}$, $time\_dev_{ij}$, and $temp\_dev_{ij}$ are the measurements for each variable that correspond to factory i during batch j. For example, $newprocess_{ij}$ indicates whether the batch produced by factory i during batch j used the new process.
- $supplier\_C_{ij}$ and $supplier\_B_{ij}$ are dummy variables that use effects (sum-to-zero) coding to indicate whether company `C` or `B`, respectively, supplied the process chemicals for the batch produced by factory i during batch j.
- $b_i \sim N(0,\sigma_b^2)$ is a random-effects intercept for each factory i that accounts for factory-specific variation in quality.

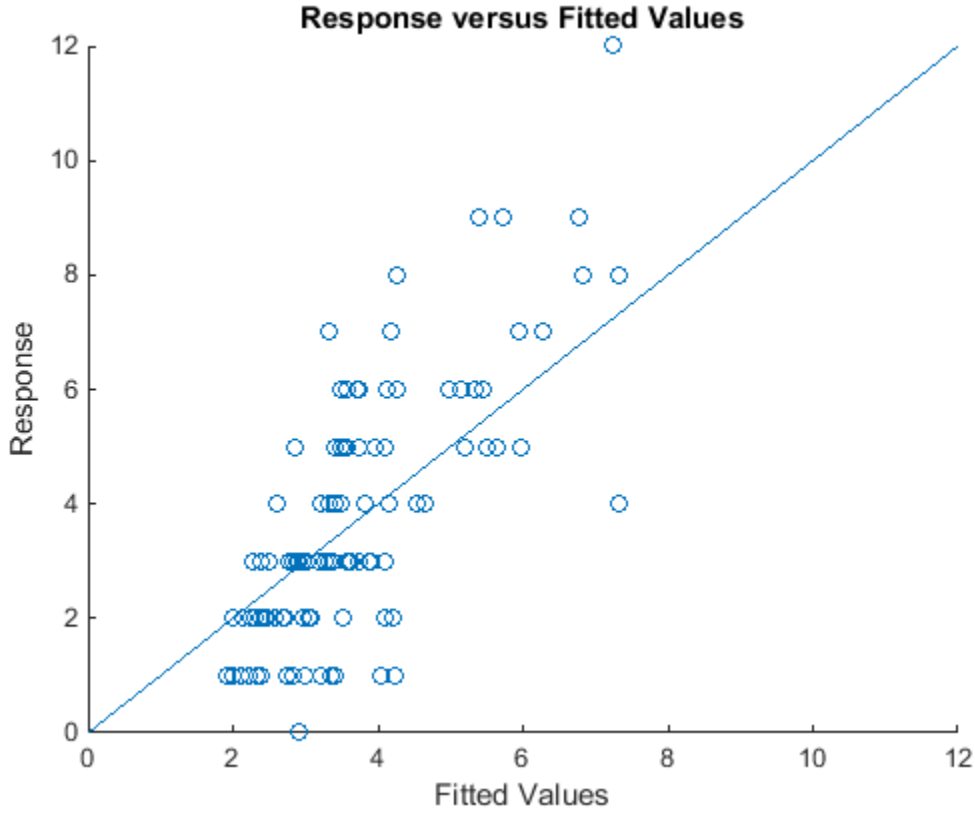
```
glme = fitglme(mfr,'defects ~ 1 + newprocess + time_dev + temp_dev + supplier + (1|fact
```

Extract the observed response values for the model, then use `fitted` to generate the fitted conditional mean values.

```
y = response(glme);   % Observed response values
yfit = fitted(glme);  % Fitted response values
```

Create a scatterplot of the observed response values versus fitted values. Add a reference line to improve the visualization.

```
figure
scatter(yfit,y)
xlim([0,12])
ylim([0,12])
refline(1,0)
title('Response versus Fitted Values')
xlabel('Fitted Values')
ylabel('Response')
```



The plot shows a positive correlation between the fitted values and the observed response values.

References

[1] Hox, J. *Multilevel Analysis, Techniques and Applications*. Lawrence Erlbaum Associates, Inc., 2002.

See Also

`GeneralizedLinearMixedModel` | `fitted` | `residuals`

response

Class: LinearMixedModel

Response vector of the linear mixed-effects model

Syntax

```
y = response(lme)
```

Description

`y = response(lme)` returns the response vector `y` used to fit the linear mixed-effects model `lme`.

Input Arguments

`lme` — Linear mixed-effects model

`LinearMixedModel` object

Linear mixed-effects model, returned as a `LinearMixedModel` object.

For properties and methods of this object, see `LinearMixedModel`.

Output Arguments

`y` — Response values

n-by-1 vector

Response values, specified as an *n*-by-1 vector, where *n* is the number of observations.

Data Types: `single` | `double`

Examples

Plot Response versus Fitted Values

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load weight
```

`weight` contains data from a longitudinal study, where 20 subjects are randomly assigned to 4 exercise programs, and their weight loss is recorded over two-week time periods. This is simulated data.

Store the data in a table. Define `Subject` and `Program` as categorical variables.

```
tbl = table(InitialWeight,Program,Subject,Week,y);
tbl.Subject = nominal(tbl.Subject);
tbl.Program = nominal(tbl.Program);
```

Fit a linear mixed-effects model where the initial weight, type of program, week, and the interaction between the week and type of program are the fixed effects. The intercept and week vary by subject.

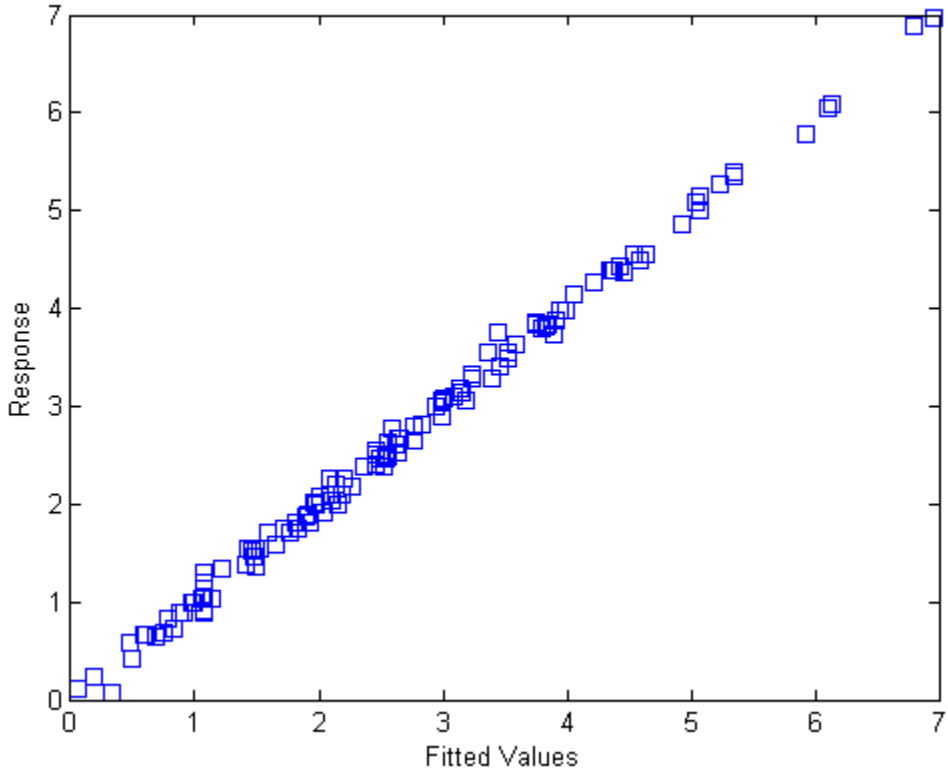
```
lme = fitlme(tbl,'y ~ InitialWeight + Program*Week + (Week|Subject)');
```

Compute the fitted values and the response.

```
F = fitted(lme);
y = response(lme);
```

Plot the response versus the fitted values.

```
plot(F,y,'bs')
xlabel('Fitted Values')
ylabel('Response')
```



See Also

`fitted` | `LinearMixedModel` | `residuals`

resubEdge

Class: ClassificationDiscriminant

Classification edge by resubstitution

Syntax

```
edge = resubEdge(obj)
```

Description

`edge = resubEdge(obj)` returns the classification edge obtained by `obj` on its training data.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

Output Arguments

`edge`

Classification edge obtained by resubstituting the training data into the calculation of edge.

Definitions

Edge

The *edge* is the weighted mean value of the classification *margin*. The weights are class prior probabilities. If you supply additional weights, those weights are normalized to

sum to the prior probabilities in the respective classes, and are then used to compute the weighted average.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

The classification margin is a column vector with the same number of rows as in the matrix X. A high value of margin indicates a more reliable prediction than a low value.

Score

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see “Posterior Probability” on page 15-7.

Examples

Esimtate the Resubstitution Edge of Discriminant Analysis Classifiers

Estimate the quality of a discriminant analysis classifier for Fisher's iris data by resubstitution.

Load Fisher's iris data set.

```
load fisheriris
```

Train a discriminant analysis classifier.

```
Mdl = fitcdiscr(meas,species);
```

Compute the resubstitution edge.

```
redge = resubEdge(Mdl)
```

```
redge =

    0.9454
```

See Also

`resubMargin` | `ClassificationDiscriminant` | `fitcdiscr` | `edge`

How To

- “Discriminant Analysis” on page 15-3

resubEdge

Class: ClassificationECOC

Classification edge for error-correcting output codes, multiclass models by resubstitution

Syntax

```
e = resubEdge(Mdl)
e = resubEdge(Mdl,Name,Value)
```

Description

`e = resubEdge(Mdl)` returns the classification edge (`e`) for the trained, error-correcting output codes (ECOC), multiclass model `Mdl` using the training data stored in `Mdl.X` and corresponding class labels stored in `Mdl.Y`.

`e = resubEdge(Mdl,Name,Value)` computes the resubstitution classification edge with additional options specified by one or more Name,Value pair arguments.

For example, specify a decoding scheme, binary learner loss function, or verbosity level.

Input Arguments

`Mdl` — ECOC multiclass model

`ClassificationECOC` model

ECOC multiclass model, specified as a `ClassificationECOC` model returned by `fitcecoc`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

  The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `Mdl.CodingMatrix`.
  - `s` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.

- L is the number of binary learners.

For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`
- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single | double`

Output Arguments

e — Classification edge
numeric scalar

Classification edge, returned as a scalar. `e` represents the (weighted) mean of the classification margins.

Definitions

Classification Edge

The *classification edge* is the weighted mean of the *classification margins*.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margin

The *classification margins* are, for each observation, the difference between the negative loss for the positive class and maximal negative loss among the negative classes. If the margins are on the same scale, then they serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [4].

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left|m_{kj}\right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$

Value	Description	Score Domain	$g(y_j,s_j)$
`'linear'`	Linear	$(-\infty,\infty)$	$(1-y_j s_j)/2$
`'quadratic'`	Quadratic	$[0,1]$	$[1-y_j(2s_j-1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Estimate the Resubstitution Edge of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

Train an ECOC model using SVM binary classifiers. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
classOrder = unique(Y)
Mdl = fitcecoc(X,Y,'Learners',t,'ClassNames',classOrder);
```

```
classOrder =

    'setosa'
    'versicolor'
    'virginica'
```

`t` is an SVM template object. The software uses default values for empty options in `t` during training. `Mdl` is a `ClassificationECOC` model.

Estimate the resubstitution edge.

```
e = resubEdge(Mdl)
```

```
e =

    0.4961
```

The mean of the training sample margins is `0.4961`.

Select ECOC Model Features by Comparing In-Sample Edges

The classifier edge measures the average of the classifier margins. One way to perform feature selection is to compare training sample edges from multiple models. Based solely on this criterion, the classifier with the highest edge is the best classifier.

Load Fisher's iris data set. Define two data sets:

- `fullX` contains all four predictors.
- `partX` contains the sepal measurements.

```
load fisheriris
X = meas;
fullX = X;
partX = X(:,1:2);
Y = species;
```

Train ECOC models using SVM binary learners for each predictor set. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template, and to compute posterior probabilities.

```
t = templateSVM('Standardize',1);
classOrder = unique(Y)
FullMdl = fitcecoc(fullX,Y,'Learners',t,'ClassNames',classOrder,...
    'FitPosterior',1);
PartMdl = fitcecoc(partX,Y,'Learners',t,'ClassNames',classOrder,...
    'FitPosterior',1);
```

```
classOrder =

    'setosa'
    'versicolor'
    'virginica'
```

The default SVM score is distance from the decision boundary. If you specify to compute posterior probabilities, then the software uses posterior probabilities as scores.

Estimate the training sample edge for each classifier. The quadratic loss function operates on scores in the domain [0,1]. Specify to use quadratic loss when aggregating the binary learners for both models.

```
fullEdge = resubEdge(FullMdl,'BinaryLoss','quadratic')
partEdge = resubEdge(PartMdl,'BinaryLoss','quadratic')
```

```
fullEdge =

    0.9896


partEdge =

    0.5058
```

The edge for the classifier trained on the complete data set is greater, suggesting that the classifier trained using every predictor has a better in-sample fit.

- “Quick Start Parallel Computing for Statistics and Machine Learning Toolbox” on page 21-2

Tip

To compare margins or edges of several classifiers, use template objects to specify a common score transform function among the classifiers when you train them using `fitcecoc`.

References

[1] Allwein, E., R. Schapire, and Y. Singer. “Reducing multiclass to binary: A unifying approach for margin classifiers.” *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. “On the decoding process in ternary error-correcting output codes.” *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. “Separability of ternary codes for sparse designs of error-correcting output codes.” *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q., X. Che, L. Zhang, and D. Yu. “Feature Evaluation and Selection Based on Neighborhood Soft Margin.” *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `edge` | `fitcecoc` | `predict` | `resbuMargin` | `resubPredict`

More About

- “Reproducibility in Parallel Statistical Computations” on page 21-13
- “Concepts of Parallel Computing in Statistics and Machine Learning Toolbox” on page 21-7

resubEdge

Class: ClassificationEnsemble

Classification edge by resubstitution

Syntax

```
edge = resubEdge(ens)
edge = resubEdge(ens,Name,Value)
```

Description

`edge = resubEdge(ens)` returns the classification edge obtained by `ens` on its training data.

`edge = resubEdge(ens,Name,Value)` calculates edge with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `resubEdge` uses only these learners for calculating edge.

Default: `1:NumTrained`

`'mode'`

String representing the meaning of the output edge:

- `'ensemble'` — `edge` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `edge` is a vector with one element per trained learner.
- `'cumulative'` — `edge` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`edge`

Classification edge obtained by ens by resubstituting the training data into the calculation of edge. Classification edge is classification margin averaged over the entire data. `edge` can be a scalar or vector, depending on the setting of the `mode` name-value pair.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in ens`.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix ens`.X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the resubstitution edge for an ensemble that classifies the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
edge = resubEdge(ens)

edge =
    3.2486
```

See Also

`resubMargin` | `resubEdge` | `resubLoss` | `resubPredict`

resubEdge

Class: ClassificationKNN

Edge of *k*-nearest neighbor classifier by resubstitution

Syntax

```
E = resubEdge(mdl)
```

Description

`E = resubEdge(mdl)` returns the classification edge for `mdl` with the data used to train `mdl` (see “Edge” on page 22-4147).

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

Output Arguments

`E`

Classification edge, a scalar that is the mean classification margin (see “Margin” on page 22-4147).

Definitions

Edge

The *edge* is the mean value of the classification *margin*.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

Margin is a column vector with the same number of rows as in the training data.

Score

The *score* of a classification is the posterior probability of the classification. The posterior probability is the number of neighbors that have that classification, divided by the number of neighbors. For a more detailed definition that includes weights and prior probabilities, see “Posterior Probability” on page 22-3654.

Examples

Resubstitution Edge Calculation

Construct a k-nearest neighbor classifier for the Fisher iris data, where $k = 5$.

Load the data.

```
load fisheriris
X = meas;
Y = species;
```

Construct a classifier for 5-nearest neighbors.

```
mdl = fitcknn(X,Y,'NumNeighbors',5);
```

Examine the resubstitution edge of the classifier.

```
E = resubEdge(mdl)
```

```
E =

    0.9253
```

- “Examine the Quality of a KNN Classifier” on page 16-29

See Also

`ClassificationKNN` | `fitcknn` | `resubLoss` | `resubMargin` | `resubPredict`

More About

- “Classification Using Nearest Neighbors” on page 16-8

resubEdge

Class: ClassificationNaiveBayes

Classification edge for naive Bayes classifiers by resubstitution

Syntax

```
e = resubEdge(Mdl)
```

Description

`e = resubEdge(Mdl)` returns the resubstitution classification edge (`e`) for the naive Bayes classifier `Mdl` using the training data stored in `Mdl.X` and corresponding class labels stored in `Mdl.Y`.

Input Arguments

`Mdl` — Fully trained naive Bayes classifier

`ClassificationNaiveBayes` model

A fully trained naive Bayes classifier, specified as a `ClassificationNaiveBayes` model trained by `fitcnb`.

Output Arguments

`e` — Classification edge

scalar

Classification edge, returned as a scalar. If you passed in weights when training the classifier, then `e` is the weighted classification edge. The software normalizes the weights so that they sum to the prior probability of their respective class.

Definitions

Classification Edge

The *classification edge* is the weighted mean of the classification margins.

If you supply weights, then the software normalizes them to sum to the prior probability of their respective class. The software uses the normalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margins

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.

- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

$$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Score

The naive Bayes *score* is the class posterior probability given the observation.

Examples

Estimate the Resubstitution Edge of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
rng(1);
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
Mdl = fitcnb(X,Y,'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier.

Estimate the resubstitution edge.

```
e = resubEdge(Mdl)
```

```
e =
```

```
    0.8944
```

The mean of the training sample margins is approximately `0.9`, which indicates that the classifier classifies in-sample observations with high confidence.

Select Naive Bayes Classifier Features by Comparing In-Sample Edges

The classifier edge measures the average of the classifier margins. One way to perform feature selection is to compare training sample edges from multiple models. Based solely on this criterion, the classifier with the highest edge is the best classifier.

Load Fisher's iris data set. Define two data sets:

- `fullX` contains all predictors.
- `partX` contains the last two predictors.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
fullX = X;
partX = X(:,3:4);
```

Train naive Bayes classifiers for each predictor set.

```
FullMdl = fitcnb(fullX,Y);
PartMdl = fitcnb(partX,Y);
```

Estimate the training sample edge for each classifier.

```
fullEdge = resubEdge(FullMdl)
partEdge = resubEdge(PartMdl)
```

```
fullEdge =

    0.8944


partEdge =

    0.9169
```

The edge for the classifier trained on predictors 3 and 4 is greater, suggesting that the classifier trained using only those predictors has a better in-sample fit.

References

[1] Hu, Q., X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `edge` | `fitcnb` | `loss` | `margin` | `predict` | `resubEdge` | `resubLoss` | `resubLoss` | `resubMargin`

More About

- "Naive Bayes Classification" on page 15-31

resubEdge

Class: ClassificationSVM

Classification edge for support vector machine classifiers by resubstitution

Syntax

```
e = resubEdge(SVMModel)
```

Description

`e = resubEdge(SVMModel)` returns the resubstitution classification edge (`e`) for the support vector machine (SVM) classifier `SVMModel` using the training data stored in `SVMModel.X` and corresponding class labels stored in `SVMModel.Y`.

Input Arguments

`SVMModel` — Full, trained SVM classifier

`ClassificationSVM` classifier

Full, trained SVM classifier, specified as a `ClassificationSVM` model trained using `fitcsvm`.

Output Arguments

`e` — Classification edge

scalar

Classification edge, returned as a scalar. `e` represents the weighted mean of the classification margins.

Definitions

Edge

The *edge* is the weighted mean of the *classification margins*.

The weights are the prior class probabilities. If you supply weights, then the software normalizes them to sum to the prior probabilities in the respective classes. The software uses the renormalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margins

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j,x) = x_j'x$ (the linear kernel), then the score function reduces to

$$f(x) = (x / s)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Examples

Estimate the Resubstitution Edge of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to standardize the predictors and define the class order.

```
SVMModel = fitcsvm(X,Y,'Standardize',true,'ClassNames',{'b','g'});
```

`SVMModel` is a trained `ClassificationSVM` classifier. `'b'` is the negative class and `'g'` is the positive class.

Estimate the resubstitution edge.

```
e = resubEdge(SVMModel)
```

```
e =

    5.0998
```

The mean of the training sample margins is `5.0999`.

Select SVM Classifier Features by Comparing In-Sample Edges

The classifier edge measures the average of the classifier margins. One way to perform feature selection is to compare training sample edges from multiple models. Based solely on this criterion, the classifier with the highest edge is the best classifier.

Load the `ionosphere` data set. Define two data sets:

- `fullX` contains all predictors (except the removed column of 0s).
- `partX` contains the last 20 predictors.

```
load ionosphere
fullX = X;
partX = X(:,end-20:end);
```

Train SVM classifiers for each predictor set.

```
FullSVMModel = fitcsvm(fullX,Y);
PartSVMModel = fitcsvm(partX,Y);
```

Estimate the training sample edge for each classifier.

```
fullEdge = resubEdge(FullSVMModel)
partEdge = resubEdge(PartSVMModel)
```

```
fullEdge =

    3.3653


partEdge =

    2.0471
```

The edge for the classifier trained on the complete data set is greater, suggesting that the classifier trained using all of the predictors has a better in-sample fit.

Algorithms

For binary classification, the software defines the margin for observation j, m_j, as

$$m_j = 2y_j f(x_j),$$

where $y_j \in \{-1,1\}$, and $f(x_j)$ is the predicted score of observation j for the positive class. However, the literature commonly uses $m_j = y_j f(x_j)$ to define the margin.

References

[1] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[2] Hu, Q., X. Che, L. Zhang, and D. Yu. “Feature Evaluation and Selection Based on Neighborhood Soft Margin.” *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `edge` | `fitcsvm` | `resubLoss` | `resubMargin`

resubEdge

Class: ClassificationTree

Classification edge by resubstitution

Syntax

```
edge = resubEdge(tree)
```

Description

`edge = resubEdge(tree)` returns the classification edge obtained by `tree` on its training data.

Input Arguments

`tree`

A classification tree created using `fitctree`.

Output Arguments

`edge`

Classification edge obtained by resubstituting the training data into the calculation of edge.

Definitions

Edge

The *edge* is the weighted mean value of the classification margin. The weights are the class probabilities in tree`.Prior`.

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix X.

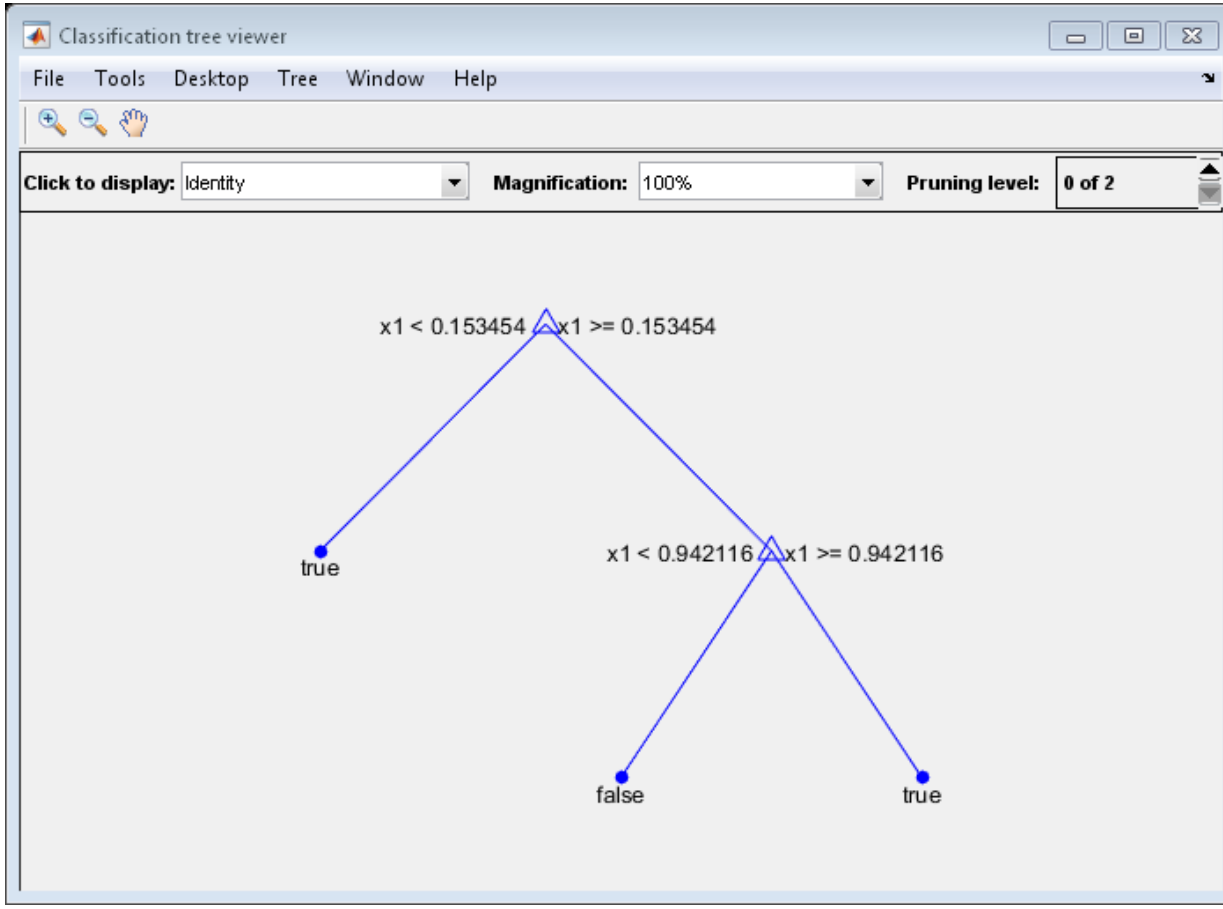
Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

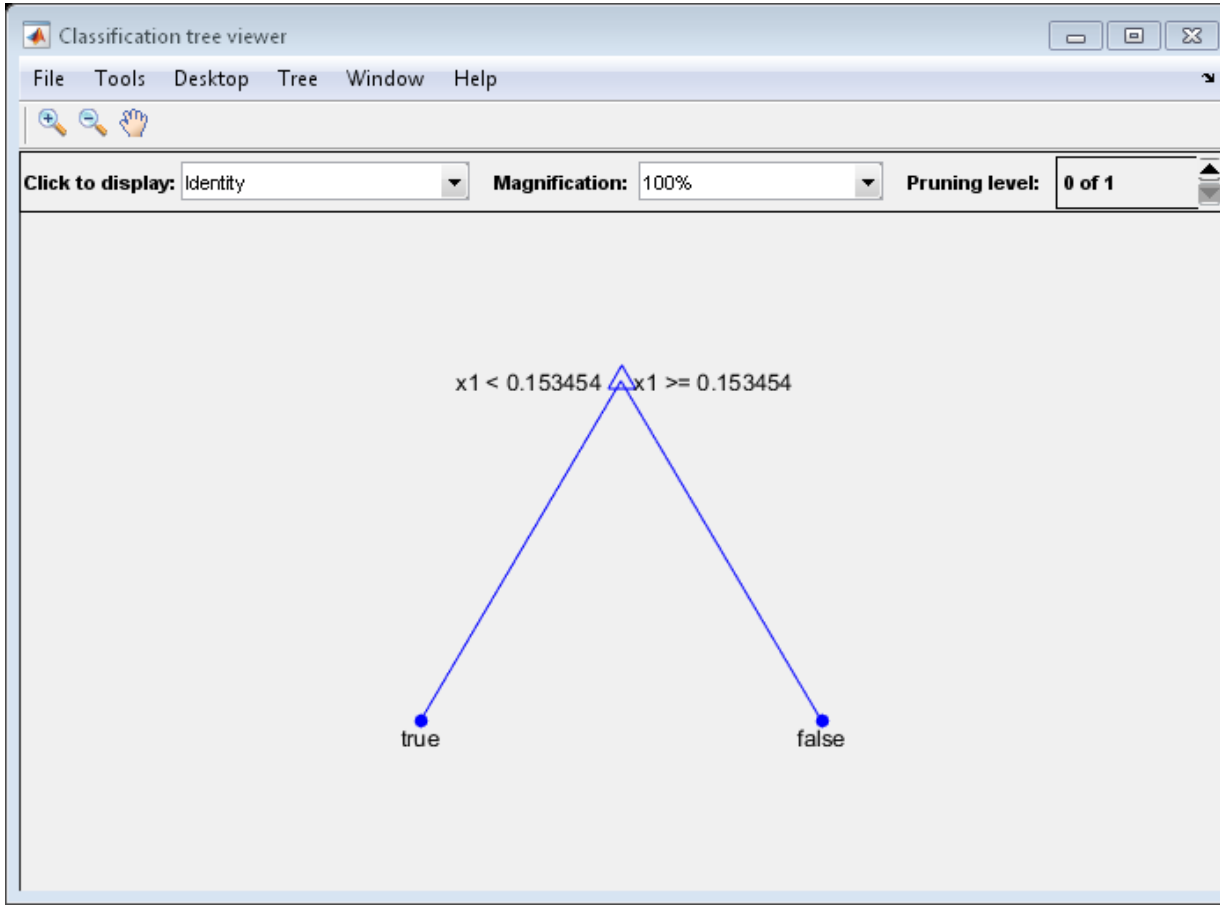
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Estimate the quality of a classification tree for the Fisher iris data by resubstitution.

```
load fisheriris
tree = fitctree(meas,species);
redge = resubEdge(tree)
```

```
redge =
    0.9384
```

See Also

`edge` | `resubLoss` | `resubPredict` | `resubMargin` | `fitctree`

resubLoss

Class: ClassificationDiscriminant

Classification error by resubstitution

Syntax

```
L = resubLoss(obj)
L = resubLoss(obj,Name,Value)
```

Description

`L = resubLoss(obj)` returns the resubstitution loss, meaning the loss computed for the data that `fitcdiscr` used to create `obj`.

`L = resubLoss(obj,Name,Value)` returns loss statistics with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'lossfun '`

Function handle or string representing a loss function. Built-in loss functions are:

- `'binodeviance'` — See “Loss Functions” on page 22-4165.

- `'classiferror'` — Fraction of misclassified observations. See "Loss Functions" on page 22-4165.
- `'exponential'` — See "Loss Functions" on page 22-4165.
- `'hinge'` — See "Loss Functions" on page 22-4181.
- `'mincost'` — Smallest misclassification cost as given by the obj`.Cost` matrix.

You can write your own loss function using the syntax described in "Loss Functions" on page 22-4165.

Default: `'mincost'`

Output Arguments

`L`

Classification error, a scalar. The meaning of the error depends on the values in `weights` and `lossfun`. See "Classification Error" on page 22-4165.

Definitions

Classification Error

The default classification error is the fraction of the training data `X` that obj misclassifies.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when obj misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

  $$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'classiferror'` — Predict the label with the largest posterior probability. The loss is then the fraction of misclassified observations.
- `'hinge'` — Classification error measure that has the form

  $$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

  where:

  - w_j is weight j.
  - For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
  - $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.
- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file in this form:

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in the classifier, represented in the `ClassNames` property.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in the `ClassNames` property.

- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST = ones(K) - eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

Posterior Probability

The posterior probability that a point z belongs to class j is the product of the prior probability and the multivariate normal density. The density function of the multivariate normal with mean μ_j and covariance Σ_j at a point z is

$$P(x \mid k) = \frac{1}{\left(2\pi|\Sigma_k|\right)^{1/2}} \exp\left(-\frac{1}{2}(x-\mu_k)^T \Sigma_k^{-1}(x-\mu_k)\right),$$

where $|\Sigma_k|$ is the determinant of Σ_k, and Σ_k^{-1} is the inverse matrix.

Let $P(k)$ represent the prior probability of class k. Then the posterior probability that an observation x is of class k is

$$\hat{P}(k \mid x) = \frac{P(x \mid k)P(k)}{P(x)},$$

where $P(x)$ is a normalization constant, the sum over k of $P(x \mid k)P(k)$.

Prior Probability

The prior probability is one of three choices:

- `'uniform'` — The prior probability of class `k` is one over the total number of classes.
- `'empirical'` — The prior probability of class `k` is the number of training samples of class `k` divided by the total number of training samples.

- Custom — The prior probability of class `k` is the `k`th element of the `prior` vector. See `fitcdiscr`.

After creating a classifier `obj`, you can set the prior using dot notation:

```
obj.Prior = v;
```

where `v` is a vector of positive elements representing the frequency with which each element occurs. You do not need to retrain the classifier when you set a new prior.

Cost

The matrix of expected costs per observation is defined in "Cost" on page 15-8.

Examples

Compute the resubstituted classification error for the Fisher iris data:

```
load fisheriris
obj = fitcdiscr(meas,species);
L = resubLoss(obj)

L =
    0.0200
```

See Also

`ClassificationDiscriminant` | `fitcdiscr` | `loss`

How To

- "Discriminant Analysis" on page 15-3

resubLoss

Class: ClassificationECOC

Classification loss for error-correcting output codes, multiclass models by resubstitution

Syntax

```
L = resubLoss(Mdl)
L = resubLoss(Mdl,Name,Value)
```

Description

`L = resubLoss(Mdl)` returns classification loss (`L`) for the trained, error-correcting output codes (ECOC), multiclass model `Mdl` using the training data stored in `Mdl.X` and corresponding class labels stored in `Mdl.Y`.

`L = resubLoss(Mdl,Name,Value)` returns the classification loss with additional options specified by one or more Name,Value pair arguments.

For example, specify the loss function, decoding scheme, or verbosity level.

Input Arguments

`Mdl` — ECOC multiclass model

`ClassificationECOC` model

ECOC multiclass model, specified as a `ClassificationECOC` model returned by `fitcecoc`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

'BinaryLoss' — Binary learner loss function

function handle | 'hamming' | 'linear' | 'exponential' | 'binodeviance' | 'hinge' | 'quadratic'

Binary learner loss function, specified as the comma-separated pair consisting of 'BinaryLoss' and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
'binodeviance'	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
'exponential'	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
'hamming'	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
'hinge'	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
'linear'	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
'quadratic'	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

  The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., customFunction, specify its function handle 'BinaryLoss',@customFunction.

  customFunction should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - M is the K-by-L coding matrix stored in Mdl.CodingMatrix.
  - s is the 1-by-L row vector of classification scores.
  - bLoss is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.

- L is the number of binary learners.

  For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`
- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'LossFun'` — Loss function

`'classiferror'` (default) | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or `'classiferror'`.

You can:

- Specify the built-in function `'classiferror'`, then the loss function is classification error, in other words, the proportion of misclassified observations.
- Specify your own function using function handle notation.

  Suppose that `n = size(X,1)` is the sample size and `k` is the number of classes. Your function must have the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

- The output argument `lossvalue` is a scalar.
- You choose the function name (*`lossfun`*).
- `C` is an `n`-by-`k` logical matrix with rows indicating to which class the corresponding observation belongs. The column order corresponds to the class order in `Mdl.ClassNames`.

  Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q` for each row. Set all other elements of row `p` to `0`.
- `S` is an `n`-by-`k` numeric matrix of negated loss values for classes. Each row corresponds to an observation. The column order corresponds to the class order in `CVMdl.ClassNames`. `S` is similar to the output argument `negLoss` of `resubPredict`.
- `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes its elements to sum to `1`.
- `Cost` is a `k`-by-`k` numeric matrix of misclassification costs. For example, `Cost = ones(K) - eye(K)` specifies a cost of 0 for correct classification, and 1 for misclassification.

Specify your function using `'LossFun',@lossfun`.

`'Options'` — Estimation options

`[ ]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single | double`

Output Arguments

L — Classification loss

scalar

Classification loss, returned as a scalar. `L` is a generalization or resubstitution quality measure. Its interpretation depends on the loss function and weighting scheme, but, in general, better classifiers yield smaller loss values.

Definitions

Classification Error

The *classification error* is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j e_j}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is the weight for observation j. The software renormalizes the weights to sum to 1.
- $e_j = 1$ if the predicted class of observation j differs from its true class, and 0 otherwise.

In other words, it is the proportion of observations that the classifier misclassifies.

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left| m_{kj} \right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left| m_{kj} \right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$

Value	Description	Score Domain	$g(y_j,s_j)$
`'linear'`	Linear	$(-\infty,\infty)$	$(1-y_js_j)/2$
`'quadratic'`	Quadratic	$[0,1]$	$[1-y_j(2s_j-1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Determine the Resubstitution Loss of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

Train an ECOC model using SVM binary classifiers. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
classOrder = unique(Y)
Mdl = fitcecoc(X,Y,'Learners',t,'ClassNames',classOrder);
```

```
classOrder =

    'setosa'
    'versicolor'
    'virginica'
```

`t` is an SVM template object. The software uses default values for empty options in `t` during training. `Mdl` is a `ClassificationECOC` model.

Estimate the resubstitution loss (i.e., the in-sample classification error).

```
L = resubLoss(Mdl)
```

```
L =

    0.0267
```

The ECOC model misclassifies 2.67% of the training sample irises.

Determine the ECOC Model Quality Using a Custom Resubstitution Loss

Suppose that it is interesting to know how well a model classifies a particular class. This example shows how to pass such a custom loss function to `resubLoss`.

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
n = numel(Y);           % Sample size
classOrder = unique(Y)  % Class order
K = numel(classOrder);  % Number of classes
```

```
classOrder =

     setosa
     versicolor
     virginica
```

Train an ECOC model using SVM binary classifiers. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
Mdl = fitcecoc(X,Y,'Learners',t,'ClassNames',classOrder);
```

`t` is an SVM template object. The software uses default values for empty options in `t` during training. `Mdl` is a `ClassificationECOC` model.

Compute the negated losses for the training observations.

```
rng(1); % For reproducibility
```

```
[~,negLoss] = resubPredict(Mdl);
```

Create a function that takes the minimal loss for each observation, and then averages the minimal losses across all observations.

```
lossfun = @(C,S,~,~)mean(min(-negLoss,[],2));
```

Compute the custom loss for the training data.

```
resubLoss(Mdl,'LossFun',lossfun)
```

```
ans =

    0.0065
```

The average, minimal, binary loss in the training data is 0.0065.

- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q., X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `fitcecoc` | `loss` | `predict` | `resubPredict`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

resubLoss

Class: ClassificationEnsemble

Classification error by resubstitution

Syntax

```
L = resubLoss(ens)
L = resubLoss(ens,Name,Value)
```

Description

`L = resubLoss(ens)` returns the resubstitution loss, meaning the loss computed for the data that `fitensemble` used to create `ens`.

`L = resubLoss(ens,Name,Value)` calculates loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `resubLoss` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'lossfun'`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-4181
- `'classiferror'` — Fraction of misclassified data
- `'exponential'` — See "Loss Functions" on page 22-4181
- `'hinge'` — See "Loss Functions" on page 22-4181.
- `'mincost'` — Smallest misclassification cost as given by the obj`.Cost` matrix. See "Loss Functions" on page 22-4181.

You can write your own loss function in the syntax described in "Loss Functions" on page 22-4181.

Default: `'classiferror'`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Loss, by default the fraction of misclassified data. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Definitions

Classification Error

The default classification error is the fraction of the training data `X` that ens misclassifies.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when tree misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

  $$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'classiferror'` — Fraction of misclassified data, weighted by w.
- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

  $$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'hinge'` — Classification error measure that has the form

  $$L=\frac{\sum_{j=1}^{n} w_j \max\left\{0,1-y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

  where:

  - w_j is weight j.

  - For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
  - $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.
- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file of the form

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of ens`.X`.
- `K` is the number of classes in ens, represented in `ens.ClassNames`.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in `tree.ClassNames`.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `score` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. The default `'classiferror'` gives a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `lossfun` name-value pair.

Examples

Compute the resubstitution loss for a classification ensemble for the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
loss = resubLoss(ens)
```

```
loss =
    0.0333
```

See Also

resubEdge | resubLoss | resubMargin | resubPredict

resubLoss

Class: ClassificationKNN

Loss of *k*-nearest neighbor classifier by resubstitution

Syntax

```
L = resubLoss(mdl)
L = resubLoss(mdl,Name,Value)
```

Description

`L = resubLoss(mdl)` returns the resubstitution loss, meaning the loss computed for the data that `fitcknn` used to create `mdl`.

`L = resubLoss(mdl,Name,Value)` returns loss statistics with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'lossfun '`

Function handle or string representing a loss function. Built-in loss functions are:

- `'binodeviance'` — See "Loss Functions" on page 22-4186.
- `'classiferror'` — Fraction of misclassified observations. See "Loss Functions" on page 22-4186.
- `'exponential'` — See "Loss Functions" on page 22-4186.
- `'hinge'` — See "Loss Functions" on page 22-4186.
- `'mincost'` — Smallest misclassification cost as given by the mdl`.Cost` matrix.

You can write your own loss function using the syntax described in "Loss Functions" on page 22-4186.

Default: `'mincost'`

Output Arguments

`L`

Classification error, a scalar. The meaning of the error depends on the values in `weights` and `lossfun`. See "Classification Error" on page 22-4185.

Definitions

Classification Error

The default classification error is the fraction of data X that mdl misclassifies, where Y represents the true classifications.

The weighted classification error is the sum of weight i times the Boolean value that is `1` when mdl misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

$$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'classiferror'` — Predict the label with the largest posterior probability. The loss is then the fraction of misclassified observations.
- `'hinge'` — Classification error measure that has the form

$$L=\frac{\sum_{j=1}^{n} w_j \max\left\{0,1-y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

  where:

  - w_j is weight j.
  - For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
  - $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.
- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost`

property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file in this form:

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in the classifier, represented in the `ClassNames` property.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in the `ClassNames` property.
- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST = ones(K) - eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

True Misclassification Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation.

You can set the true misclassification cost per class in the `Cost` name-value pair when you run `fitcknn`. `Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

Expected Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation. The third output of `predict` is the expected misclassification cost per observation.

Suppose you have `Nobs` observations that you want to classify with a trained classifier `mdl`. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row. The command

```
[label,score,cost] = predict(mdl,Xnew)
```

returns, among other outputs, a `cost` matrix of size `Nobs`-by-`K`. Each row of the `cost` matrix contains the expected (average) cost of classifying the observation into each of the `K` classes. `cost(n,k)` is

$$\sum_{i=1}^{K} \hat{P}(i \mid Xnew(n)) C(k \mid i),$$

where

- K is the number of classes.
- $\hat{P}(i \mid Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.
- $C(k \mid i)$ is the true misclassification cost of classifying an observation as k when its true class is i.

Examples

Loss Calculation

Construct a k-nearest neighbor classifier for the Fisher iris data, where $k = 5$.

Load the data.

```
load fisheriris
```

Construct a classifier for 5-nearest neighbors.

```
mdl = fitcknn(meas,species,'NumNeighbors',5);
```

Examine the resubstitution loss of the classifier.

```
L = resubLoss(mdl)
```

```
L =
```

```
0.0333
```

The classifier predicts incorrect classifications for 1/30 of its training data.

- “Examine the Quality of a KNN Classifier” on page 16-29
- “Predict Classification Based on a KNN Classifier” on page 16-30
- “Modify a KNN Classifier” on page 16-30

See Also

`ClassificationKNN` | `fitcknn` | `resubEdge` | `resubMargin` | `resubPredict`

More About

- “Classification Using Nearest Neighbors” on page 16-8

resubLoss

Class: ClassificationNaiveBayes

Classification loss for naive Bayes classifiers by resubstitution

Syntax

```
L = resubLoss(Mdl)
L = resubLoss(Mdl,Name,Value)
```

Description

`L = resubLoss(Mdl)` returns the in-sample minimum misclassification cost loss (`L`), which is a scalar representing how well the trained naive Bayes classifer Mdl classifies the predictor data sotred in `Mdl.X` as compared to the true class labels stored in `Mdl.Y`.

`L = resubLoss(Mdl,Name,Value)` returns the in-sample classification loss with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`Mdl` — Fully trained naive Bayes classifier

`ClassificationNaiveBayes` model

A fully trained naive Bayes classifier, specified as a `ClassificationNaiveBayes` model trained by `fitcnb`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun'` — Loss function

`'classiferror'` (default) | `'binodeviance'` | `'exponential'` | `'hinge'` | `'mincost'` | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or string.

- This table describes the built-in loss functions. Specify one using its corresponding string.

String	Loss Function
`'binodeviance'`	Binomial deviance
`'classiferror'`	Classification error
`'exponential'`	Exponential loss
`'hinge'`	Hinge loss
`'mincost'`	Minimum misclassification cost loss

- Specify your own function using function handle notation.

  Suppose that `n = size(X,1)` is the sample size and `k = size(Mdl.ClassNames,1)` is the number of classes. Your function must have the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

  - The output argument `lossvalue` is a scalar.
  - You choose the function name (*`lossfun`*).
  - `C` is an `n`-by-`k` logical matrix with rows indicating to which class the corresponding observation belongs. The column order corresponds to the class order in `Mdl.ClassNames`.

    Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q`, for each row. Set all other elements of row `p` to `0`.
  - `S` is an `n`-by-`k` numeric matrix of classification scores. The column order corresponds to the class order in `Mdl.ClassNames`. `S` is a matrix of posterior probabilities, similar to the output of `predict`.
  - `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes the weights to sum to the prior probability of their respective class. If `Mdl` is a compact model, then you must also supply the weights using the `'Weights'` name-value pair argument.

- `Cost` is a `k`-by-`k` numeric matrix of misclassification costs. For example, `Cost = ones(K) - eye(K)` specifies a cost of `0` for correct classification, and `1` for misclassification.

Specify your function using `'LossFun',@lossfun`.

Output Arguments

`L` — Classification loss

scalar

Classification loss, returned as a scalar. `L` is a generalization or resubstitution quality measure. Its interpretation depends on the loss function and weighting scheme, but, in general, better classifiers yield smaller loss values.

Definitions

Binomial Deviance

The *binomial deviance* (or *multinomial deviance* for number of classes $K > 3$) is a classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \log\left(1 + \exp\left(-2 y_j' f\left(X_j\right)\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.

- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

The binomial deviance has connections to the maximization of the binomial likelihood function. For details on binomial deviance, see [1].

Classification Error

The *classification error* is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j e_j}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is the weight for observation j. The software renormalizes the weights to sum to 1.
- $e_j = 1$ if the predicted class of observation j differs from its true class, and 0 otherwise.

In other words, it is the proportion of observations that the classifier misclassifies.

Exponential Loss

Exponential loss is a classification error measure that is similar to binomial deviance, and has the form

$$L = \frac{\sum_{j=1}^{n} w_j \exp\left(-y_j' f\left(X_j\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.

- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

Hinge Loss

Hinge loss is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j.
- For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
- $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.

Hinge loss linearly penalizes for misclassified observations, and is related to the support vector machine (SVM) objective function used for optimization. For more details on hinge loss, see [1].

Minimum Misclassification Cost Loss

The *minimum misclassification cost loss* is the weighted average of the minimum expected misclassification costs for each observation.

In other words, the minimum misclassification cost is

$$L = \frac{\sum_{j=1}^{n} w_j c_j}{\sum_{j}^{n} w_j},$$

where:

- w_j is the weight of observation j.
- c_j is the minimum of the expected misclassification costs for observation j.

Misclassification Cost

A *misclassification cost* is the relative severity of a classifier labeling an observation into the wrong class.

There are two types of misclassification costs: true and expected. Let K be the number of classes.

- *True misclassification cost* — A K-by-K matrix, where element (i,j) indicates the misclassification cost of predicting an observation into class j if its true class is i. The software stores the misclassification cost in the property `Mdl.Cost`, and used in computations. By default, `Mdl.Cost(i,j)` = 1 if `i` ≠ `j`, and `Mdl.Cost(i,j)` = 0 if `i` = `j`. In other words, the cost is `0` for correct classification, and `1` for any incorrect classification.
- *Expected misclassification cost* — A K-dimensional vector, where element k is the weighted average misclassification cost of classifying an observation into class k, weighted by the class posterior probabilities. In other words,

$$c_k = \sum_{j=1}^{K} \hat{P}(Y = j \mid x_1,...,x_P)\texttt{Cost}_{jk}.$$

the software classifies observations to the class corresponding with the lowest expected misclassification cost.

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.
- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

  $$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Examples

Determine the Resubstitution Loss of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
Mdl = fitcnb(X,Y,'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier.

Estimate the default resubstitution loss, which is the in-sample minimum misclassification cost.

```
L = resubLoss(Mdl)
```

```
L =

    0.0400
```

The average, in-sample cost of classification is 0.04.

Determine Resubstitution Classification Error of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
Mdl = fitcnb(X,Y,'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a trained `ClassificationNaiveBayes` classifier.

Estimate the in-sample proportion of misclassified observations.

```
L = resubLoss(Mdl,'LossFun','classiferror')
```

```
L =

    0.0400
```

The naive Bayes classifier misclassifies 4% of the training observations.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, second edition. Springer, New York, 2008.

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `fitcnb` | `loss` | `predict` | `resubPredict`

More About

- "Naive Bayes Classification" on page 15-31

resubLoss

Class: ClassificationSVM

Classification loss for support vector machine classifiers by resubstitution

Syntax

```
L = resubLoss(SVMModel)
L = resubLoss(SVMModel,Name,Value)
```

Description

`L = resubLoss(SVMModel)` returns the classification loss by resubstitution (`L`), the in-sample classification loss, for the support vector machine (SVM) classifier `SVMModel` using the training data stored in `SVMModel.X` and corresponding class labels stored in `SVMModel.Y`.

`L = resubLoss(SVMModel,Name,Value)` returns the classification loss by resubstitution with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`SVMModel` — Full, trained SVM classifier

`ClassificationSVM` classifier

Full, trained SVM classifier, specified as a `ClassificationSVM` model trained using `fitcsvm`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun'` — Loss function
`'classiferror'` (default) | `'binodeviance'` | `'exponential'` | `'hinge'` | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or string.

- The following lists available loss functions. Specify one using its corresponding string.

Value	Loss Function
`'binodeviance'`	Binomial deviance
`'classiferror'`	Classification error
`'exponential'`	Exponential loss
`'hinge'`	Hinge loss

- Specify your own function using function handle notation.

  Suppose that `n = size(X,1)` is the sample size and `K= size(SVMModel.ClassNames,1)` is the number of classes. Your function must have the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

  - The output argument `lossvalue` is a scalar.
  - You choose the function name (*`lossfun`*).
  - `C` is an `n`-by-`K` logical matrix with rows indicating which class the corresponding observation belongs. The column order corresponds to the class order in `SVMModel.ClassNames`.

    Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q`, for each row. Set all other elements of row `p` to `0`.
  - `S` is an `n`-by-`K` numeric matrix of classification scores. The column order corresponds to the class order in `SVMModel.ClassNames`. `S` is a matrix of classification scores, similar to the output of `predict`.
  - `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes them to sum to `1`.

- `Cost` is a `K`-by-`K` numeric matrix of misclassification costs. For example, `Cost = ones(K) - eye(K)` specifies a cost of `0` for correct classification, and `1` for misclassification.

Specify your function using `'LossFun',@lossfun`.

Data Types: `char | function_handle`

Output Arguments

`L` — Classification loss

scalar

Classification loss, returned as a scalar. `L` is a generalization or resubstitution quality measure. Its interpretation depends on the loss function and weighting scheme, but, in general, better classifiers yield smaller loss values.

Definitions

Binomial Deviance

The binomial deviance is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \log\left(1 + \exp\left(-2 y_j' f\left(X_j\right)\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j. The software renormalizes the weights to sum to 1.
- $y_j = \{-1,1\}$.
- $f(X_j)$ is the score for observation j.

The binomial deviance has connections to the maximization of the binomial likelihood function. For details on binomial deviance, see [1].

Classification Error

The *classification error* is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j e_j}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is the weight for observation j. The software renormalizes the weights to sum to 1.
- e_j = 1 if the predicted class of observation j differs from its true class, and 0 otherwise.

In other words, it is the proportion of observations that the classifier misclassifies.

Exponential Loss

A binary classification error measure that is similar to binomial deviance, and has the form

$$L = \frac{\sum_{j=1}^{n} w_j \exp\left(-y_j' f\left(X_j\right)\right)}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j. The software renormalizes the weights to sum to 1.
- y_j = {-1,1}.
- $f(X_j)$ is the score for observation j.

Hinge Loss

Hinge loss is a binary classification error measure that has the form

$$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

where:

- w_j is weight j. The software renormalizes the weights to sum to 1.
- $y_j = \{-1,1\}$.
- $f(X_j)$ is the score for observation j.

Hinge loss linearly penalizes for misclassified observations, and is related to the SVM objective function used for optimization. For more details on hinge loss, see [1].

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j, x) = x_j' x$ (the linear kernel), then the score function reduces to

$$f(x) = (x / s)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Examples

Determine the Resubstitution Loss of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to standardize the data.

```
SVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true);
```

`SVMModel` is a trained `ClassificationSVM` classifier. The negative class is `'b'` and the positive class is `'g'`.

Estimate the resubstitution loss (i.e., the in-sample classification error).

```
L = resubLoss(SVMModel)
```

```
L =

    0.0570
```

The SVM classifier misclassifies 5.7% of the training sample radar returns.

Determine the Resubstitution Hinge Loss of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to standardize the data.

```
SVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true);
```

`SVMModel` is a trained `ClassificationSVM` classifier. The negative class is `'b'` and the positive class is `'g'`.

Estimate the in-sample hinge loss.

```
L = resubLoss(SVMModel,'LossFun','Hinge')
```

```
L =

    0.1603
```

The hinge loss is `0.1603`. Classifiers with hinge losses close to 0 are desirable.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, second edition. Springer, New York, 2008.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm` | `loss` | `resubMargin` | `resubPredict`

resubLoss

Class: ClassificationTree

Classification error by resubstitution

Syntax

```
L = resubLoss(tree)
L = resubLoss(tree,Name,Value)
L = resubLoss(tree,'Subtrees',subtreevector)
[L,se] = resubLoss(tree,'Subtrees',subtreevector)
[L,se,NLeaf] = resubLoss(tree,'Subtrees',subtreevector)
[L,se,NLeaf,bestlevel] = resubLoss(tree,'Subtrees',subtreevector)
[L,...] = resubLoss(tree,'Subtrees',subtreevector,Name,Value)
```

Description

`L = resubLoss(tree)` returns the resubstitution loss, meaning the loss computed for the data that `fitctree` used to create `tree`.

`L = resubLoss(tree,Name,Value)` returns the loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

`L = resubLoss(tree,'Subtrees',subtreevector)` returns a vector of classification errors for the trees in the pruning sequence `subtreevector`.

`[L,se] = resubLoss(tree,'Subtrees',subtreevector)` returns the vector of standard errors of the classification errors.

`[L,se,NLeaf] = resubLoss(tree,'Subtrees',subtreevector)` returns the vector of numbers of leaf nodes in the trees of the pruning sequence.

`[L,se,NLeaf,bestlevel] = resubLoss(tree,'Subtrees',subtreevector)` returns the best pruning level as defined in the `TreeSize` name-value pair. By default,

`bestlevel` is the pruning level that gives loss within one standard deviation of minimal loss.

`[L,...] = resubLoss(tree,'Subtrees',subtreevector,Name,Value)` returns loss statistics with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`tree`

A classification tree constructed by `fitctree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun'`

Function handle or string representing a loss function. Built-in loss functions:

- `'binodeviance'` — See "Loss Functions" on page 22-4209
- `'classiferror'` — Fraction of misclassified observations. See "Loss Functions" on page 22-4209.
- `'exponential'` — See "Loss Functions" on page 22-4209
- `'hinge'` — See "Loss Functions" on page 22-4209.
- `'mincost'` — Smallest misclassification cost as given by the tree`.Cost` matrix. See "Loss Functions" on page 22-4209.

You can write your own loss function in the syntax described in "Loss Functions" on page 22-4209.

Default: `'mincost'`

Name,Value arguments associated with pruning subtrees:

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `ClassificationTree.resubLoss` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`ClassificationTree.resubLoss` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

`'TreeSize'`

One of the following strings:

- `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `Subtrees`).
- `'min'` — `loss` returns the element of `Subtrees` with smallest loss, usually the smallest element of `Subtrees`.

Output Arguments

`L`

Classification error, a vector the length of `Subtrees`. The meaning of the error depends on the values in `Weights` and `LossFun`; see “Classification Error” on page 22-4209.

`se`

Standard error of loss, a vector the length of `Subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `Subtrees`.

`bestlevel`

A scalar whose value depends on `TreeSize`:

- `TreeSize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L+se`, where `L` and `se` relate to the smallest value in `Subtrees`).
- `TreeSize` = `'min'` — `loss` returns the element of `Subtrees` with smallest loss, usually the smallest element of `Subtrees`.

Definitions

Classification Error

The default classification error is the fraction of the training data `X` that tree misclassifies.

Weighted classification error is the sum of weight i times the Boolean value that is `1` when tree misclassifies the ith row of `X`, divided by the sum of the weights.

Loss Functions

The built-in loss functions are:

- `'binodeviance'` — For binary classification, assume the classes y_n are `-1` and `1`. With weight vector w normalized to have sum `1`, and predictions of row n of data X as $f(X_n)$, the binomial deviance is

$$\sum w_n \log\left(1+\exp\left(-2y_n f\left(X_n\right)\right)\right).$$

- `'exponential'` — With the same definitions as for `'binodeviance'`, the exponential loss is

  $$\sum w_n \exp\left(-y_n f\left(X_n\right)\right).$$

- `'classiferror'` — Predict the label with the largest posterior probability. The loss is then the fraction of misclassified observations.
- `'hinge'` — Classification error measure that has the form

  $$L = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

  where:

  - w_j is weight j.
  - For binary classification, $y_j = 1$ for the positive class and -1 for the negative class. For problems where the number of classes $K > 3$, y_j is a vector of 0s, but with a 1 in the position corresponding to the true class, e.g., if the second observation is in the third class and $K = 4$, then $y_2 = [0\ 0\ 1\ 0]'$.
  - $f(X_j)$ is, for binary classification, the posterior probability or, for $K > 3$, a vector of posterior probabilities for each class given observation j.
- `'mincost'` — Predict the label with the smallest expected misclassification cost, with expectation taken over the posterior probability, and cost as given by the `Cost` property of the classifier (a matrix). The loss is then the true misclassification cost averaged over the observations.

To write your own loss function, create a function file in this form:

```
function loss = lossfun(C,S,W,COST)
```

- `N` is the number of rows of X.
- `K` is the number of classes in the classifier, represented in the `ClassNames` property.
- `C` is an `N`-by-`K` logical matrix, with one `true` per row for the true class. The index for each class is its position in the `ClassNames` property.

- `S` is an `N`-by-`K` numeric matrix. `S` is a matrix of posterior probabilities for classes with one row per observation, similar to the `posterior` output from `predict`.
- `W` is a numeric vector with `N` elements, the observation weights. If you pass `W`, the elements are normalized to sum to the prior probabilities in the respective classes.
- `COST` is a `K`-by-`K` numeric matrix of misclassification costs. For example, you can use `COST = ones(K) - eye(K)`, which means a cost of `0` for correct classification, and `1` for misclassification.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

True Misclassification Cost

There are two costs associated with classification: the true misclassification cost per class, and the expected misclassification cost per observation.

You can set the true misclassification cost per class in the `Cost` name-value pair when you create the classifier using the `fitctree` method. `Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

Expected Misclassification Cost

There are two costs associated with classification: the true misclassification cost per class, and the expected misclassification cost per observation.

Suppose you have `Nobs` observations that you want to classify with a trained classifier. Suppose you have `K` classes. You place the observations into a matrix `Xnew` with one observation per row.

The expected cost matrix `CE` has size `Nobs`-by-`K`. Each row of `CE` contains the expected (average) cost of classifying the observation into each of the `K` classes. `CE(n,k)` is

$$\sum_{i=1}^{K} \hat{P}(i \mid Xnew(n)) C(k \mid i),$$

where

- K is the number of classes.
- $\hat{P}(i \mid Xnew(n))$ is the posterior probability of class i for observation $Xnew(n)$.
- $C(k \mid i)$ is the true misclassification cost of classifying an observation as k when its true class is i.

Examples

Compute the In-Sample Classification Error

Compute the resubstitution classification error for the `ionosphere` data.

```
load ionosphere
tree = fitctree(X,Y);
L = resubLoss(tree)
```

```
L =

    0.0114
```

Examine the Classification Error for Each Subtree

Unpruned decision trees tend to overfit. One way to balance model complexity and out-of-sample performance is to prune a tree (or restrict its growth) so that in-sample and out-of-sample performance are satisfactory.

Load Fisher's iris data set. Partition the data into training (50%) and validation (50%) sets.

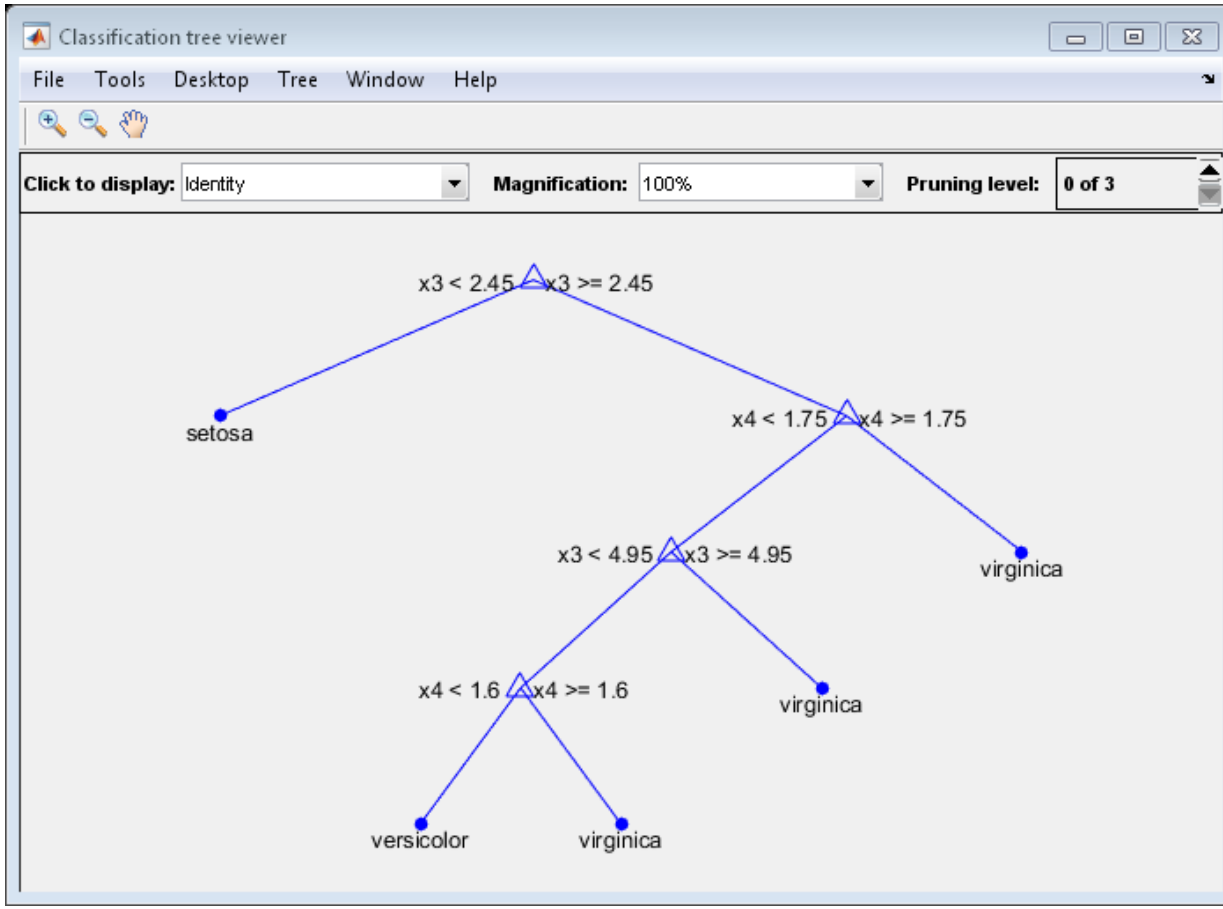
```
load fisheriris
n = size(meas,1);
rng(1) % For reproducibility
idxTrn = false(n,1);
idxTrn(randsample(n,round(0.5*n))) = true; % Training set logical indices
idxVal = idxTrn == false;                  % Validation set logical indices
```

Grow a classification tree using the training set.

```
Mdl = fitctree(meas(idxTrn,:),species(idxTrn));
```

View the classification tree.

```
view(Mdl,'Mode','graph');
```



The classification tree has four pruning levels. Level 0 is the full, unpruned tree (as displayed). Level 3 is just the root node (i.e., no splits).

Examine the training sample classification error for each subtree (or pruning level) excluding the highest level.

```
m = max(Mdl.PruneList) - 1;
trnLoss = resubLoss(Mdl,'SubTrees',0:m)
```

```
trnLoss =

    0.0267
    0.0533
    0.3067
```

- The full, unpruned tree misclassifies about 2.7% of the training observations.
- The tree pruned to level 1 misclassifies about 5.3% of the training observations.
- The tree pruned to level 2 (i.e., a stump) misclassifies about 30.6% of the training observations.

Examine the validation sample classification error at each level excluding the highest level.

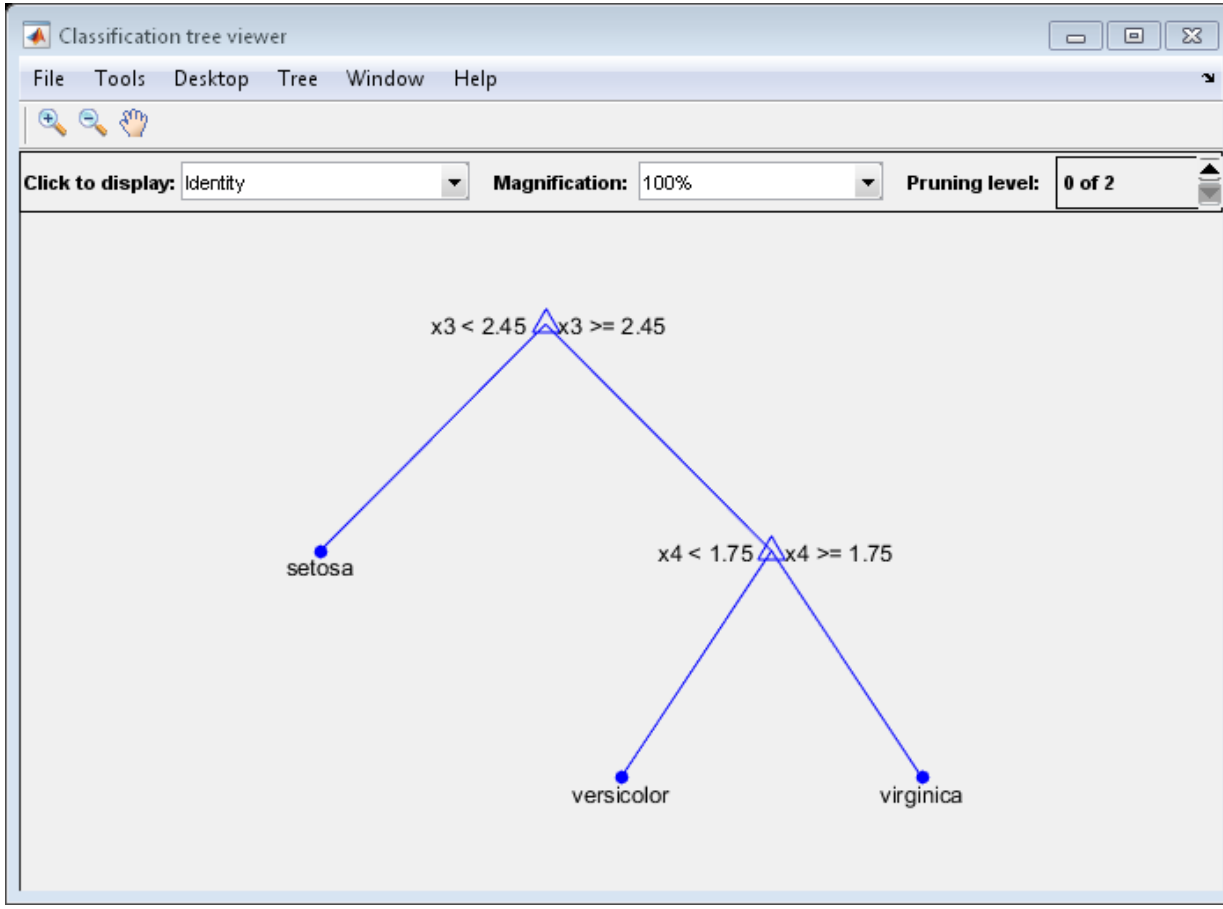
```
valLoss = loss(Mdl,meas(idxVal,:),species(idxVal),'SubTrees',0:m)
```

```
valLoss =

    0.0369
    0.0237
    0.3067
```

- The full, unpruned tree misclassifies about 3.7% of the validation observations.
- The tree pruned to level 1 misclassifies about 2.4% of the validation observations.
- The tree pruned to level 2 (i.e., a stump) misclassifies about 30.7% of the validation observations.

To balance model complexity and out-of-sample performance, consider pruning `Mdl` to level 1.

```
pruneMdl = prune(Mdl,'Level',1);
view(pruneMdl,'Mode','graph')
```



See Also

`loss` | `resubMargin` | `resubPredict` | `resubEdge` | `fitctree`

resubLoss

Class: RegressionEnsemble

Regression error by resubstitution

Syntax

```
L = resubLoss(ens)
L = resubLoss(ens,Name,Value)
```

Description

`L = resubLoss(ens)` returns the resubstitution loss, meaning the mean squared error computed for the data that `fitensemble` used to create `ens`.

`L = resubLoss(ens,Name,Value)` calculates loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `resubLoss` uses only these learners for calculating loss.

Default: `1:NumTrained`

`'lossfun'`

Function handle for loss function, or the string `'mse'`, meaning mean squared error. If you pass a function handle `fun`, `resubLoss` calls it as

```
FUN(Y,Yfit,W)
```

where `Y`, `Yfit`, and `W` are numeric vectors of the same length. `Y` is the observed response, `Yfit` is the predicted response, and `W` is the observation weights.

Default: `'mse'`

`'mode'`

String representing the meaning of the output L:

- `'ensemble'` — `L` is a scalar value, the loss for the entire ensemble.
- `'individual'` — `L` is a vector with one element per trained learner.
- `'cumulative'` — `L` is a vector in which element `J` is obtained by using learners `1:J` from the input list of learners.

Default: `'ensemble'`

Output Arguments

`L`

Loss, by default the mean squared error. `L` can be a vector, and can mean different things, depending on the name-value pair settings.

Examples

Find the resubstitution predictions of mileage from the `carsmall` data based on horsepower and weight, and look at their mean square difference from the training data.

```
load carsmall
X = [Horsepower Weight];
```

```
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
MSE = resubLoss(ens)

MSE =
    6.4336
```

See Also

`resubPredict` | `loss` | `resubLoss`

resubLoss

Class: RegressionTree

Regression error by resubstitution

Syntax

```
L = resubLoss(tree)
L = resubLoss(tree,Name,Value)
L = resubLoss(tree,'Subtrees',subtreevector)
[L,se] = resubLoss(tree,'Subtrees',subtreevector)
[L,se,NLeaf] = resubLoss(tree,'Subtrees',subtreevector)
[L,se,NLeaf,bestlevel] = resubLoss(tree,'Subtrees',subtreevector)
[L,...] = resubLoss(tree,'Subtrees',subtreevector,Name,Value)
```

Description

`L = resubLoss(tree)` returns the resubstitution loss, meaning the loss computed for the data that `fitrtree` used to create `tree`.

`L = resubLoss(tree,Name,Value)` returns the loss with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

`L = resubLoss(tree,'Subtrees',subtreevector)` returns a vector of mean squared errors for the trees in the pruning sequence `subtreevector`.

`[L,se] = resubLoss(tree,'Subtrees',subtreevector)` returns the vector of standard errors of the classification errors.

`[L,se,NLeaf] = resubLoss(tree,'Subtrees',subtreevector)` returns the vector of numbers of leaf nodes in the trees of the pruning sequence.

`[L,se,NLeaf,bestlevel] = resubLoss(tree,'Subtrees',subtreevector)` returns the best pruning level as defined in the `TreeSize` name-value pair. By default,

`bestlevel` is the pruning level that gives loss within one standard deviation of minimal loss.

`[L,...] = resubLoss(tree,'Subtrees',subtreevector,Name,Value)` returns loss statistics with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`tree`

A regression tree constructed using `fitrtree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'LossFun'`

Function handle, or the string `'mse'` meaning mean squared error.

You can write your own loss function in the syntax described in “Loss Functions” on page 22-4222.

Default: `'mse'`

Name,Value arguments associated with pruning subtrees:

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `RegressionTree.resubLoss` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`RegressionTree.resubLoss` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

`'TreeSize'`

One of the following strings:

- `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L` + `se`, where `L` and `se` relate to the smallest value in `Subtrees`).
- `'min'` — `loss` returns the element of `Subtrees` with smallest loss, usually the smallest element of `Subtrees`.

Output Arguments

`L`

Mean squared error, a vector the length of `Subtrees`. The meaning of the error depends on the values in `Weights` and `LossFun`.

`se`

Standard error of loss, a vector the length of `Subtrees`.

`NLeaf`

Number of leaves (terminal nodes) in the pruned subtrees, a vector the length of `Subtrees`.

`bestlevel`

A scalar whose value depends on `TreeSize`:

- `TreeSize` = `'se'` — `loss` returns the highest pruning level with loss within one standard deviation of the minimum (`L` + `se`, where `L` and `se` relate to the smallest value in `Subtrees`).
- `TreeSize` = `'min'` — `loss` returns the element of `Subtrees` with smallest loss, usually the smallest element of `Subtrees`.

Definitions

Loss Functions

The built-in loss function is `'mse'`, meaning mean squared error.

To write your own loss function, create a function file of the form

```
function loss = lossfun(Y,Yfit,W)
```

- `N` is the number of rows of tree`.X`.
- `Y` is an `N`-element vector representing the observed response.
- `Yfit` is an `N`-element vector representing the predicted responses.
- `W` is an `N`-element vector representing the observation weights.
- The output `loss` should be a scalar.

Pass the function handle `@lossfun` as the value of the `LossFun` name-value pair.

Examples

Compute the In-Sample MSE

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
```

```
X = [Displacement Horsepower Weight];
```

Grow a regression tree using all observations.

```
Mdl = fitrtree(X,MPG);
```

Compute the resubstitution MSE.

```
resubLoss(Mdl)
```

```
ans =

    4.8952
```

Examine the MSE for Each Subtree

Unpruned decision trees tend to overfit. One way to balance model complexity and out-of-sample performance is to prune a tree (or restrict its growth) so that in-sample and out-of-sample performance are satisfactory.

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
X = [Displacement Horsepower Weight];
Y = MPG;
```

Partition the data into training (50%) and validation (50%) sets.

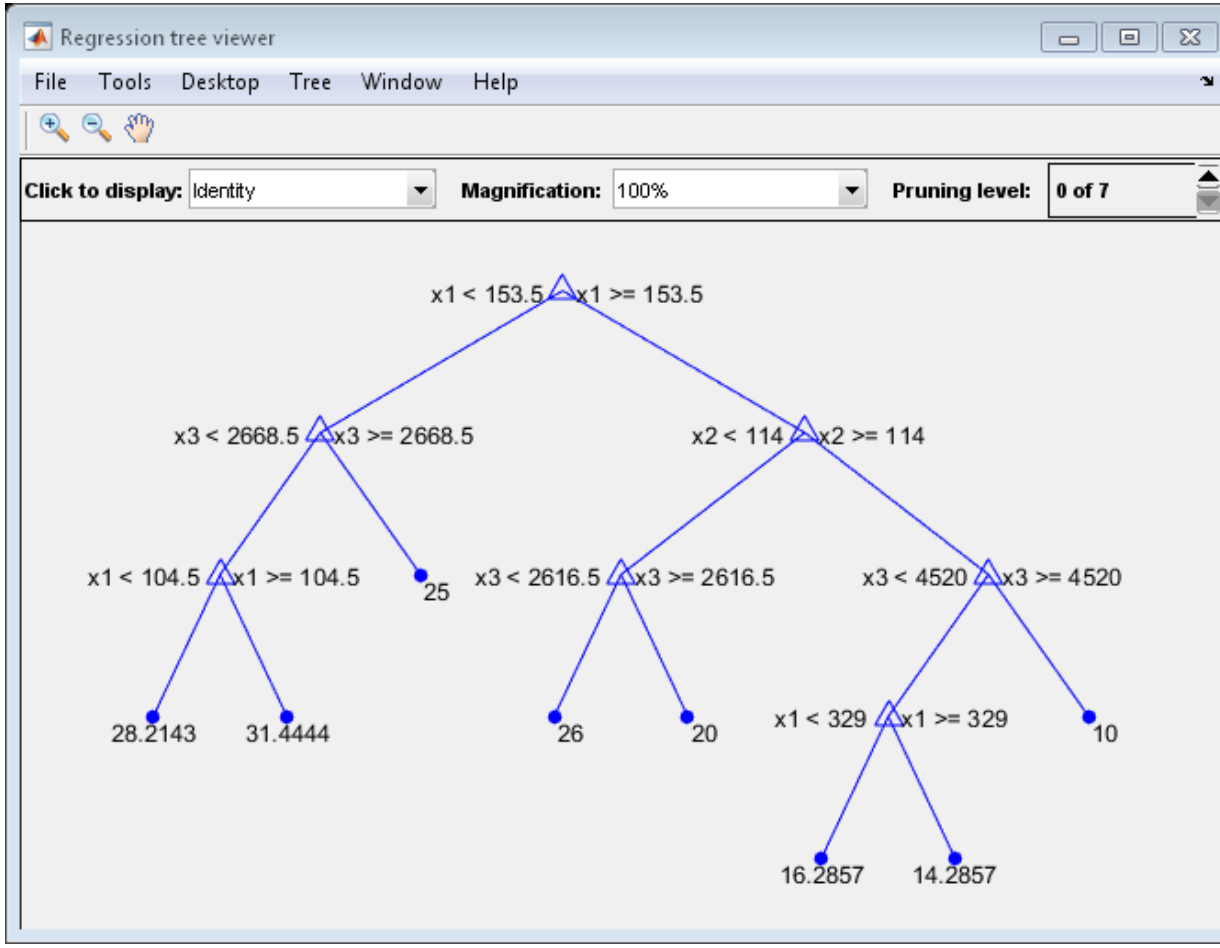
```
n = size(X,1);
rng(1) % For reproducibility
idxTrn = false(n,1);
idxTrn(randsample(n,round(0.5*n))) = true; % Training set logical indices
idxVal = idxTrn == false;                  % Validation set logical indices
```

Grow a regression tree using the training set.

```
Mdl = fitrtree(X(idxTrn,:),Y(idxTrn));
```

View the regression tree.

```
view(Mdl,'Mode','graph');
```



The regression tree has seven pruning levels. Level 0 is the full, unpruned tree (as displayed). Level 7 is just the root node (i.e., no splits).

Examine the training sample MSE for each subtree (or pruning level) excluding the highest level.

```
m = max(Mdl.PruneList) - 1;
trnLoss = resubLoss(Mdl,'SubTrees',0:m)
```

```
trnLoss =

    5.9789
    6.2768
    6.8316
    7.5209
    8.3951
   10.7452
   14.8445
```

- The MSE for the full, unpruned tree is about 6 units.
- The MSE for the tree pruned to level 1 is about 6.3 units.
- The MSE for the tree pruned to level 6 (i.e., a stump) is about 14.8 units.

Examine the validation sample MSE at each level excluding the highest level.

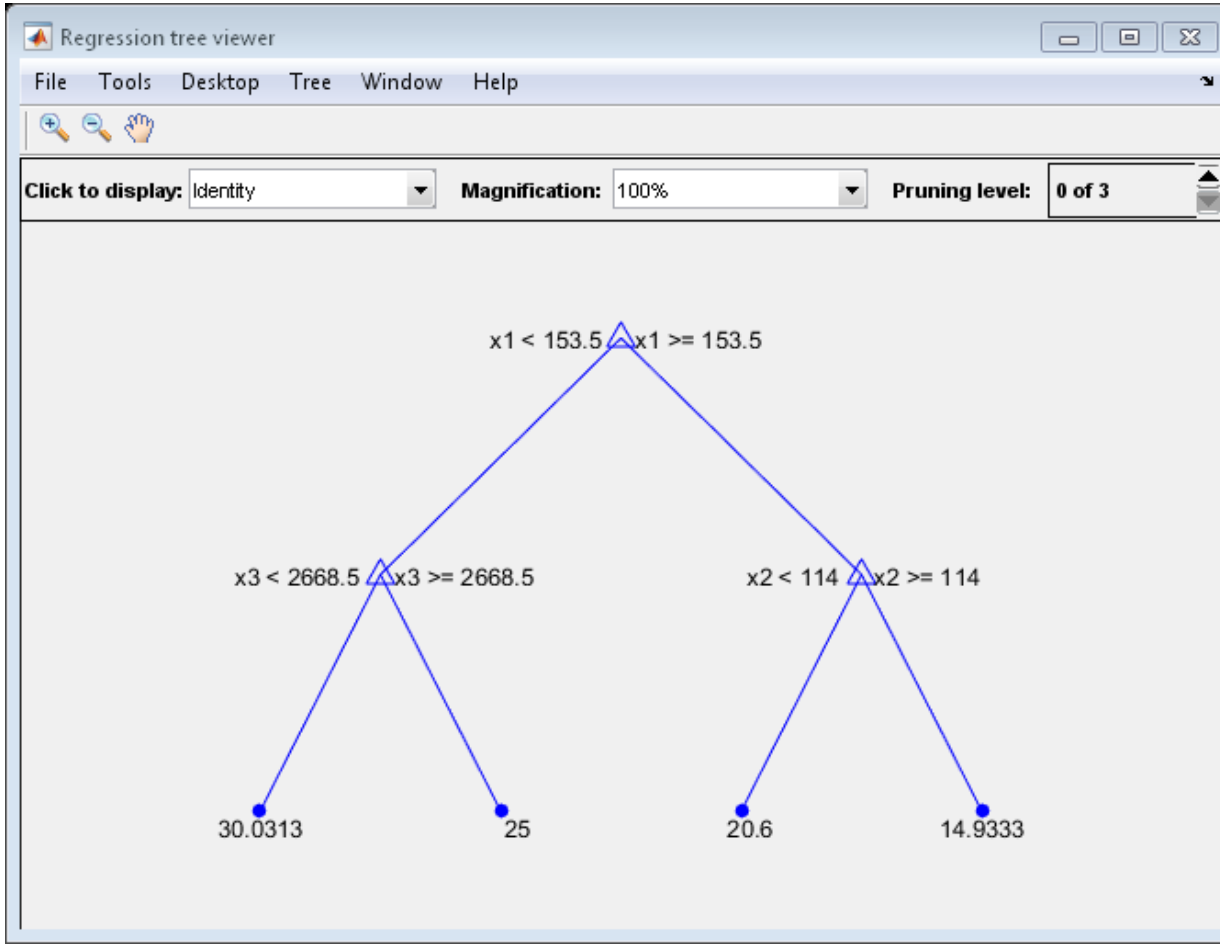
```
valLoss = loss(Mdl,X(idxVal,:),Y(idxVal),'SubTrees',0:m)
```

```
valLoss =

   32.1205
   31.5035
   32.0541
   30.8183
   26.3535
   30.0137
   38.4695
```

- The MSE for the full, unpruned tree (level 0) is about 32.1 units.
- The MSE for the tree pruned to level 4 is about 26.4 units.
- The MSE for the tree pruned to level 5 is about 30.0 units.
- The MSE for the tree pruned to level 6 (i.e., a stump) is about 38.5 units.

To balance model complexity and out-of-sample performance, consider pruning `Mdl` to level 4.

```
pruneMdl = prune(Mdl,'Level',4);
view(pruneMdl,'Mode','graph')
```



See Also

`resubPredict` | `loss` | `fitrtree`

resubMargin

Class: ClassificationDiscriminant

Classification margins by resubstitution

Syntax

```
M = resubMargin(obj)
```

Description

`M = resubMargin(obj)` returns resubstitution classification margins for `obj`.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

Output Arguments

`M`

Numeric column-vector of length `size(obj.X,1)` containing the classification margins.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

The classification margin is a column vector with the same number of rows as in the matrix X. A high value of margin indicates a more reliable prediction than a low value.

Score

For discriminant analysis, the *score* of a classification is the posterior probability of the classification. For the definition of posterior probability in discriminant analysis, see “Posterior Probability” on page 15-7.

Examples

Estimate Resubstitution Margins for Discriminant Analysis Classifiers

Find the margins for a discriminant analysis classifier for Fisher's iris data by resubstitution. Examine several entries.

Load Fisher's iris data set.

```
load fisheriris
```

Train a discriminant analysis classifier.

```
Mdl = fitcdiscr(meas,species);
```

Compute the resubstitution margins, and display several of them.

```
m = resubMargin(Mdl);
m(1:25:end)
```

```
ans =

    1.0000
    1.0000
    0.9998
    0.9998
    1.0000
    0.9946
```

See Also

`ClassificationDiscriminant` | `fitcdiscr` | `margin`

How To

- “Discriminant Analysis” on page 15-3

resubMargin

Class: ClassificationECOC

Classification margins for error-correcting output codes, multiclass models by resubstitution

Syntax

```
m = margin(Mdl)
m = margin(Mdl,Name,Value)
```

Description

`m = margin(Mdl)` returns the classification margins (`m`) for the trained, error-correcting output codes (ECOC), multiclass model `Mdl` using the training data stored in `Mdl.X` and corresponding class labels stored in `Mdl.Y`.

`m = margin(Mdl,Name,Value)` returns the classification margins with additional options specified by one or more Name,Value pair arguments.

For example, specify a decoding scheme, binary learner loss function, or verbosity level.

Input Arguments

`Mdl` — ECOC multiclass model

`ClassificationECOC` model

ECOC multiclass model, specified as a `ClassificationECOC` model returned by `fitcecoc`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

  The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `Mdl.CodingMatrix`.
  - `s` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.

- L is the number of binary learners.

For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`
- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single | double`

Output Arguments

`m` — Classification margins

numeric column vector

Classification margins, returned as a numeric column vector.

`m` has the same length as `Mdl.Y`. The software estimates each entry of `m` using the trained ECOC model Mdl, the corresponding row of Mdl.X, and the true class label Mdl.Y.

Definitions

Classification Margin

The *classification margins* are, for each observation, the difference between the negative loss for the positive class and maximal negative loss among the negative classes. If the margins are on the same scale, then they serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [4].

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left|m_{kj}\right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$

Value	Description	Score Domain	$g(y_j,s_j)$
`'quadratic'`	Quadratic	[0,1]	$[1-y_j(2s_j-1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Estimate In-Sample Classification Margins of ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = species;
```

Train an ECOC model using SVM binary classifiers. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

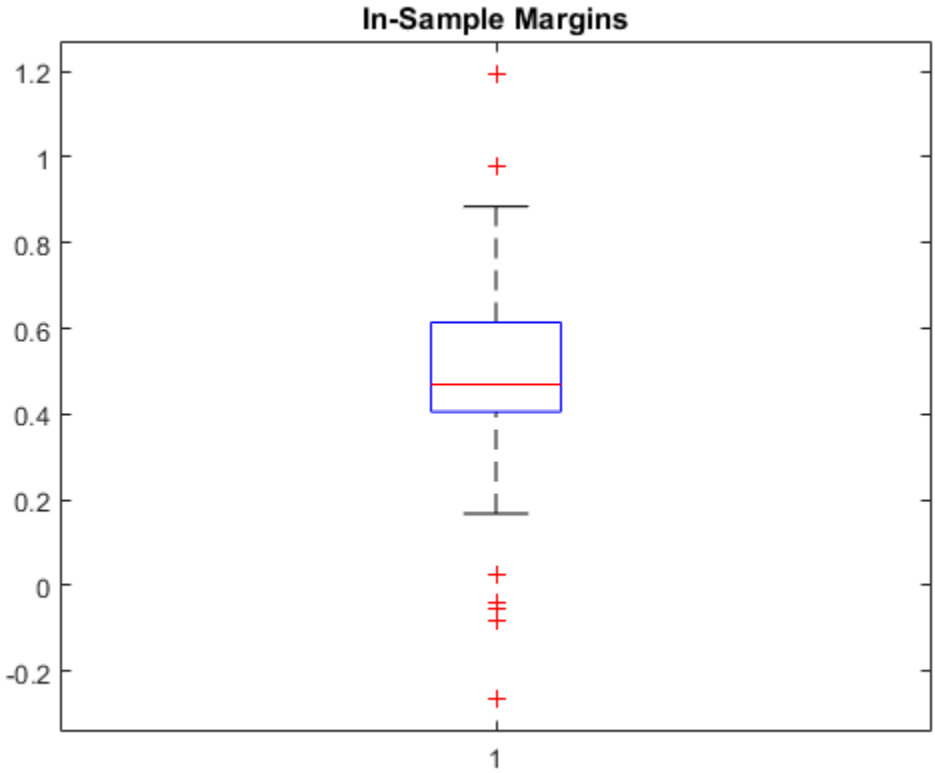
```
t = templateSVM('Standardize',1);
classOrder = unique(Y)
Mdl = fitcecoc(X,Y,'Learners',t,'ClassNames',classOrder);
```

```
classOrder =

    'setosa'
    'versicolor'
    'virginica'
```

`t` is an SVM template object. The software uses default values for empty options in `t` during training. `Mdl` is a `ClassificationECOC` model.

Estimate the in-sample classification margins. Display the distribution of the margins using a boxplot.

```
m = resubMargin(Mdl);

figure;
boxplot(m);
title 'In-Sample Margins'
```



An observation margin is the positive-class, negated loss minus the maximum negative-class, negated loss. Classifiers that yield relatively large margins are desirable.

Select ECOC Model Features by Examining In-Sample Margins

The classifier margins measure, for each observation, the difference between the positive-class, negated loss score and the maximal negative-class, negated loss. One way to

perform feature selection is to compare in-sample margins from multiple models. Based solely on this criterion, the model with the highest margins is the best model.

Load Fisher's iris data set. Define two data sets:

- `fullX` contains all 4 predictors.
- `partX` contains the sepal measurements.

```
load fisheriris
X = meas;
fullX = X;
partX = X(:,1:2);
Y = species;
```

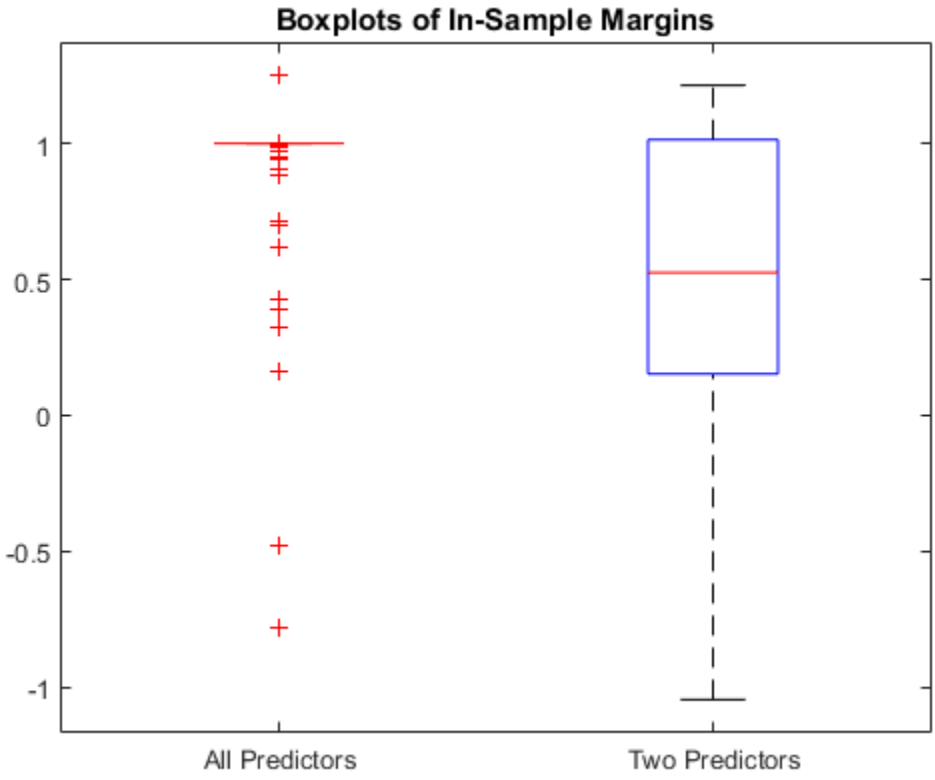
Train ECOC models using SVM binary learners for each predictor set. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template, and to compute posterior probabilities.

```
t = templateSVM('Standardize',1);
classOrder = unique(Y)
FullMdl = fitcecoc(fullX,Y,'Learners',t,'ClassNames',classOrder,...
    'FitPosterior',1);
PartMdl = fitcecoc(partX,Y,'Learners',t,'ClassNames',classOrder,...
    'FitPosterior',1);
```

```
classOrder =

    'setosa'
    'versicolor'
    'virginica'
```

Estimate the in-sample margins for each classifier. For each model, display the distribution of the margins using a boxplot.

```
fullMargins = resubMargin(FullMdl);
partMargins = resubMargin(PartMdl);

figure;
boxplot([fullMargins partMargins],'Labels',{'All Predictors','Two Predictors'});
title('Boxplots of In-Sample Margins')
```



The margin distribution of CMdl is situated higher, and with less variablility than the margin distribution of PCMdl.

- “Quick Start Parallel Computing for Statistics and Machine Learning Toolbox” on page 21-2

Tip

To compare margins or edges of several classifiers, use template objects to specify a common score transform function among the classifiers when you train them using `fitcecoc`.

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[3] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[4] Hu, Q., X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationECOC` | `fitcecoc` | `margin` | `predict` | `resubEdge` | `resubPredict`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

resubMargin

Class: ClassificationEnsemble

Classification margins by resubstitution

Syntax

```
margin = resubMargin(ens)
margin = resubMargin(ens,Name,Value)
```

Description

`margin = resubMargin(ens)` returns the classification margin obtained by `ens` on its training data.

`margin = resubMargin(ens,Name,Value)` calculates margins with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `resubMargin` uses only these learners for calculating margin.

Default: `1:NumTrained`

Output Arguments

`margin`

A numeric column-vector of length `size(ens.X,1)` containing the classification margins.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes. Margin is a column vector with the same number of rows as in the matrix `ens.X`.

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the resubstitution margins for an ensemble that classifies the Fisher iris data:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
margin = resubMargin(ens);
[min(margin) mean(margin) max(margin)]
```

```
ans =
   -0.5674    3.2486    4.6245
```

See Also

`resubEdge` | `resubMargin` | `resubLoss` | `resubPredict`

resubMargin

Class: ClassificationKNN

Margin of *k*-nearest neighbor classifier by resubstitution

Syntax

```
m = resubMargin(mdl)
```

Description

`m = resubMargin(mdl)` returns the classification margins of the data used to train `mdl`. For the definition, see "Margin" on page 22-4244.

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

Output Arguments

`m`

A numeric column vector of length `size(mdl.X,1)`, where `mdl.X` is the training data for `mdl`. Each entry in `m` represents the margin for the corresponding row of mdl.X and (true class) mdl.Y.

Definitions

Margin

The classification *margin* is the difference between the classification *score* for the true class and maximal classification score for the false classes.

Margin is a column vector with the same number of rows as in the training data.

Score

The *score* of a classification is the posterior probability of the classification. The posterior probability is the number of neighbors that have that classification, divided by the number of neighbors. For a more detailed definition that includes weights and prior probabilities, see “Posterior Probability” on page 22-3654.

Examples

Resubstitution Margin Calculation

Construct a k-nearest neighbor classifier for the Fisher iris data, where $k = 5$.

Load the data.

```
load fisheriris
X = meas;
Y = species;
```

Construct a classifier for 5-nearest neighbors.

```
mdl = fitcknn(X,Y,'NumNeighbors',5);
```

Examine some statistics of the resubstitution margin of the classifier.

```
m = resubMargin(mdl);
[max(m) min(m) mean(m)]
```

```
ans =

    1.0000   -0.6000    0.9253
```

The mean margin is over 0.9, indicating fairly high classification accuracy for resubstitution. For more reliable assessment of model accuracy, consider cross validation, such as `kfoldLoss`.

- "Examine the Quality of a KNN Classifier" on page 16-29

See Also

`ClassificationKNN` | `fitcknn` | `resubEdge` | `resubLoss` | `resubPredict`

More About

- "Classification Using Nearest Neighbors" on page 16-8

resubMargin

Class: ClassificationNaiveBayes

Classification margins for naive Bayes classifiers by resubstitution

Syntax

```
m = resubMargin(Mdl)
```

Description

`m = resubMargin(Mdl)` returns the resubstitution classification margins (`m`) for the naive Bayes classifier `Mdl` using the training data stored in `Mdl.X` and corresponding class labels stored in `Mdl.Y`.

Input Arguments

`Mdl` — Fully trained naive Bayes classifier

`ClassificationNaiveBayes` model

A fully trained naive Bayes classifier, specified as a `ClassificationNaiveBayes` model trained by `fitcnb`.

Output Arguments

`m` — Classification margins

numeric vector

Classification margins, returned as a numeric vector.

`m` has the same length equal to `size(Mdl.X,1)`. Each entry of `m` is the classification margin of the corresponding observation (row) of Mdl.X and element of Mdl.Y.

Definitions

Classification Edge

The *classification edge* is the weighted mean of the classification margins.

If you supply weights, then the software normalizes them to sum to the prior probability of their respective class. The software uses the normalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Classification Margin

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.

- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

$$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Score

The naive Bayes *score* is the class posterior probability given the observation.

Examples

Estimate In-Sample Classification Margins of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

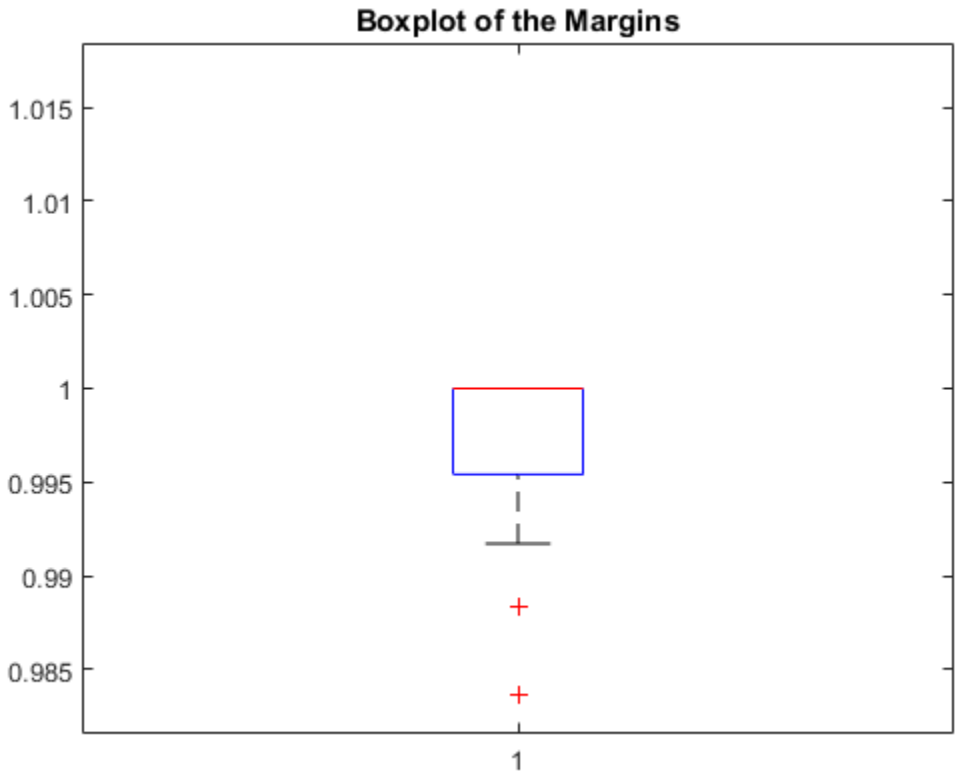
```
Mdl = fitcnb(X,Y,'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationNaiveBayes` classifier.

Estimate the in-sample classification margins. Display the distribution of the margins using a boxplot.

```
m = resubMargin(Mdl);

figure;
boxplot(m);
h = gca;
iqr = quantile(m,0.75) - quantile(m,0.25);
h.YLim = median(m) + iqr*[-4 4];
```

```
title 'Boxplot of the Margins';
```



An observation margin is the observed (true) class score minus the maximum false class score among all scores in the respective class. Classifiers that yield relatively large margins are desirable.

Select Naive Bayes Classifier Features by Examining In-Sample Margins

The classifier margins measure, for each observation, the difference between the true class observed score and the maximal false class score for a particular class. One way to perform feature selection is to compare in-sample margins from multiple models. Based solely on this criterion, the model with the highest margins is the best model.

Load Fisher's iris data set. Define two data sets:

- `fullX` contains all predictors (except the removed column of 0s).
- `partX` contains the last 20 predictors.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
fullX = X;
partX = X(:,3:4);
```

Train naive Bayes classifiers for each predictor set.

```
FullMdl = fitcnb(fullX,Y);
PartMdl = fitcnb(partX,Y);
```

Estimate the in-sample margins for each classifier. Compute confidence intervals for each sample.

```
fullM = resubMargin(FullMdl);
partM = resubMargin(PartMdl);
n = size(X,1);
fullMCI = mean(fullM) + 2*[-std(fullM)/n std(fullM)/n]
partMCI = mean(partM) + 2*[-std(partM)/n std(partM)/n]
```

```
fullMCI =

    0.8898    0.8991


partMCI =

    0.9129    0.9209
```

The confidence intervals are tight, and mutually exclusive. The margin confidence interval of the classifier trained using just predictors 3 and 4 has higher values than that of the full model. Therefore, the model trained on two predictors has better in-sample performance.

References

[1] Hu, Q., X. Che, L. Zhang, and D. Yu. “Feature Evaluation and Selection Based on Neighborhood Soft Margin.” *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm` | `margin` | `resubEdge` | `resubLoss`

resubMargin

Class: ClassificationSVM

Classification margins for support vector machine classifiers by resubstitution

Syntax

```
m = resubMargin(SVMModel)
```

Description

`m = resubMargin(SVMModel)` returns the resubstitution classification margins (`m`) for the support vector machine (SVM) classifier `SVMModel` using the training data stored in `SVMModel.X` and corresponding class labels stored in `SVMModel.Y`.

Input Arguments

`SVMModel` — Full, trained SVM classifier

`ClassificationSVM` classifier

Full, trained SVM classifier, specified as a `ClassificationSVM` model trained using `fitcsvm`.

Output Arguments

`m` — Classification margins

numeric vector

Classification margins, returned as a numeric vector.

`m` has the same length as `Y`. The software estimates each entry of `m` using the trained SVM classifier SVMModel, the corresponding row of X, and the true class label Y.

Definitions

Margins

The *classification margins* are, for each observation, the difference between the score for the true class and maximal score for the false classes. Provided that they are on the same scale, margins serve as a classification confidence measure, i.e., among multiple classifiers, those that yield larger margins are better [2].

Edge

The *edge* is the weighted mean of the *classification margins*.

The weights are the prior class probabilities. If you supply weights, then the software normalizes them to sum to the prior probabilities in the respective classes. The software uses the renormalized weights to compute the weighted mean.

One way to choose among multiple classifiers, e.g., to perform feature selection, is to choose the classifier that yields the highest edge.

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j,x) = x_j'x$ (the linear kernel), then the score function reduces to

$$f(x) = (x / s)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Examples

Estimate In-Sample Classification Margins of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to specify the class order and standardize the data.

```
SVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier. The negative class is `'b'` and the positive class is `'g'`.

Estimate the in-sample classification margins.

```
m = resubMargin(SVMModel);
m(10:20)
```

```
ans =

    5.5622
    4.2918
    1.9993
    4.5520
   -1.4897
    3.2816
    4.0260
    4.5419
   16.4449
```

```
    2.0006
   23.3782
```

An observation margin is the observed (true) class score minus the maximum false class score among all scores in the respective class. Classifiers that yield relatively large margins are desirable.

Select SVM Classifier Features by Examining In-Sample Margins

The classifier margins measure, for each observation, the difference between the true class observed score and the maximal false class score for a particular class. One way to perform feature selection is to compare in-sample margins from multiple models. Based solely on this criterion, the model with the highest margins is the best model.

Load the `ionosphere` data set. Define two data sets:

- `fullX` contains all predictors (except the removed column of 0s).
- `partX` contains the last 20 predictors.

```
load ionosphere
fullX = X;
partX = X(:,end-20:end);
```

Train SVM classifiers for each predictor set.

```
FullSVMModel = fitcsvm(fullX,Y);
PartSVMModel = fitcsvm(partX,Y);
```

Estimate the in-sample margins for each classifier.

```
fullMargins = resubMargin(FullSVMModel);
partMargins = resubMargin(PartSVMModel);
n = size(X,1);
p = sum(fullMargins < partMargins)/n
```

```
p =

    0.2222
```

Approximately 22% of the margins from the full model are less than those from the model with fewer predictors. This suggests that the model trained using all of the predictors is better.

Algorithms

For binary classification, the software defines the margin for observation j, m_j, as

$$m_j = 2y_j f(x_j),$$

where $y_j \in \{-1,1\}$, and $f(x_j)$ is the predicted score of observation j for the positive class. However, the literature commonly uses $m_j = y_j f(x_j)$ to define the margin.

References

[1] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[2] Hu, Q., X. Che, L. Zhang, and D. Yu. "Feature Evaluation and Selection Based on Neighborhood Soft Margin." *Neurocomputing*. Vol. 73, 2010, pp. 2114–2124.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm` | `margin` | `resubEdge` | `resubLoss`

resubMargin

Class: ClassificationTree

Classification margins by resubstitution

Syntax

```
M = resubMargin(tree)
```

Description

`M = resubMargin(tree)` returns resubstitution classification margins for `tree`.

Input Arguments

`tree`

A classification tree created by `fitctree`.

Output Arguments

`M`

A numeric column-vector of length `size(tree.X,1)` containing the classification margins.

Definitions

Margin

Classification *margin* is the difference between classification *score* for the true class and maximal classification score for the false classes. A high value of margin indicates a more reliable prediction than a low value.

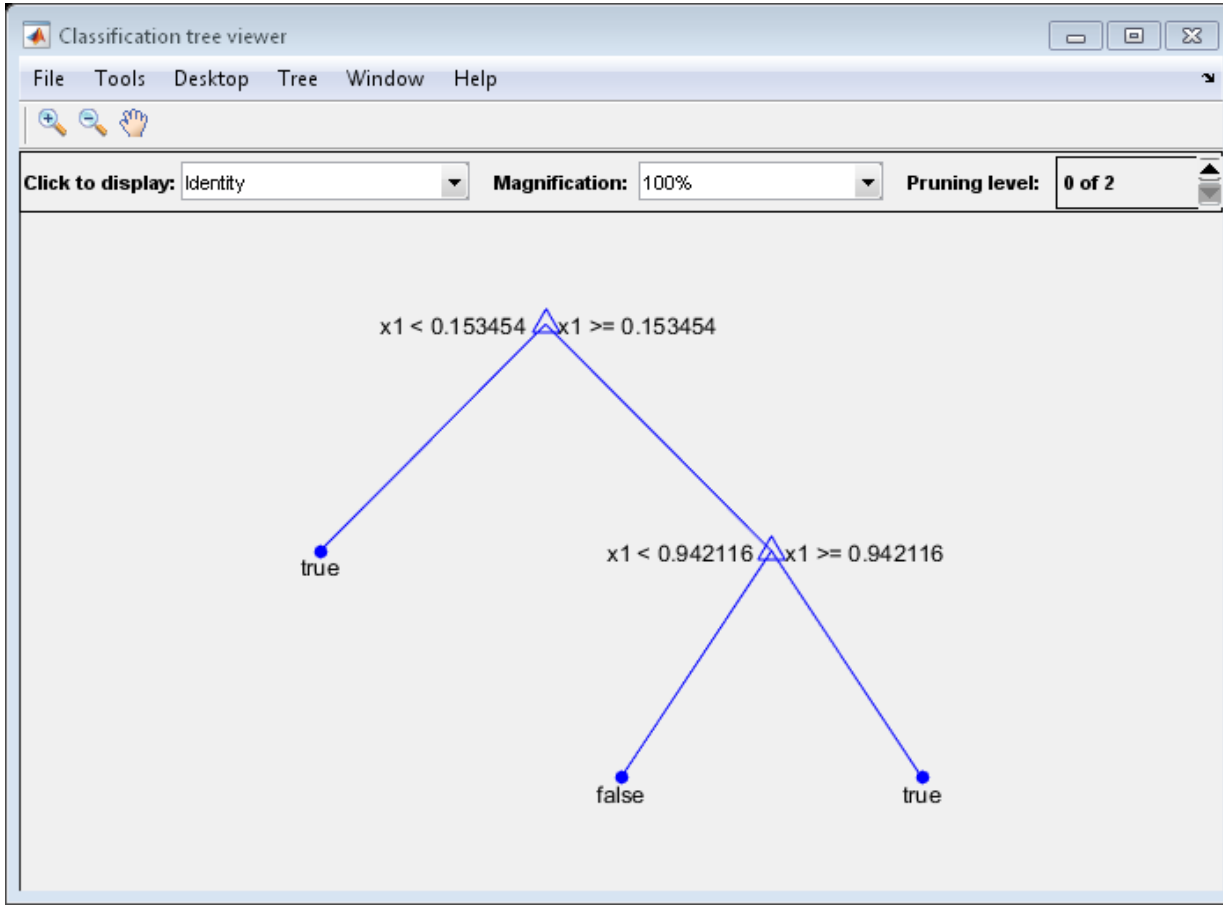
Score (tree)

For trees, the *score* of a classification of a leaf node is the posterior probability of the classification at that node. The posterior probability of the classification at a node is the number of training sequences that lead to that node with the classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X < 0.15` or `X > 0.95`, and `X` is false otherwise.

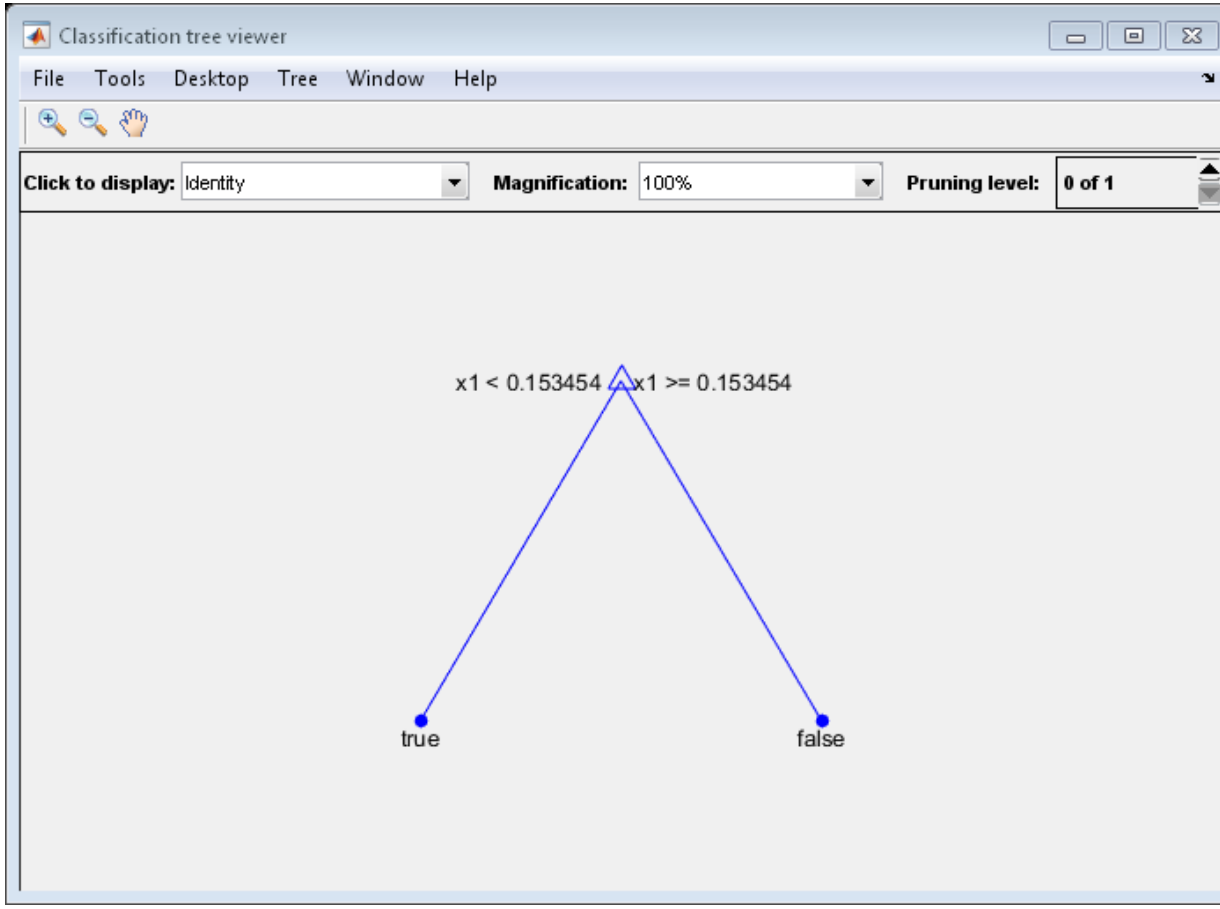
Generate 100 random points and classify them:

```
rng(0,'twister') % for reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','Graph')
```



Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','Graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations from .15 to .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore, the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]
```

```
ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the right-most column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.91` and `0.09`. The difference (score `0.09` instead of the expected `.06`) is due to a statistical fluctuation: there are `8` observations in `X` in the range `(.95,1)` instead of the expected `5` observations.

Examples

Find the margins for a classification tree for the Fisher iris data by resubstitution. Examine several entries:

```
load fisheriris
tree = fitctree(meas,species);
M = resubMargin(tree);
M(1:25:end)
```

```
ans =
    1.0000
    1.0000
    1.0000
    1.0000
    0.9565
    0.9565
```

See Also

`margin` | `resubEdge` | `fitctree` | `resubLoss` | `resubPredict`

resubPredict

Class: ClassificationDiscriminant

Predict resubstitution response of classifier

Syntax

```
label = resubPredict(obj)
[label,posterior] = resubPredict(obj)
[label,posterior,cost] = resubPredict(obj)
```

Description

`label = resubPredict(obj)` returns the labels `obj` predicts for the data `obj.X`. `label` is the predictions of `obj` on the data that `fitcdiscr` used to create `obj`.

`[label,posterior] = resubPredict(obj)` returns the posterior class probabilities for the predictions.

`[label,posterior,cost] = resubPredict(obj)` returns the predicted misclassification costs per class for the resubstituted data.

Input Arguments

`obj`

Discriminant analysis classifier, produced using `fitcdiscr`.

Output Arguments

`label`

Response obj predicts for the training data. `label` is the same data type as the training response data `obj.Y`. The predicted class labels are those with minimal expected misclassification cost; see “How the predict Method Classifies” on page 15-6.

`posterior`

N-by-K matrix of posterior probabilities for classes obj predicts, where N is the number of observations and K is the number of classes.

`cost`

N-by-K matrix of predicted misclassification costs. Each cost is the average misclassification cost with respect to the posterior probability.

Definitions

Posterior Probability

`posterior(i,k)` is the posterior probability of class `k` for observation `i`. For the mathematical definition, see "Posterior Probability" on page 15-7.

Examples

Find the total number of misclassifications of the Fisher iris data for a discriminant analysis classifier:

```
load fisheriris
obj = fitcdiscr(meas,species);
Ypredict = resubPredict(obj); % the predictions
Ysame = strcmp(Ypredict,species); % true when ==
sum(~Ysame) % how many are different?

ans =
     3
```

See Also

`predict` | `ClassificationDiscriminant` | `fitcdiscr`

How To

- "Discriminant Analysis" on page 15-3

resubPredict

Class: ClassificationECOC

Predict error-correcting output codes, multiclass model resubstitution responses

Syntax

```
label = resubPredict(Mdl)
label = resubPredict(Mdl,Name,Value)
[label,NegLoss,PBScore] = resubPredict( ___ )
[label,NegLoss,PBScore,Posterior] = resubPredict( ___ )
```

Description

`label = resubPredict(Mdl)` returns a vector of predicted class labels for the predictor data (stored in `Mdl.X`) based on the trained error-correcting output codes, multiclass model `Mdl`.

The software predicts the classification of an observation by assigning the observation to the class yielding the largest negated average binary loss (or, equivalently, the smallest average binary loss).

`label = resubPredict(Mdl,Name,Value)` returns predicted class labels with additional options specified by one or more Name,Value pair arguments.

For example, specify the posterior probability estimation method, decoding scheme, or verbosity level.

`[label,NegLoss,PBScore] = resubPredict( ___ )` additionally returns negated average binary loss per class (`NegLoss`) for observations, and positive-class scores (`PBScore`) for the observations classified by each binary learner.

`[label,NegLoss,PBScore,Posterior] = resubPredict( ___ )` additionally returns posterior class probability estimates for observations (`Posterior`).

To obtain posterior class probabilities, you must set `'FitPosterior',1` when training the ECOC model using `fitcecoc`. Otherwise, `resubPredict` throws an error.

Input Arguments

`Mdl` — ECOC multiclass model

`ClassificationECOC` model

ECOC multiclass model, specified as a `ClassificationECOC` model returned by `fitcecoc`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BinaryLoss'` — Binary learner loss function

function handle | `'hamming'` | `'linear'` | `'exponential'` | `'binodeviance'` | `'hinge'` | `'quadratic'`

Binary learner loss function, specified as the comma-separated pair consisting of `'BinaryLoss'` and a function handle or string.

- If the value is a string, then it must correspond to a built-in function. This table summarizes the built-in functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$ is the binary loss formula.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	(-∞,∞)	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	(-∞,∞)	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	(-∞,∞)	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	(-∞,∞)	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$. Also, the software calculates the mean binary loss for each class.

- For a custom binary loss function, e.g., `customFunction`, specify its function handle `'BinaryLoss',@customFunction`.

  `customFunction` should have this form

  ```
  bLoss = customFunction(M,s)
  ```
  where:

  - `M` is the K-by-L coding matrix stored in `Mdl.CodingMatrix`.
  - `s` is the 1-by-L row vector of classification scores.
  - `bLoss` is the classification loss. This scalar aggregates the binary losses for every learner in a particular class. For example, you can use the mean binary loss to aggregate the loss over the learners for each class.
  - K is the number of classes.
  - L is the number of binary learners.

  For an example on passing a custom binary loss function, see "Predict Test-Sample Labels of ECOC Models Using Custom Binary Loss Function".

This list describes the default values of `BinayLoss`. If all binary learners are:

- SVMs, then `BinaryLoss` is `'hinge'`
- Ensembles trained by `AdaboostM1` or `GentleBoost`, then `BinaryLoss` is `'exponential'`
- Ensembles trained by `LogitBoost`, then `BinaryLoss` is `'binodeviance'`
- Predicting class posterior probabilities (i.e., set `'FitPosterior',1` in `fitcecoc`), then `BinaryLoss` is `'quadratic'`

Otherwise, the default `BinaryLoss` is `'hamming'`.

Example: `'BinaryLoss','binodeviance'`

Data Types: `char` | `function_handle`

`'Decoding'` — Decoding scheme

`'lossweighted'` (default) | `'lossbased'`

Decoding scheme that aggregates the binary losses, specified as the comma-separated pair consisting of `'Decoding'` and `'lossweighted'` or `'lossbased'`.

Example: `'Decoding','lossbased'`

Data Types: `char`

`'NumKLInitializations'` — Number of random initial values

`0` (default) | nonnegative integer

Number of random initial values for fitting posterior probabilities by Kullback-Leibler divergence minimization, specified as the comma-separated pair consisting of `'NumKLInitializations'` and a nonnegative integer.

If you do not request the fourth output argument (Posterior) and set `'PosteriorMethod','kl'` (the default), then the software ignores the value of `NumKLInitializations`.

For more details, see "Posterior Estimation Using Kullback-Leibler Divergence" on page 22-3679.

Example: `'NumKLInitializations',5`

Data Types: `single` | `double`

`'Options'` — Estimation options

`[]` (default) | structure array returned by `statset`

Estimation options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`.

To invoke parallel computing:

- You need a Parallel Computing Toolbox license.
- Specify `'Options',statset('UseParallel',1)`.

`'PosteriorMethod'` — Posterior probability estimation method

`'kl'` (default) | `'qp'`

Posterior probability estimation method, specified as the comma-separated pair consisting of `'PosteriorMethod'` and `'kl'` or `'qp'`.

- If `PosteriorMethod` is `'kl'`, then the software estimates multiclass posterior probabilities by minimizing the Kullback-Leibler divergence between the predicted

and expected posterior probabilities returned by binary learners. For details, see "Posterior Estimation Using Kullback-Leibler Divergence".

- If `PosteriorMethod` is `'qp'`, then the software estimates multiclass posterior probabilities by solving a least-squares problem using quadratic programming. You need an Optimization Toolbox license to use this option. For details, see "Posterior Estimation Using Quadratic Programming".
- If you do not request the fourth output argument (Posterior), then the software ignores the value of `PosteriorMethod`.

Example: `'PosteriorMethod','qp'`

Data Types: `char`

`'Verbose'` — Verbosity level

`0` (default) | `1`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0` or `1`. `Verbose` controls the amount of diagnostic messages that the software displays in the Command Window.

If `Verbose` is `0`, then the software does not display diagnostic messages. Otherwise, the software displays diagnostic messages.

Example: `'Verbose',1`

Data Types: `single` | `double`

Output Arguments

`label` — Predicted class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Predicted class labels, returned as a categorical or character array, logical or numeric vector, or cell array of strings.

`label` is the same data type as the Mdl.ClassNames, and has length equal to the number of rows of Mdl.X.

The software predicts the classification of an observation by assigning the observation to the class yielding the largest negated average binary loss (or, equivalently, the smallest average binary loss).

`NegLoss` — Negated average binary losses

numeric matrix

Negated, average binary losses, returned as a numeric matrix. `NegLoss` is an `n`-by-`K` matrix, where `n` is the number of observations (`size(Mdl.X,1)`) and `K` is the number of unique classes (`size(Mdl.ClassNames,1)`).

`PBScore` — Positive-class scores

numeric matrix

Positive-class scores for each binary learner, returned as a numeric matrix. `PBScore` is an `n`-by-`L` matrix, where `n` is the number of observations (`size(Mdl.X,1)`) and `L` is the number of binary learners (`size(Mdl.CodingMatrix,2)`).

`Posterior` — Posterior class probabilities

numeric matrix

Posterior class probabilities, returned as a numeric matrix. `Posterior` is an `n`-by-`K` matrix, where `n` is the number of observations (`size(Mdl.X,1)`) and `K` is the number of unique classes (`size(Mdl.ClassNames,1)`).

You must set `'FitPosterior',1` when training the ECOC model using `fitcecoc` to request `Posterior`. Otherwise, the software throws an error.

Definitions

Binary Loss

A *binary loss* is a function of the class and classification score that determines how well a binary learner classifies an observation into the class.

Let:

- m_{kj} be element (k,j) of the coding design matrix M (i.e., the code corresponding to class k of binary learner j)
- s_j be the score of binary learner j for an observation
- g be the binary loss function
- $\hat{k}$ be the predicted class for the observation

In *loss-based decoding* [3], the class producing the minimum sum of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j).$$

In *loss-weighted decoding* [3], the class producing the minimum average of the binary losses over binary learners determines the predicted class of an observation, that is,

$$\hat{k} = \underset{k}{\operatorname{argmin}} \frac{\sum_{j=1}^{L} \left|m_{kj}\right| g(m_{kj}, s_j)}{\sum_{j=1}^{L} \left|m_{kj}\right|}.$$

Allwein et al. [1] suggest that loss-weighted decoding improves classification accuracy by keeping loss values for all classes in the same dynamic range.

This table summarizes the supported loss functions, where y_j is a class label for a particular binary learner (in the set {-1,1,0}), s_j is the score for observation j, and $g(y_j,s_j)$.

Value	Description	Score Domain	$g(y_j,s_j)$
`'binodeviance'`	Binomial deviance	$(-\infty,\infty)$	$\log[1 + \exp(-2y_js_j)]/[2\log(2)]$
`'exponential'`	Exponential	$(-\infty,\infty)$	$\exp(-y_js_j)/2$
`'hamming'`	Hamming	{-1,1}	$[1 - \text{sign}(y_js_j)]/2$
`'hinge'`	Hinge	$(-\infty,\infty)$	$\max(0,1 - y_js_j)/2$
`'linear'`	Linear	$(-\infty,\infty)$	$(1 - y_js_j)/2$
`'quadratic'`	Quadratic	[0,1]	$[1 - y_j(2s_j - 1)]^2/2$

The software normalizes the binary losses such that the loss is 0.5 when $y_j = 0$, and aggregates using the average of the binary learners [1].

Do not confuse the binary loss with the overall classification loss (specified by the LossFun name-value pair argument of `predict` and `loss`), e.g., classification error, which measures how well an ECOC classifier performs as a whole.

Examples

Predict Labels of Training Data Using ECOC Models

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
n = numel(Y); % Sample size
classOrder = unique(Y);
```

Train an ECOC model using SVM binary classifiers. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
Mdl = fitcecoc(X,Y,'Learners',t,'ClassNames',classOrder);
```

`t` is an SVM template object. The software uses default values for empty options in `t` during training. `Mdl` is a `ClassificationECOC` model.

Predict the labels of the training data. Print a random subset of true and predicted labels.

```
labels = resubPredict(Mdl);
rng(1);
idx = randsample(n,10);
table(Y(idx),labels(idx),'VariableNames',{'TrueLabels','PredictedLabels'})
```

```
ans =

    TrueLabels    PredictedLabels
    __________    _______________

    setosa        setosa
    versicolor    versicolor
    virginica     virginica
    setosa        setosa
    versicolor    versicolor
    setosa        setosa
    versicolor    versicolor
    versicolor    versicolor
    setosa        setosa
```

```
    setosa        setosa
```

`Mdl` correctly labeled the observations with indices `idx`.

Predict Resubstitution Labels of ECOC Models Using a Custom Binary Loss Function

Load Fisher's iris data set.

```
load fisheriris
X = meas;
Y = categorical(species);
n = numel(Y);           % Sample size
classOrder = unique(Y); % Class order
K = numel(classOrder);  % Number of classes
```

Train an ECOC model using SVM binary classifiers. It is good practice to standardize the predictors and define the class order. Specify to standardize the predictors using an SVM template.

```
t = templateSVM('Standardize',1);
Mdl = fitcecoc(X,Y,'Learners',t,'ClassNames',classOrder);
```

`t` is an SVM template object. The software uses default values for empty options in `t` during training. `Mdl` is a `ClassificationECOC` model.

SVM scores are signed distances from the observation to the decision boundary. Therefore, the domain is $(-\infty,\infty)$. Create a custom binary loss function that:

- Maps the coding design matrix (*M*) and positive-class classification scores (*s*) for each learner to the binary loss for each observation
- Uses linear loss
- Aggregates the binary learner loss using the median

You can create a separate function for the binary loss function, and then save it on the MATLAB® path. Or, you can specify an anonymous binary loss function.

```
customBL = @(M,s)nanmedian(1 - bsxfun(@times,M,s),2)/2;
```

Predict resubstitution labels and estimate the median binary loss per class. Print the median negative binary losses per class for a random set of 10 observations.

```
[label,NegLoss] = resubPredict(Mdl,'BinaryLoss',customBL);

rng(1); % For reproducibility
```

```
idx = randsample(n,10);
classOrder
table(Y(idx),label(idx),NegLoss(idx,:),'VariableNames',...
    {'TrueLabel','PredictedLabel','NegLoss'})
```

```
classOrder =

     setosa
     versicolor
     virginica


ans =

    TrueLabel     PredictedLabel               NegLoss
    __________    ______________    ___________________________________

    setosa        versicolor        0.12376      1.9575     -3.5812
    versicolor    versicolor        -1.0171     0.62948     -1.1123
    virginica     virginica         -1.9088    -0.21759     0.62641
    setosa        versicolor        0.43846      2.2448     -4.1833
    versicolor    versicolor        -1.0735      0.3965    -0.82299
    setosa        versicolor        0.26658       2.201     -3.9675
    versicolor    versicolor        -1.1237     0.69927     -1.0756
    versicolor    versicolor        -1.2716     0.51847    -0.74687
    setosa        versicolor        0.35211      2.0683     -3.9204
    setosa        versicolor        0.23342      2.1892     -3.9226
```

The column order corresponds to the elements of `classOrder`. The software predicts the label based on the maximum negated loss. The results seem to indicate that the median of the linear losses might not perform as well as other losses.

Estimate Posterior Probabilities Using ECOC Classifiers

Load Fisher's iris data set. Train the classifier using the petal dimensions as predictors.

```
load fisheriris
X = meas(:,3:4);
Y = species;
rng(1); % For reproducibility
```

Create an SVM template, and specify the Gaussian kernel. It is good practice to standardize the predictors.

```
t = templateSVM('Standardize',1,'KernelFunction','gaussian');
```

`t` is an SVM template. Most of its properties are empty. When the software trains the ECOC classifier, it sets the applicable properties to their default values.

Train the ECOC classifier using the SVM template. Transform classification scores to class posterior probabilities (which are returned by `predict` or `resubPredict`) using the `'FitPosterior'` name-value pair argument. Display diagnostic messages during the training using the `'Verbose'` name-value pair argument. It is good practice to specify the class order.

```
Mdl = fitcecoc(X,Y,'Learners',t,'FitPosterior',1,...
    'ClassNames',{'setosa','versicolor','virginica'},...
    'Verbose',2);

Training binary learner 1 (SVM) out of 3 with 50 negative and 50 positive observations
Negative class indices: 2
Positive class indices: 1

Fitting posterior probabilities for learner 1 (SVM).
Training binary learner 2 (SVM) out of 3 with 50 negative and 50 positive observations
Negative class indices: 3
Positive class indices: 1

Fitting posterior probabilities for learner 2 (SVM).
Training binary learner 3 (SVM) out of 3 with 50 negative and 50 positive observations
Negative class indices: 3
Positive class indices: 2

Fitting posterior probabilities for learner 3 (SVM).
```

`Mdl` is a `ClassificationECOC` model. The same SVM template applies to each binary learner, but you can adjust options for each binary learner by passing in a cell vector of templates.

Predict the in-sample labels and class posterior probabilities. Display diagnostic messages during the computation of labels and class posterior probabilities using the `'Verbose'` name-value pair argument.

```
[label,~,~,Posterior] = resubPredict(Mdl,'Verbose',1);
Mdl.BinaryLoss

Predictions from all learners have been computed.
Loss for all observations has been computed.
```

```
Computing posterior probabilities...

ans =

quadratic
```

The software assigns an observation to the class that yields the smallest average binary loss. Since all binary learners are computing posterior probabilities, the binary loss function is `quadratic`.

Display a random set of results.

```
idx = randsample(size(X,1),10,1);
Mdl.ClassNames
table(Y(idx),label(idx),Posterior(idx,:),...
    'VariableNames',{'TrueLabel','PredLabel','Posterior'})
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

     TrueLabel       PredLabel                  Posterior
    ____________    ____________    ____________________________________

    'virginica'     'virginica'      0.0039321     0.0039869       0.99208
    'virginica'     'virginica'       0.017067      0.018263       0.96467
    'virginica'     'virginica'       0.014948      0.015856        0.9692
    'versicolor'    'versicolor'    2.2197e-14       0.87317       0.12683
    'setosa'        'setosa'             0.999    0.00025091    0.00074639
    'versicolor'    'virginica'     2.2195e-14      0.059429       0.94057
    'versicolor'    'versicolor'    2.2194e-14       0.97001      0.029986
    'setosa'        'setosa'             0.999     0.0002499    0.00074741
    'versicolor'    'versicolor'     0.0085646       0.98259      0.008849
    'setosa'        'setosa'             0.999    0.00025013    0.00074718
```

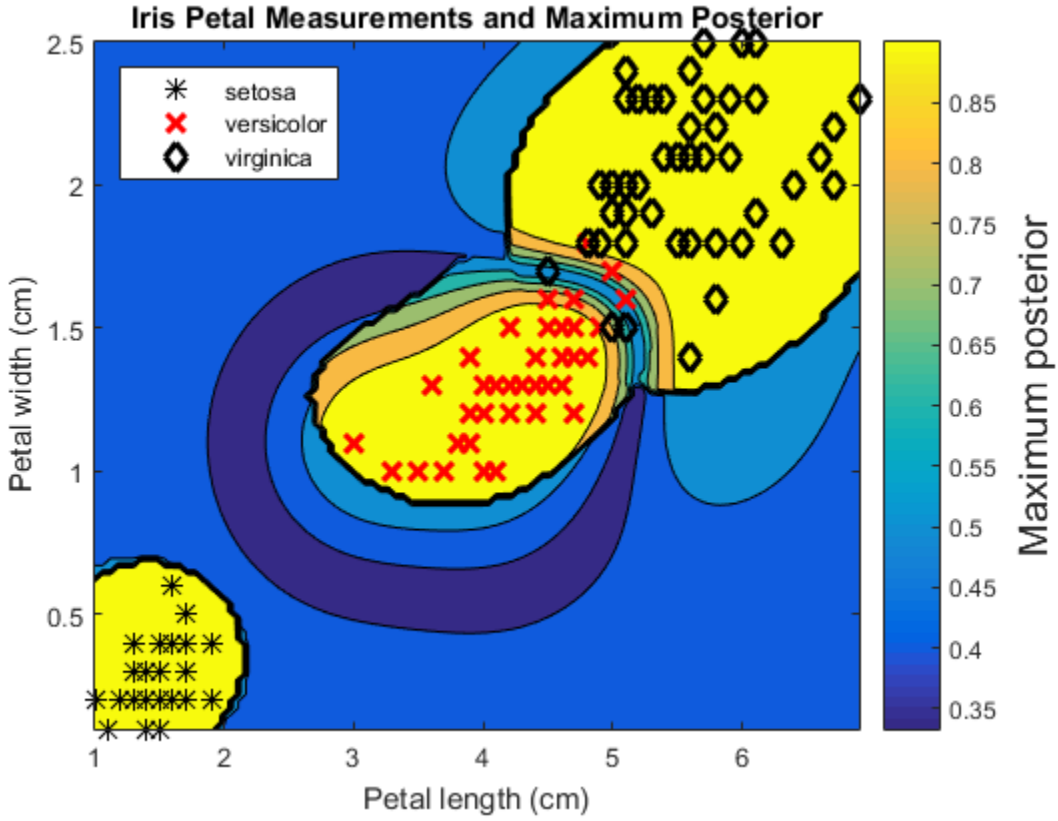
The columns of `Posterior` correspond to the class order of `Mdl.ClassNames`.

Define a grid of values in the observed predictor space. Predict the posterior probabilities for each instance in the grid.

```
xMax = max(X);
xMin = min(X);

x1Pts = linspace(xMin(1),xMax(1));
x2Pts = linspace(xMin(2),xMax(2));
[x1Grid,x2Grid] = meshgrid(x1Pts,x2Pts);

[~,~,~,PosteriorRegion] = predict(Mdl,[x1Grid(:),x2Grid(:)]);
```

For each coordinate on the grid, plot the maximum class posterior probability among all classes.

```
figure;
contourf(x1Grid,x2Grid,...
        reshape(max(PosteriorRegion,[],2),size(x1Grid,1),size(x1Grid,2)));
h = colorbar;
h.YLabel.String = 'Maximum posterior';
h.YLabel.FontSize = 15;
hold on
gh = gscatter(X(:,1),X(:,2),Y,'krk','*xd',8);
gh(2).LineWidth = 2;
gh(3).LineWidth = 2;

title 'Iris Petal Measurements and Maximum Posterior';
xlabel 'Petal length (cm)';
ylabel 'Petal width (cm)';
axis tight
legend(gh,'Location','NorthWest')
hold off
```



Estimate Posterior Probabilities Using Parallel Computing

Train an error-correcting output codes, multiclass model and estimate posterior probabilities using parallel computing.

Load the `arrhythmia` data set.

```
load arrhythmia
Y = categorical(Y);
tabulate(Y)
n = numel(Y);
K = numel(unique(Y));
```

```
  Value    Count   Percent
      1      245     54.20%
```

```
     2        44       9.73%
     3        15       3.32%
     4        15       3.32%
     5        13       2.88%
     6        25       5.53%
     7         3       0.66%
     8         2       0.44%
     9         9       1.99%
    10        50      11.06%
    14         4       0.88%
    15         5       1.11%
    16        22       4.87%
```

Several classes are not represented in the data, and many other classes have low relative frequencies.

Specify an ensemble learning template that uses the GentleBoost method and 50 weak, classification tree learners.

```
t = templateEnsemble('GentleBoost',50,'Tree');
```

`t` is a template object. Most of the options are empty (`[ ]`). The software uses default values for all empty options during training.

Since there are many classes, specify a sparse random coding design.

```
rng(1); % For reproducibility
Coding = designecoc(K,'sparserandom');
```

Train an ECOC model using parallel computing. Specify to fit posterior probabilities.

```
pool = parpool;                       % Invokes workers
options = statset('UseParallel',1);
Mdl = fitcecoc(X,Y,'Learner',t,'Options',options,'Coding',Coding,...
    'FitPosterior',1);

Starting parallel pool (parpool) using the 'local' profile ... connected to 4 workers.
```

`Mdl` is a `ClassificationECOC` model. You can access its properties using dot notation. The pool invokes four workers. The number of workers might vary among systems.

Estimate posterior probabilities, and display the posterior probability of being classified as not having arrythmia (class 1) given the data.

```
[~,~,~,posterior] = resubPredict(Mdl);
idx = randsample(n,10,1);
```

```
table(idx,Y(idx),posterior(idx,1),...
    'VariableNames',{'ObservationIndex','TrueLabel','PosteriorNoArrythmia'})
```

```
ans =

    ObservationIndex    TrueLabel    PosteriorNoArrythmia
    ________________    _________    ____________________

     79                 1             0.91522
    248                 1             0.95376
    398                 10           0.032369
    207                 1             0.97965
    340                 1             0.93628
    206                 1             0.97795
    345                 10           0.015643
    296                 2             0.14796
    391                 1             0.96494
    406                 1             0.94867
```

- "Quick Start Parallel Computing for Statistics and Machine Learning Toolbox" on page 21-2

Algorithms

The software can estimate class posterior probabilities using quadratic programming or by minimizing the Kullback-Leibler divergence. For the following descriptions of the posterior estimation algorithms, let:

- m_{kj} be the element (k,j) of the coding design matrix M.
- I be the indicator function.
- $\hat{p}_k$ be the class posterior probability estimate for class k of an observation, $k = 1,...,K$.
- r_j be the positive-class posterior probability for binary learner j. That is, r_j is the probability that binary learner j classifies an observation into the positive class, given the training data.

Posterior Estimation Using Kullback-Leibler Divergence

By default, the software minimizes the Kullback-Leibler divergence to estimate class posterior probabilities. The Kullback-Leibler divergence between the expected and observed positive-class posterior probabilities is

$$\Delta(r,r) = \sum_{j=1}^{L} w_j \left[r_j \log \frac{r_j}{r_j} + \left(1 - r_j\right) \log \frac{1 - r_j}{1 - r_j} \right],$$

where $w_j = \sum_{S_j} w_i^*$ is the weight for binary learner j with S_j the set of observation indices that binary learner j is trained on and w_i^* is the weight of observation i. The software minimizes the divergence iteratively. The first step is to choose initial values $\hat{p}_k^{(0)};\ k = 1,\ldots,K$ for the class posterior probabilities.

- If you do not specify NumKLIterations, then the software uses both sets of deterministic initial values described next, and uses the one that minimizes Δ.
  - $\hat{p}_k^{(0)} = 1/K;\ k = 1,\ldots,K.$
  - $\hat{p}_k^{(0)};\ k = 1,\ldots,K$ is the solution of the system

    $$M_{01}\hat{p}^{(0)} = r,$$

    where M_{01} is M with all m_{kj} = -1 replaced with 0, and r is a vector of positive-class posterior probabilities returned by the L binary learners [2]. The software uses `lsqnonneg` to solve the system.
- If you specify `'NumKLIterations',c`, where `c` is a natural number, then the software does the following to choose $\hat{p}_k^{(0)};\ k = 1,\ldots,K$, and uses the one that minimizes Δ.
  - The software chooses both sets of deterministic initial values as described previously.
  - The software randomly generates `c` vectors of length K using `rand`, and then normalizes each vector to sum to 1.

At iteration t, the software:

1 Computes

$$\hat{r}_j^{(t)} = \frac{\sum_{k=1}^{K} \hat{p}_k^{(t)} I(m_{kj} = +1)}{\sum_{k=1}^{K} \hat{p}_k^{(t)} I(m_{kj} = +1 \cup m_{kj} = -1)}.$$

2 Estimates the next class posterior probability using

$$\hat{p}_k^{(t+1)} = \hat{p}_k^{(t)} \frac{\sum_{j=1}^{L} w_j \left[r_j I\left(m_{kj} = +1\right) + \left(1 - r_j\right) I\left(m_{kj} = -1\right) \right]}{\sum_{j=1}^{L} w_j \left[\hat{r}_j^{(t)} I\left(m_{kj} = +1\right) + \left(1 - \hat{r}_j^{(t)}\right) I\left(m_{kj} = -1\right) \right]}.$$

3 Normalizes $\hat{p}_k^{(t+1)};\ k = 1,...,K$ so that they sum to 1.

4 Checks for convergence.

For more details, see [5] and [7].

Posterior Estimation Using Quadratic Programming

Posterior probability estimation using quadratic programming requires an Optimization Toolbox license. To estimate posterior probabilities for an observation using this method, the software:

1 Estimates the positive-class posterior probabilities, r_j, for binary learners $j = 1,...,L$.

2 Using the relationship between r_j and $\hat{p}_k$ [6], minimizes

$$\sum_{j=1}^{L} \left[-r_j \sum_{k=1}^{K} \hat{p}_k I\left(m_{kj} = -1\right) + \left(1 - r_j\right) \sum_{k=1}^{K} \hat{p}_k I\left(m_{kj} = +1\right) \right]^2$$

with respect to $\hat{p}_k$ and the restrictions

$$0 \le \hat{p}_k \le 1$$
$$\sum_k \hat{p}_k = 1.$$

The software performs minimization using `quadprog`.

References

[1] Allwein, E., R. Schapire, and Y. Singer. "Reducing multiclass to binary: A unifying approach for margin classifiers." *Journal of Machine Learning Research*. Vol. 1, 2000, pp. 113–141.

[2] Dietterich, T., and G. Bakiri. "Solving Multiclass Learning Problems Via Error-Correcting Output Codes." *Journal of Artificial Intelligence Research*. Vol. 2, 1995, pp. 263–286.

[3] Escalera, S., O. Pujol, and P. Radeva. "On the decoding process in ternary error-correcting output codes." *IEEE Transactions on Pattern Analysis and Machine Intelligence*. Vol. 32, Issue 7, 2010, pp. 120–134.

[4] Escalera, S., O. Pujol, and P. Radeva. "Separability of ternary codes for sparse designs of error-correcting output codes." *Pattern Recogn*. Vol. 30, Issue 3, 2009, pp. 285–297.

[5] Hastie, T., and R. Tibshirani. "Classification by Pairwise Coupling." *Annals of Statistics*. Vol. 26, Issue 2, 1998, pp. 451–471.

[6] Wu, T. F., C. J. Lin, and R. Weng. "Probability Estimates for Multi-Class Classification by Pairwise Coupling." *Journal of Machine Learning Research*. Vol. 5, 2004, pp. 975–1005.

[7] Zadrozny, B. "Reducing Multiclass to Binary by Coupling Probability Estimates." *NIPS 2001: Proceedings of Advances in Neural Information Processing Systems 14*, 2001, pp. 1041–1048.

See Also

`ClassificationECOC` | `fitcecoc` | `predict` | `quadprog` | `statset`

More About

- "Reproducibility in Parallel Statistical Computations" on page 21-13
- "Concepts of Parallel Computing in Statistics and Machine Learning Toolbox" on page 21-7

resubPredict

Class: ClassificationEnsemble

Predict ensemble response by resubstitution

Syntax

```
label = resubPredict(ens)
[label,score] = resubPredict(ens)
[label,score] = resubPredict(ens,Name,Value)
```

Description

`label = resubPredict(ens)` returns the labels `ens` predicts for the data `ens.X`. `label` is the predictions of `ens` on the data that `fitensemble` used to create `ens`.

`[label,score] = resubPredict(ens)` also returns scores for all classes.

`[label,score] = resubPredict(ens,Name,Value)` finds resubstitution predictions with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A classification ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NumTrained`

Output Arguments

`label`

The response ens predicts for the training data. `label` is the same data type as the training response data `ens.Y`, and has the same number of entries as the number of rows in `ens.X`.

`score`

An `N`-by-`K` matrix, where `N` is the number of rows in `ens.X`, and `K` is the number of classes in ens. High score value indicates that an observation likely comes from this class.

Definitions

Score (ensemble)

For ensembles, a classification *score* represents the confidence of a classification into a class. The higher the score, the higher the confidence.

Different ensemble algorithms have different definitions for their scores. Furthermore, the range of scores depends on ensemble type. For example:

- `AdaBoostM1` scores range from $-\infty$ to ∞.
- `Bag` scores range from `0` to `1`.

Examples

Find the total number of misclassifications of the Fisher iris data for a classification ensemble:

```
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,'Tree');
Ypredict = resubPredict(ens); % the predictions
Ysame = strcmp(Ypredict,species); % true when ==
sum(~Ysame) % how many are different?

ans =
     5
```

See Also

resubEdge | resubLoss | resubPredict | resubMargin

resubPredict

Class: ClassificationKNN

Predict resubstitution response of *k*-nearest neighbor classifier

Syntax

```
label = resubPredict(mdl)
[label,score] = resubPredict(mdl)
[label,score,cost] = resubPredict(mdl)
```

Description

`label = resubPredict(mdl)` returns the labels `mdl` predicts for the data `mdl.X`. `label` is the predictions of `mdl` on the data that `fitcknn` used to create `mdl`.

`[label,score] = resubPredict(mdl)` returns the posterior class probabilities for the predictions.

`[label,score,cost] = resubPredict(mdl)` returns the misclassification costs.

Input Arguments

`mdl` — Classifier model

classifier model object

k-nearest neighbor classifier model, returned as a classifier model object.

Note that using the `'CrossVal'`, `'KFold'`, `'Holdout'`, `'Leaveout'`, or `'CVPartition'` options results in a model of class `ClassificationPartitionedModel`. You cannot use a partitioned tree for prediction, so this kind of tree does not have a `predict` method.

Otherwise, mdl is of class `ClassificationKNN`, and you can use the `predict` method to make predictions.

Output Arguments

`label`

Predicted class labels for the points in the training data `X`, a vector with length equal to the number of rows in the training data `X`. The label is the class with minimal expected cost (see "Expected Cost" on page 22-4289).

`score`

Numeric matrix of size `N`-by-`K`, where `N` is the number of observations (rows) in the training data `X`, and `K` is the number of classes (in `mdl.ClassNames`). `score(i,j)` is the posterior probability that row `i` of `X` is of class `j`. See "Posterior Probability" on page 22-4288.

`cost`

Matrix of expected costs of size `N`-by-`K`, where `N` is the number of observations (rows) in the training data `X`, and `K` is the number of classes (in `mdl.ClassNames`). `cost(i,j)` is the cost of classifying row `i` of `X` as class `j`. See "Expected Cost" on page 22-4289.

Definitions

Posterior Probability

For a vector (single query point) `X` and model `mdl`, let

- `K` be the number of nearest neighbors used in prediction, `mdl.NumNeighbors`
- `nbd(mdl,X)` be the `K` nearest neighbors to `X` in `mdl.X`
- `Y(nbd)` be the classifications of the points in `nbd(mdl,X)`, namely `mdl.Y(nbd)`
- `W(nbd)` be the weights of the points in `nbd(mdl,X)`
- `prior` be the priors of the classes in `mdl.Y`

If there is a vector of prior probabilities, then the observation weights `W` are normalized by class to sum to the priors. This might involve a calculation for the point `X`, because weights can depend on the distance from `X` to the points in `mdl.X`.

The posterior probability $p(j|X)$ is

$$p(j\,|\,\mathrm{X}) = \frac{\sum_{i\in \mathrm{nbd}} W(i)1_{Y(X(i)=j)}}{\sum_{i\in \mathrm{nbd}} W(i)}.$$

Here $1_{Y(X(i)=j)}$ means `1` when `mdl.Y(i) = j`, and `0` otherwise.

Expected Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation. The third output of `predict` is the expected misclassification cost per observation.

Suppose you have `Nobs` observations that you want to classify with a trained classifier `mdl`. Suppose you have `K` classes. You place the observations into a matrix `X` with one observation per row. The command

```
[label,score,cost] = predict(mdl,X)
```

returns, among other outputs, a `cost` matrix of size `Nobs`-by-`K`. Each row of the `cost` matrix contains the expected (average) cost of classifying the observation into each of the `K` classes. `cost(n,k)` is

$$\sum_{i=1}^{K} \hat{P}(i\,|\,X(n))C(k\,|\,i),$$

where

- K is the number of classes.
- $\hat{P}(i\,|\,X(n))$ is the posterior probability of class i for observation $X(n)$.
- $C(k\,|\,i)$ is the true misclassification cost of classifying an observation as k when its true class is i.

True Misclassification Cost

There are two costs associated with KNN classification: the true misclassification cost per class, and the expected misclassification cost per observation.

You can set the true misclassification cost per class in the `Cost` name-value pair when you run `fitcknn`. `Cost(i,j)` is the cost of classifying an observation into class `j` if its true class is `i`. By default, `Cost(i,j)=1` if `i~=j`, and `Cost(i,j)=0` if `i=j`. In other words, the cost is `0` for correct classification, and `1` for incorrect classification.

Algorithms

If you specified to standardize the predictor data, that is, `mdl.Mu` and `mdl.Sigma` are not empty (`[ ]`), then `resubPredict` standardizes the predictor data before predicting labels.

Examples

Predict the Labels of the Training Data

Examine the quality of a classifier by its resubstitution predictions.

Load the data.

```
load fisheriris
X = meas;
Y = species;
```

Construct a classifier for 5-nearest neighbors.

```
mdl = fitcknn(X,Y,'NumNeighbors',5);
```

Generate the resubstitution predictions.

```
label = resubPredict(mdl);
```

Calculate the number of differences between the predictions `label` and the original data `Y`.

```
mydiff = not(strcmp(Y,label)); % mydiff(i) = 1 means they differ
sum(mydiff) % Number of differences
```

```
ans =

     5
```

A values of `1` in `mydiff` indicates that the observed label differs from the corresponding predicted label. There are `5` misclassifications.

See Also

`ClassificationKNN` | `fitcknn` | `predict` | `resubEdge` | `resubLoss` | `resubMargin`

resubPredict

Class: ClassificationNaiveBayes

Predict naive Bayes classifier resubstitution response

Syntax

```
label = resubPredict(Mdl)
[label,Posterior,Cost] = predict(Mdl)
```

Description

`label = resubPredict(Mdl)` returns a vector of predicted class labels (`label`) for the trained naive Bayes classifier `Mdl` using the predictor data `Mdl.X`.

`[label,Posterior,Cost] = predict(Mdl)` additionally returns posterior probabilities (`Posterior`) and predicted (expected) misclassification costs (`Cost`) corresponding to the observations (rows) in `Mdl.X`.

Input Arguments

`Mdl` — Fully trained naive Bayes classifier

`ClassificationNaiveBayes` model

A fully trained naive Bayes classifier, specified as a `ClassificationNaiveBayes` model trained by `fitcnb`.

Output Arguments

`label` — Predicted class labels

categorical vector | character array | logical vector | numeric vector | cell vector of strings

Predicted class labels, returned as a categorical vector, character array, logical or numeric vector, or cell vector of strings.

`label`:

- Is the same data type as the observed class labels (`Y`) that trained `Mdl`
- Has length equal to the number of rows of `X`
- Is the class yielding the lowest expected misclassification cost (`Cost`)

`Posterior` — Class posterior probabilities
numeric matrix

Class posterior probabilities, returned as a numeric matrix. `Posterior` has rows equal to the number of rows of `Mdl.X` and columns equal to the number of distinct classes in the training data (`size(Mdl.ClassNames,1)`).

`Posterior(j,k)` is the predicted posterior probability of class `k` (i.e., in class `Mdl.ClassNames(k)`) given the observation in row `j` of `Mdl.X`.

Data Types: `double`

`Cost` — Expected misclassification costs
numeric matrix

Expected misclassification costs, returned as a numeric matrix. `Cost` has rows equal to the number of rows of `Mdl.X` and columns equal to the number of distinct classes in the training data (`size(Mdl.ClassNames,1)`).

`Cost(j,k)` is the expected misclassification cost of the observation in row `j` of `Mdl.X` being predicted into class `k` (i.e., in class `Mdl.ClassNames(k)`).

Definitions

Misclassification Cost

A *misclassification cost* is the relative severity of a classifier labeling an observation into the wrong class.

There are two types of misclassification costs: true and expected. Let K be the number of classes.

- *True misclassification cost* — A K-by-K matrix, where element (i,j) indicates the misclassification cost of predicting an observation into class j if its true class is i.

The software stores the misclassification cost in the property `Mdl.Cost`, and used in computations. By default, `Mdl.Cost(i,j)` = 1 if `i` ≠ `j`, and `Mdl.Cost(i,j)` = 0 if `i` = `j`. In other words, the cost is `0` for correct classification, and `1` for any incorrect classification.

- *Expected misclassification cost* — A K-dimensional vector, where element k is the weighted average misclassification cost of classifying an observation into class k, weighted by the class posterior probabilities. In other words,

$$c_k = \sum_{j=1}^{K} \hat{P}(Y = j \mid x_1,...,x_P)\texttt{Cost}_{jk}.$$

the software classifies observations to the class corresponding with the lowest expected misclassification cost.

Posterior Probability

The *posterior probability* is the probability that an observation belongs in a particular class, given the data.

For naive Bayes, the posterior probability that a classification is k for a given observation $(x_1,...,x_P)$ is

$$\hat{P}(Y = k \mid x_1,..,x_P) = \frac{P(X_1,...,X_P \mid y = k)\pi(Y = k)}{P(X_1,...,X_P)},$$

where:

- $P(X_1,...,X_P \mid y = k)$ is the conditional joint density of the predictors given they are in class k. `Mdl.DistributionNames` stores the distribution names of the predictors.
- $\pi(Y = k)$ is the class prior probability distribution. `Mdl.Prior` stores the prior distribution.
- $P(X_1,..,X_P)$ is the joint density of the predictors. The classes are discrete, so

$$P(X_1,...,X_P) = \sum_{k=1}^{K} P(X_1,...,X_P \mid y = k)\pi(Y = k).$$

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Examples

Label Training Sample Observations for Naive Bayes

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
Mdl = fitcnb(X,Y,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationNaiveBayes` classifier.

Predict the training sample labels. Display the results for the 10 observations.

```
label = resubPredict(Mdl);
rng(1); % For reproducibility
idx = randsample(size(X,1),10);
table(Y(idx),label(idx),'VariableNames',...
    {'TrueLabel','PredictedLabel'})
```

```
ans =

     TrueLabel      PredictedLabel
    ____________    _______________

    'setosa'        'setosa'
    'versicolor'    'versicolor'
    'virginica'     'virginica'
    'setosa'        'setosa'
    'versicolor'    'versicolor'
    'setosa'        'setosa'
```

```
    'versicolor'    'versicolor'
    'versicolor'    'versicolor'
    'setosa'        'setosa'
    'setosa'        'setosa'
```

Estimate In-Sample Posterior Probabilities of Naive Bayes Classifiers

Load Fisher's iris data set.

```
load fisheriris
X = meas;    % Predictors
Y = species; % Response
```

Train a naive Bayes classifier. It is good practice to specify the class order. Assume that each predictor is conditionally, normally distributed given its label.

```
Mdl = fitcnb(X,Y,...
    'ClassNames',{'setosa','versicolor','virginica'});
```

`Mdl` is a `ClassificationNaiveBayes` classifier.

Estimate posterior probabilities and expected misclassification costs for the training data. Display the results for 10 observations.

```
[label,Posterior,MisclassCost] = resubPredict(Mdl);
rng(1); % For reproducibility
idx = randsample(size(X,1),10);
Mdl.ClassNames
table(Y(idx),label(idx),Posterior(idx,:),'VariableNames',...
    {'TrueLabel','PredictedLabel','PosteriorProbability'})
MisclassCost(idx,:)
```

```
ans =

    'setosa'
    'versicolor'
    'virginica'


ans =

     TrueLabel      PredictedLabel              PosteriorProbability
    ____________    _______________    ____________________________________________
```

```
    'setosa'        'setosa'                  1     3.8821e-16     5.5878e-24
    'versicolor'    'versicolor'       1.2516e-54              1     4.5001e-06
    'virginica'     'virginica'       5.5646e-188     0.00058232        0.99942
    'setosa'        'setosa'                  1     4.5352e-20     3.1301e-27
    'versicolor'    'versicolor'       5.0002e-69        0.99989     0.00010716
    'setosa'        'setosa'                  1     2.9813e-18     2.1524e-25
    'versicolor'    'versicolor'       4.6313e-60        0.99999     7.5413e-06
    'versicolor'    'versicolor'      7.9205e-100        0.94293       0.057072
    'setosa'        'setosa'                  1      1.799e-19     6.0606e-27
    'setosa'        'setosa'                  1     1.5426e-17     1.2744e-24


ans =

    0.0000    1.0000    1.0000
    1.0000    0.0000    1.0000
    1.0000    0.9994    0.0006
    0.0000    1.0000    1.0000
    1.0000    0.0001    0.9999
    0.0000    1.0000    1.0000
    1.0000    0.0000    1.0000
    1.0000    0.0571    0.9429
    0.0000    1.0000    1.0000
    0.0000    1.0000    1.0000
```

The order of the columns of `Posterior` and `MisclassCost` corresponds to the order of the classes in `Mdl.ClassNames`.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

See Also

`ClassificationNaiveBayes` | `CompactClassificationNaiveBayes` | `fitcnb` | `loss` | `predict`

More About

- "Naive Bayes Classification" on page 15-31

- “Grouping Variables” on page 2-52

resubPredict

Class: ClassificationSVM

Predict support vector machine classifier resubstitution responses

Syntax

```
label = resubPredict(SVMModel)
[label,Score] = resubPredict(SVMModel)
```

Description

`label = resubPredict(SVMModel)` returns a vector of predicted class labels (`label`) for the trained support vector machine (SVM) classifier `SVMModel` using the predictor data `SVMModel.X`.

`[label,Score] = resubPredict(SVMModel)` additionally returns class likelihood measures, that is, either scores or posterior probabilities.

Input Arguments

`SVMModel` — Full, trained SVM classifier

`ClassificationSVM` classifier

Full, trained SVM classifier, specified as a `ClassificationSVM` model trained using `fitcsvm`.

Output Arguments

`label` — Predicted class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Predicted class labels, returned as a categorical or character array, logical or numeric vector, or cell array of strings.

`label`:

- Is the same data type as the observed class labels (`SVMModel.Y`)
- Has length equal to the number of rows of SVMModel.X

For one-class learning, the elements of `label` are the one class represented in `SVMModel.Y`

`Score` — Predicted class scores or posterior probabilities

numeric column vector | numeric matrix

Predicted class scores or posterior probabilities, returned as a numeric column vector or numeric matrix.

- For one-class learning, `Score` is a column vector with the same number of rows as `SVMModel.X`. The elements are the positive class scores for the corresponding observations. You cannot obtain posterior probabilities for one-class learning.
- For two-class learning, `Score` is a two column matrix with the same number of rows as `SVMModel.X`.
  - If you fit the optimal score-to-posterior probability transformation function using `fitPosterior` or `fitSVMPosterior`, then `Score` contains class posterior probabilities. That is, if the value of `SVMModel.ScoreTransform` is not `none`, then the elements of the first and second columns of `Score` are the negative class (`SVMModel.ClassNames{1}`) and positive class (`SVMModel.ClassNames{2}`) posterior probabilities for the corresponding observations, respectively.
  - Otherwise, the elements of the first column are the negative class scores and the elements of the second column are the positive class scores for the corresponding observations.

If SVMModel`.KernelParameters.Function` is `'linear'`, then the software estimates the classification score for the observation x using

$$f(x) = (x / s)'\beta + b.$$

SVMModel stores β, b, and s in the properties Beta, Bias, and KernelParameters`.Scale`, respectively.

Data Types: `double` | `single`

Definitions

Score

The SVM *score* for classifying observation x is the signed distance from x to the decision boundary ranging from -∞ to +∞. A positive score for a class indicates that x is predicted to be in that class, a negative score indicates otherwise.

The score is also the numerical, predicted response for x, $f(x)$, computed by the trained SVM classification function

$$f(x) = \sum_{j=1}^{n} \alpha_j y_j G(x_j, x) + b,$$

where $(\alpha_1, ..., \alpha_n, b)$ are the estimated SVM parameters, $G(x_j, x)$ is the dot product in the predictor space between x and the support vectors, and the sum includes the training set observations.

If $G(x_j,x) = x_j'x$ (the linear kernel), then the score function reduces to

$$f(x) = (x / s)'\beta + b.$$

s is the kernel scale and β is the vector of fitted linear coefficients.

Posterior Probability

The probability that an observation belongs in a particular class, given the data.

For SVM, the posterior probability is a function of the score, $P(s)$, that observation j is in class $k = \{-1,1\}$.

- For separable classes, the posterior probability is the step function

$$P(s_j) = \begin{cases} 0; & s < \max_{y_k=-1} s_k \\ \pi; & \max_{y_k=-1} s_k \le s_j \le \min_{y_k=+1} s_k \\ 1; & s_j > \min_{y_k=+1} s_k \end{cases},$$

where:

- s_j is the score of observation j.
- +1 and –1 denote the positive and negative classes, respectively.
- π is the prior probability that an observation is in the positive class.

- For inseparable classes, the posterior probability is the sigmoid function

$$P(s_j) = \frac{1}{1+\exp(As_j + B)},$$

where the parameters A and B are the slope and intercept parameters.

Prior Probability

The *prior probability* is the believed relative frequency that observations from a class occur in the population for each class.

Examples

Label Training Sample Observations for SVM Classifiers Using resubPredict

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to specify the class order and standardize the data.

```
SVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier. The positive class is `'g'`.

Predict the training sample labels and scores. Display the results for the first 10 observations.

```
[label,score] = resubPredict(SVMModel);
table(Y(1:10),label(1:10),score(1:10,2),'VariableNames',...
    {'TrueLabel','PredictedLabel','Score'})
```

```
ans =

    TrueLabel    PredictedLabel     Score
    _________    ______________    _______

    'g'          'g'                1.4861
    'b'          'b'               -1.0004
    'g'          'g'                1.8685
    'b'          'b'               -2.6458
    'g'          'g'                1.2805
    'b'          'b'               -1.4617
    'g'          'g'                2.1672
    'b'          'b'               -5.7085
    'g'          'g'                2.4797
    'b'          'b'               -2.7811
```

Estimate In-Sample Posterior Probabilities of SVM Classifiers

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. It is good practice to specify the class order and standardize the data.

```
SVMModel = fitcsvm(X,Y,'ClassNames',{'b','g'},'Standardize',true);
```

`SVMModel` is a `ClassificationSVM` classifier. The positive class is `'g'`.

Fit the optimal score-to-posterior-probability transformation function.

```
rng(1); % For reproducibility
ScoreSVMModel = fitPosterior(SVMModel)
```

```
ScoreSVMModel =

  ClassificationSVM
      PredictorNames: {1x34 cell}
        ResponseName: 'Y'
          ClassNames: {'b'  'g'}
      ScoreTransform: '@(S)sigmoid(S,-9.481802e-01,-1.218745e-01)'
     NumObservations: 351
               Alpha: [90x1 double]
                Bias: -0.1343
    KernelParameters: [1x1 struct]
                  Mu: [1x34 double]
               Sigma: [1x34 double]
      BoxConstraints: [351x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [351x1 logical]
              Solver: 'SMO'
```

Since the classes are inseparable, the score transformation function (`ScoreSVMModel.ScoreTransform`) is the sigmoid function.

Estimate scores and positive class posterior probabilities for the training data. Display the results for the first 10 observations.

```
[label,scores] = resubPredict(SVMModel);
[~,postProbs] = resubPredict(ScoreSVMModel);
table(Y(1:10),label(1:10),scores(1:10,2),postProbs(1:10,2),'VariableNames',...
    {'TrueLabel','PredictedLabel','Score','PosteriorProbability'})
```

```
ans =

    TrueLabel    PredictedLabel     Score     PosteriorProbability
    _________    ______________    _______    ____________________

    'g'          'g'                1.4861      0.82215
    'b'          'b'               -1.0004      0.30436
    'g'          'g'                1.8685      0.86916
    'b'          'b'               -2.6458     0.084183
    'g'          'g'                1.2805      0.79184
    'b'          'b'               -1.4617      0.22028
    'g'          'g'                2.1672      0.89814
    'b'          'b'               -5.7085    0.0050122
```

```
'g'          'g'                2.4797      0.92223
'b'          'b'               -2.7811     0.074805
```

Algorithms

- By default, the software computes optimal posterior probabilities using Platt's method [1]:

  1. Performing 10-fold cross validation
  2. Fitting the sigmoid function parameters to the scores returned from the cross validation
  3. Estimating the posterior probabilities by entering the cross-validation scores into the fitted sigmoid function

- The software incorporates prior probabilities in the SVM objective function during training.
- For SVM, `predict` classifies observations into the class yielding the largest score (i.e., the largest posterior probability). The software accounts for misclassification costs by applying the average-cost correction before training the classifier. That is, given the class prior vector P, misclassification cost matrix C, and observation weight vector w, the software defines a new vector of observation weights (W) such that

$$W_j = w_j P_j \sum_{k=1}^{K} C_{jk}.$$

References

[1] Platt, J. "Probabilistic outputs for support vector machines and comparisons to regularized likelihood methods." *In Advances in Large Margin Classifiers*. MIT Press, 1999, pp. 61–74.

See Also

`ClassificationSVM` | `CompactClassificationSVM` | `fitcsvm` | `fitPosterior` | `fitSVMPosterior` | `predict`

resubPredict

Class: ClassificationTree

Predict resubstitution response of tree

Syntax

```
label = resubPredict(tree)
[label,posterior] = resubPredict(tree)
[label,posterior,node] = resubPredict(tree)
[label,posterior,node,cnum] = resubPredict(tree)
[label,...] = resubPredict(tree,Name,Value)
```

Description

`label = resubPredict(tree)` returns the labels `tree` predicts for the data `tree.X`. `label` is the predictions of `tree` on the data that `fitctree` used to create `tree`.

`[label,posterior] = resubPredict(tree)` returns the posterior class probabilities for the predictions.

`[label,posterior,node] = resubPredict(tree)` returns the node numbers of `tree` for the resubstituted data.

`[label,posterior,node,cnum] = resubPredict(tree)` returns the predicted class numbers for the predictions.

`[label,...] = resubPredict(tree,Name,Value)` returns resubstitution predictions with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

A classification tree constructed by `fitctree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `ClassificationTree.resubPredict` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`ClassificationTree.resubPredict` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

Output Arguments

`label`

The response tree predicts for the training data. `label` is the same data type as the training response data `tree.Y`.

If the `Subtrees` name-value argument contains `m>1` entries, `label` has `m` columns, each of which represents the predictions of the corresponding subtree. Otherwise, `label` is a vector.

`posterior`

Matrix or array of posterior probabilities for classes tree predicts.

If the `Subtrees` name-value argument is a scalar or is missing, `posterior` is an `n`-by-`k` matrix, where `n` is the number of rows in the training data `tree.X`, and `k` is the number of classes.

If `Subtrees` contains `m>1` entries, `posterior` is an `n`-by-`k`-by-`m` array, where the matrix for each `m` gives posterior probabilities for the corresponding subtree.

`node`

The node numbers of `tree` where each data row resolves.

If the `Subtrees` name-value argument is a scalar or is missing, `node` is a numeric column vector with `n` rows, the same number of rows as `tree.X`.

If `Subtrees` contains `m>1` entries, `node` is a `n`-by-`m` matrix. Each column represents the node predictions of the corresponding subtree.

`cnum`

The class numbers that tree predicts for the resubstituted data.

If the `Subtrees` name-value argument is a scalar or is missing, `cnum` is a numeric column vector with `n` rows, the same number of rows as `tree.X`.

If `Subtrees` contains `m>1` entries, `cnum` is a `n`-by-`m` matrix. Each column represents the class predictions of the corresponding subtree.

Definitions

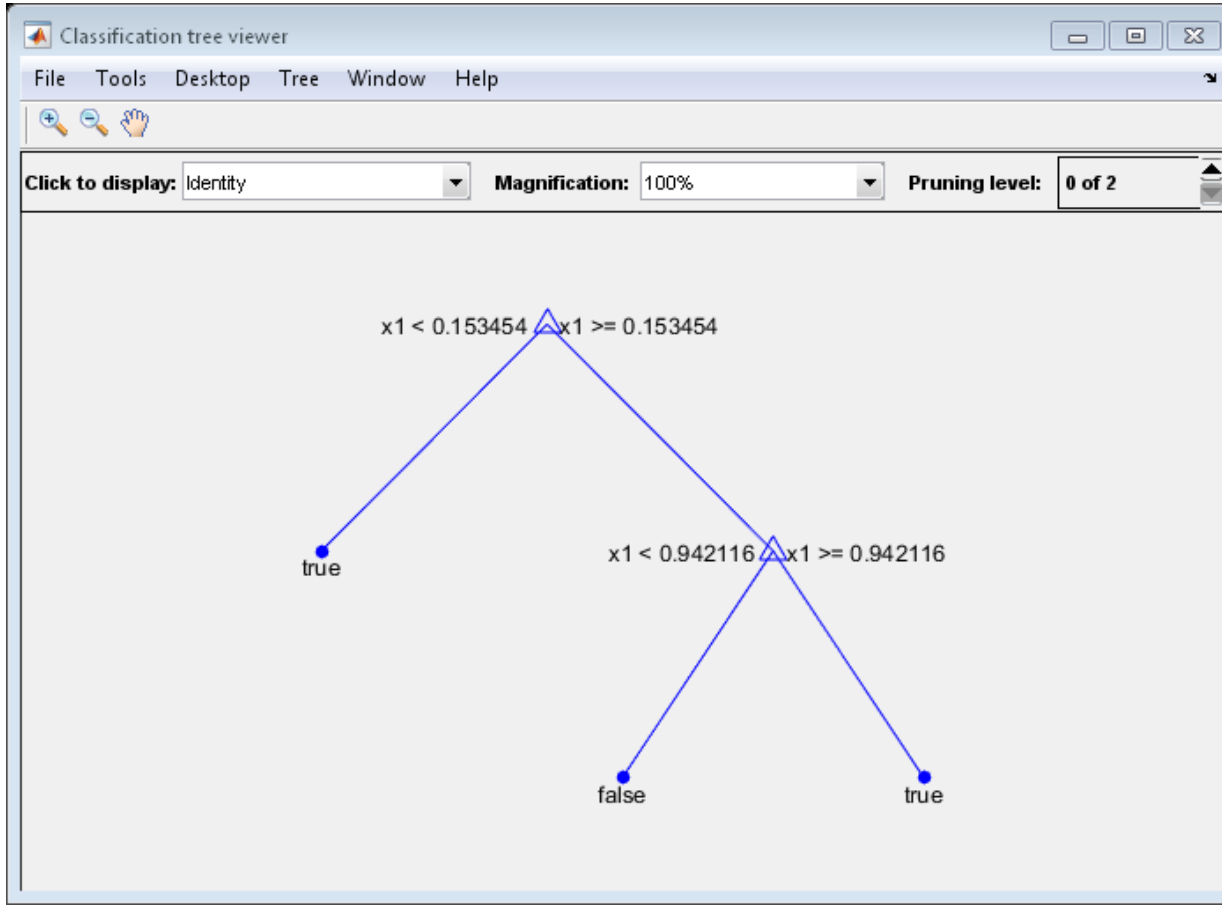
Posterior Probability

The posterior probability of the classification at a node is the number of training sequences that lead to that node with this classification, divided by the number of training sequences that lead to that node.

For example, consider classifying a predictor `X` as `true` when `X<0.15` or `X>0.95`, and `X` is false otherwise.

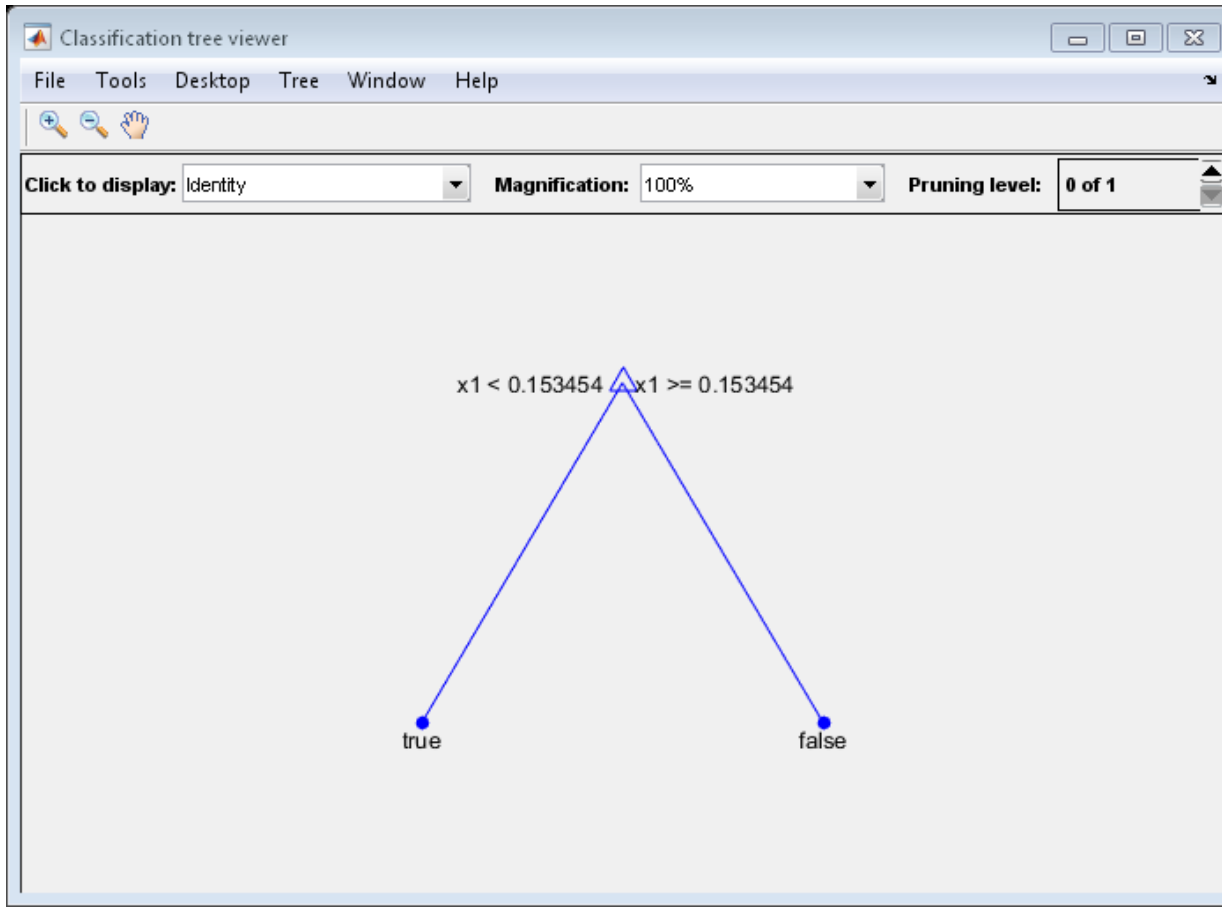
1 Generate 100 random points and classify them:

```
rng(0) % For reproducibility
X = rand(100,1);
Y = (abs(X - .55) > .4);
tree = fitctree(X,Y);
view(tree,'Mode','graph')
```



2 Prune the tree:

```
tree1 = prune(tree,'Level',1);
view(tree1,'Mode','graph')
```



The pruned tree correctly classifies observations that are less than 0.15 as `true`. It also correctly classifies observations between .15 and .94 as `false`. However, it incorrectly classifies observations that are greater than .94 as `false`. Therefore the score for observations that are greater than .15 should be about .05/.85=.06 for `true`, and about .8/.85=.94 for `false`.

3 Compute the prediction scores for the first 10 rows of `X`:

```
[~,score] = predict(tree1,X(1:10));
[score X(1:10,:)]

ans =

    0.9059    0.0941    0.8147
    0.9059    0.0941    0.9058
         0    1.0000    0.1270
    0.9059    0.0941    0.9134
    0.9059    0.0941    0.6324
         0    1.0000    0.0975
    0.9059    0.0941    0.2785
    0.9059    0.0941    0.5469
    0.9059    0.0941    0.9575
    0.9059    0.0941    0.9649
```

Indeed, every value of `X` (the rightmost column) that is less than 0.15 has associated scores (the left and center columns) of `0` and `1`, while the other values of `X` have associated scores of `0.94` and `0.06`.

Examples

Compute Number of Misclassified Observations

Find the total number of misclassifications of the Fisher iris data for a classification tree.

```
load fisheriris
tree = fitctree(meas,species);
Ypredict = resubPredict(tree);    % The predictions
Ysame = strcmp(Ypredict,species); % True when ==
sum(~Ysame) % How many are different?

ans =

     3
```

Compare In-Sample Posterior Probabilities for Each Subtree

Load Fisher's iris data set. Partition the data into training (50%)

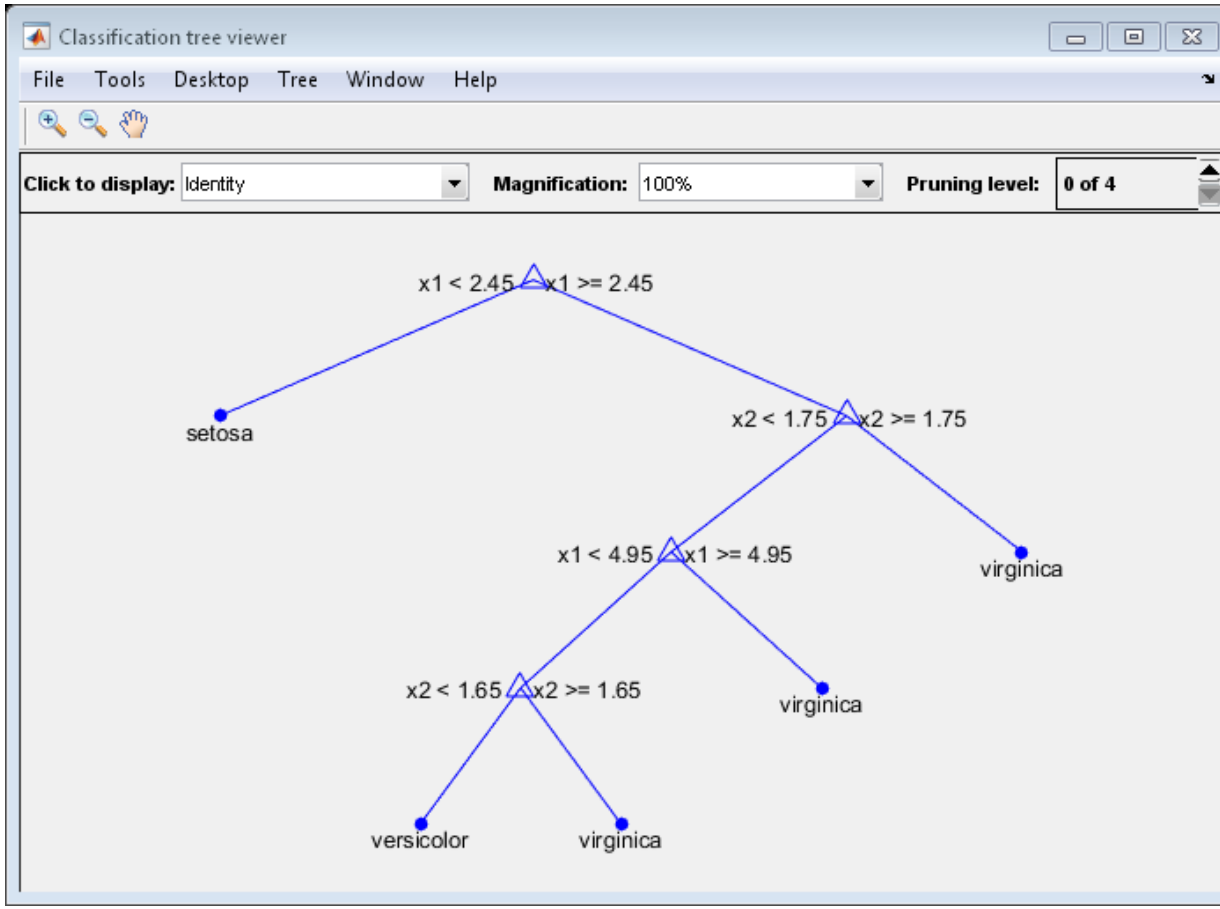
```
load fisheriris
```

Grow a classification tree using the all petal measurements.

```
Mdl = fitctree(meas(:,3:4),species);
n = size(meas,1); % Sample size
K = numel(Mdl.ClassNames); % Number of classes
```

View the classification tree.

```
view(Mdl,'Mode','graph');
```



The classification tree has four pruning levels. Level 0 is the full, unpruned tree (as displayed). Level 4 is just the root node (i.e., no splits).

Estimate the posterior probabilities for each class using the subtrees pruned to levels 1 and 3.

```
[~,Posterior] = resubPredict(Mdl,'SubTrees',[1 3]);
```

`Posterior` is an `n`-by- `K`-by- 2 array of posterior probabilities. Rows of `Posterior` correspond to observations, columns correspond to the classes with order `Mdl.ClassNames`, and pages correspond to pruning level.

Display the class posterior probabilities for iris 125 using each subtree.

```
Posterior(125,:,:)
```

```
ans(:,:,1) =

         0    0.0217    0.9783


ans(:,:,2) =

         0    0.5000    0.5000
```

The decision stump (page 2 of `Posterior`) has trouble predicting whether iris 125 is versicolor or virginica.

See Also

`resubEdge` | `resubLoss` | `predict` | `fitctree` | `resubMargin`

resubPredict

Class: RegressionEnsemble

Predict response of ensemble by resubstitution

Syntax

```
Yfit = resubPredict(ens)
Yfit = resubPredict(ens,Name,Value)
```

Description

`Yfit = resubPredict(ens)` returns the response `ens` predicts for the data `ens.X`. `Yfit` is the predictions of `ens` on the data that `fitensemble` used to create `ens`.

`Yfit = resubPredict(ens,Name,Value)` predicts responses with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'learners'`

Indices of weak learners in the ensemble ranging from `1` to `NumTrained`. `oobLoss` uses only these learners for calculating loss.

Default: `1:NumTrained`

Output Arguments

`Yfit`

A vector of predicted responses to the training data, with `ens.X` elements.

Examples

Find the resubstitution predictions of mileage from the `carsmall` data based on horsepower and weight, and look at their mean square difference from the training data.

```
load carsmall
X = [Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,'Tree');
Yfit = resubPredict(ens);
MSE = mean((Yfit - ens.Y).^2)

MSE =
    6.4336
```

This is the same as the result of `resubLoss`:

```
resubLoss(ens)

ans =
    6.4336
```

See Also

`resubLoss` | `predict` | `resubPredict`

resubPredict

Class: RegressionTree

Predict resubstitution response of tree

Syntax

```
Yfit = resubPredict(tree)
[Yfit,node] = resubPredict(tree)
[Yfit,node] = resubPredict(tree,Name,Value)
```

Description

`Yfit = resubPredict(tree)` returns the responses `tree` predicts for the data `tree.X`. `Yfit` is the predictions of `tree` on the data that `fitrtree` used to create `tree`.

`[Yfit,node] = resubPredict(tree)` returns the node numbers of `tree` for the resubstituted data.

`[Yfit,node] = resubPredict(tree,Name,Value)` predicts with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

A regression tree constructed using `fitrtree`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Subtrees'`

A vector of nonnegative integers in ascending order or `'all'`.

If you specify a vector, then all elements must be at least `0` and at most `max(tree.PruneList)`. `0` indicates the full, unpruned tree and `max(tree.PruneList)` indicates the a completely pruned tree (i.e., just the root node).

If you specify `'all'`, then `RegressionTree.resubPredict` operates on all subtrees (i.e., the entire pruning sequence). This specification is equivalent to using `0:max(tree.PruneList)`.

`RegressionTree.resubPredict` prunes tree to each level indicated in `Subtrees`, and then estimates the corresponding output arguments. The size of `Subtrees` determines the size of some output arguments.

To invoke `Subtrees`, the properties `PruneList` and `PruneAlpha` of tree must be nonempty. In other words, grow `tree` by setting `'Prune','on'`, or by pruning `tree` using `prune`.

Default: `0`

Output Arguments

`Yfit`

The response tree predicts for the training data.

If the `Subtrees` name-value argument is a scalar or is missing, `label` is the same data type as the training response data `tree.Y`.

If `Subtrees` contains `m>1` entries, `label` has `m` columns, each of which represents the predictions of the corresponding subtree.

`node`

The `tree` node numbers where `tree` sends each data row.

If the `Subtrees` name-value argument is a scalar or is missing, `node` is a numeric column vector with `n` rows, the same number of rows as `tree.X`.

If `Subtrees` contains `m>1` entries, `node` is a `n`-by-`m` matrix. Each column represents the node predictions of the corresponding subtree.

Examples

Compute the In-Sample MSE

Load the `carsmall` data set. Consider `Displacement`, `Horsepower`, and `Weight` as predictors of the response `MPG`.

```
load carsmall
X = [Displacement Horsepower Weight];
```

Grow a regression tree using all observations.

```
Mdl = fitrtree(X,MPG);
```

Compute the resubstitution MSE.

```
Yfit = resubPredict(Mdl);
mean((Yfit - Mdl.Y).^2)
```

```
ans =

    4.8952
```

You can get the same result using resubLoss (RegressionTree).

```
resubLoss(Mdl)
```

```
ans =

    4.8952
```

Estimate In-Sample Responses For Each Subtree

Load the `carsmall` data set. Consider `Weight` as a predictor of the response `MPG`.

```
load carsmall
idxNaN = isnan(MPG + Weight);
X = Weight(~idxNaN);
Y = MPG(~idxNaN);
n = numel(X);
```

Grow a regression tree using all observations.

```
Mdl = fitrtree(X,Y);
```

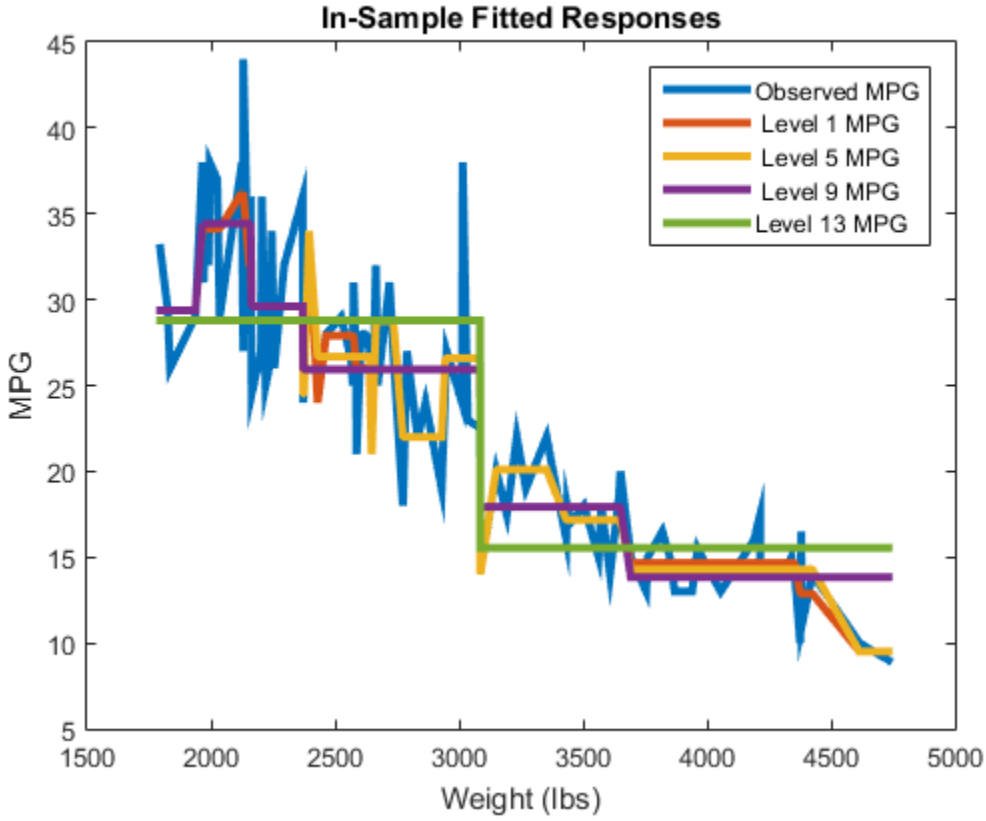
Compute resubstitution fitted values for the subtrees at several pruning levels.

```
m = max(Mdl.PruneList);
pruneLevels = 1:4:m; % Pruning levels to consider
z = numel(pruneLevels);
Yfit = resubPredict(Mdl,'SubTrees',pruneLevels);
```

`Yfit` is an `n`-by- `z` matrix of fitted values in which the rows correspond to observations and the columns correspond to a subtree.

Plot several columns of `Yfit` and `Y` against `X`.

```
figure;
sortDat = sortrows([X Y Yfit],1); % Sort all data with respect to X
plot(repmat(sortDat(:,1),1,size(Yfit,2) + 1),sortDat(:,2:end))...
    % Vectorize for efficiency
lev = cellstr(num2str((pruneLevels)','Level %d MPG'));
legend(['Observed MPG'; lev])
title 'In-Sample Fitted Responses'
xlabel 'Weight (lbs)';
ylabel 'MPG';
h = findobj(gcf);
set(h(4:end),'LineWidth',3) % Widen all lines
```



The values of `Yfit` for lower pruning levels tend to follow the data more closely than higher levels. Higher pruning levels tend to be flat for large `X` intervals.

See Also

`resubLoss` | `predict` | `fitrtree`

resume

Class: ClassificationEnsemble

Resume training ensemble

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

Note: You cannot `resume` training when `ens` is a `Subspace` ensemble created with `'AllPredictorCombinations'` number of learners.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A classification ensemble, created with `fitensemble`.

`nlearn`

A positive integer, the number of cycles for additional training of ens.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'nprint'`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The classification ensemble ens, augmented with additional training.

Examples

Train a classification ensemble for 10 cycles. Examine the resubstitution error. Then train for 10 more cycles and examine the new resubstitution error.

```
load ionosphere
ens = fitensemble(X,Y,'GentleBoost',10,'Tree');
L = resubLoss(ens)

L =
    0.0484

ens1 = resume(ens,10);
L = resubLoss(ens1)

L =
    0.0256
```

The new ensemble has much less resubstitution error than the original.

See Also

`fitensemble`

resume

Class: ClassificationPartitionedEnsemble

Resume training learners on cross-validation folds

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` in every fold for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A cross-validated classification ensemble. `ens` is the result of either:

- The `fitensemble` function with a cross-validation name-value pair. The names are `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.
- The `crossval` method applied to a classification ensemble.

`nlearn`

A positive integer, the number of cycles for additional training of ens.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'nprint'`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The cross-validated classification ensemble ens, augmented with additional training.

Examples

Train a partitioned classification ensemble for 10 cycles. Examine the error. Then train for 10 more cycles and examine the new error.

```
load ionosphere
cvens = fitensemble(X,Y,'GentleBoost',10,'Tree',...
    'crossval','on');
L = kfoldLoss(cvens)

L =
    0.0883

cvens = resume(cvens,10);
L = kfoldLoss(cvens)

L =
    0.0769
```

The ensemble has less cross-validation error after training for ten more cycles.

See Also

`kfoldEdge` | `kfoldMargin` | `kfoldLoss` | `kfoldPredict`

resume

Class: ClassificationSVM

Resume training support vector machine classifier

Syntax

```
UpdatedSVMModel = resume(SVMModel,numIter)
UpdatedSVMModel = resume(SVMModel,numIter,Name,Value)
```

Description

`UpdatedSVMModel = resume(SVMModel,numIter)` returns an updated support vector machine (SVM) classifier (`UpdatedSVMModel`) by training the support vector machine classifier `SVMModel` for `numIter` more iterations.

`resume` continues applying the training options that you set for `fitcsvm` to train `SVMModel`.

`UpdatedSVMModel = resume(SVMModel,numIter,Name,Value)` returns an updated support vector machine classifier (`UpdatedSVMModel`) with additional options specified by one or more Name,Value pair arguments.

Tips

If optimization has not converged and the solver is `'SMO'` or `'ISDA'`, then try to resume training the SVM classifier.

Input Arguments

`SVMModel` — Full, trained SVM classifier

`ClassificationSVM` classifier

Full, trained SVM classifier, specified as a `ClassificationSVM` model trained using `fitcsvm`.

`numIter` — Number of iterations

Positive integer

Number of iterations to continue training the SVM classifier, specified as a positive integer.

Data Types: `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Verbose'` — Verbosity level

`0 | 1 | 2`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and either `0`, `1`, or `2`. `Verbose` controls the amount of optimization information that the software displays to the Command Window and is saved as a structure to `SVMModel.ConvergenceInfo.History`.

This table summarizes the available verbosity level options.

Value	Description
0	The software does not display or save convergence information.
1	The software displays diagnostic messages and saves convergence criteria every *`numprint`* iterations, where *`numprint`* is the value of the name-value pair argument `'NumPrint'`.
2	The software displays diagnostic messages and saves convergence criteria at every iteration.

By default, `Verbose` is the value that `fitcsvm` used to train SVMModel.

Example: `'Verbose',1`

Data Types: `double`

`'NumPrint'` — Number of iterations between diagnostic message printouts
nonnegative integer

Number of iterations between diagnostic message printouts, specified as the comma-separated pair consisting of `'NumPrint'` and a nonnegative integer.

If you set `'Verbose',1` and `'NumPrint',numprint`, then the software displays all optimization diagnostic messages from SMO [1] and ISDA [2] every *`numprint`* iterations to the Command Window.

By default, `NumPrint` is the value that `fitcsvm` used to train SVMModel.

Example: `'NumPrint',500`

Data Types: `double`

Output Arguments

`UpdatedSVMModel` — Updated SVM classifier
`ClassificationSVM` classifier

Updated SVM classifier, returned as a `ClassificationSVM` classifier.

Examples

Resume Training an SVM Classifier

If you trained an SVM classifier, and the solver failed to converge onto a solution, then you can resume training the classifier without having to restart the entire learning process.

Load the `ionosphere` data set.

```
load ionosphere
rng(1); % For reproducibility
```

Train an SVM classifier. For illustration, specify that the optimization routine uses at most 50 iterations.

```
SVMModel = fitcsvm(X,Y,'IterationLimit',50);
DidConverge = SVMModel.ConvergenceInfo.Converged
Reason = SVMModel.ConvergenceInfo.ReasonForConvergence
```

```
DidConverge =

     0


Reason =

NoConvergence
```

`DidConverge = 0` indicates that the optimization routine did not converge onto a solution. `Reason` states the reaon why the routine did not converge. Therefore, `SVMModel` is a partially trained, SVM classifier.

Resume training the SVM classifier for another `1500` iterations.

```
UpdatedSVMModel = resume(SVMModel,1500);
DidConverge = UpdatedSVMModel.ConvergenceInfo.Converged
Reason = UpdatedSVMModel.ConvergenceInfo.ReasonForConvergence
```

```
DidConverge =

     1


Reason =

DeltaGradient
```

`DidConverge` indicates that the optimization routine converged onto a solution. `Reason` indicates that the gradient difference (`DeltaGradient`) reached its tolerance level (`DelatGradientTolerance`). Therefore, `SVMModel` is a fully trained SVM classifier.

Monitor Training of an SVM Classifier

Load the `ionosphere` data set.

```
load ionosphere
```

Train an SVM classifier. For illustration, specify that the optimization routine uses at most 100 iterations. Monitor the algorithm specifying that the software prints diagnostic inofrmation every 50 iterations.

```
SVMModel = fitcsvm(X,Y,'IterationLimit',100,'Verbose',1,'NumPrint',50);
```

```
|=============================================================================================|
|   Iteration   | Set  |   Set Size    |  Feasibility  |     Delta     |      KKT      |
|               |      |               |      Gap      |    Gradient   |   Violation   |
|=============================================================================================|
|             0 |active|           351 |  9.971591e-01 |  2.000000e+00 |  1.000000e+00 |
|            50 |active|           351 |  8.064425e-01 |  3.736929e+00 |  2.161317e+00 |

SVM optimization did not converge to the required tolerance.
```

The software prints an iterative display to the Command Window. The printout indicates that the optimization routine has not converged onto a solution.

Estimate the resubstitution loss of the partially trained SVM classifier.

```
partialLoss = resubLoss(SVMModel)
```

```
partialLoss =

    0.1054
```

The training sample misclassification error is approximately 11%.

Resume training the classifier for another 1500 iterations. Specify that the software print diagnostic information every 250 iterations.

```
UpdatedSVMModel = resume(SVMModel,1500,'NumPrint',250)
```

```
|=============================================================================================|
|   Iteration   | Set  |   Set Size    |  Feasibility  |     Delta     |      KKT      |
|               |      |               |      Gap      |    Gradient   |   Violation   |
|=============================================================================================|
|           250 |active|           351 |  1.441556e-01 |  1.701201e+00 |  1.015454e+00 |
|           500 |active|           351 |  3.277736e-03 |  9.155364e-02 |  4.830095e-02 |
|           750 |active|           351 |  3.928360e-04 |  1.367091e-02 |  9.155316e-03 |
|          1000 |active|           351 |  4.802547e-05 |  1.551900e-03 |  7.765843e-04 |
|          1044 |active|           351 |  3.602828e-05 |  9.382457e-04 |  5.182592e-04 |

 Exiting Active Set upon convergence due to DeltaGradient.
```

```
UpdatedSVMModel =

  ClassificationSVM
      PredictorNames: {1x34 cell}
        ResponseName: 'Y'
          ClassNames: {'b'  'g'}
      ScoreTransform: 'none'
     NumObservations: 351
               Alpha: [103x1 double]
                Bias: -3.8828
    KernelParameters: [1x1 struct]
      BoxConstraints: [351x1 double]
     ConvergenceInfo: [1x1 struct]
     IsSupportVector: [351x1 logical]
              Solver: 'SMO'
```

The software resumes at iteration `1000`, and uses the same verbosity level as you set when you trained the model using `fitcsvm`. The printout indicates that the algorithm converged. Therefore, `UpdatedSVMModel` is a fully trained `ClassificationSVM` classifier.

```
updatedLoss = resubLoss(UpdatedSVMModel)
```

```
updatedLoss =

    0.0769
```

The trainig sample misclassification error of the fully trained classifier is approximately 8%.

References

[1] Fan, R.-E., P.-H. Chen, and C.-J. Lin. “Working set selection using second order information for training support vector machines.” *Journal of Machine Learning Research*, Vol 6, 2005, pp. 1889–1918.

[2] Kecman V., T. -M. Huang, and M. Vogt. “Iterative Single Data Algorithm for Training Kernel Machines from Huge Data Sets: Theory and Performance.” In *Support*

Vector Machines: Theory and Applications. Edited by Lipo Wang, 255–274. Berlin: Springer-Verlag, 2005.

See Also

`ClassificationSVM` | `fitcsvm`

resume

Class: RegressionEnsemble

Resume training ensemble

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A regression ensemble, created with `fitensemble`.

`nlearn`

A positive integer, the number of cycles for additional training of ens.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'nprint'`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The regression ensemble ens, augmented with additional training.

Examples

Train a regression ensemble for 50 cycles. Examine the resubstitution error. Then train for 50 more cycles and examine the new resubstitution error.

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',50,'Tree');
 L = resubLoss(ens)

L =
    6.2681

ens = resume(ens,50);
L = resubLoss(ens)

L =
    4.3904
```

The new ensemble has much less resubstitution error than the original.

See Also

`fitensemble`

resume

Class: RegressionPartitionedEnsemble

Resume training ensemble

Syntax

```
ens1 = resume(ens,nlearn)
ens1 = resume(ens,nlearn,Name,Value)
```

Description

`ens1 = resume(ens,nlearn)` trains `ens` in every fold for `nlearn` more cycles. `resume` uses the same training options `fitensemble` used to create `ens`.

`ens1 = resume(ens,nlearn,Name,Value)` trains `ens` with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`ens`

A cross-validated regression ensemble. `ens` is the result of either:

- The `fitensemble` function with a cross-validation name-value pair. The names are `'crossval'`, `'kfold'`, `'holdout'`, `'leaveout'`, or `'cvpartition'`.
- The `crossval` method applied to a regression ensemble.

`nlearn`

A positive integer, the number of cycles for additional training of ens.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'nprint'`

Printout frequency, a positive integer scalar or `'off'` (no printouts). Returns to the command line the number of weak learners trained so far. Useful when you train ensembles with many learners on large data sets.

Default: `'off'`

Output Arguments

`ens1`

The cross-validated regression ensemble ens, augmented with additional training.

Examples

Train a regression ensemble for 50 cycles, and cross validate it. Examine the cross-validation error. Then train for 50 more cycles and examine the new cross-validation error.

```
load carsmall
X = [Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',50,'Tree');
cvens = crossval(ens);
L = kfoldLoss(cvens)

L =
   25.6573

cvens = resume(cvens,50);
L = kfoldLoss(cvens)

L =
   26.7563
```

The additional training did not improve the cross-validation error.

See Also

`kfoldLoss` | `fitensemble`

prob.RicianDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Rician probability distribution object

Description

`prob.RicianDistribution` is an object consisting of parameters, a model description, and sample data for a Rician probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Rician')` creates a Rician probability distribution object using the default parameter values.

`pd = makedist('Rician','s',s,'sigma',sigma)` creates a Rician probability distribution object using the specified parameter values.

Input Arguments

`s` — Noncentrality parameter

1 (default) | nonnegative scalar value

Noncentrality parameter for the Rician distribution, specified as a nonnegative scalar value.

Data Types: `single` | `double`

`sigma` — scale parameter

1 (default) | positive scalar value

Scale parameter for the Rician distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

`s` — Noncentrality parameter

nonnegative scalar value

Noncentrality parameter of the Rician distribution, stored as a nonnegative scalar value.

Data Types: `single | double`

`sigma` — scale parameter

positive scalar value

Scale parameter for the Rician distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object

truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Rician Distribution

The Rician distribution is used in communications theory to model scattered signals that reach a receiver using multiple paths.

The Rician distribution uses the following parameters.

Name	Description	Support
`s`	Noncentrality parameter	$s \geq 0$
`sigma`	Scale parameter	$\sigma > 0$

The probability density function (pdf) is

$$f(x \mid s,\sigma) = I_0\left(\frac{xs}{\sigma^2}\right)\left(\frac{x}{\sigma^2}\right)\exp\left\{-\frac{x^2+s^2}{2\sigma^2}\right\} \quad ; \quad x \geq 0 \, ,$$

where I_0 is the zero-order modified Bessel function of the first kind.

Examples

Create a Rician Distribution Object Using Default Parameters

Create a Rician distribution object using the default parameter values.

```
pd = makedist('Rician')
```

```
pd =

  RicianDistribution

  Rician distribution
        s = 1
    sigma = 1
```

Create a Rician Distribution Object Using Specified Parameters

Create a Rician distribution object by specifying the parameter values.

```
pd = makedist('Rician','s',0,'sigma',2)
```

```
pd =

  RicianDistribution

  Rician distribution
        s = 0
    sigma = 2
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =
```

```
2.5066
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Rician Distribution"
- Class Attributes
- Property Attributes

ridge

Ridge regression

Syntax

```
b = ridge(y,X,k)
b = ridge(y,X,k,scaled)
```

Description

`b = ridge(y,X,k)` returns a vector `b` of coefficient estimates for a multilinear ridge regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses. `k` is a vector of ridge parameters. If `k` has m elements, `b` is p-by-m. By default, `b` is computed after centering and scaling the predictors to have mean 0 and standard deviation 1. The model does not include a constant term, and `X` should not contain a column of 1s.

`b = ridge(y,X,k,scaled)` uses the {0,1}-valued flag `scaled` to determine if the coefficient estimates in `b` are restored to the scale of the original data. `ridge(y,X,k,0)` performs this additional transformation. In this case, `b` contains p+1 coefficients for each value of `k`, with the first row corresponding to a constant term in the model. `ridge(y,X,k,1)` is the same as `ridge(y,X,k)`. In this case, `b` contains p coefficients, without a coefficient for a constant term.

The relationship between `b0 = ridge(y,X,k,0)` and `b1 = ridge(y,X,k,1)` is given by

```
m = mean(X);
s = std(X,0,1)';
b1_scaled = b1./s;
b0 = [mean(y)-m*b1_scaled; b1_scaled]
```

This can be seen by replacing the x_i (i = 1, ..., n) in the multilinear model $y = b_0{}^0 + b_1{}^0 x_1 + ... + b_n{}^0 x_n$ with the z-scores $z_i = (x_i - \mu_i)/\sigma_i$, and replacing y with $y - \mu_y$.

In general, `b1` is more useful for producing plots in which the coefficients are to be displayed on the same scale, such as a *ridge trace* (a plot of the regression coefficients as a function of the ridge parameter). `b0` is more useful for making predictions.

Coefficient estimates for multiple linear regression models rely on the independence of the model terms. When terms are correlated and the columns of the design matrix X have an approximate linear dependence, the matrix $(X^TX)^{-1}$ becomes close to singular. As a result, the least-squares estimate

$$\hat{\beta} = (X^T X)^{-1} X^T y$$

becomes highly sensitive to random errors in the observed response y, producing a large variance. This situation of *multicollinearity* can arise, for example, when data are collected without an experimental design.

Ridge regression addresses the problem by estimating regression coefficients using

$$\hat{\beta} = (X^T X + kI)^{-1} X^T y$$

where k is the *ridge parameter* and I is the identity matrix. Small positive values of k improve the conditioning of the problem and reduce the variance of the estimates. While biased, the reduced variance of ridge estimates often result in a smaller mean square error when compared to least-squares estimates.

Examples

Ridge Regression

Load the sample data.

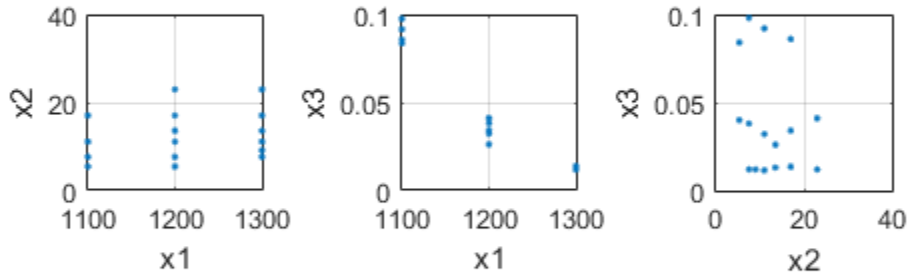
```
load acetylene
```

`acetylene` has observations for the predictor variables `x1` , `x2` , `x3` , and the response variable `y` .

Plot the predictor variables against each other.

```
subplot(1,3,1)
plot(x1,x2,'.')
xlabel('x1'); ylabel('x2'); grid on; axis square

subplot(1,3,2)
```

```
plot(x1,x3,'.')
xlabel('x1'); ylabel('x3'); grid on; axis square

subplot(1,3,3)
plot(x2,x3,'.')
xlabel('x2'); ylabel('x3'); grid on; axis square
```



Note the correlation between `x1` and the other two predictor variables.

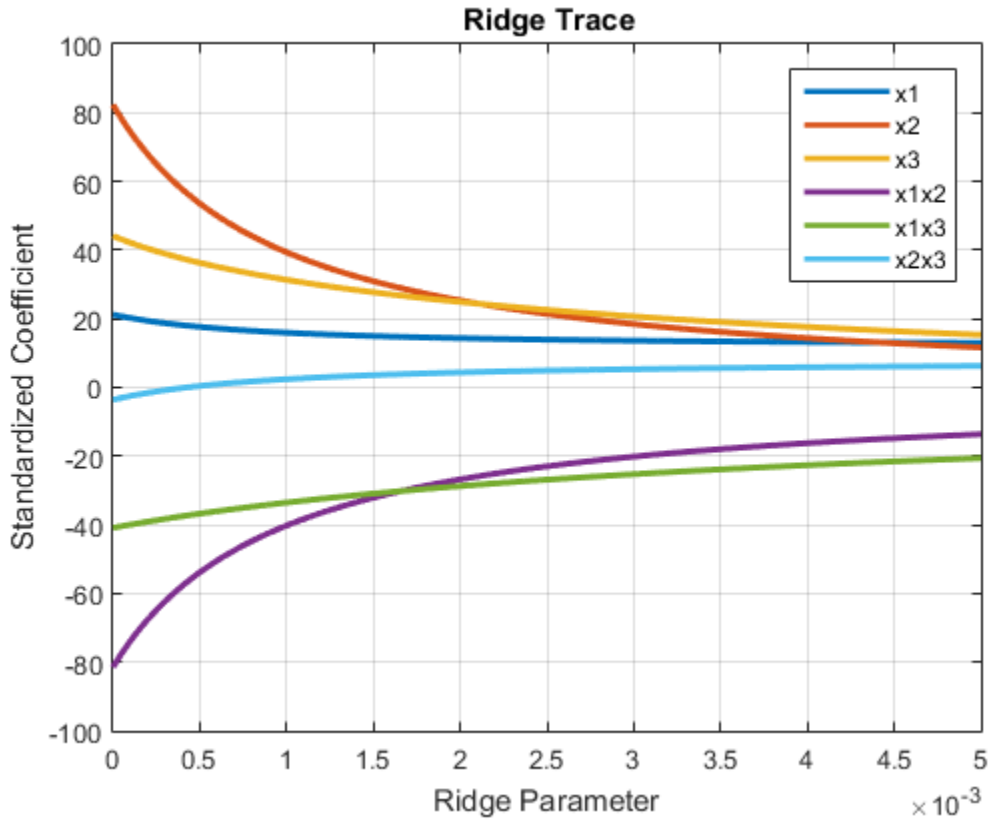
Compute coefficient estimates for a multilinear model with interaction terms, for a range of ridge parameters using `ridge` and `x2fx` .

```
X = [x1 x2 x3];
D = x2fx(X,'interaction');
```

```
D(:,1) = []; % No constant term
k = 0:1e-5:5e-3;
b = ridge(y,D,k);
```

Plot the ridge trace.

```
figure
plot(k,b,'LineWidth',2)
ylim([-100 100])
grid on
xlabel('Ridge Parameter')
ylabel('Standardized Coefficient')
title('{\bf Ridge Trace}')
legend('x1','x2','x3','x1x2','x1x3','x2x3')
```



The estimates stabilize to the right of the plot. Note that the coefficient of the `x2x3` interaction term changes sign at a value of the ridge parameter $\approx 5 * 10^{-4}$.

References

[1] Hoerl, A. E., and R. W. Kennard. "Ridge Regression: Biased Estimation for Nonorthogonal Problems." *Technometrics*. Vol. 12, No. 1, 1970, pp. 55–67.

[2] Hoerl, A. E., and R. W. Kennard. "Ridge Regression: Applications to Nonorthogonal Problems." *Technometrics*. Vol. 12, No. 1, 1970, pp. 69–82.

[3] Marquardt, D.W. "Generalized Inverses, Ridge Regression, Biased Linear Estimation, and Nonlinear Estimation." *Technometrics*. Vol. 12, No. 3, 1970, pp. 591–612.

[4] Marquardt, D. W., and R.D. Snee. "Ridge Regression in Practice." *The American Statistician*. Vol. 29, No. 1, 1975, pp. 3–20.

See Also

`regress` | `stepwise`

risk

Class: classregtree

Node risks

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
r = risk(t)
r = risk(t,nodes)
```

Description

`r = risk(t)` returns an *n*-element vector `r` of the risk of the nodes in the tree `t`, where *n* is the number of nodes. The risk `r(i)` for node `i` is the node error `e(i)` (computed by `nodeerr`) weighted by the node probability `p(i)` (computed by `nodeprob`).

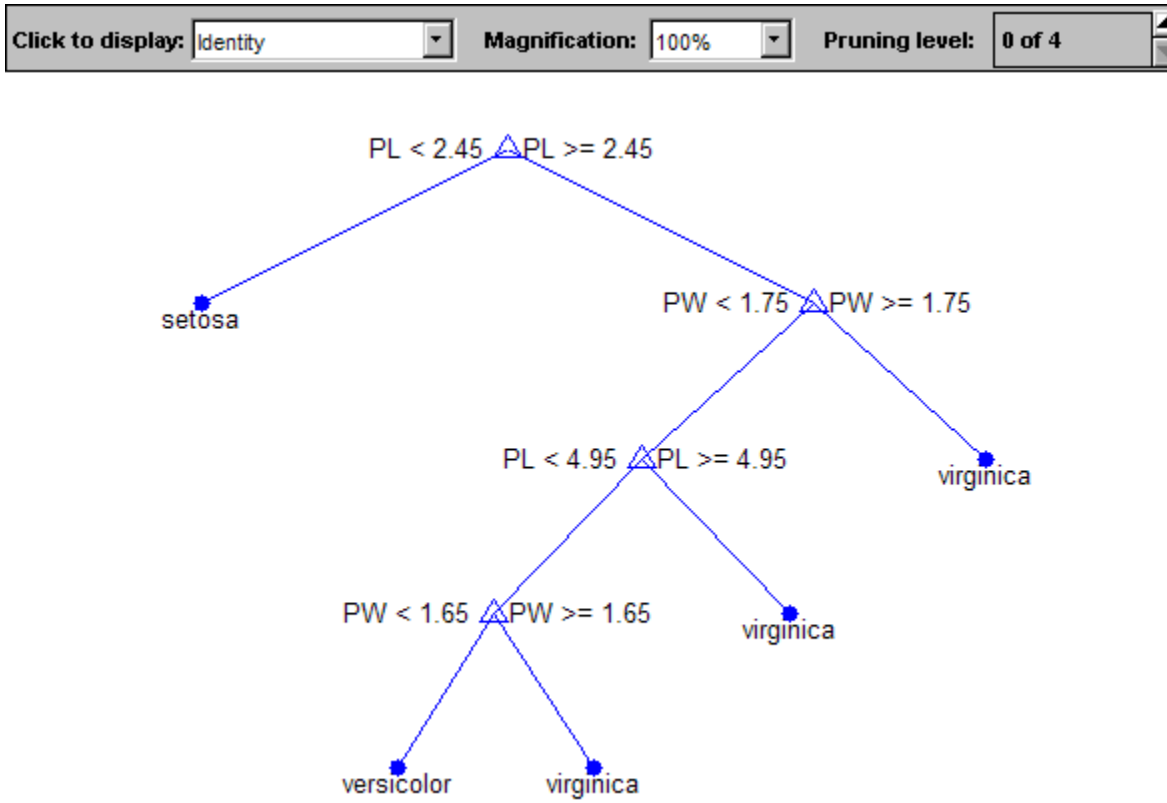
`r = risk(t,nodes)` takes a vector `nodes` of node numbers and returns the risk values for the specified nodes.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
```

```
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```




```
e = nodeerr(t);
p = nodeprob(t);
r = risk(t);

r
r =
```

```
    0.6667
         0
    0.3333
    0.0333
    0.0067
    0.0067
    0.0133
         0
         0

e.*p
ans =
    0.6667
         0
    0.3333
    0.0333
    0.0067
    0.0067
    0.0133
         0
         0
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `nodeprob` | `nodeerr`

robustdemo

Interactive robust regression

Syntax

```
robustdemo
robustdemo(x,y)
```

Description

`robustdemo` shows the difference between ordinary least squares and robust regression for data with a single predictor. With no input arguments, `robustdemo` displays a scatter plot of a sample of roughly linear data with one outlier. The bottom of the figure displays equations of lines fitted to the data using ordinary least squares and robust methods, together with estimates of the root mean squared errors.

Use the right mouse button to click on a point and view its least-squares leverage and robust weight.

Use the left mouse button to click-and-drag a point. The displays will update.

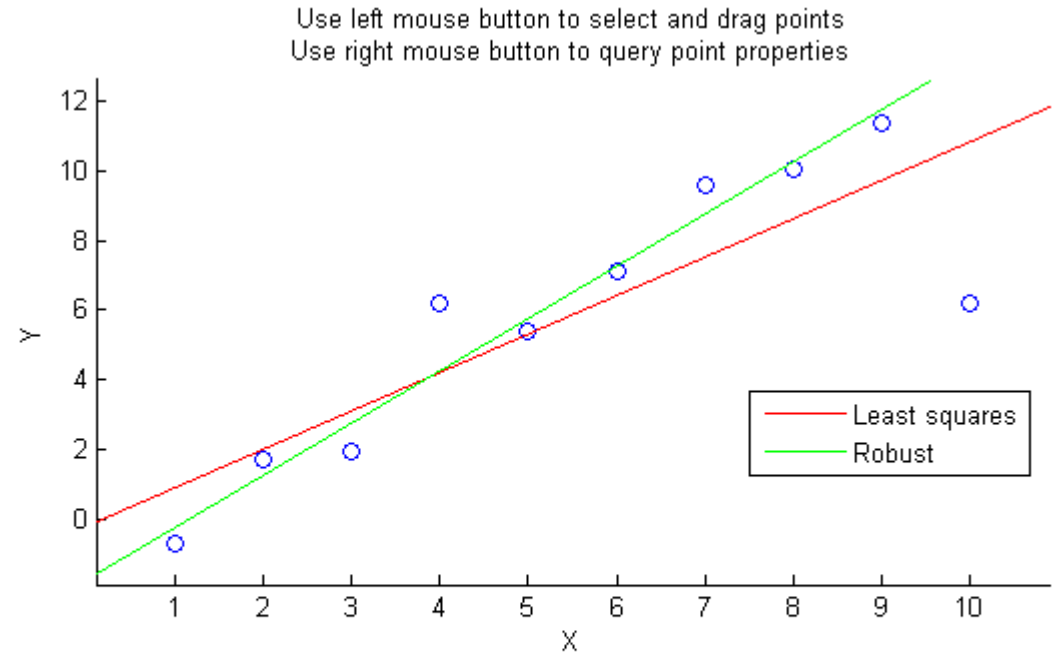
`robustdemo(x,y)` uses `x` and `y` data vectors you supply, in place of the sample data supplied with the function.

Examples

The following steps show you how to use `robustdemo`.

1 **Start the example.** To begin using `robustdemo` with the built-in data, simply type the function name:

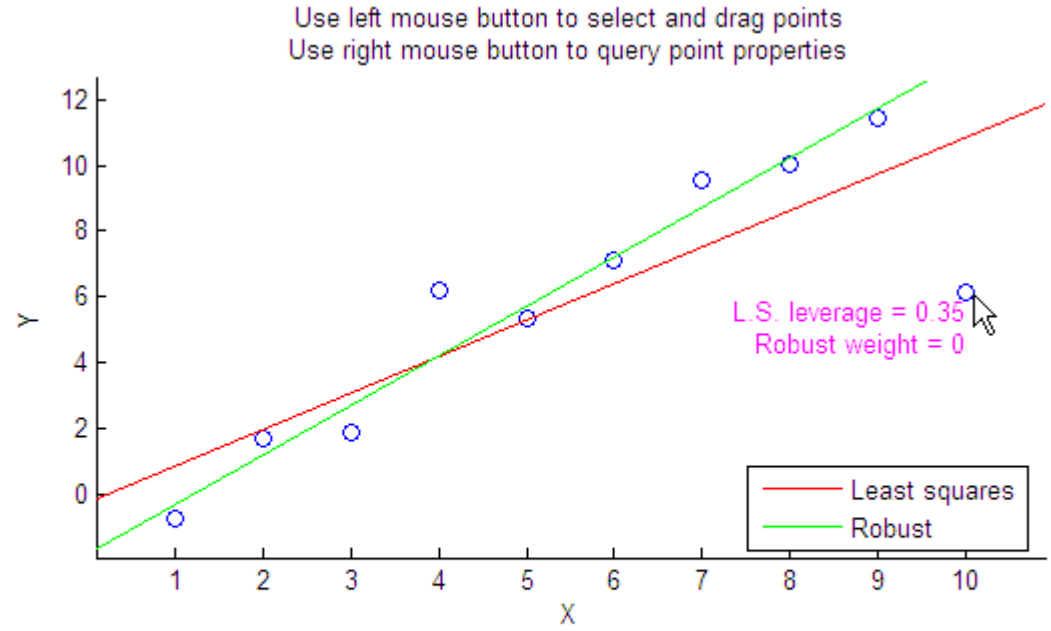
```
robustdemo
```



Least squares:	Y = -0.188327 + 1.10351*X	RMS error = 2.21375
Robust:	Y = -1.77278 + 1.50415*X	RMS error = 1.43663

The resulting figure shows a scatter plot with two fitted lines. The red line is the fit using ordinary least-squares regression. The green line is the fit using robust regression. At the bottom of the figure are the equations for the fitted lines, together with the estimated root mean squared errors for each fit.

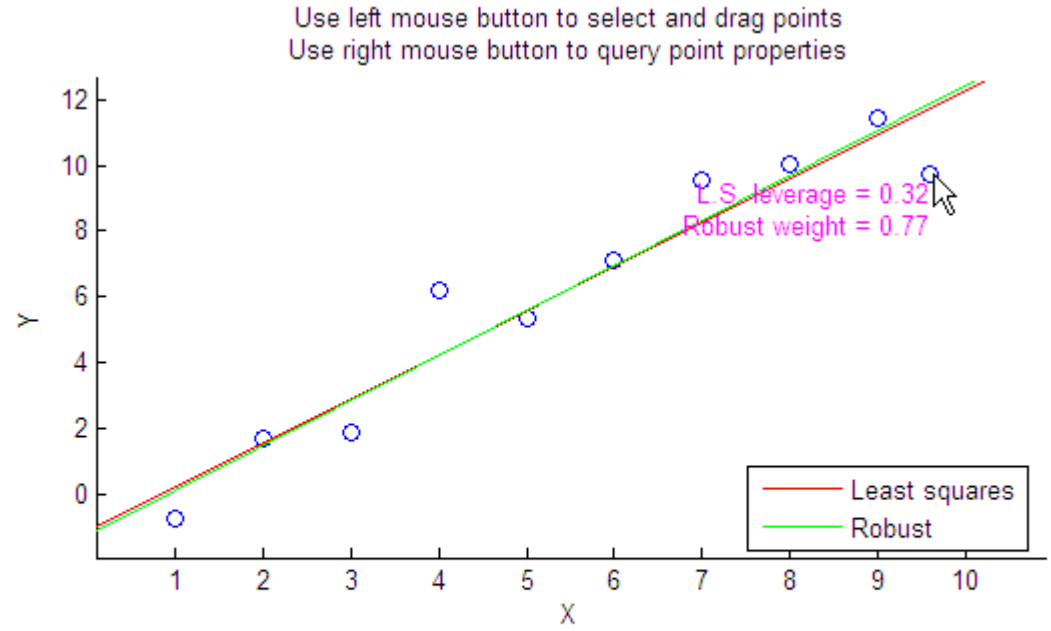
2 **View leverages and robust weights.** Right-click on any data point to see its least-squares leverage and robust weight:



Least squares:	Y = -0.188327 + 1.10351*X	RMS error = 2.21375
Robust:	Y = -1.77278 + 1.50415*X	RMS error = 1.43663

In the built-in data, the right-most point has a relatively high leverage of 0.35. The point exerts a large influence on the least-squares fit, but its small robust weight shows that it is effectively excluded from the robust fit.

3 **See how changes in the data affect the fits.** With the left mouse button, click and hold on any data point and drag it to a new location. When you release the mouse button, the displays update:



Least squares:	Y = -1.0661 + 1.33785*X	RMS error = 1.21477
Robust:	Y = -1.18916 + 1.36459*X	RMS error = 1.27697

Bringing the right-most data point closer to the least-squares line makes the two fitted lines nearly identical. The adjusted right-most data point has significant weight in the robust fit.

See Also

`robustfit` | `leverage`

robustfit

Robust regression

Syntax

```
b = robustfit(X,y)
b = robustfit(X,y,wfun,tune)
b = robustfit(X,y,wfun,tune,const)
[b,stats] = robustfit(...)
```

Description

`b = robustfit(X,y)` returns a (p + 1)-by-1 vector `b` of coefficient estimates for a robust multilinear regression of the responses in `y` on the predictors in `X`. `X` is an n-by-p matrix of p predictors at each of n observations. `y` is an n-by-1 vector of observed responses. By default, the algorithm uses iteratively reweighted least squares with a bisquare weighting function.

Note: By default, `robustfit` adds a first column of 1s to `X`, corresponding to a constant term in the model. Do not enter a column of 1s directly into `X`. You can change the default behavior of `robustfit` using the input *`const`*, below.

`robustfit` treats `NaN`s in `X` or `y` as missing values, and removes them.

`b = robustfit(X,y,wfun,tune)` specifies a weighting function *`wfun`*. `tune` is a tuning constant that is divided into the residual vector before computing weights.

The weighting function *`wfun`* can be any one of the following strings:

Weight Function	Equation	Default Tuning Constant
`'andrews'`	`w = (abs(r)<pi) .* sin(r) ./ r`	1.339
`'bisquare'` (default)	`w = (abs(r)<1) .* (1 - r.^2).^2`	4.685

Weight Function	Equation	Default Tuning Constant
'cauchy'	w = 1 ./ (1 + r.^2)	2.385
'fair'	w = 1 ./ (1 + abs(r))	1.400
'huber'	w = 1 ./ max(1, abs(r))	1.345
'logistic'	w = tanh(r) ./ r	1.205
'ols'	Ordinary least squares (no weighting function)	None
'talwar'	w = 1 * (abs(r)<1)	2.795
'welsch'	w = exp(-(r.^2))	2.985

If `tune` is unspecified, the default value in the table is used. Default tuning constants give coefficient estimates that are approximately 95% as statistically efficient as the ordinary least-squares estimates, provided the response has a normal distribution with no outliers. Decreasing the tuning constant increases the downweight assigned to large residuals; increasing the tuning constant decreases the downweight assigned to large residuals.

The value `r` in the weight functions is

```
r = resid/(tune*s*sqrt(1-h))
```

where `resid` is the vector of residuals from the previous iteration, `h` is the vector of leverage values from a least-squares fit, and `s` is an estimate of the standard deviation of the error term given by

```
s = MAD/0.6745
```

Here `MAD` is the median absolute deviation of the residuals from their median. The constant 0.6745 makes the estimate unbiased for the normal distribution. If there are p columns in `X`, the smallest p absolute deviations are excluded when computing the median.

You can write your own weight function. The function must take a vector of scaled residuals as input and produce a vector of weights as output. In this case, *`wfun`* is specified using a function handle `@` (as in `@myfun`), and the input `tune` is required.

`b = robustfit(X,y,`*`wfun`*`,tune,`*`const`*`)` controls whether or not the model will include a constant term. *`const`* is `'on'` to include the constant term (the default), or

`'off'` to omit it. When *`const`* is `'on'`, `robustfit` adds a first column of 1s to `X` and `b` becomes a (p + 1)-by-1 vector . When *`const`* is `'off'`, `robustfit` does not alter `X`, then `b` is a p-by-1 vector.

`[b,stats] = robustfit(...)` returns the structure `stats`, whose fields contain diagnostic statistics from the regression. The fields of `stats` are:

- `ols_s` — Sigma estimate (RMSE) from ordinary least squares
- `robust_s` — Robust estimate of sigma
- `mad_s` — Estimate of sigma computed using the median absolute deviation of the residuals from their median; used for scaling residuals during iterative fitting
- `s` — Final estimate of sigma, the larger of `robust_s` and a weighted average of `ols_s` and `robust_s`
- `resid` — Residual
- `rstud` — Studentized residual (see `regress` for more information)
- `se` — Standard error of coefficient estimates
- `covb` — Estimated covariance matrix for coefficient estimates
- `coeffcorr` — Estimated correlation of coefficient estimates
- `t` — Ratio of `b` to `se`
- `p` — p-values for `t`
- `w` — Vector of weights for robust fit
- `R` — R factor in QR decomposition of `X`
- `dfe` — Degrees of freedom for error
- `h` — Vector of leverage values for least-squares fit

The `robustfit` function estimates the variance-covariance matrix of the coefficient estimates using `inv(X'*X)*stats.s^2`. Standard errors and correlations are derived from this estimate.

Examples

Compare Robust and Least-Squares Regression

Generate data with the trend y = 10 - 2* x , then change one value to simulate an outlier.

```
x = (1:10)';
rng default; % For reproducibility
y = 10 - 2*x + randn(10,1);
y(10) = 0;
```

Fit a straight line using ordinary least squares regression.

```
bls = regress(y,[ones(10,1) x])
```

```
bls =

    7.8518
   -1.3644
```

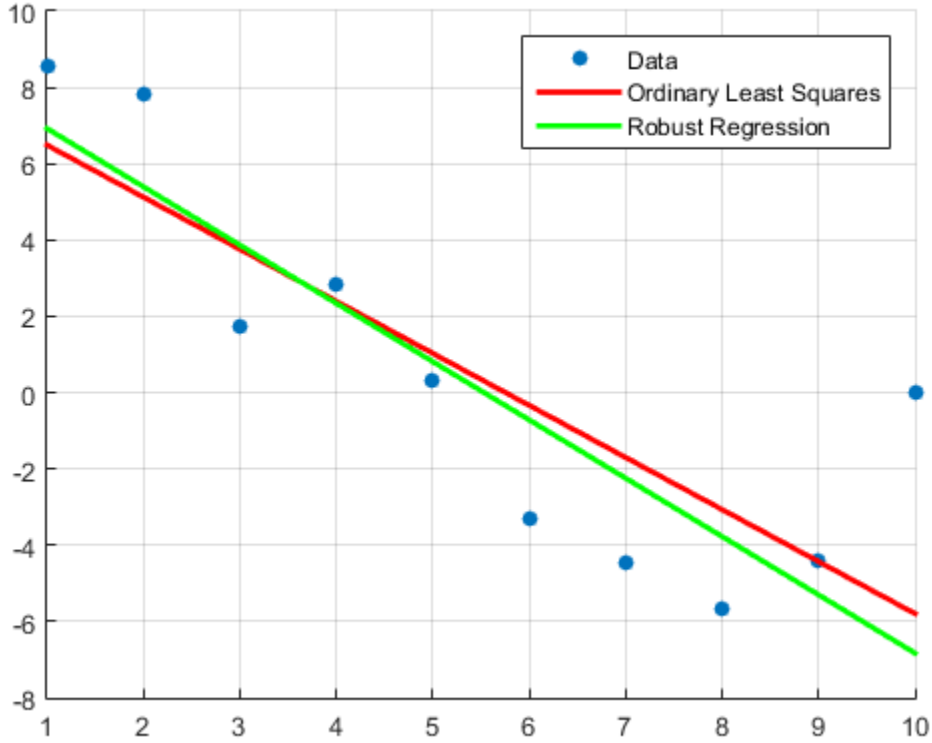
Now use robust regression to estimate a straight-line fit.

```
brob = robustfit(x,y)
```

```
brob =

    8.4504
   -1.5278
```

Create scatter plot of the data together with the fits.

```
scatter(x,y,'filled'); grid on; hold on
plot(x,bls(1)+bls(2)*x,'r','LineWidth',2);
plot(x,brob(1)+brob(2)*x,'g','LineWidth',2)
legend('Data','Ordinary Least Squares','Robust Regression')
```



The robust fit is less influenced by the outlier than the least-squares fit.

References

[1] DuMouchel, W. H., and F. L. O'Brien. "Integrating a Robust Option into a Multiple Regression Computing Environment." *Computer Science and Statistics*: *Proceedings of the 21st Symposium on the Interface*. Alexandria, VA: American Statistical Association, 1989.

[2] Holland, P. W., and R. E. Welsch. "Robust Regression Using Iteratively Reweighted Least-Squares." *Communications in Statistics: Theory and Methods*, *A6*, 1977, pp. 813–827.

[3] Huber, P. J. *Robust Statistics*. Hoboken, NJ: John Wiley & Sons, Inc., 1981.

[4] Street, J. O., R. J. Carroll, and D. Ruppert. "A Note on Computing Robust Regression Estimates via Iteratively Reweighted Least Squares." *The American Statistician*. Vol. 42, 1988, pp. 152–154.

See Also

`regress` | `robustdemo`

rotatefactors

Rotate factor loadings

Syntax

```
B = rotatefactors(A)
B = rotatefactors(A,'Method','orthomax','Coeff',gamma)
B = rotatefactors(A,'Method','procrustes','Target',target)
B = rotatefactors(A,'Method','pattern','Target',target)
B = rotatefactors(A,'Method','promax')
[B,T] = rotatefactors(A,...)
```

Description

`B = rotatefactors(A)` rotates the d-by-m loadings matrix `A` to maximize the varimax criterion, and returns the result in `B`. Rows of `A` and `B` correspond to variables and columns correspond to factors, for example, the (i, j)th element of `A` is the coefficient for the i th variable on the j th factor. The matrix `A` usually contains principal component coefficients created with `pca` or `pcacov`, or factor loadings estimated with `factoran`.

`B = rotatefactors(A,'Method','orthomax','Coeff',gamma)` rotates `A` to maximize the orthomax criterion with the coefficient `gamma`, i.e., `B` is the orthogonal rotation of `A` that maximizes

```
sum(D*sum(B.^4,1) - GAMMA*sum(B.^2,1).^2)
```

The default value of 1 for `gamma` corresponds to varimax rotation. Other possibilities include `gamma` = 0, $m/2$, and $d(m - 1)/(d + m - 2)$, corresponding to quartimax, equamax, and parsimax. You can also supply the strings `'varimax'`, `'quartimax'`, `'equamax'`, or `'parsimax'` for the `'method'` parameter and omit the `'Coeff'` parameter.

If `'Method'` is `'orthomax'`, `'varimax'`, `'quartimax'`, `'equamax'`, or `'parsimax'`, then additional parameters are

- `'Normalize'` — Flag indicating whether the loadings matrix should be row-normalized for rotation. If `'on'` (the default), rows of `A` are normalized prior to rotation to have unit Euclidean norm, and unnormalized after rotation. If `'off'`, the raw loadings are rotated and returned.

- `'Reltol'` — Relative convergence tolerance in the iterative algorithm used to find `T`. The default is `sqrt(eps)`.
- `'Maxit'` — Iteration limit in the iterative algorithm used to find `T`. The default is `250`.

`B = rotatefactors(A,'Method','procrustes','Target',target)` performs an oblique procrustes rotation of `A` to the *d*-by-*m* target loadings matrix `target`.

`B = rotatefactors(A,'Method','pattern','Target',target)` performs an oblique rotation of the loadings matrix `A` to the *d*-by-*m* target pattern matrix `target`, and returns the result in `B`. `target` defines the "restricted" elements of `B`, i.e., elements of `B` corresponding to zero elements of `target` are constrained to have small magnitude, while elements of `B` corresponding to nonzero elements of `target` are allowed to take on any magnitude.

If `'Method'` is `'procrustes'` or `'pattern'`, an additional parameter is `'Type'`, the type of rotation. If `'Type'` is `'orthogonal'`, the rotation is orthogonal, and the factors remain uncorrelated. If `'Type'` is `'oblique'` (the default), the rotation is oblique, and the rotated factors might be correlated.

When `'Method'` is `'pattern'`, there are restrictions on `target`. If `A` has *m* columns, then for orthogonal rotation, the *j*th column of `target` must contain at least *m* - *j* zeros. For oblique rotation, each column of `target` must contain at least *m* - 1 zeros.

`B = rotatefactors(A,'Method','promax')` rotates A to maximize the promax criterion, equivalent to an oblique Procrustes rotation with a target created by an orthomax rotation. Use the four orthomax parameters to control the orthomax rotation used internally by promax.

An additional parameter for 'promax' is `'Power'`, the exponent for creating promax target matrix. `'Power'` must be `1` or greater. The default is `4`.

`[B,T] = rotatefactors(A,...)` returns the rotation matrix `T` used to create `B`, that is, `B = A*T`. You can find the correlation matrix of the rotated factors by using `inv(T'*T)`. For orthogonal rotation, this is the identity matrix, while for oblique rotation, it has unit diagonal elements but nonzero off-diagonal elements.

Examples

```
rng('default') % for reproducibility
```

```
X = randn(100,10);

% Default (normalized varimax) rotation:
% first three principal components.
LPC = pca(X);
[L1,T] = rotatefactors(LPC(:,1:3));

% Equamax rotation:
% first three principal components.
[L2,T] = rotatefactors(LPC(:,1:3),...
                       'method','equamax');

% Promax rotation:
% first three factors.
LFA = factoran(X,3,'Rotate','none');
[L3,T] = rotatefactors(LFA(:,1:3),...
                       'method','promax',...
                       'power',2);

% Pattern rotation:
% first three factors.
Tgt = [1 1 1 1 1 0 1 0 1 1; ...
       0 0 0 1 1 1 0 0 0 0; ...
       1 0 0 1 0 1 1 1 1 0]';
[L4,T] = rotatefactors(LFA(:,1:3),...
                       'method','pattern',...
                       'target',Tgt);
inv(T'*T) % Correlation matrix of the rotated factors
ans =

    1.0000   -0.9593   -0.7098
   -0.9593    1.0000    0.5938
   -0.7098    0.5938    1.0000
```

References

[1] Harman, H. H. *Modern Factor Analysis*. 3rd ed. Chicago: University of Chicago Press, 1976.

[2] Lawley, D. N., and A. E. Maxwell. *Factor Analysis as a Statistical Method*. 2nd ed. New York: American Elsevier Publishing, 1971.

See Also

`biplot` | `factoran` | `pca` | `pcacov` | `procrustes`

rowexch

Row exchange

Syntax

```
dRE = rowexch(nfactors,nruns)
[dRE,X] = rowexch(nfactors,nruns)
[dRE,X] = rowexch(nfactors,nruns,model)
[dRE,X] = rowexch(...,param1,val1,param2,val2,...)
```

Description

`dRE = rowexch(nfactors,nruns)` uses a row-exchange algorithm to generate a *D*-optimal design `dRE` with `nruns` runs (the rows of `dRE`) for a linear additive model with `nfactors` factors (the columns of `dRE`). The model includes a constant term.

`[dRE,X] = rowexch(nfactors,nruns)` also returns the associated design matrix `X`, whose columns are the model terms evaluated at each treatment (row) of `dRE`.

`[dRE,X] = rowexch(nfactors,nruns,model)` uses the linear regression model specified in *`model`*. *`model`* is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

The order of the columns of `X` for a full quadratic model with n terms is:

1. The constant term
2. The linear terms in order 1, 2, ..., n
3. The interaction terms in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n)
4. The squared terms in order 1, 2, ..., n

Other models use a subset of these terms, in the same order.

Alternatively, *model* can be a matrix specifying polynomial terms of arbitrary order. In this case, *model* should have one column for each factor and one row for each term in the model. The entries in any row of *model* are powers for the factors in the columns. For example, if a model has factors X1, X2, and X3, then a row [0 1 2] in *model* specifies the term (X1.^0).*(X2.^1).*(X3.^2). A row of all zeros in *model* specifies a constant term, which can be omitted.

[dRE,X] = rowexch(...,*param1*,*val1*,*param2*,*val2*,...) specifies additional parameter/value pairs for the design. Valid parameters and their values are listed in the following table.

Parameter	Value
'bounds'	Lower and upper bounds for each factor, specified as a 2-by-nfactors matrix. Alternatively, this value can be a cell array containing nfactors elements, each element specifying the vector of allowable values for the corresponding factor.
'categorical'	Indices of categorical predictors.
'display'	Either 'on' or 'off' to control display of the iteration counter. The default is 'on'.
'excludefun'	Handle to a function that excludes undesirable runs. If the function is *f*, it must support the syntax $b = f(S)$, where S is a matrix of treatments with nfactors columns and b is a vector of Boolean values with the same number of rows as S. $b(i)$ is true if the ith row S should be excluded.
'init'	Initial design as an nruns-by-nfactors matrix. The default is a randomly selected set of points.
'levels'	Vector of number of levels for each factor.
'maxiter'	Maximum number of iterations. The default is 10.
options	A structure that specifies whether to run in parallel, and specifies the random stream or streams. Create the options structure with statset. Option fields: • UseParallel — Set to true to compute in parallel. Default is false. • UseSubstreams — Set to true to compute in parallel in a reproducible fashion. Default is false. To compute

Parameter	Value

	reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`.
	• `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `rowexch` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case
	  • You have an open Parallel pool
	  • `UseParallel` is `true`
	  • `UseSubstreams` is `false`
	  In that case, use a cell array the same size as the Parallel pool.

`'tries'`	Number of times to try to generate a design from a new starting point. The algorithm uses random points for each try, except possibly the first. The default is `1`.

Examples

Suppose you want a design to estimate the parameters in the following three-factor, seven-term interaction model:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{12} x_1 x_2 + \beta_{13} x_1 x_3 + \beta_{23} x_2 x_3 + \varepsilon$$

Use `rowexch` to generate a *D*-optimal design with seven runs:

```
nfactors = 3;
nruns = 7;
[dRE,X] = rowexch(nfactors,nruns,'interaction','tries',10)
dRE =
     -1     -1      1
      1     -1      1
      1     -1     -1
      1      1      1
     -1     -1     -1
     -1      1     -1
     -1      1      1
X =
```

```
     1    -1    -1     1     1    -1    -1
     1     1    -1     1    -1     1    -1
     1     1    -1    -1    -1    -1     1
     1     1     1     1     1     1     1
     1    -1    -1    -1     1     1     1
     1    -1     1    -1    -1     1    -1
     1    -1     1     1    -1    -1     1
```

Columns of the design matrix `X` are the model terms evaluated at each row of the design `dRE`. The terms appear in order from left to right: constant term, linear terms (1, 2, 3), interaction terms (12, 13, 23). Use `X` to fit the model, as described in "Linear Regression" on page 9-11, to response data measured at the design points in `dRE`.

More About

Algorithms

Both `cordexch` and `rowexch` use iterative search algorithms. They operate by incrementally changing an initial design matrix X to increase $D = |X^TX|$ at each step. In both algorithms, there is randomness built into the selection of the initial design and into the choice of the incremental changes. As a result, both algorithms may return locally, but not globally, D-optimal designs. Run each algorithm multiple times and select the best result for your final design. Both functions have a `'tries'` parameter that automates this repetition and comparison.

At each step, the row-exchange algorithm exchanges an entire row of X with a row from a design matrix C evaluated at a candidate set of feasible treatments. The `rowexch` function automatically generates a C appropriate for a specified model, operating in two steps by calling the `candgen` and `candexch` functions in sequence. Provide your own C by calling `candexch` directly. In either case, if C is large, its static presence in memory can affect computation.

See Also

`candgen` | `candexch` | `cordexch`

rsmdemo

Interactive response surface demonstration

Syntax

```
rsmdemo
```

Description

`rsmdemo` opens a group of three graphical user interfaces for interactively investigating response surface methodology (RSM), nonlinear fitting, and the design of experiments.

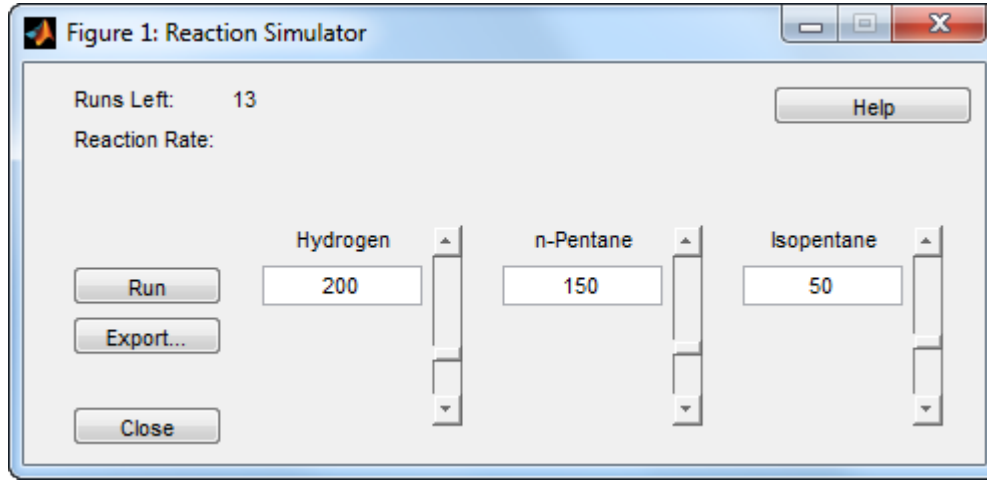
The interfaces allow you to collect and model data from a simulated chemical reaction. Experimental predictors are concentrations of three reactants (hydrogen, *n*-Pentane, and isopentane) and the response is the reaction rate. The reaction rate is simulated by a Hougen-Watson model (Bates and Watts, [2], pp. 271–272):

$$rate = \frac{\beta_1 x_2 - x_3 \,/\, \beta_5}{1 + \beta_2 x_1 + \beta_3 x_2 + \beta_4 x_3}$$

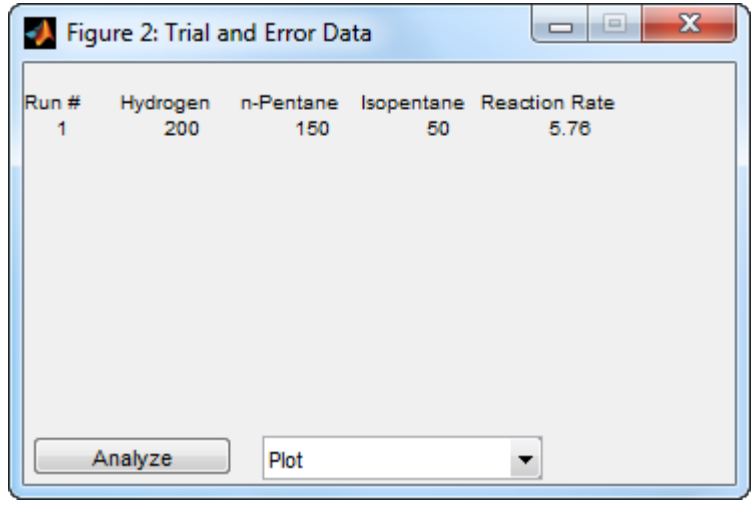
where *rate* is the reaction rate, x_1, x_2, and x_3 are the concentrations of hydrogen, *n*-pentane, and isopentane, respectively, and β_1, β_2, ... , β_5 are fixed parameters. Random errors are used to perturb the reaction rate for each combination of reactants.

Collect data using one of two methods:

1. Manually set reactant concentrations in the **Reaction Simulator** interface by editing the text boxes or by adjusting the associated sliders.

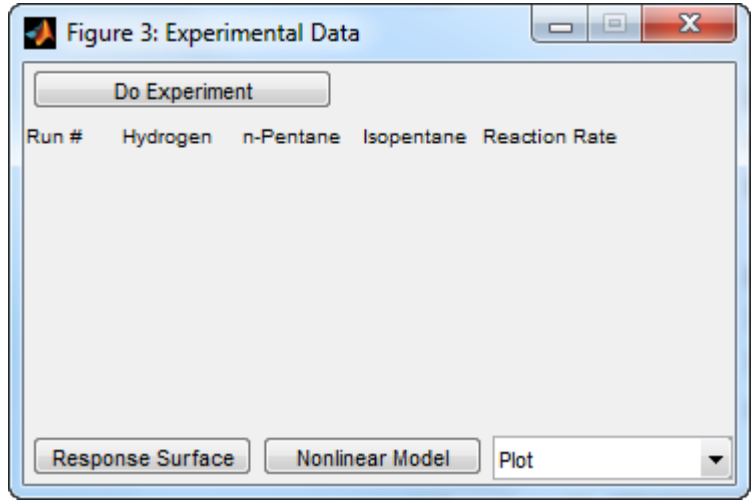


When you click **Run**, the concentrations and simulated reaction rate are recorded on the **Trial and Error Data** interface.

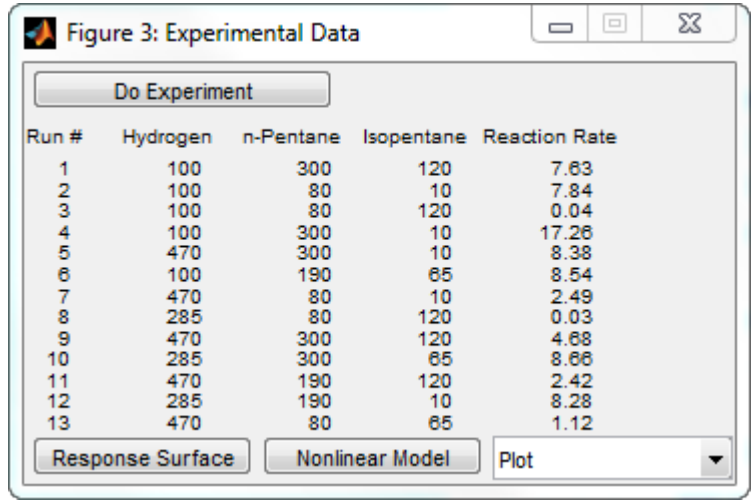


You are allowed up to 13 independent experimental runs for data collection.

2 Use a designed experiment to set reactant concentrations in the **Experimental Data** interface by clicking the **Do Experiment** button.



A 13-run *D*-optimal design for a full quadratic model is generated by the `cordexch` function, and the concentrations and simulated reaction rates are recorded on the same interface.



Once data is collected, scatter plots of reaction rates vs. individual predictors are generated by selecting one of the following from the **Plot** pop-up menu below the recorded data:

- **Hydrogen vs. Rate**
- **n-Pentane vs. Rate**
- **Isopentane vs. Rate**

Fit a response surface model to the data by clicking the **Analyze** button below the trial-and-error data or the **Response Surface** button below the experimental data. Both buttons load the data into the Response Surface Tool `rstool`. By default, trial-and-error data is fit with a linear additive model and experimental data is fit with a full quadratic model, but the models can be adjusted in the Response Surface Tool.

For experimental data, you have the additional option of fitting a Hougen-Watson model. Click the **Nonlinear Model** button to load the data and the model in `hougen` into the Nonlinear Fitting Tool `nlintool`.

See Also

`hougen` | `cordexch` | `rstool` | `nlintool`

rstool

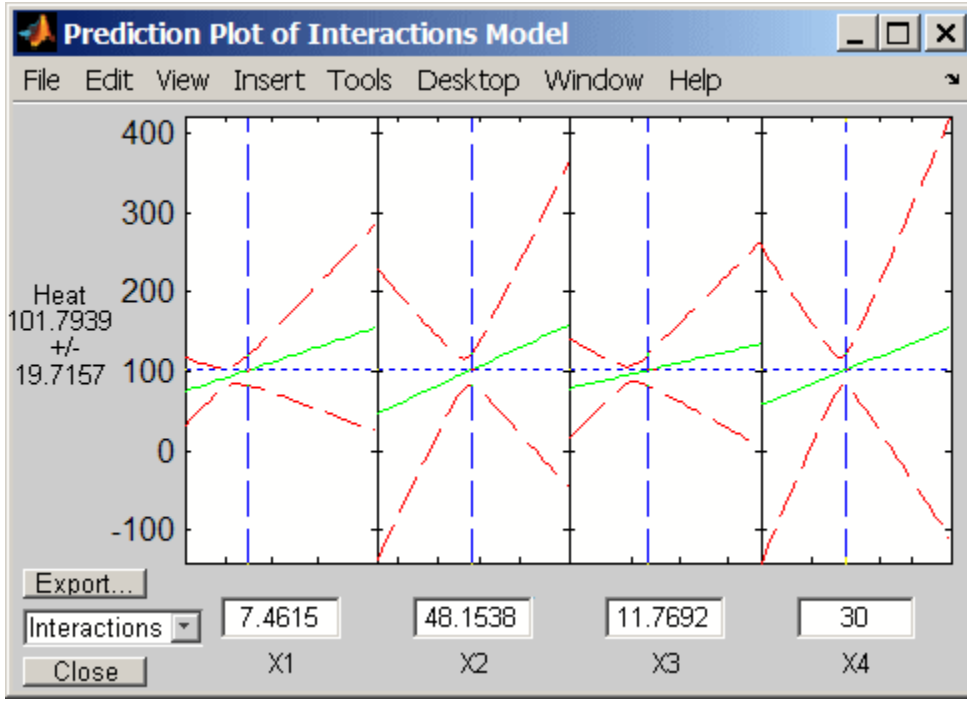
Interactive response surface modeling

Syntax

```
rstool
rstool(X,Y,model)
rstool(x,y,model,alpha)
rstool(x,y,model,alpha,xname,yname)
```

Description

`rstool` opens a graphical user interface for interactively investigating one-dimensional contours of multidimensional response surface models.



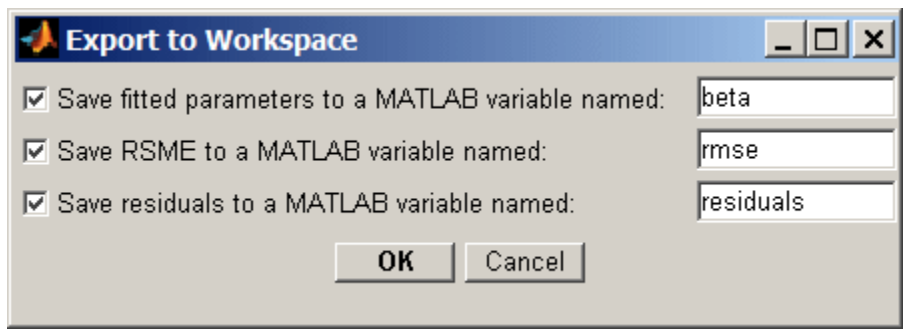
By default, the interface opens with the data from `hald.mat` and a fitted response surface with constant, linear, and interaction terms.

A sequence of plots is displayed, each showing a contour of the response surface against a single predictor, with all other predictors held fixed. `rstool` plots a 95% simultaneous confidence band for the fitted response surface as two red curves. Predictor values are displayed in the text boxes on the horizontal axis and are marked by vertical dashed blue lines in the plots. Predictor values are changed by editing the text boxes or by dragging the dashed blue lines. When you change the value of a predictor, all plots update to show the new point in predictor space.

The pop-up menu at the lower left of the interface allows you to choose among the following models:

- `Linear` — Constant and linear terms (the default)
- `Pure Quadratic` — Constant, linear, and squared terms
- `Interactions` — Constant, linear, and interaction terms
- `Full Quadratic` — Constant, linear, interaction, and squared terms

Click **Export** to open the following dialog box:



The dialog allows you to save information about the fit to MATLAB workspace variables with valid names.

`rstool(X,Y,`*`model`*`)` opens the interface with the predictor data in `X`, the response data in `Y`, and the fitted model *`model`*. Distinct predictor variables should appear in different columns of `X`. `Y` can be a vector, corresponding to a single response, or a matrix, with

columns corresponding to multiple responses. `Y` must have as many elements (or rows, if it is a matrix) as `X` has rows.

The optional input *`model`* can be any one of the following strings:

- `'linear'` — Constant and linear terms (the default)
- `'purequadratic'` — Constant, linear, and squared terms
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms

To specify a polynomial model of arbitrary order, or a model without a constant term, use a matrix for *`model`* as described in `x2fx`.

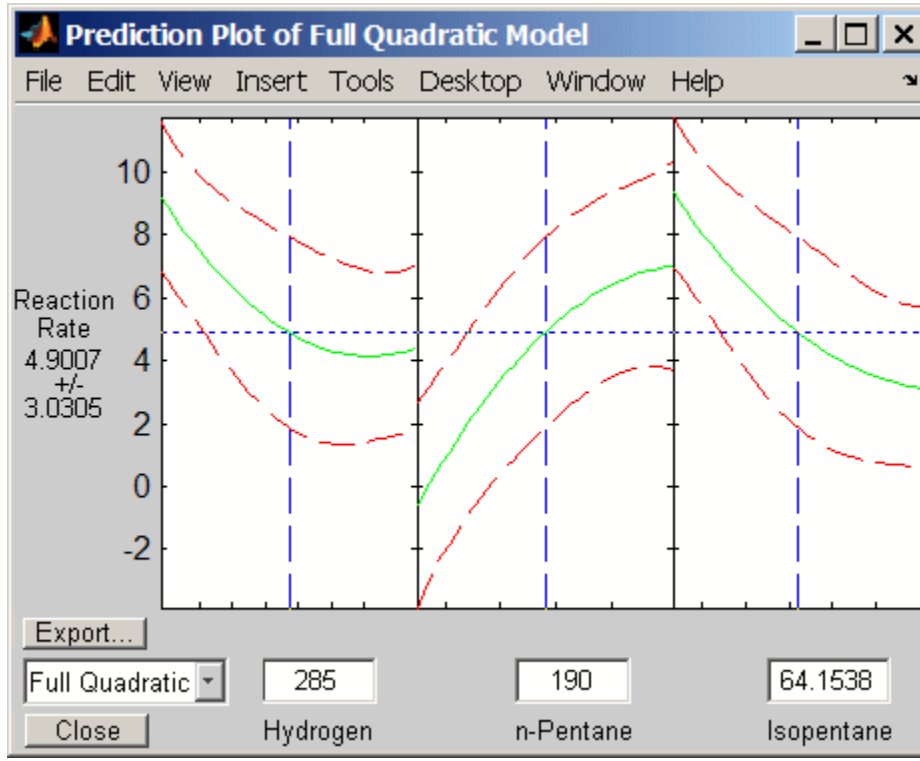
`rstool(x,y,model,alpha)` uses `100(1-alpha)`% global confidence intervals for new observations in the plots.

`rstool(x,y,model,alpha,xname,yname)` labels the axes using the strings in `xname` and `yname`. To label each subplot differently, `xname` and `yname` can be cell arrays of strings.

Examples

The following uses `rstool` to visualize a quadratic response surface model of the 3-D chemical reaction data in `reaction.mat`:

```
load reaction
alpha = 0.01; % Significance level
rstool(reactants,rate,'quadratic',alpha,xn,yn)
```



The `rstool` interface is used by `rsmdemo` to visualize the results of simulated experiments with data like that in `reaction.mat`. As described in "Response Surface Designs" on page 19-9, `rsmdemo` uses a response surface model to generate simulated data at combinations of predictors specified by either the user or by a designed experiment.

See Also

`x2fx` | `rsmdemo` | `nlintool`

runstest

Run test for randomness

Syntax

```
h = runstest(x)
h = runstest(x,v)
h = runstest(x,'ud')
h = runstest(___,Name,Value)
[h,p,stats] = runstest(___)
```

Description

`h = runstest(x)` returns a test decision for the null hypothesis that the values in the data vector x come in random order, against the alternative that they do not. The test is based on the number of runs of consecutive values above or below the mean of x. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, or `0` otherwise.

`h = runstest(x,v)` returns a test decision based on the number of runs of consecutive values above or below the specified reference value v. Values exactly equal to `v` are discarded.

`h = runstest(x,'ud')` returns a test decision based on the number of runs up or down. Too few runs indicate a trend, while too many runs indicate an oscillation. Values exactly equal to the preceding value are discarded.

`h = runstest(___,Name,Value)` returns a test decision using additional options specified by one or more name-value pair arguments. For example, you can change the significance level of the test, specify the algorithm used to calculate the *p*-value, or conduct a one-sided test.

`[h,p,stats] = runstest(___)` also returns the *p*-value of the test p, and a structure stats containing additional data about the test.

Examples

Test Data for Randomness Using Sample Median

Generate a vector of 40 random numbers from a standard normal distribution.

```
rng default;  % for reproducibility
x = randn(40,1);
```

Test whether the values in `x` appear in random order, using the sample median as the reference value.

```
[h,p] = runstest(x,median(x))
```

```
h =

     0


p =

    0.8762
```

The returned value of `h = 0` indicates that `runstest` does not reject the null hypothesis that the values in `x` are in random order at the default 5% significance level.

Input Arguments

x — Data vector

vector of scalar values

Data vector, specified as a vector of scalar values. `runstest` treats `NaN` values in `x` as missing values, and ignores them.

Data Types: `single` | `double`

v — Reference value

mean of `x` (default) | scalar value

Reference value, specified as a scalar value. If you specify a value for v, then `runstest` performs the hypothesis test based on the number of runs of consecutive values above or below v. `runstest` discards values exactly equal to v.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example:

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Method'` — Method used to compute *p*-value

`'exact'` | `'approximate'`

Method used to compute *p*-value, specified as the comma-separated pair consisting of `'Method'` and either `'exact'` to use an exact algorithm, or `'approximate'` to use a normal approximation. The default is `'exact'` for runs above/below, and for runs up/down when the length of x is less than or equal to 50. If `runstest` tests for runs up/down and the length of x is greater than 50, then the default is `'approximate'`, and the `'exact'` method is not available.

Example: `'Method','approximate'`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Two-tailed test (sequence is not random)

`'right'`	Right-tailed test (like values separate for runs above/below, direction alternates for runs up/down)
`'left'`	Left-tailed test (like values cluster for runs above/below, values trend for runs up/down)

Example: `'Tail','right'`

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

- If h = `1`, then `runstest` rejects the null hypothesis at the Alpha significance level.
- If h = `0`, then `runstest` fails to reject the null hypothesis at the Alpha significance level.

The result in `runstest` is based on the number of runs of consecutive values above or below the mean of `x`. Too few runs indicate a tendency for high and low values to cluster. Too many runs indicate a tendency for high and low values to alternate.

`runstest` uses a test statistic which is the difference between the number of runs and its mean, divided by its standard deviation. The test statistic is approximately normally distributed when the null hypothesis is true.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

p is computed from either the test statistic or the exact distribution of the number of runs, depending on the value specified for the `'Method'` name-value pair argument.

stats — Test data

structure

Test data, returned as a structure with the following fields.

- `nruns` — The number of runs
- `n1` — The number of values above `v`
- `n0` — The number of values below `v`
- `z` — The test statistic

See Also

`signrank` | `signtest`

SampleWithReplacement property

Class: TreeBagger

Flag to sample with replacement

Description

The `SampleWithReplacement` property is a logical flag specifying if data are sampled for each decision tree with replacement. True if `TreeBagger` samples data with replacement and false otherwise. True by default.

sampsizepwr

Sample size and power of test

`sampsizepwr` computes the sample size, power, or alternative parameter value for a hypothesis test, given the other two values. For example, you can compute the sample size required to obtain a particular power for a hypothesis test, given the parameter value of the alternative hypothesis.

Syntax

```
nout = sampsizepwr(testtype,p0,p1)
nout = sampsizepwr(testtype,p0,p1,pwr)

pwrout = sampsizepwr(testtype,p0,p1,[],n)

p1out = sampsizepwr(testtype,p0,[],pwr,n)

___ = sampsizepwr(testtype,p0,p1,n,pwr,Name,Value)
```

Description

`nout = sampsizepwr(testtype,p0,p1)` returns the sample size, nout, required for a two-sided test of the type specified by testtype to have a power (probability of rejecting the null hypothesis when the alternative hypothesis is true) of 0.90 when the significance level (probability of rejecting the null hypothesis when the null hypothesis is true) is 0.05. p0 specifies parameter values under the null hypothesis. p1 specifies the value, or an array of values, of the single parameter being tested under the alternative hypothesis.

`nout = sampsizepwr(testtype,p0,p1,pwr)` returns the sample size, nout, that corresponds to the specified power, pwr, and the parameter value under the alternative hypothesis, p1.

`pwrout = sampsizepwr(testtype,p0,p1,[],n)` returns the power achieved for a sample size of n when the true parameter value is p1.

`p1out = sampsizepwr(testtype,p0,[],pwr,n)` returns the parameter value detectable with the specified sample size, n, and the specified power, pwr.

`___ = sampsizepwr(testtype,p0,p1,n,pwr,Name,Value)` returns any of the previous arguments using one or more name-value pair arguments. For example, you can change the significance level of the test, or specify a right- or left-tailed test. The name-value pairs can appear in any order but must begin in the sixth argument position.

Examples

Compute Sample Size for Selected Power Value

A company runs a manufacturing process that fills empty bottles with 100 mL of liquid. To monitor quality, the company randomly selects several bottles and measures the volume of liquid inside.

Determine the sample size the company must use if it wants to detect a difference between 100 mL and 102 mL with a power of 0.80. Assume that prior evidence indicates a standard deviation of 5 mL.

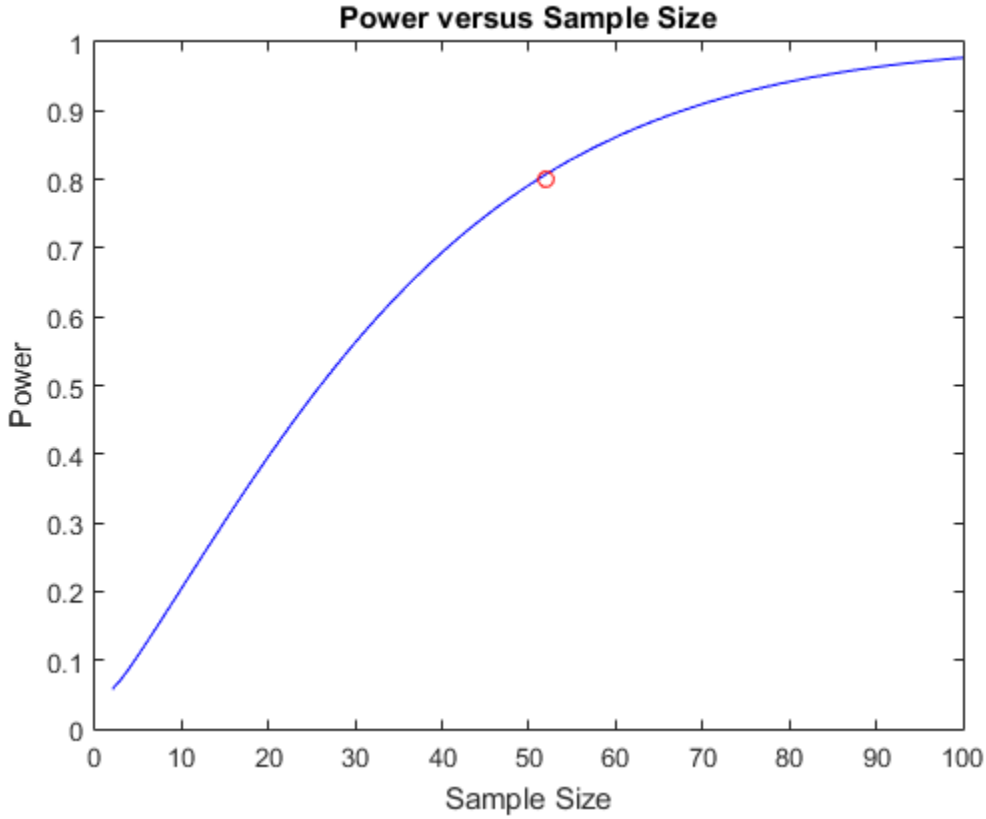
```
nout = sampsizepwr('t',[100 5],102,0.80)
```

```
nout =

    52
```

The company must test 52 bottles to detect the difference between a mean volume of 100 mL and 102 mL with a power of 0.80.

Generate a power curve to visualize how the sample size affects the power of the test.

```
nn = 1:100;
pwrout = sampsizepwr('t',[100 5],102,[],nn);

figure;
plot(nn,pwrout,'b-',nout,0.8,'ro')
title('Power versus Sample Size')
xlabel('Sample Size')
ylabel('Power')
```



Compute Power amd Sample Size for One-Sided Test

An employee wants to buy a house near her office. She decides to eliminate from consideration any house that has a mean morning commute time greater than 20 minutes. The null hypothesis for this right-sided test is H0: $\mu = 20$, and the alternative hypothesis is HA: $\mu > 20$. The selected significance level is 0.05.

To determine the mean commute time, the employee takes a test drive from the house to her office during rush hour every morning for one week, so her total sample size is 5. She assumes that the standard deviation, σ, is equal to 5.

The employee decides that a true mean commute time of 25 minutes is too different from her targeted 20-minute limit, so she wants to detect a significant departure if the

true mean is 25 minutes. Find the probability of incorrectly concluding that the mean commute time is no greater than 20 minutes.

Compute the power of the test, and then subtract the power from 1 to obtain β.

```
power = sampsizepwr('t',[20 5],25,[],5,'Tail','right');
beta = 1 - power
```

```
beta =

    0.4203
```

The β value indicates a probability of 0.4203 that the employee concludes incorrectly that the morning commute is not greater than 20 minutes.

The employee decides tha this risk is too high, and she wants no more than a 0.01 probability of reaching an incorrect conclusion. Calculate the number of test drives the employee must take to obtain a power of 0.99.

```
nout = sampsizepwr('t',[20 5],25,0.99,[],'Tail','right')
```

```
nout =

    18
```

The results indicate that she must take 18 test drives from a candidate house to achieve this power level.

The employee decides that she only has time to take 10 test drives. She also accepts a 0.05 probability of making an incorrect conclusion. Calculate the smallest true parameter value that produces a detectable difference in mean commute time.

```
p1out = sampsizepwr('t',[20 5],[],0.95,10,'Tail','right')
```

```
p1out =

   25.6532
```

Given the employee's target power level and sample size, her test detects a significant difference from a mean commute time of at least 25.6532 minutes.

Compute Sample Size for a Binomial Test

Compute the sample size, n, required to distinguish $p = 0.30$ from $p = 0.36$, using a binomial test with a power of 0.8.

```
napprox = sampsizepwr('p',0.30,0.36,0.8)
```

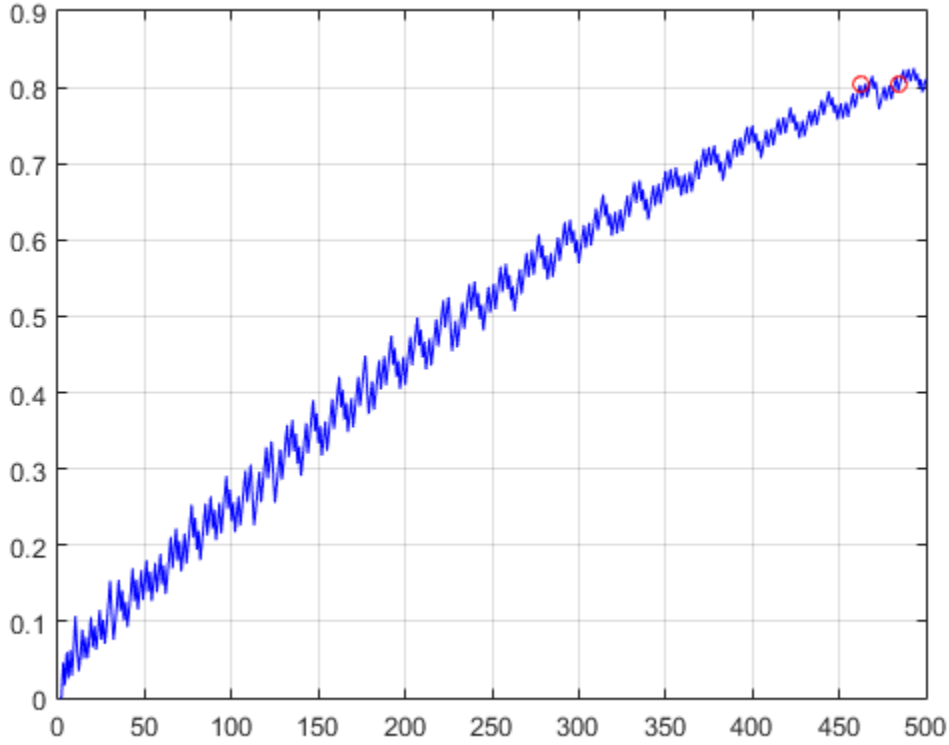
```
Warning: Values N>200 are approximate.  Plotting the power as a function
of N may reveal lower N values that have the required power.

napprox =

   485
```

The result indicates that a power of 0.8 requires a sample size of 485. However, this result is approximate.

Make a plot to see if any smaller n values provide the required power of 0.8.

```
nn = 1:500;
pwrout = sampsizepwr('p',0.3,0.36,[],nn);
nexact = min(nn(pwrout>=0.8))

figure
plot(nn,pwrout,'b-',[napprox nexact],pwrout([napprox nexact]),'ro')
grid on
```

```
nexact =

   462
```



The result indicates that a sample size of 462 also provides a power of 0.8 for this test.

Compute Power for a Two-Sample t-Test

A farmer wants to test the impact of two different types of fertilizer on the yield of his bean crops. He currently uses Fertilizer A, but believes that Fertilizer B might improve crop yield. Because Fertilizer B is more expensive than Fertilizer A, the farmer wants to limit the number of plans he treats with Fertilizer B in this experiment.

The farmer uses a 2:1 ratio of plants in each treatment group. He tests 10 plants with Fertilizer A, and 5 plants with Fertilizer B. The mean yield using Fertilizer A is 1.4 kg per plant, with a standard deviation of 0.2. The mean yield using Fertilizer B is 1.7 kg per plant. The significance level of the test is 0.05.

Compute the power of the test.

```
pwr = sampsizepwr('t2',[1.4 0.2],1.7,[],5,'Ratio',2)
```

```
pwr =

    0.7165
```

The farmer wants to increase the power of the test to 0.90. Calculate how many plants he must treat with each type of fertilizer.

```
n = sampsizepwr('t2',[1.4 0.2],1.7,0.9,[])
```

```
n =

    11
```

To increase the power of the test to 0.90, the farmer must test 11 plants with each type of fertilizer.

The farmer wants to reduce the number of plants he must treat with Fertilizer B, but keep the power of the test at 0.90. but maintain the initial 2:1 ratio of plants in each treatment group

Using a 2:1 ratio of plants in each treatment group, calculate how many plants the farmer must test to obtain a power of 0.90. Use the mean and standard deviation values obtained in the previous test.

```
[n1out,n2out] = sampsizepwr('t2',[1.4,0.2],1.7,0.9,[],'Ratio',2)
```

```
n1out =

     8


n2out =

    16
```

To obtain a power of 0.90. the farmer must treat 16 plants with Fertilizer A and 8 plants with Fertilizer B.

Input Arguments

`testtype` — Test type

`'z'` | `'t'` | `'t2'` | `'var'` | `'p'`

Test type, specified as one of the following.

- `'z'` — *z*-test for normally distributed data with known standard deviation.
- `'t'` — *t*-test for normally distributed data with unknown standard deviation.
- `'t2'` — Two-sample pooled *t*-test for normally distributed data with unknown standard deviation and equal variances.
- `'var'` — Chi-square test of variance for normally distributed data.
- `'p'` — Test of the *p* parameter (success probability) for a binomial distribution. The `'p'` test is a discrete test for which increasing the sample size does not always increase the power. For `n` values larger than 200, there may exist values smaller than the returned `n` value that also produce the specified power.

`p0` — Parameter value under null hypothesis

scalar value | two-element array of scalar values

Parameter value under the null hypothesis, specified as a scalar value or a two-element array of scalar values.

- If testtype is `'z'`or `'t'`, then `p0` is a two-element array `[mu0,sigma0]` of the mean and standard deviation, respectively, under the null hypothesis.
- If testtype is `'t2'`, then `p0` is a two-element array `[mu0,sigma0]` of the mean and standard deviation, respectively, of the first sample under the null and alternative hypotheses.
- If testtype is `'var'`, then `p0` is the variance under the null hypothesis.
- If testtype is `'p'`, then `p0` is the value of *p* under the null hypothesis.

Data Types: `single` | `double`

`p1` — Parameter value under alternative hypothesis

scalar value | array of scalar values | `[]`

Parameter value under the alternative hypothesis, specified as a scalar value or as an array of scalar values.

- If testtype is `'z'` or `'t'`, then `p1` is the value of the mean under the alternative hypothesis.
- If testtype is `'t2'`, then `p1` is the value of the mean of the second sample under the alternative hypothesis.
- If testtype is `'var'`, then `p1` is the variance under the alternative hypothesis.
- If testtype is `'p'`, then `p1` is the value of *p* under the alternative hypothesis.

If you specify p1 as an array, then `sampsizepwr` returns an array for nout or pwrout that is the same length as p1.

To return the alternative parameter value, p1out, specify p1 using empty brackets ([ ]), as shown in the syntax description.

Data Types: `single | double`

pwr — Power of the test

0.90 (default) | scalar value in the range (0,1) | array of scalar values in the range (0,1) | [ ]

Power of the test, specified as a scalar value in the range (0,1) or as an array of scalar values in the range (0,1). The power of a test is the probability of rejecting the null hypothesis when the alternative hypothesis is true, given a particular significance level.

If you specify pwr as an array, then `sampsizepwr` returns an array for nout or p1out that is the same length as pwr.

To return a power value, pwrout, specify pwr using empty brackets ([ ]), as shown in the syntax description.

Data Types: `single | double`

n — Sample size

positive integer value | array of positive integer values

Sample size, specified as a positive integer value or as an array of positive integer values.

If testtype is `'t2'`, then `sampsizepwr` assumes that the two sample sizes are equal. For unequal sample sizes, specify n as the smaller of the two sample sizes, and use the

'Ratio' name-value pair argument to indicate the sample size ratio. For example, if the smaller sample size is 5 and the larger sample size is 10, specify n as 5, and the 'Ratio' name-value pair as 2.

If you specify n as an array, then sampsizepwr returns an array for pwrout or p1out that is the same length as n.

Data Types: single | double

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. Name is the argument name and Value is the corresponding value. Name must appear inside single quotes (' '). You can specify several name and value pair arguments in any order as Name1,Value1,...,NameN,ValueN.

Example: 'Alpha',0.01,'Tail','right' specifies a right-tailed test with a 0.01 significance level.

'Alpha' — Significance level

0.05 (default) | scalar value in the range (0,1)

Significance value of the test, specified as the comma-separated pair consisting of 'Alpha' and a scalar value in the range (0,1).

Example: 'Alpha',0.01

Data Types: single | double

'Ratio' — Sample size ratio

1 (default) | scalar value greater than or equal to 1

Sample size ratio for a two-sample *t*-test, specified as the comma-separated pair consisting of 'Ratio' and a scalar value greater than or equal to 1. The value of Ratio is equal to n2/n1, where n2 is the larger sample size, and n1 is the smaller sample size.

To return the power, pwrout, or alternative parameter value, p1out, specify the smaller of the two sample sizes for n, and use 'Ratio' to indicate the sample size ratio.

Example: 'Ratio',2

'Tail' — Test type

'both' (default) | 'right' | 'left'

Test type, specified as the comma-separated pair consisting of `'Tail'` and one of the following:

- `'both'` — Two-sided test for an alternative not equal to `p0`
- `'right'` — One-sided test for an alternative larger than `p0`
- `'left'` — One-sided test for an alternative smaller than `p0`

Example: `'Tail','right'`

Output Arguments

`nout` — Sample size

positive integer value | array of positive integer values

Sample size, returned as a positive integer value or as an array of positive integer values.

If testtype is `t2`, and you use the `'Ratio'` name-value pair argument to specify the ratio of the two unequal sample sizes, then nout returns the smaller of the two sample sizes.

Alternatively, to return both sample sizes, specify this argument as `[n1out,n2out]`. In this case, `sampsizepwr` returns the smaller sample size as `n1out`, and the larger sample size as `n2out`.

If you specify pwr or p1 as an array, then `sampsizepwr` returns an array for nout that is the same length as pwr or p1.

`pwrout` — Power

scalar value in the range (0,1) | array of scalar values in the range (0,1)

Power achieved by the test, returned as a scalar value in the range (0,1) or as an array of scalar values in the range (0,1).

If you specify n or p1 as an array, then `sampsizepwr` returns an array for pwrout that is the same length as n or p1.

`p1out` — Parameter value for the alternative hypothesis

scalar value | array of scalar values

Parameter value for the alternative hypothesis, returned as a scalar value or as an array of scalar values.

When computing `p1out` for the `'p'` test, if no alternative can be rejected for a given null hypothesis and significance level, the function displays a warning message and returns `NaN`.

See Also

`binocdf` | `ttest` | `vartest` | `ztest`

scatterhist

Scatter plot with marginal histograms

Syntax

```
scatterhist(x,y)
scatterhist(x,y,Name,Value)

h = scatterhist( ___ )
```

Description

`scatterhist(x,y)` creates a 2-D scatter plot of the data in vectors x and y, and puts a univariate histogram on the horizontal and vertical axes of the plot.

`scatterhist(x,y,Name,Value)` creates the plot using additional options specified by one or more name-value pair arguments. For example, you can specify a grouping variable or change the display options.

`h = scatterhist( ___ )` returns a vector of three axis handles for the scatter plot, the histogram along the horizontal axis, and the histogram along the vertical axis, respectively, using any of the input arguments in the previous syntaxes.

Examples

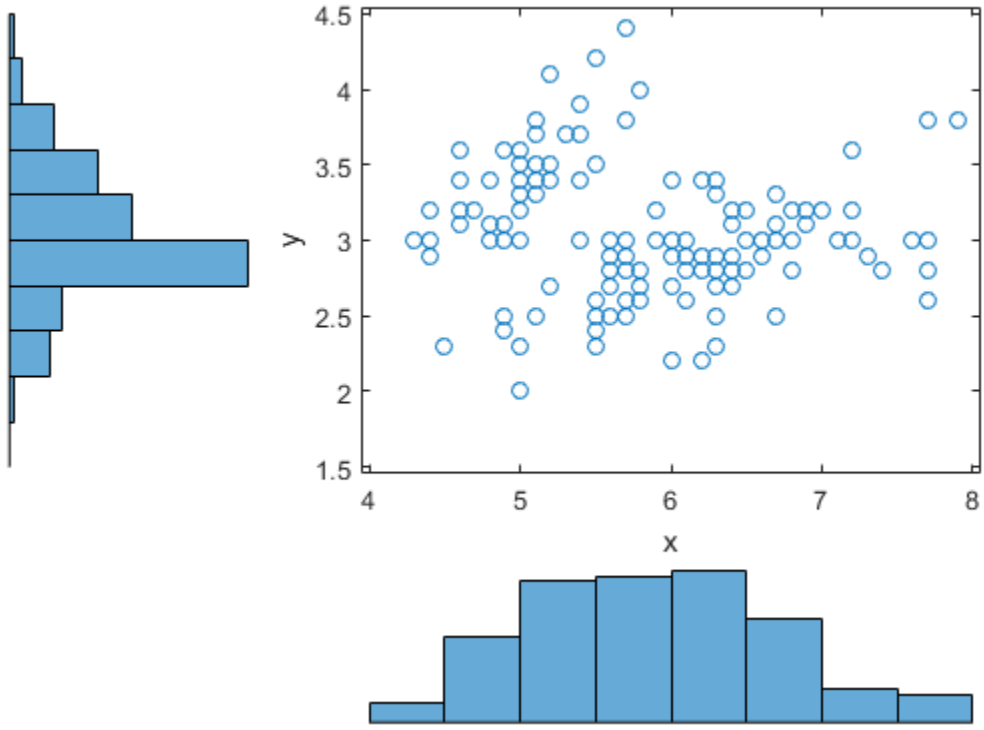
Create a Scatterhist Plot

Load the sample data. Create data vector `x` from the first column of the data matrix, which contains sepal length measurements from iris flowers. Create data vector `y` from the second column of the data matrix, which contains sepal width measurements from the same flowers.

```
load fisheriris.mat;
x = meas(:,1);
y = meas(:,2);
```

Create a scatter plot and two marginal histograms to visualize the relationship between sepal length and sepal width.

```
scatterhist(x,y)
```



Plot Grouped Data

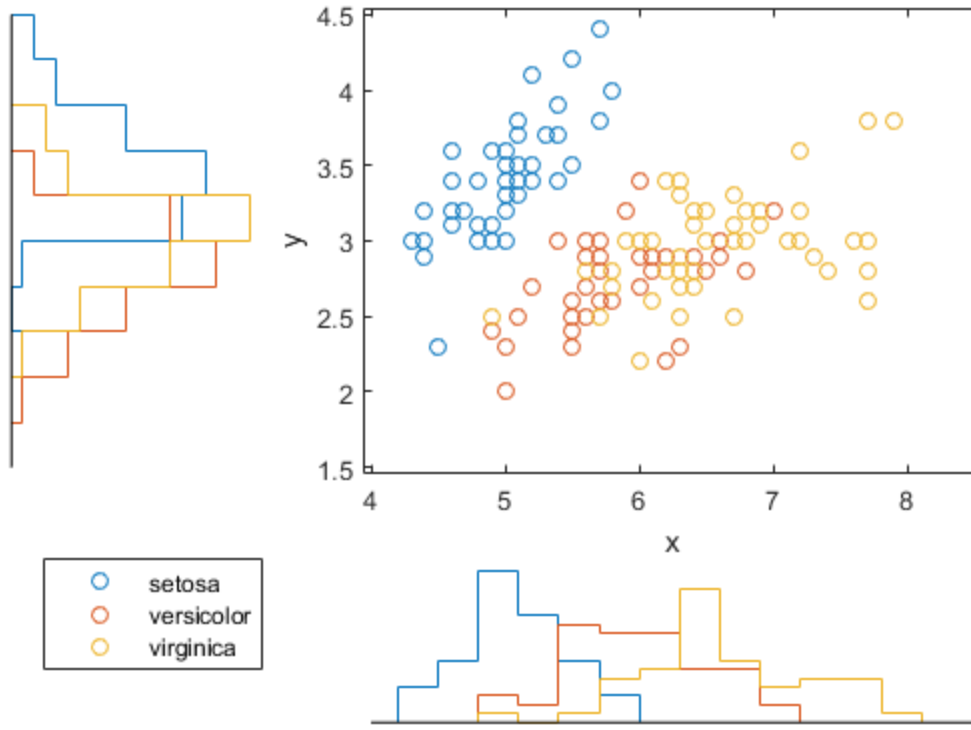
Load the sample data. Create data vector `x` from the first column of the data matrix, which contains sepal length measurements from three species of iris flowers. Create data vector `y` from the second column of the data matrix, which contains sepal width measurements from the same flowers.

```
load fisheriris.mat;
x = meas(:,1);
```

```
y = meas(:,2);
```

Create a scatter plot and six kernel density plots to visualize the relationship between sepal length and sepal width, grouped by species.

```
scatterhist(x,y,'Group',species)
```



The plot shows that the relationship between sepal length and width varies depending on the flower species.

Customize the Plot Display

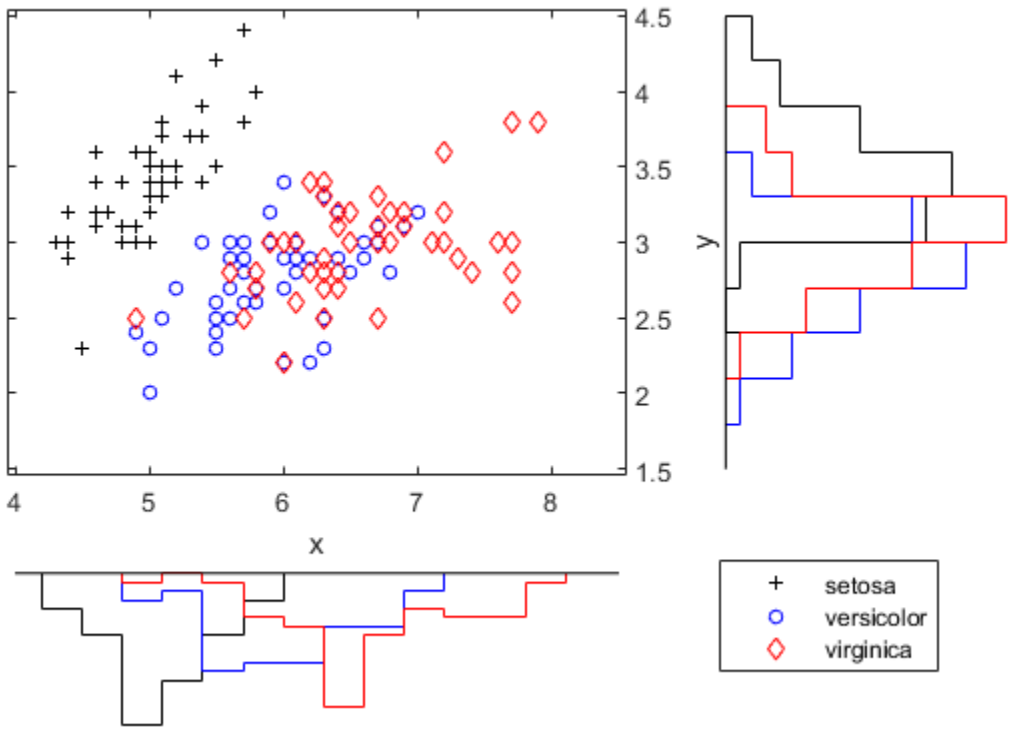
Load the sample data. Create data vector `x` from the first column of the data matrix, which contains sepal length measurements from three different species of iris flowers.

Create data vector `y` from the second column of the data matrix, which contains sepal width measurements from the same flowers.

```
load fisheriris.mat;
x = meas(:,1);
y = meas(:,2);
```

Create a scatter plot and six kernel density plots to visualize the relationship between sepal length and sepal width as measured on three species of iris flowers, grouped by species. Customize the appearance of the plots.

```
scatterhist(x,y,'Group',species,'Location','SouthEast',...
    'Direction','out','Color','kbr','LineStyle',{'-','-.',':'},...
    'LineWidth',[2,2,2],'Marker','+od','MarkerSize',[4,5,6]);
```



Customize Plots Using Axes Handles

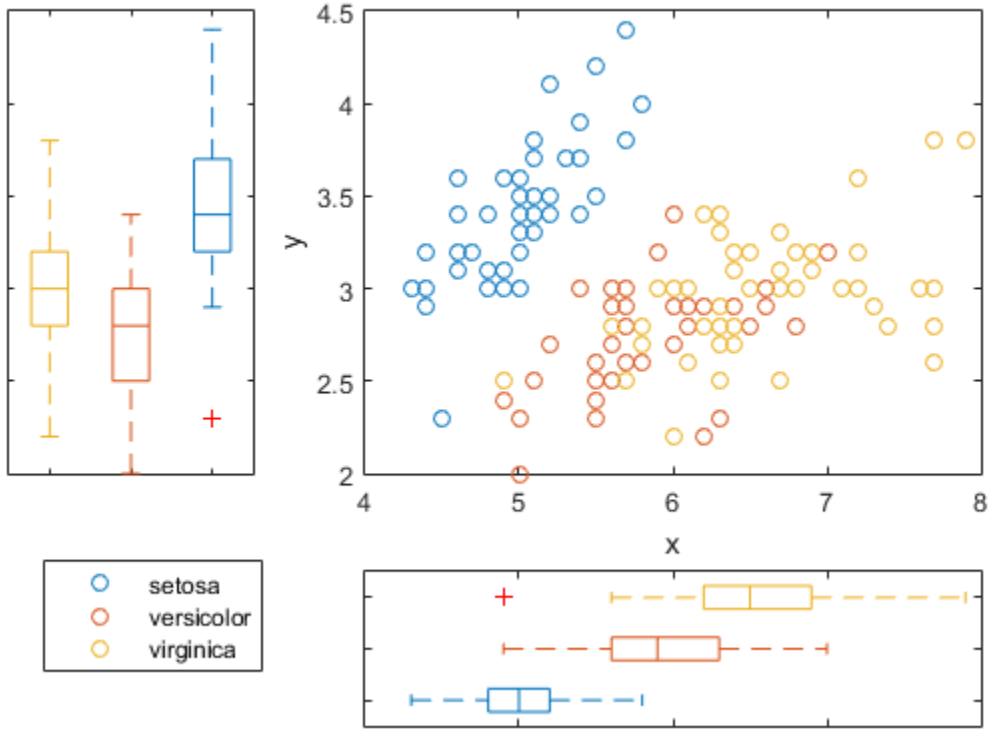
Load the sample data. Create data vector `x` from the first column of the data matrix, which contains sepal length measurements from three species of iris flowers. Create data vector `y` from the second column of the data matrix, which contains sepal width measurements from the same flowers.

```
load fisheriris.mat;
x = meas(:,1);
y = meas(:,2);
```

Use axis handles to replace the marginal histograms with box plots.

```
h = scatterhist(x,y,'Group',species);
```

```
hold on;
clr = get(h(1),'colororder');
boxplot(h(2),x,species,'orientation','horizontal',...
     'label',{'','',''},'color',clr);
boxplot(h(3),y,species,'orientation','horizontal',...
     'label', {'','',''},'color',clr);
set(h(2:3),'XTickLabel','');
view(h(3),[270,90]);  % Rotate the Y plot
axis(h(1),'auto');  % Sync axes
hold off;
```



Create a scatterhist Plot in a Specified Parent Container

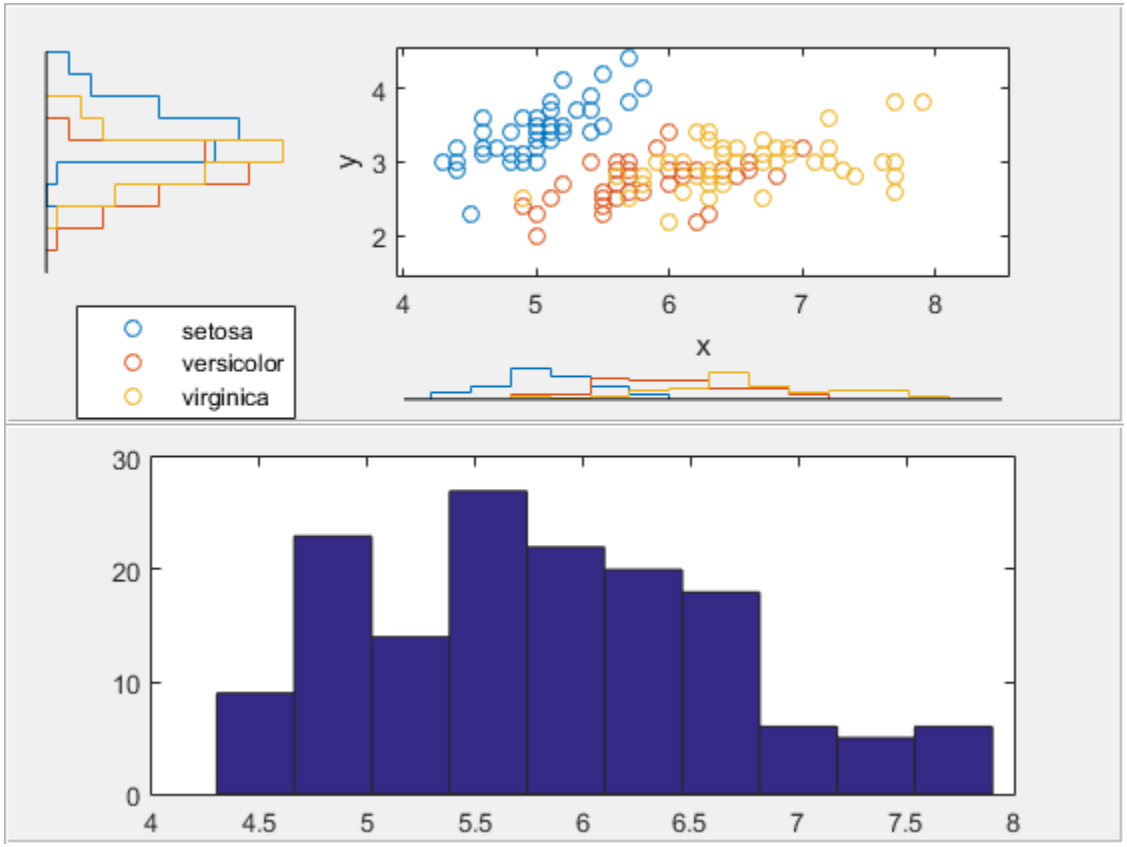
Load the sample data. Create data vector `x` from the first column of the data matrix, which contains sepal length measurements from iris flowers. Create data vector `y` from the second column of the data matrix, which contains sepal width measurements from the same flowers.

```
load fisheriris
x = meas(:,1);
y = meas(:,2);
```

Create a new figure and define two uipanel objects to divide the figure into two parts. In the upper half of the figure, plot the sample data using `scatterhist`. Include marginal

kernel density plots grouped by species. In the lower half of the figure, plot a histogram of the sepal length measurements contained in `x`.

```
figure
hp1 = uipanel('position',[0 .5 1 .5]);
hp2 = uipanel('position',[0 0 1 .5]);
scatterhist(x,y,'Group',species,'Parent',hp1);
axes('Parent',hp2);
hist(x);
```



Input Arguments

x — Sample data

vector

Sample data, specified as a vector. The data vectors x and y must be the same length.

If x or y contain `NaN` values, then `scatterhist`:

- Removes rows with `NaN` values in either x or y from both data vectors when generating the scatter plot

- Removes rows with `NaN` values only from the corresponding x or y data vector when generating the marginal histograms

Data Types: `single` | `double`

y — Sample data

vector

Sample data, specified as a vector. The data vectors x and y must be the same length.

If x or y contain `NaN` values, then `scatterhist`:

- Removes rows with `NaN` values in either x or y from both data vectors when generating the scatter plot
- Removes rows with `NaN` values only from the corresponding x or y data vector when generating the marginal histograms

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Location','SouthEast','Direction','out'` specifies a plot with histograms located below and to the right of the scatter plot, with the bars directed away from the scatter plot.

'NBins' — Number of bins for histograms

positive integer value | vector

Number of bins for histograms, specified as the comma-separated pair consisting of `'NBins'` and a positive integer value greater than or equal to 2, or vector of two such values. If the number of bins is specified as a positive integer value, that value is the number of bins for both the x and y histograms. If the number of bins is specified by a vector, the first value is the number of bins for the x data, and the second value is the number of bins for the y data. By default, the number of bins is computed based on the sample standard deviation using Scott's rule.

Example: `'NBins',[5,7]`

Data Types: `single` | `double`

`'Location'` — Location of marginal histograms

`'SouthWest'` (default) | `'SouthEast'` | `'NorthEast'` | `'NorthWest'`

Location of the marginal histograms in the figure, specified as the comma-separated pair consisting of `'Location'` and one of the following.

`'SouthWest'`	Plot the histograms below and to the left of the scatter plot.
`'SouthEast'`	Plot the histograms below and to the right of the scatter plot.
`'NorthEast'`	Plot the histograms above and to the right of the scatter plot.
`'NorthWest'`	Plot the histograms above and to the left of the scatter plot.

Example: `'Location','SouthEast'`

`'Direction'` — Direction of marginal histograms

`'in'` (default) | `'out'`

Direction of the marginal histograms, specified as the comma-separated pair consisting of `'Direction'` and one of the following.

`'in'`	Plot the histograms with the bars directed toward the scatter plot.
`'out'`	Plot the histograms with the bars directed away from the scatter plot.

Example: `'Direction','out'`

`'Group'` — Grouping variable

categorical array | logical or numeric vector | cell array of strings

Grouping variable, specified as the comma-separated pair consisting of `'Group'` and a categorical array, logical or numeric vector, or cell array of strings. Each unique value in a grouping variable defines a group.

For example, if `Gender` is a cell array of strings with values `'Male'` and `'Female'`, you can use `Gender` as a grouping variable to plot your data by gender.

Multiple grouping variables can be used by specifying a cell array of grouping variable names. Observations are placed in the same group if they have common values of all specified grouping variables.

For example, if `Smoker` is a logical vector with values `0` for nonsmokers and `1` for smokers, then specifying the cell array `{Gender,Smoker}` divides observations into four groups: Male Smoker, Male Nonsmoker, Female Smoker, and Female Nonsmoker.

Example: `'Group',{Gender,Smoker}`

Data Types: `single | double | logical | cell | char`

`'PlotGroup'` — Grouped plot indicator

`'on' | 'off'`

Grouped plot indicator, specified as the comma-separated pair consisting of `'PlotGroup'` and one of the following.

`'on'`	Displays grouped histograms or grouped kernel density plots. This is the default if a Group parameter is specified.
`'off'`	Displays histograms or kernel density plots of the whole data set. This is the default if a Group parameter is not specified.

Example: `'PlotGroup','off'`

`'Style'` — Histogram display style

`'stairs' | 'bar'`

Histogram display style, specified as the comma-separated pair consisting of `'PlotGroup'` and one of the following.

`'stairs'`	Displays a stairstep plot that shows the outline of the histogram without filling the bars. This is the default if you specify a grouping variable that contains more than one group.
`'bar'`	Displays a histogram bar plot. This is the default if you specify a grouping variable that contains only one group or if PlotGroup is specified as `'off'`.

Example: `'Style','bar'`

`'Kernel'` — Grouped kernel density plot indicator

`'off'` (default) | `'on'` | `'overlay'`

Grouped kernel density plot indicator, specified as the comma-separated pair consisting of `'Kernel'` and one of the following.

`'off'`	Display the overall marginal distribution as histograms.
`'on'`	Display kernel density plots for each group.
`'overlay'`	Display the overall marginal distribution as kernel density plots overlaid onto histograms, similar to `histfit`.

Example: `'Kernel','overlay'`

`'Bandwidth'` — Bandwidth of kernel smoothing window

matrix

Bandwidth of kernel smoothing window, specified as the comma-separated pair consisting of `'Bandwidth'` and a matrix of size 2-by-K, where K is the number of unique groups. The first row of the matrix gives the bandwidth of each group in `x`, and the second row gives the bandwidth of each group in `y`. By default, `scatterhist` finds the optimal bandwidth for estimating normal densities. Specifying a different bandwidth value changes the smoothing characteristics of the resulting kernel density plot. The value specified is a scaling factor for the normal distribution used to generate the kernel density plot.

Example: `'Bandwidth',[.5,.2,.1;.15,.25,.35]`

Data Types: `single` | `double`

`'Legend'` — Legend visibility indicator

`'on'` | `'off'`

Legend visibility indicator, specified as the comma-separated pair consisting of `'Legend'` and one of the following.

`'on'`	Set legend visible. This is the default if a Group parameter is specified.
`'off'`	Set legend invisible. This is the default if a Group parameter is not specified.

Example: `'Legend','on'`

`'Parent'` — Parent container of the plot

`uipanel` container object | `figure` container object

Parent container for the plot, specified as a `uipanel` container object or `figure` container object. You can create panel container objects using `uipanel` or `figure`, respectively.

For example, if `h1` is a panel container object, specify the parent container of the plot as follows.

Example: `'Parent',h1`

`'LineStyle'` — Style of kernel density plot line

valid line style string | cell array of strings

Style of kernel density plot line, specified as the comma-separated pair consisting of `'LineStyle'` and a valid line style string or a cell array of valid line style strings. See `plot` for valid line style strings. The default is a solid line. Use a cell array to specify different line styles for each group. When the total number of groups exceeds the number of specified values, `scatterhist` cycles through the specified values.

Example: `'LineStyle',{'-',':','-.'}`

`'LineWidth'` — Width of kernel density plot line

`0.5` (default) | nonnegative scalar value | vector

Width of kernel density plot line, specified as the comma-separated pair consisting of `'LineWidth'` and a nonnegative scalar value or vector of nonnegative scalar values. The specified value is the size of the kernel density plot line measured in points. The default size is 0.5 points. Use a vector to specify different line widths for each group. When the total number of groups is greater than the number of specified values, `scatterhist` cycles through the specified values.

Example: `'LineWidth',[0.5,1,2]`

Data Types: `single` | `double`

`'Color'` — Marker color for each scatter plot group

valid color designation char | string of chars | matrix of RGB values

Marker color for each scatter plot group, specified as the comma-separated pair consisting of `'Color'` and a valid color designation character, a string of valid color designation characters, or a three-column matrix of RGB values in the range [0,1]. See `ColorSpec` for predefined colors and their RGB equivalents. If colors are specified using a matrix, each row of the matrix represents a group, and the three columns represent the R value, G value, and B value, respectively. When the total number of groups exceeds the number of specified colors, `scatterhist` cycles through the specified colors.

Example: `'Color','kcm'`

Example: `'Color',[.5,0,1;0,.5,.5]`

Data Types: `single` | `double` | `char`

`'Marker'` — Marker symbol for each scatterplot group

`'o'` (default) | valid marker symbol | string of valid marker symbols

Marker symbol for each scatter plot group, specified as the comma-separated pair consisting of `'Marker'` and a valid marker symbol or string of valid marker symbols. See `plot` for valid symbols. The default is `'o'`, a circle. When the total number of groups exceeds the number of specified symbols, `scatterhist` cycles through the specified symbols.

Example: `'Marker','+do'`

`'MarkerSize'` — Marker size for each scatter plot group

6 (default) | nonnegative scalar value | vector

Marker size for each scatter plot group, specified as the comma-separated pair consisting of `'MarkerSize'` and a nonnegative scalar value or a vector of nonnegative scalar values, measured in points. When the total number of groups exceeds the number of specified values, `scatterhist` cycles through the specified values.

Example: `'MarkerSize',10`

Data Types: `single` | `double`

Output Arguments

`h` — Axes handles

vector

Axes handles for the three plots, returned as a vector. The vector contains the handles for the scatter plot, the histogram along the horizontal axis, and the histogram along the vertical axis, respectively.

More About

- “Grouping Variables” on page 2-52

See Also

`gscatter` | `histogram`

scramble

Class: qrandset

Scramble quasi-random point set

Syntax

```
ps = scramble(p,type)
ps = scramble(p,'clear')
ps = scramble(p)
```

Description

`ps = scramble(p,type)` returns a scrambled copy `ps` of the point set `p` of the `qrandset` class, created using the scramble type specified in the string *`type`*. Point sets from different subclasses of `qrandset` support different scramble types, as indicated in the following table.

Subclass	Scramble Types
`haltonset`	`'RR2'` — A permutation of the radical inverse coefficients derived by applying a reverse-radix operation to all of the possible coefficient values. The scramble is described in [1].
`sobolset`	`'MatousekAffineOwen'` — A random linear scramble combined with a random digital shift. The scramble is described in [2].

`ps = scramble(p,'clear')` removes all scramble settings from `p` and returns the result in `ps`.

`ps = scramble(p)` removes all scramble settings from `p` and then adds them back in the order they were originally applied. This typically results in a different point set because of the randomness of the scrambling algorithms.

Examples

Use `haltonset` to generate a 3-D Halton point set, skip the first 1000 values, and then retain every 101st point:

```
p = haltonset(3,'Skip',1e3,'Leap',1e2)
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
```

Use `scramble` to apply reverse-radix scrambling:

```
p = scramble(p,'RR2')
p =
    Halton point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : RR2
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.0928    0.6950    0.0029
    0.6958    0.2958    0.8269
    0.3013    0.6497    0.4141
    0.9087    0.7883    0.2166
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.0928    0.6950    0.0029
    0.9087    0.7883    0.2166
    0.3843    0.9840    0.9878
    0.6831    0.7357    0.7923
```

References

[1] Kocis, L., and W. J. Whiten. "Computational Investigations of Low-Discrepancy Sequences." *ACM Transactions on Mathematical Software*. Vol. 23, No. 2, 1997, pp. 266–294.

[2] Matousek, J. "On the L2-Discrepancy for Anchored Boxes." *Journal of Complexity*. Vol. 14, No. 4, 1998, pp. 527–556.

See Also

`haltonset` | `sobolset`

ScrambleMethod property

Class: qrandset

Settings that control scrambling

Description

The `ScrambleMethod` property contains a structure that defines which scrambles to apply to the sequence. The structure consists of two fields:

- `Type`: A string containing the name of the scramble.
- `Options`: A cell array of parameter values for the scramble.

Different point sets support different scramble types as outlined in the help for each point set class. An error occurs if you set an invalid scramble type for a given point set.

The `ScrambleMethod` property also accepts an empty matrix as a value. This will clear all scrambling and set the property to contain a (`0x0`) structure.

The `scramble` method provides an alternative, easier way to set scrambles.

Examples

Apply a random linear scramble combined with a random digital shift to a `sobolset` point set class:

```
P = sobolset(5);
P = scramble(P, 'MatousekAffineOwen');
P.ScrambleMethod
```

See Also

`sobolset` | `scramble`

segment

Class: piecewisedistribution

Segments containing values

Syntax

```
S = segment(obj,X,P)
```

Description

`S = segment(obj,X,P)` returns an array `S` of integers indicating which segment of the piecewise distribution object `obj` contains each value of `X` or, alternatively, `P`. One of `X` and `P` must be empty (`[]`). If `X` is nonempty, `S` is determined by comparing `X` with the quantile boundary values defined for `obj`. If `P` is nonempty, `S` is determined by comparing `P` with the probability boundary values.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

pvals = 0:0.2:1;
s = segment(obj,[],pvals)
s =
     1     2     2     2     2     3
```

See Also

`paretotails` | `boundary` | `nsegments`

sequentialfs

Sequential feature selection

Syntax

```
inmodel = sequentialfs(fun,X,y)
inmodel = sequentialfs(fun,X,Y,Z,...)
[inmodel,history] = sequentialfs(fun,X,...)
[] = sequentialfs(...,param1,val1,param2,val2,...)
```

Description

`inmodel = sequentialfs(fun,X,y)` selects a subset of features from the data matrix `X` that best predict the data in `y` by sequentially selecting features until there is no improvement in prediction. Rows of `X` correspond to observations; columns correspond to variables or features. `y` is a column vector of response values or class labels for each observation in `X`. `X` and `y` must have the same number of rows. `fun` is a function handle to a function that defines the criterion used to select features and to determine when to stop. The output `inmodel` is a logical vector indicating which features are finally chosen.

Starting from an empty feature set, `sequentialfs` creates candidate feature subsets by sequentially adding each of the features not yet selected. For each candidate feature subset, `sequentialfs` performs 10-fold cross-validation by repeatedly calling `fun` with different training subsets of `X` and `y`, `XTRAIN` and `ytrain`, and test subsets of `X` and `y`, `XTEST` and `ytest`, as follows:

```
criterion = fun(XTRAIN,ytrain,XTEST,ytest)
```

`XTRAIN` and `ytrain` contain the same subset of rows of `X` and `Y`, while `XTEST` and `ytest` contain the complementary subset of rows. `XTRAIN` and `XTEST` contain the data taken from the columns of `X` that correspond to the current candidate feature set.

Each time it is called, `fun` must return a scalar value `criterion`. Typically, `fun` uses `XTRAIN` and `ytrain` to train or fit a model, then predicts values for `XTEST` using that model, and finally returns some measure of distance, or *loss*, of those predicted values from `ytest`. In the cross-validation calculation for a given candidate feature

set, `sequentialfs` sums the values returned by `fun` and divides that sum by the total number of test observations. It then uses that mean value to evaluate each candidate feature subset.

Typical loss measures include sum of squared errors for regression models (`sequentialfs` computes the mean-squared error in this case), and the number of misclassified observations for classification models (`sequentialfs` computes the misclassification rate in this case).

Note: `sequentialfs` divides the sum of the values returned by `fun` across all test sets by the total number of test observations. Accordingly, `fun` should not divide its output value by the number of test observations.

After computing the mean `criterion` values for each candidate feature subset, `sequentialfs` chooses the candidate feature subset that minimizes the mean criterion value. This process continues until adding more features does not decrease the criterion.

`inmodel = sequentialfs(fun,X,Y,Z,...)` allows any number of input variables `X`, `Y`, `Z`, ... `sequentialfs` chooses features (columns) only from `X`, but otherwise imposes no interpretation on `X`, `Y`, `Z`, ... All data inputs, whether column vectors or matrices, must have the same number of rows. `sequentialfs` calls `fun` with training and test subsets of `X`, `Y`, `Z`, ... as follows:

```
criterion = fun(XTRAIN,YTRAIN,ZTRAIN,...,
                XTEST,YTEST,ZTEST,...)
```

`sequentialfs` creates `XTRAIN`, `YTRAIN`, `ZTRAIN`, ... , `XTEST`, `YTEST`, `ZTEST`, ... by selecting subsets of the rows of `X`, `Y`, `Z`, ... `fun` must return a scalar value `criterion`, but may compute that value in any way. Elements of the logical vector `inmodel` correspond to columns of `X` and indicate which features are finally chosen.

`[inmodel,history] = sequentialfs(fun,X,...)` returns information on which feature is chosen at each step. `history` is a scalar structure with the following fields:

- `Crit` — A vector containing the criterion values computed at each step.
- `In` — A logical matrix in which row `i` indicates the features selected at step `i`.

`[] = sequentialfs(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs from the following table.

Parameter	Value
`'cv'`	The validation method used to compute the criterion for each candidate feature subset. • When the value is a positive integer `k`, `sequentialfs` uses `k`-fold cross-validation without stratification. • When the value is an object of the `cvpartition` class, other forms of cross-validation can be specified. • When the value is `'resubstitution'`, the original data are passed to `fun` as both the training and test data to compute the criterion. • When the value is `'none'`, `sequentialfs` calls `fun` as `criterion = fun(X,Y,Z,...)`, without separating test and training sets. The default value is `10`, that is, 10-fold cross-validation without stratification. So-called *wrapper methods* use a function `fun` that implements a learning algorithm. These methods usually apply cross-validation to select features. So-called *filter methods* use a function `fun` that measures characteristics of the data (such as correlation) to select features.
`'mcreps'`	A positive integer indicating the number of Monte-Carlo repetitions for cross-validation. The default value is `1`. The value must be `1` if the value of `'cv'` is `'resubstitution'` or `'none'`.
`'direction'`	The direction of the sequential search. The default is `'forward'`. A value of `'backward'` specifies an initial candidate set including all features and an algorithm that removes features sequentially until the criterion increases.
`'keepin'`	A logical vector or a vector of column numbers specifying features that must be included. The default is empty.
`'keepout'`	A logical vector or a vector of column numbers specifying features that must be excluded. The default is empty.

Parameter	Value
`'nfeatures'`	The number of features at which `sequentialfs` should stop. `inmodel` includes exactly this many features. The default value is empty, indicating that `sequentialfs` should stop when a local minimum of the criterion is found. A nonempty value overrides values of `'MaxIter'` and `'TolFun'` in `'options'`.
`'nullmodel'`	A logical value, indicating whether or not the null model (containing no features from `X`) should be included in feature selection and in the `history` output. The default is `false`.
`'options'`	Options structure for the iterative sequential search algorithm, as created by `statset`. `sequentialfs` uses the following `statset` parameters: • `Display` — Amount of information displayed by the algorithm. The default is `'off'`. • `MaxIter` — Maximum number of iterations allowed. The default is `Inf`. • `TolFun` — Termination tolerance for the objective function value. The default is `1e-6` if `'direction'` is `'forward'`; `0` if `'direction'` is `'backward'`. • `TolTypeFun` — Use absolute or relative objective function tolerances. The default is `'rel'`. • `UseParallel` — Set to `true` to compute in parallel. Default is `false`. • `UseSubstreams` — Set to `true` to compute in parallel in a reproducible fashion. Default is `false`. To compute reproducibly, set `Streams` to a type allowing substreams: `'mlfg6331_64'` or `'mrg32k3a'`. • `Streams` — A `RandStream` object or cell array consisting of one such object. If you do not specify `Streams`, `sequentialfs` uses the default stream.

Examples

Perform sequential feature selection for classification of noisy features:

```
load fisheriris;
X = randn(150,10);
X(:,[1 3 5 7 ])= meas;
y = species;

c = cvpartition(y,'k',10);
opts = statset('display','iter');
fun = @(XT,yT,Xt,yt)...
      (sum(~strcmp(yt,classify(Xt,XT,yT,'quadratic'))));

[fs,history] = sequentialfs(fun,X,y,'cv',c,'options',opts)

Start forward sequential feature selection:
Initial columns included: none
Columns that can not be included: none
Step 1, added column 7, criterion value 0.04
Step 2, added column 5, criterion value 0.0266667
Final columns included:  5 7

fs =
     0  0  0  0  1  0  1  0  0  0
history =
      In: [2x10 logical]
    Crit: [0.0400 0.0267]

history.In
ans =
     0  0  0  0  0  0  1  0  0  0
     0  0  0  0  1  0  1  0  0  0
```

More About

- “Sequential Feature Selection” on page 13-68

See Also

`crossval` | `cvpartition` | `statset` | `stepwisefit`

set

Class: dataset

Set and display properties

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
set(A)
set(A,PropertyName)
A = set(A,PropertyName,PropertyValue,...)
B = set(A,PropertyName,value)
```

Description

`set(A)` displays all properties of the dataset array `A` and their possible values.

`set(A,PropertyName)` displays possible values for the property specified by the string *`PropertyName`*.

`A = set(A,PropertyName,PropertyValue,...)` sets property name/value pairs.

`B = set(A,PropertyName,value)` returns a dataset array `B` that is a copy of `A`, but with the property `'PropertyName'` set to the value `value`.

Note: Using `set(A,'PropertyName',value)` without assigning to a variable does not modify A's properties. Use `A = set(A,'PropertyName',value)` to modify `A`.

Examples

Create a dataset array from Fisher's iris data and add a description:

```
load fisheriris
NumObs = size(meas,1);
NameObs = strcat({'Obs'},num2str((1:NumObs)','%-d'));
iris = dataset({nominal(species),'species'},...
               {meas,'SL','SW','PL','PW'},...
               'ObsNames',NameObs);
iris = set(iris,'Description','Fisher''s Iris Data');
get(iris)
   Description: 'Fisher's Iris Data'
   Units: {}
   DimNames: {'Observations' 'Variables'}
   UserData: []
   ObsNames: {150x1 cell}
   VarNames: {'species' 'SL' 'SW' 'PL' 'PW'}
```

See Also

`get` | `summary`

setDefaultYfit

Class: CompactTreeBagger

Set default value for `predict`

Syntax

```
B = setDefaultYfit(B,Yfit)
```

Description

`B = setDefaultYfit(B,Yfit)` sets the default prediction for ensemble `B` to `Yfit`. The default prediction must be a character variable for classification or a numeric scalar for regression. This setting controls what predicted value `CompactTreeBagger` returns when no prediction is possible, for example when the `predict` method needs to predict for an observation which has only false values in the matrix supplied through `'useifort'` argument.

See Also

`predict` | `TreeBagger.DefaultYfit`

setdiff

Class: dataset

Set difference for dataset array observations

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
C = setdiff(A,B)
C = setdiff(A,B,vars)
C = setxor(A,B,vars,setOrder)
[C,iA] = setxor( ___ )
```

Description

`C = setdiff(A,B)` for `dataset` arrays `A` and `B` returns the set of observations that are in `A` but not `B`, with repetitions removed. The observations in the dataset array `C` are sorted.

`C = setdiff(A,B,vars)` returns the set of observations that are in `A` but not `B`, considering only the variables specified in `vars`, with repetitions removed. The observations in the dataset array `C` are sorted by these variables. The values for variables not specified in `vars` for each observation in `C` are taken from the corresponding observation in `A`. If there are multiple observations in `A` that correspond to an observation in `C`, those values are taken from the first occurrence.

`C = setxor(A,B,vars,setOrder)` returns the observations in C in the order specified by `setOrder`.

`[C,iA] = setxor( ___ )` also returns the index vector iA such that `C = A(iA,:)`. If there are repeated observations in `A`, then `setxor` returns the index of the first occurrence. You can use any of the previous input arguments.

Input Arguments

`A,B`

Input dataset arrays.

`vars`

Cell array of strings containing variable names or a vector of integers containing variable column numbers, indicating the variables that `setdiff` considers.

Specify `vars` as `[]` to use its default value of all variables.

`setOrder`

Flag indicating the sorting order for the observations in C. The possible values of `setOrder` are:

`'sorted'`	Observations in C are in sorted order (default).
`'stable'`	Observations in C are in the same order that they appear in `A`.

Output Arguments

`C`

Dataset array with the observations that are in `A` but not `B`, with repetitions removed. C is in sorted order (by default), or the order specified by setOrder.

`iA`

Index vector, indicating the observations from `A` that are in `C`. The vector `iA` contains the index to the first occurrence of any repeated observations in `A`.

Examples

Set Difference of Two Dataset Arrays

Create a scalar structure array, and then convert it into two dataset arrays.

```
S(1,1).Name = 'CLARK';
S(1,1).Gender = 'M';
S(1,1).SystolicBP = 124;
S(1,1).DiastolicBP = 93;

S(2,1).Name = 'BROWN';
S(2,1).Gender = 'F';
S(2,1).SystolicBP = 122;
S(2,1).DiastolicBP = 80;

S(3,1).Name = 'MARTIN';
S(3,1).Gender = 'M';
S(3,1).SystolicBP = 130;
S(3,1).DiastolicBP = 92;

A = struct2dataset(S(1:2));
B = struct2dataset(S(2:3));
```

The intersection of A and B is the second observation, with last name BROWN.

Return the set difference of A and B.

```
[C,iA] = setdiff(A,B)
```

```
C =

    Name            Gender     SystolicBP    DiastolicBP
    'CLARK'         'M'        124           93


iA =

     1
```

The first observation in A is not present in B.

See Also

dataset | intersect | ismember | setxor | sortrows | union | unique

More About

- “Dataset Arrays” on page 2-132

setlabels

Assign labels to levels of nominal or ordinal arrays

Compatibility

The `nominal` and `ordinal` array data types might be removed in a future release. To represent ordered and unordered discrete, nonnumeric data, use the MATLAB `categorical` data type instead.

Syntax

```
B = setlabels(A,labels)
B = setlabels(A,labels,levels)
```

Description

`B = setlabels(A,labels)` returns a `nominal` or `ordinal` array object the same as A but with levels labeled in the order specified by labels.

`B = setlabels(A,labels,levels)` labels only the levels specified in levels.

Examples

- “Change Category Labels” on page 2-9

Input Arguments

A — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, specified as a `nominal` or `ordinal` array object created using `nominal` or `ordinal`.

`labels` — Labels to assign

cell array of strings | 2-D character matrix

Labels to assign to levels, specified as a cell array of strings or 2-D character matrix.

Data Types: `char` | `cell`

`levels` — Levels to assign labels

cell array of strings | 2-D character matrix

Level to assign labels to, specified as a cell array of strings or 2-D character matrix.

Data Types: `char` | `cell`

Output Arguments

`B` — Nominal or ordinal array

`nominal` array | `ordinal` array

Nominal or ordinal array, returned as a `nominal` or `ordinal` array object.

More About

- Using nominal Objects
- Using ordinal Objects

See Also

`getlabels` | `nominal` | `ordinal`

setxor

Class: dataset

Set exclusive or for dataset array observations

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
C = setxor(A,B)
C = setxor(A,B,vars)
C = setxor(A,B,vars,setOrder)
[C,iA,iB] = setxor( ___ )
```

Description

`C = setxor(A,B)` for `dataset` arrays `A` and `B` returns the set of observations that are not in the intersection of the two arrays, with repetitions removed. The observations in the dataset array `C` are sorted.

`C = setxor(A,B,vars)` returns the set of observations that are not in the intersection of the two arrays, considering only the variables specified in `vars`, with repetitions removed. The observations in the dataset array `C` are sorted by these variables. The values for variables not specified in `vars` for each observation in `C` are taken from the corresponding observation in `A` or `B`. If there are multiple observations in `A` or `B` that correspond to an observation in `C`, those values are taken from the first occurrence.

`C = setxor(A,B,vars,setOrder)` returns the observations in C in the order specified by `setOrder`.

`[C,iA,iB] = setxor( ___ )` also returns index vectors iA and iB such that `C` is a sorted combination of the values `A(iA,:)` and `B(iB,:)`. If there are repeated

observations in A or B, then setxor returns the index of the first occurrence. You can use any of the previous input arguments.

Input Arguments

A,B

Input dataset arrays.

vars

Cell array of strings containing variable names or a vector of integers containing variable column numbers, indicating the variables in A and B that setxor considers.

Specify vars as [] to use its default value of all variables.

setOrder

Flag indicating the sorting order for the observations in C. The possible values of setOrder are:

'sorted'	Observations in C are in sorted order (default).
'stable'	Observations in C are in the same order that they appear in A, then B.

Output Arguments

C

Dataset array with the observations not in the intersection of A and B, with repetitions removed. C is in sorted order (by default), or the order specified by setOrder.

iA

Index vector, indicating the observations from A that are in C. The vector iA contains the index to the first occurrence of any repeated observations in A.

`iB`

Index vector, indicating the observations from `B` that are in `C`. The vector `iB` contains the index to the first occurrence of any repeated observations in `B`.

Examples

Symmetric Difference of Two Dataset Arrays

Create a scalar structure array, and then convert it into two dataset arrays.

```
S(1,1).Name = 'CLARK';
S(1,1).Gender = 'M';
S(1,1).SystolicBP = 124;
S(1,1).DiastolicBP = 93;

S(2,1).Name = 'BROWN';
S(2,1).Gender = 'F';
S(2,1).SystolicBP = 122;
S(2,1).DiastolicBP = 80;

S(3,1).Name = 'MARTIN';
S(3,1).Gender = 'M';
S(3,1).SystolicBP = 130;
S(3,1).DiastolicBP = 92;

A = struct2dataset(S(1:2));
B = struct2dataset(S(2:3));
```

The intersection of `A` and `B` is the second observation, with last name `BROWN`.

Return the symmetric difference of `A` and `B`.

```
[C,iA,iB] = setxor(A,B);
C
```

```
C =

    Name            Gender     SystolicBP    DiastolicBP
    'CLARK'         'M'        124           93
    'MARTIN'        'M'        130           92
```

```
[iA iB]
```

```
ans =

     1     2
```

The symmetric difference contains the first observation from A, and the second observation from B.

See Also

dataset | intersect | ismember | setdiff | sortrows | union | unique

More About

- “Dataset Arrays” on page 2-132

SharedCovariance property

Class: gmdistribution

`true` if all covariance matrices are restricted to be the same

Description

Logical `true` if all the covariance matrices are restricted to be the same (pooled estimate); logical `false` otherwise.

shrink

Class: RegressionEnsemble

Prune ensemble

Syntax

```
cmp = shrink(ens)
cmp = shrink(ens,Name,Value)
```

Description

`cmp = shrink(ens)` returns a compact shrunken version of `ens`, a regularized ensemble. `cmp` retains only learners with weights above a threshold.

`cmp = shrink(ens,Name,Value)` returns an ensemble with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

`ens`

A regression ensemble created with `fitensemble`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'lambda'`

Vector of nonnegative regularization parameter values for lasso. If `ens.Regularization` is nonempty (populate it with `regularize`), `shrink` regularizes

`ens` using `lambda`. If `ens` contains a `Regularization` structure, you cannot pass `lambda`.

Default: `[ ]`

`'threshold'`

Lower cutoff on weights for weak learners, a numeric nonnegative scalar. `shrink` creates cmp from those learners with weights above `threshold`.

Default: `0`

`'weightcolumn'`

Column index of ens`.Regularization.TrainedWeights`, a positive integer. `shrink` creates cmp with learner weights from this column.

Default: `1`

Output Arguments

`cmp`

A regression ensemble of class `CompactRegressionEnsemble`. Use `cmp` for making predictions exactly as you use ens, with the `predict` method.

`shrink` orders the members of `cmp` from largest to smallest.

Examples

Shrink a 300-member bagged regression ensemble using `0.1` for the parameter `lambda`, and view the number of members of the resulting ensemble:

```
X = rand(2000,20);
Y = repmat(-1,2000,1);
Y(sum(X(:,1:5),2)>2.5) = 1;
bag = fitensemble(X,Y,'Bag',300,'Tree','type','regression');
cmp = shrink(bag,'lambda',0.1);
cmp.NumTrained
```

```
ans =
    83
```

See Also

`regularize` | `predict` | `cvshrink`

Sigma property

Class: gmdistribution

Input array of covariances

Description

Input array of covariances `SIGMA`.

signrank

Wilcoxon signed rank test

Syntax

```
p = signrank(x)
p = signrank(x,y)
p = signrank(x,y,Name,Value)
[p,h] = signrank( ___ )
[p,h,stats] = signrank( ___ )

[ ___ ] = signrank(x,m)
[ ___ ] = signrank(x,m,Name,Value)
```

Description

`p = signrank(x)` returns the *p*-value of a two-sided Wilcoxon signed rank test.

`signrank` tests the null hypothesis that data in the vector `x` come from a distribution whose median is zero at the 5% significance level. The test assumes that the data in `x` come from a continuous distribution symmetric about its median.

`p = signrank(x,y)` returns the *p*-value of a paired, two-sided test for the null hypothesis that `x` – `y` comes from a distribution with zero median.

`p = signrank(x,y,Name,Value)` returns the *p*-value for the sign test with additional options specified by one or more `Name`,`Value` pair arguments.

`[p,h] = signrank( ___ )` also returns a logical value indicating the test decision. `h = 1` indicates a rejection of the null hypothesis, and `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level. You can use any of the input arguments in the previous syntaxes.

`[p,h,stats] = signrank( ___ )` also returns the structure `stats` with information about the test statistic.

`[ ___ ] = signrank(x,m)` returns any of the output arguments in the previous syntaxes for the null hypothesis that the data in `x` are observations from a distribution with median `m`.

`[ ___ ] = signrank(x,m,Name,Value)` returns any of the output arguments in the previous syntaxes for the signed rank test with additional options specified by one or more `Name,Value` pair arguments.

Examples

Test for Zero Median of a Single Population

Test the hypothesis of zero median.

Generate the sample data.

```
rng('default') % for reproducibility
x = randn(1,25) + 1.30;
```

Test the hypothesis that the data in `x` has zero median.

```
[p,h] = signrank(x)
```

```
p =

   3.2229e-05


h =

     1
```

At the default 5% significance level, the value `h = 1` indicates that the test rejects the null hypothesis of zero median.

Test the Median of Differences of Paired Samples

Test the hypothesis of zero median for the difference between paired samples.

Generate the sample data.

```
rng('default') % for reproducibility
```

```
x = lognrnd(2,.25,10,1);
y = x + trnd(2,10,1);
```

Test the hypothesis that `x – y` has zero median.

```
[p,h] = signrank(x,y)
```

```
p =
    0.3223

h =
     0
```

The results indicate that the test fails to reject the null hypothesis of zero median in the difference at the default 5% significance level.

Signed Rank Test for Large Samples

Conduct a -sided test on a large sample using approximation.

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load gradespaired
```

Test the null hypothesis that the median of the grade differences of students before and after participating in a tutoring program is 0 against the alternate that it is less than 0.

```
[p,h,stats] = signrank(gradespaired(:,1),...
       gradespaired(:,2),'tail','left')
```

```
p =

    0.0047


h =

     1
```

```
stats =

          zval: -2.5982
    signedrank: 2.0175e+03
```

Because the sample size is greater than 15, `signrank` uses an approximate method to calculate the *p*-value and also returns the value of the *z*-statistic. The value `h = 1` indicates that the test rejects the null hypothesis that there is no difference between the grade medians at the 5% significance level. There is enough statistical evidence to conclude that the median grade before the tutoring program is less than the median grade after the tutoring program.

Repeat the test using the exact method.

```
[p,h,stats] = signrank(gradespaired(:,1),gradespaired(:,2),...
       'tail','left','method','exact')
```

```
p =

    0.0045


h =

     1


stats =

    signedrank: 2.0175e+03
```

The results obtained using the approximate method are consistent with the exact method.

Two-Sided Test for the Median of a Single Population

Load the sample data.

```
load mileage
```

The data contains the mileages per gallon for three different types of cars in columns 1 to 3.

Test the hypothesis that the median mileage for the type of cars in the second column differs from 33.

```
[p,h,stats] = signrank(mileage(:,2),33)
```

```
p =
    0.0313

h =
     1

stats =
    signedrank: 21
```

At the 5% significance level, the results indicate that the median mileage for the second type of cars differs from 33. Note that `signrank` uses an exact method to calculate the *p*-value for small samples and does not return the *z*-statistic.

Right-Sided Test for the Median of a Single Population

Use the name-value pair arguments in `signrank`.

Load the sample data.

```
load mileage
```

The data contains the mileage per gallon for three different types of cars in columns 1 to 3.

Test the hypothesis that the median mileage for the type of cars in the second row are larger than 33.

```
[p,h,stats] = signrank(mileage(:,2),33,'tail','right')
```

```
p =
    0.0156

h =
     1

stats =
    signedrank: 21
```

Repeat the same test at the 1% significance level using the approximate method.

```
[p,h,stats] = signrank(mileage(:,2),33,'tail','right',...
'alpha',0.01,'method','approximate')

p =

    0.0180

h =

     0

stats =

          zval: 2.0966
    signedrank: 21
```

This result, `h` = 0, indicates that the null hypothesis cannot be rejected at the 1% significance level.

Input Arguments

`x` — Sample data

vector

Sample data, specified as a vector.

Data Types: `single` | `double`

`y` — Sample data

vector

Sample data, specified as a vector. `y` must be the same length as `x`.

Data Types: `single` | `double`

`m` — Hypothesized value of the median

scalar

Hypothesized value of the median, specified as a scalar.

Example: `signrank(x,10)`

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'alpha',0.01,'method','approximate','tail','right'` specifies a right-tailed signed rank test with 1% significance level, which returns the approximate p-value.

`'alpha'` — Significance level

0.05 (default) | scalar value in the range 0 to 1

Significance level of the decision of a hypothesis test, specified as the comma-separated pair consisting of `'alpha'` and a scalar value in the range 0 to 1. Significance level of `h` is 100 * `alpha`%.

Example: `'alpha', 0.01`

Data Types: `double | single`

`'method'` — Computation method of `p`

`'exact' | 'approximate'`

Computation method of `p`, specified as the comma-separated pair consisting of `'method'` and one of the following.

`'exact'`	Exact computation of the *p*-value, `p`. Default value for 15 or fewer observations in `x`, `x – m`, or `x – y` when `method` is unspecified.
`'approximat`	Normal approximation while computing the *p*-value, `p`. Default value for more than 15 observations in `x`, `x – m`, or `x – y` when `'method'` is unspecified because the exact method can be slow on large samples.

Example: `'method','exact'`

Data Types: `char`

`'tail'` — Type of test

`'both'` (default) | `'right'` | `'left'`

Type of test, specified as the comma-separated pair consisting of `'tail'` and one of the following:

`'both'`	Two-sided hypothesis test, which is the default test type. • For a one-sample test, the alternate hypothesis states that the data in `x` come from a continuous distribution with median different than 0 or `m`. • For a two-sample test, the alternate hypothesis states that the data in `x – y` come from a distribution with median different than 0.
`'right'`	Right-tailed hypothesis test. • For a one-sample test, the alternate hypothesis states that the data in `x` come from a continuous distribution with median greater than 0 or `m`. • For a two-sample test, the alternate hypothesis states the data in `x – y` come from a distribution with median greater than 0.
`'left'`	Left-tailed hypothesis test. • For a one-sample test, the alternate hypothesis states that the data in `x` come from a continuous distribution with median less than 0 or `m`. • For a two-sample test, the alternate hypothesis states the data in `x – y` come from a distribution with median less than 0.

Example: `'tail','left'`

Output Arguments

`p` — *p*-value of the test

nonnegative scalar

p-value of the test, returned as a nonnegative scalar from 0 to 1. `p` is the probability of observing a test statistic as or more extreme than the observed value under the null hypothesis. `signrank` computes the two-sided *p*-value by doubling the most significant one-sided value.

`h` — Result of the hypothesis test

1 | 0

Result of the hypothesis test, returned as a logical value.

- If `h` = 1, this indicates the rejection of the null hypothesis at the 100 * `alpha`% significance level.

- If `h` = 0, this indicates a failure to reject the null hypothesis at the 100 * `alpha`% significance level.

`stats` — Test statistics

structure

Test statistics, returned as a structure. The test statistics stored in `stats` are:

- `signrank`: Value of the sign rank test statistic.
- `zval`: Value of the *z*- statistic (computed when `'method'` is `'approximate'`).

More About

Wilcoxon Signed Rank Test

The Wilcoxon signed rank test is a nonparametric test for two populations when the observations are paired. In this case, the test statistic, W, is the sum of the ranks of positive differences between the observations in the two samples (that is, `x – y`). When you use the test for one sample, then W is the sum of the ranks of positive differences between the observations and the hypothesized median value M_0 (which is 0 when you use `signrank(x)` and `m` when you use `signrank(x,m)`).

z-Statistic

For large samples, or when `method` is `approximate`, the `signrank` function calculates the *p*-value using the *z*-statistic, given by

$$z = \frac{\left(W - n(n+1)/4\right)}{\sqrt{\frac{n(n+1)(2n+1) - tieadj}{24}}},$$

where *n* is the sample size of the difference `x – y` or `x – m`. For the two-sample case, `signrank` uses `[tie_rank,tieadj] = tiedrank(abs(diffxy),0,0,epsdiff)` to obtain the tie adjustment value `tieadj`.

Algorithms

`signrank` treats `NaN`s in `x` and `y` as missing values and ignores them.

For the two-sample case, `signrank` uses a tolerance based on the values `epsdiff = eps(x) + eps(y)`. The `signrank` function treats any pair of values with difference `d(i) = x(i) - y(i)` that differ by no more than the sum of their two `eps` values (`abs(d(i)) < epsdiff(i)`) as ties.

References

[1] Gibbons, J. D., and S. Chakraborti. *Nonparametric Statistical Inference*, 5th Ed., Boca Raton, FL: Chapman & Hall/CRC Press, Taylor & Francis Group, 2011.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`ranksum` | `signtest` | `ttest` | `ztest`

signtest

Sign test

Syntax

```
p = signtest(x)
p = signtest(x,y)
p = signtest(x,y,Name,Value)
[p,h] = signtest( ___ )
[p,h,stats] = signtest( ___ )

[ ___ ] = signtest(x,m)
[ ___ ] = signtest(x,m,Name,Value)
```

Description

`p = signtest(x)` returns the *p*-value for a two-sided sign test.

`signtest` tests the hypothesis that data in `x` has a continuous distribution with zero median against the alternative that the distribution does not have zero median at the 5% significance level.

`p = signtest(x,y)` returns the *p*-value of a two-sided sign test. Here,`signtest` tests for the hypothesis that the data in `x – y` has a distribution with zero median against the alternative that the distribution does not have zero median. Note that a hypothesis of zero median for `x – y` is not equivalent to a hypothesis of equal median for `x` and `y`.

`p = signtest(x,y,Name,Value)` returns the *p*-value for the sign test with additional options specified by one or more `Name`,`Value` pair arguments.

`[p,h] = signtest( ___ )` also returns a logical value indicating the test decision. The value `h = 1` indicates a rejection of the null hypothesis, and `h = 0` indicates a failure to reject the null hypothesis at the 5% significance level. You can use any of the input arguments in the previous syntaxes.

`[p,h,stats] = signtest( ___ )` also returns the structure `stats` containing information about the test statistic.

`[ ___ ] = signtest(x,m)` returns any of the output arguments in the previous syntaxes for the test whether the data in `x` are observations from a distribution with median `m` against the alternative that the median is different from `m`.

`[ ___ ] = signtest(x,m,Name,Value)` returns any of the output arguments in the previous syntaxes for the sign test with additional options specified by one or more `Name,Value` pair arguments.

Examples

Test for Zero Median of a Single Population

Test the hypothesis of zero median.

Generate the sample data.

```
rng('default') % for reproducibility
x = randn(1,25);
```

The sampling distribution of `x` is symmetric with zero median.

Test the null hypothesis that `x` comes from a distribution with a median different from zero median.

```
[p,h,stats] = signtest(x,0)
```

```
p =
    0.1078

h =
     0

stats =
    zval: NaN
    sign: 17
```

At the default 5% significance level, the result `h` = 0 indicates that `signtest` fails to reject to the null hypothesis of zero median. `signtest` calculates the *p*-value using the exact method, hence it does not calculate `zval` and returns it as a `NaN`.

Test for Zero Median for the Difference of Paired Samples

Test the hypothesis of zero median for the difference between paired samples.

Generate the sample data.

```
rng('default') % for reproducibility
before = lognrnd(2,.25,10,1);
after = before + (lognrnd(0,.5,10,1) - 1);
```

The sampling distribution of the difference between `before` and `after` is symmetric with zero median.

Test the null hypothesis that the difference of `before` and `after` has zero median.

```
[p,h] = signtest(before,after)
```

```
p =

    0.7539


h =

     0
```

At the default 5% significance level, the value `h` = 0 indicates that `signtest` fails to reject to the null hypothesis of zero median in the difference.

Medians of Paired Samples

Test the hypothesis of zero median for the difference between two paired samples using the exact and approximate methods.

Generate the sample data.

```
rng('default') % for reproducibility
x = lognrnd(2,.25,15,1);
y = x + trnd(2,15,1);
display([x y])
```

```
ans =

    8.4521    7.8047
   11.6869   11.4094
    4.2009    5.1133
    9.1664   12.1655
    8.0020   10.0300
    5.3285    6.0153
```

```
    6.6300    5.1235
    8.0499    8.6737
   18.0763   19.2164
   14.7665   15.3380
    5.2726    8.4187
   15.7798   16.2093
    8.8583    8.5575
    7.2735    7.4783
    8.8347    7.8894
```

Test the hypothesis that `x – y` has zero median.

```
[p,h,stats] = signtest(x,y)
```

```
p =

    0.3018


h =

     0


stats =

    zval: NaN
    sign: 5
```

At the default 5% significance level, the value `h = 0` indicates that the test fails to reject the null hypothesis of zero median in the difference.

Repeat the test using the approximate method.

```
[p,h,stats] = signtest(x,y,'method','approximate')
```

```
p =

    0.3017


h =

     0
```

```
stats =

    zval: -1.0328
    sign: 5
```

The approximate p-value, which `signtest` obtains using the z-statistic, is really close to the exact p-value.

Test for Large Samples

Perform a left-sided sign test for large samples.

Navigate to a folder containing sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')
```

Load the sample data.

```
load gradespaired
```

Test the null hypothesis that the median of the grade differences before and after the tutoring program is 0 against the alternate that it is less than 0.

```
[p,h,stats] = signtest(gradespaired(:,1),gradespaired(:,2),...
'tail','left')
```

```
p =

    0.0013


h =

     1


stats =

    zval: -3.0110
    sign: 37
```

Because the sample size is large (greater than 100), `signtest` uses an approximate method to calculate the p-value and also returns the value of the z-statistic. The test

rejects the null hypothesis that there is no difference between the grade medians at the 5% significance level.

Test for Median of a Single Population

Test the hypothesis that the population median is different from a specified value.

Load the sample data.

```
load lawdata
```

The data set has 15 observations for variables `gpa` and `lsat`.

Test the hypothesis that the median `lsat` score is higher than 570.

```
[p,h,stats] = signtest(lsat,570,'tail','right')
```

```
p =

    0.0176


h =

     1


stats =

    zval: NaN
    sign: 12
```

Both the *p*-value, 0.0176, and `h` = 1 indicate that at the 5% significance level the test concludes in favor of the alternate hypothesis.

Input Arguments

x — Sample data

vector

Sample data, specified as a vector.

Data Types: `single` | `double`

y — Sample data

vector

Sample data, specified as a vector. `y` must be the same length as `x`.

Data Types: `single | double`

m — Hypothesized value of the median

scalar

Hypothesized value of the median, specified as a scalar.

Example: `signtest(x,35)`

Data Types: `single | double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'alpha',0.01,'method','approximate','tail','right'` specifies a right-tailed sign test with 1% significance level , which returns the approximate p-value.

'alpha' — Significance level

0.05 (default) | scalar value in the range 0 to 1

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'alpha'` and a scalar value in the range 0 to 1. The default value of `alpha` is 0.05. Significance level of `h` is 100 * `alpha`%.

Example: `'alpha', 0.01`

Data Types: `double | single`

'method' — *p*-value computation method

`'exact' | 'approximate'`

p-value computation method, specified as the comma-separated pair consisting of `'method'` and one of the following:

`'exact'`	Exact computation of the *p*-value, `p`.

`'approximate'`	Normal approximation for computing the *p*-value, `p`.

The default computation method is `'exact'`, if there are fewer than 100 observations and `'approximate'` if there are 100 observations or more.

Example: `'method','exact'`

Data Types: `char`

`'tail'` — Type of test

`'both'` (default) | `'right'` | `'left'`

Type of test, specified as the comma-separated pair consisting of `'tail'` and one of the following:

`'both'`	Two-sided hypothesis test, which is the default test type. • For a one-sample test, the alternate hypothesis states that the data in `x` come from a continuous distribution with median different than zero (or `m`). • For a two-sample test, the alternate hypothesis states that the data in `x-y` come from a distribution with median different than zero.
`'right'`	Right-tailed hypothesis test. • For a one-sample test, the alternate hypothesis states that the data in `x` come from a continuous distribution with median greater than zero (or `m`). • For a two-sample test, the alternate hypothesis states the data in `x-y` come from a distribution with median greater than zero.
`'left'`	Left-tailed hypothesis test. • For a one-sample test, the alternate hypothesis states that the data in `x` come from a continuous distribution with median less than zero (or `m`). • For a two-sample test, the alternative hypothesis states the data in `x-y` come from a distribution with median less than zero.

Example: `'tail','left'`

Output Arguments

`p` — *p*-value of the test

nonnegative scalar

p-value of the test, returned as a nonnegative scalar from 0 to 1. `p` is the probability of observing a test statistic as or more extreme than the observed value under the null hypothesis. `signtest` computes the two-sided *p*-value by doubling the most significant one-sided value.

`h` — Result of the hypothesis test

1 | 0

Result of the hypothesis test, returned as a logical value.

- If `h` = 1, this indicates rejection of the null hypothesis at the 100 * `alpha`% significance level.
- If `h` = 0, this indicates a failure to reject the null hypothesis at the 100 * `alpha`% significance level.

`stats` — Test statistics

structure

Test statistics, returned as a structure. The test statistics stored in `stats` are:

- `sign`: Value of the sign test statistic.
- `zval`: Value of the z-statistic (computed only for large samples).

More About

Sign Test

The sign test is a nonparametric test for the median of a population or median of the difference of two populations.

For example, for tests on a single population median:

- If the test is two-sided, then the test statistic, S, is the minimum of the number of observations that are smaller or larger than the hypothesized median value, M_0.
- If the test is right-sided, then S is the number of observations that are larger than the hypothesized median value M_0.
- If the test is left-sided, then S is the number of observations that are smaller than the hypothesized median value M_0.

z-Statistic

For a large sample, `signtest` uses the *z*-statistic to approximate the *p*-value.

The `signtest` test statistic is the number of elements that are greater than `0` (for `signtest(x)` or `signtest(x-y)`), or `m` (for `signtest(x,m)`). Hence, the *z*-statistic of the sign test, with the continuity correction, is:

$$z = \frac{\left(S - E(S)\right)}{\sqrt{V(S)}} = \frac{\left(S - (0.5)n - 0.5 sign(npos - nneg)\right)}{\sqrt{(0.5)(0.5)n}},$$

where *npos* and *nneg* are the number of positive and negative differences from the hypothesized median value, respectively.

Algorithms

For a one-sample test, `signtest` omits values in `x` that are zero or `NaN`.

For a two-sample test, `signtest` omits values in `x – y` that are zero or `NaN`.

References

[1] Gibbons, J. D., and S. Chakraborti. *Nonparametric Statistical Inference*, 5th Ed. Boca Raton, FL: Chapman & Hall/CRC Press, Taylor & Francis Group, 2011.

[2] Hollander, M., and D. A. Wolfe. *Nonparametric Statistical Methods*. Hoboken, NJ: John Wiley & Sons, Inc., 1999.

See Also

`ranksum` | `signrank` | `ttest` | `ztest`

silhouette

Silhouette plot

Syntax

```
silhouette(X,clust)
s = silhouette(X,clust)
[s,h] = silhouette(X,clust)
[...] = silhouette(X,clust,metric)
[...] = silhouette(X,clust,distfun,p1,p2,...)
```

Description

`silhouette(X,clust)` plots cluster silhouettes for the n-by-p data matrix `X`, with clusters defined by `clust`. Rows of `X` correspond to points, columns correspond to coordinates. `clust` can be a categorical variable, numeric vector, character matrix, or cell array of strings containing a cluster name for each point. `silhouette` treats `NaN`s or empty strings in `clust` as missing values, and ignores the corresponding rows of `X`. By default, `silhouette` uses the squared Euclidean distance between points in `X`.

`s = silhouette(X,clust)` returns the silhouette values in the n-by-1 vector `s`, but does not plot the cluster silhouettes.

`[s,h] = silhouette(X,clust)` plots the silhouettes, and returns the silhouette values in the n-by-1 vector `s`, and the figure handle in `h`.

`[...] = silhouette(X,clust,metric)` plots the silhouettes using the inter-point distance function specified in `metric`. Choices for `metric` are given in the following table.

Metric	Description
`'Euclidean'`	Euclidean distance
`'sqEuclidean'`	Squared Euclidean distance (default)
`'cityblock'`	Sum of absolute differences

Metric	Description
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors)
`'correlation'`	One minus the sample correlation between points (treated as sequences of values)
`'Hamming'`	Percentage of coordinates that differ
`'Jaccard'`	Percentage of nonzero coordinates that differ
Vector	A numeric distance matrix in upper triangular vector form, such as is created by `pdist`. `X` is not used in this case, and can safely be set to `[]`.

For more information on each metric, see "Distance Metrics".

`[...] = silhouette(X,clust,distfun,p1,p2,...)` accepts a function handle `distfun` to a metric of the form

```
d = distfun(X0,X,p1,p2,...)
```

where `X0` is a `1`-by-`p` point, `X` is an `n`-by-`p` matrix of points, and `p1,p2,...` are optional additional arguments. The function `distfun` returns an `n`-by-`1` vector `d` of distances between `X0` and each point (row) in `X`. The arguments `p1`, `p2`,`...` are passed directly to the function `distfun`.

Examples

Create Silhouette Plot

Create a silhouette plot from clustered data.

Generate random sample data.

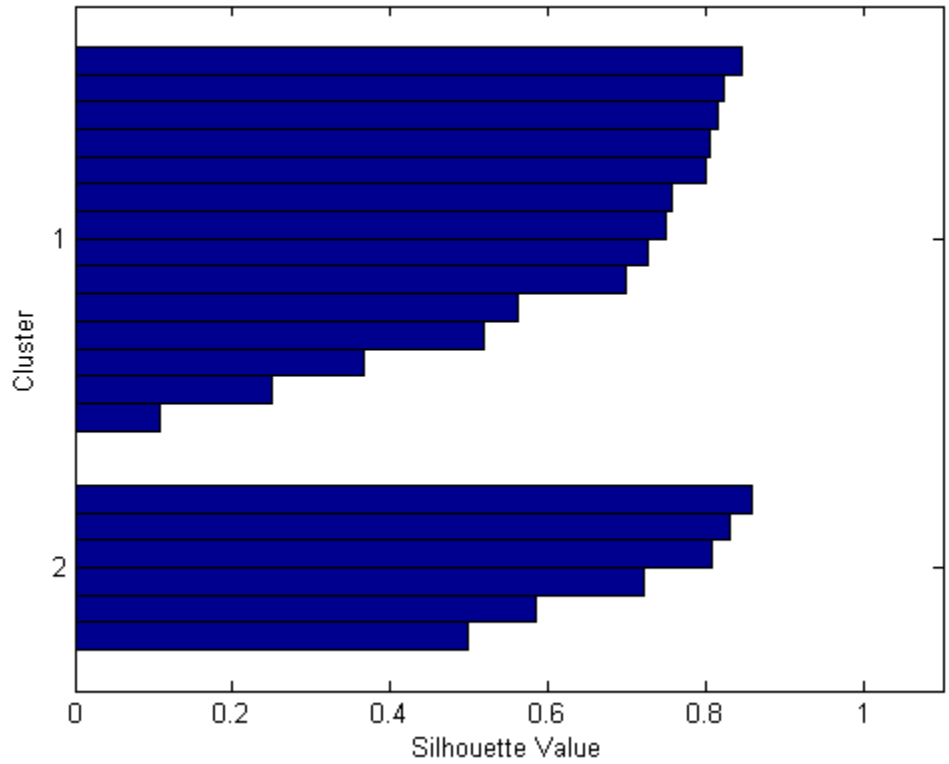
```
rng('default');  % For reproducibility
X = [randn(10,2)+ones(10,2);randn(10,2)-ones(10,2)];
```

Cluster the data in `X` using `kmeans`.

```
cidx = kmeans(X,2);
```

Create a silhouette plot from the clustered data.

```
silhouette(X,cidx)
```



Compute Silhouette Values

Compute the silhouette values from clustered data.

Generate random sample data.

```
rng('default');  % For reproducibility
X = [randn(10,2)+ones(10,2);randn(10,2)-ones(10,2)];
```

Use `kmeans` to cluster the data in `X` based on the sum of absolute differences in distance.

```
cidx = kmeans(X,2,'distance','cityblock');
```

Compute the silhouette values from the clustered data. Specify `metric` as `'cityblock'` to indicate that the `kmeans` clustering is based on the sum of absolute differences.

```
s = silhouette(X,cidx,'cityblock')
```

```
s =

    0.0816
    0.5848
    0.1906
    0.2781
    0.3954
    0.4050
    0.0897
    0.5416
    0.6203
    0.6664
    0.5814
    0.6022
    0.6540
    0.5223
    0.5566
    0.4227
    0.6225
    0.6558
    0.5284
    0.6034
```

More About

Silhouette Value

The silhouette value for each point is a measure of how similar that point is to points in its own cluster, when compared to points in other clusters. The silhouette value for the `i`th point, `Si`, is defined as

```
Si = (bi-ai)/ max(ai,bi)
```

where `ai` is the average distance from the `i`th point to the other points in the same cluster as `i`, and `bi` is the minimum average distance from the `i`th point to points in a different cluster, minimized over clusters.

The silhouette value ranges from -1 to +1. A high silhouette value indicates that `i` is well-matched to its own cluster, and poorly-matched to neighboring clusters. If most points have a high silhouette value, then the clustering solution is appropriate. If many points have a low or negative silhouette value, then the clustering solution may have either too many or too few clusters. The silhouette clustering evaluation criterion can be used with any distance metric.

- "Grouping Variables" on page 2-52

References

[1] Kaufman L., and P. J. Rousseeuw. *Finding Groups in Data: An Introduction to Cluster Analysis*. Hoboken, NJ: John Wiley & Sons, Inc., 1990.

See Also

`dendrogram` | `kmeans` | `linkage` | `pdist` | `evalclusters`

clustering.evaluation.SilhouetteEvaluation class

Package: clustering.evaluation
Superclasses: clustering.evaluation.ClusterCriterion

Silhouette criterion clustering evaluation object

Description

`clustering.evaluation.SilhouetteEvaluation` is an object consisting of sample data, clustering data, and silhouette criterion values used to evaluate the optimal number of data clusters. Create a silhouette criterion clustering evaluation object using `evalclusters`.

Construction

`eva = evalclusters(x,clust,'Silhouette')` creates a silhouette criterion clustering evaluation object.

`eva = evalclusters(x,clust,'Silhouette',Name,Value)` creates a silhouette criterion clustering evaluation object using additional options specified by one or more name-value pair arguments.

Input Arguments

x — Input data

matrix

Input data, specified as an *N*-by-*P* matrix. *N* is the number of observations, and *P* is the number of variables.

Data Types: `single` | `double`

clust — Clustering algorithm

`'kmeans'` | `'linkage'` | `'gmdistribution'` | matrix of clustering solutions | function handle

Clustering algorithm, specified as one of the following.

`'kmeans'`	Cluster the data in x using the `kmeans` clustering algorithm, with `'EmptyAction'` set to `'singleton'` and `'Replicates'` set to `5`.
`'linkage'`	Cluster the data in x using the `clusterdata` agglomerative clustering algorithm, with `'Linkage'` set to `'ward'`.
`'gmdistribution'`	Cluster the data in x using the `gmdistribution` Gaussian mixture distribution algorithm, with `'SharedCov'` set to `true` and `'Replicates'` set to `5`.

If `Criterion` is `'CalinskHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can specify a clustering algorithm using the `function_handle` (`@`) operator. The function must be of the form `C = clustfun(DATA,K)`, where `DATA` is the data to be clustered, and `K` is the number of clusters. The output of `clustfun` must be one of the following:

- A vector of integers representing the cluster index for each observation in `DATA`. There must be `K` unique values in this vector.
- A numeric n-by-K matrix of score for n observations and K classes. In this case, the cluster index for each observation is determined by taking the largest score value in each row.

If `Criterion` is `'CalinskHarabasz'`, `'DaviesBouldin'`, or `'silhouette'`, you can also specify `clust` as a n-by-K matrix containing the proposed clustering solutions. n is the number of observations in the sample data, and K is the number of proposed clustering solutions. Column j contains the cluster indices for each of the N points in the jth clustering solution.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'KList',[1:5],'Distance','cityblock'` specifies to test 1, 2, 3, 4, and 5 clusters using the sum of absolute differences distance measure.

`'ClusterPriors'` — Prior probabilities for each cluster

`'empirical'` (default) | `'equal'`

Prior probabilities for each cluster, specified as the comma-separated pair consisting of `'ClusterPriors'` and one of the following.

`'empirical'`	Compute the overall silhouette value for the clustering solution by averaging the silhouette values for all points. Each cluster contributes to the overall silhouette value proportionally to its size.
`'equal'`	Compute the overall silhouette value for the clustering solution by averaging the silhouette values for all points within each cluster, and then averaging those values across all clusters. Each cluster contributes equally to the overall silhouette value, regardless of its size.

Example: `'ClusterPriors','empirical'`

`'Distance'` — Distance metric

`'sqEuclidean'` (default) | `'Euclidean'` | `'cityblock'` | vector | function | ...

Distance metric used for computing the criterion values, specified as the comma-separated pair consisting of `'Distance'` and one of the following.

`'sqEuclidean'`	Squared Euclidean distance
`'Euclidean'`	Euclidean distance
`'cityblock'`	Sum of absolute differences
`'cosine'`	One minus the cosine of the included angle between points (treated as vectors)
`'correlation'`	One minus the sample correlation between points (treated as sequences of values)
`'Hamming'`	Percentage of coordinates that differ
`'Jaccard'`	Percentage of nonzero coordinates that differ

For detailed information about each distance metric, see `pdist`.

You can also specify a function for the distance metric by using the `function_handle` (`@`) operator. The distance function must be of the form `d2 = distfun(XI,XJ)`, where `XI` is a 1-by-n vector corresponding to a single row of the input matrix `X`, and `XJ` is an m_2-

by-n matrix corresponding to multiple rows of `X`. `distfun` must return an m_2-by-1 vector of distances `d2`, whose kth element is the distance between `XI` and `XJ(k,:)`.

If `Criterion` is `'silhouette'`, you can also specify `Distance` as the output vector output created by the function `pdist`.

When `Clust` a string representing a built-in clustering algorithm, `evalclusters` uses the distance metric specified for `Distance` to cluster the data, except for the following:

- If `Clust` is `'linkage'`, and `Distance` is either `'sqEuclidean'` or `'Euclidean'`, then the clustering algorithm uses Euclidean distance and Ward linkage.
- If `Clust` is `'linkage'` and `Distance` is any other metric, then the clustering algorithm uses the specified distance metric and average linkage.

In all other cases, the distance metric specified for Distance must match the distance metric used in the clustering algorithm to obtain meaningful results.

Example: `'Distance','Euclidean'`

`'KList'` — List of number of clusters to evaluate

vector

List of number of clusters to evaluate, specified as the comma-separated pair consisting of `'KList'` and a vector of positive integer values. You must specify `KList` when clust is a clustering algorithm name string or a function handle. When criterion is `'gap'`, clust must be a string or a function handle, and you must specify KList.

Example: `'KList',[1:6]`

Properties

`ClusteringFunction`

Clustering algorithm used to cluster the input data, stored as a valid clustering algorithm name string or function handle. If the clustering solutions are provided in the input, `ClusteringFunction` is empty.

`ClusterPriors`

Prior probabilities for each cluster, stored as valid prior probability name string.

`ClusterSilhouettes`

Silhouette values corresponding to each proposed number of clusters in `InspectedK`, stored as a cell array of vectors.

`CriterionName`

Name of the criterion used for clustering evaluation, stored as a valid criterion name string.

`CriterionValues`

Criterion values corresponding to each proposed number of clusters in `InspectedK`, stored as a vector of numerical values.

`Distance`

Distance measure used for clustering data, stored as a valid distance measure name string.

`InspectedK`

List of the number of proposed clusters for which to compute criterion values, stored as a vector of positive integer values.

`Missing`

Logical flag for excluded data, stored as a column vector of logical values. If `Missing` equals `true`, then the corresponding value in the data matrix `x` is not used in the clustering solution.

`NumObservations`

Number of observations in the data matrix `X`, minus the number of missing (`NaN`) values in `X`, stored as a positive integer value.

`OptimalK`

Optimal number of clusters, stored as a positive integer value.

`OptimalY`

Optimal clustering solution corresponding to `OptimalK`, stored as a column vector of positive integer values. If the clustering solutions are provided in the input, `OptimalY` is empty.

X

Data used for clustering, stored as a matrix of numerical values.

Methods

Inherited Methods

addK	Evaluate additional numbers of clusters
plot	Plot clustering evaluation object criterion values
compact	Compact clustering evaluation object

Definitions

Silhouette Value

The silhouette value for each point is a measure of how similar that point is to points in its own cluster, when compared to points in other clusters. The silhouette value for the `i`th point, `Si`, is defined as

```
Si = (bi-ai)/ max(ai,bi)
```

where `ai` is the average distance from the `i`th point to the other points in the same cluster as `i`, and `bi` is the minimum average distance from the `i`th point to points in a different cluster, minimized over clusters.

The silhouette value ranges from -1 to +1. A high silhouette value indicates that `i` is well-matched to its own cluster, and poorly-matched to neighboring clusters. If most points have a high silhouette value, then the clustering solution is appropriate. If many points have a low or negative silhouette value, then the clustering solution may have

either too many or too few clusters. The silhouette clustering evaluation criterion can be used with any distance metric.

Examples

Evaluate the Clustering Solution Using Silhouette Criterion

Evaluate the optimal number of clusters using the silhouette clustering evaluation criterion.

Generate sample data containing random numbers from three multivariate distributions with different parameter values.

```
rng('default');  % For reproducibility
mu1 = [2 2];
sigma1 = [0.9 -0.0255; -0.0255 0.9];

mu2 = [5 5];
sigma2 = [0.5 0 ; 0 0.3];

mu3 = [-2, -2];
sigma3 = [1 0 ; 0 0.9];

N = 200;

X = [mvnrnd(mu1,sigma1,N);...
     mvnrnd(mu2,sigma2,N);...
     mvnrnd(mu3,sigma3,N)];
```

Evaluate the optimal number of clusters using the silhouette criterion. Cluster the data using `kmeans`.

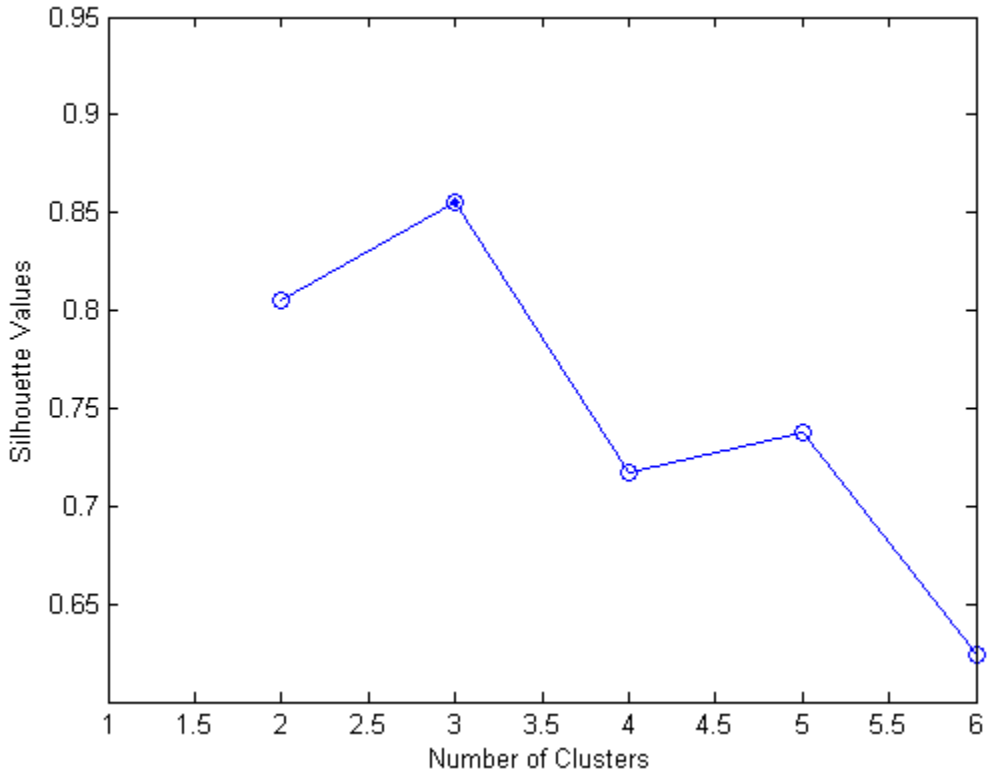
```
E = evalclusters(X,'kmeans','silhouette','klist',[1:6])
```

```
E =

  SilhouetteEvaluation with properties:

    NumObservations: 600
         InspectedK: [1 2 3 4 5 6]
    CriterionValues: [NaN 0.8055 0.8551 0.7170 0.7376 0.6239]
           OptimalK: 3
```

The `OptimalK` value indicates that, based on the silhouette criterion, the optimal number of clusters is three.

Plot the silhouette criterion values for each number of clusters tested.

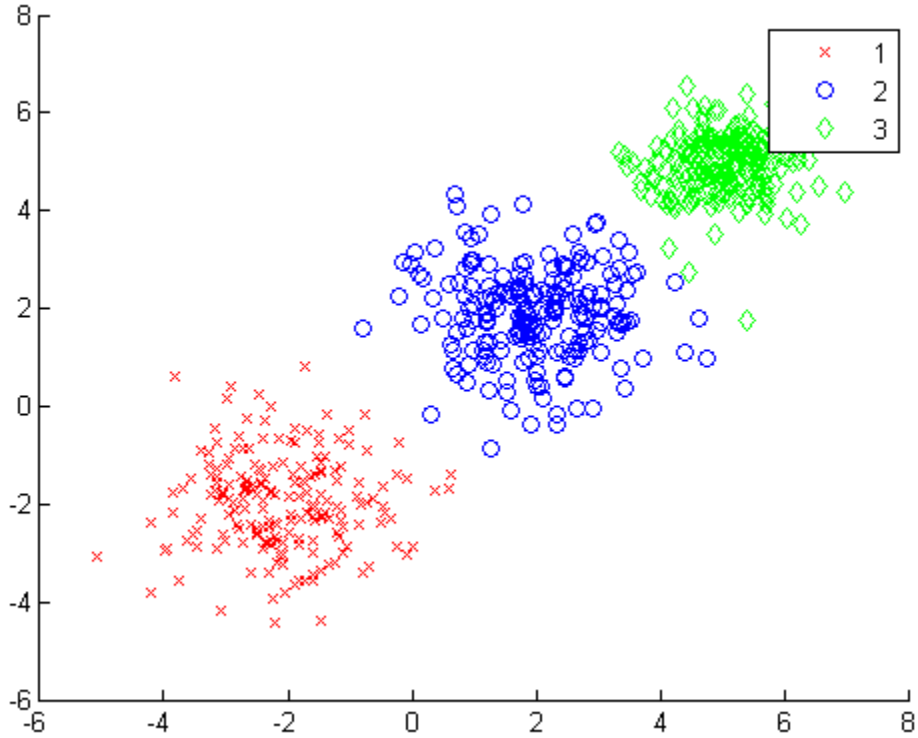
```
figure;
plot(E)
```



The plot shows that the highest silhouette value occurs at three clusters, suggesting that the optimal number of clusters is three.

Create a grouped scatter plot to visually examine the suggested clusters.

```
figure;
gscatter(X(:,1),X(:,2),E.OptimalY,'rbg','xod')
```



The plot shows three distinct clusters within the data: Cluster 1 is in the lower-left corner, cluster 2 is near the center of the plot, and cluster 3 is in the upper-right corner.

References

[1] Kaufman L. and P. J. Rouseeuw. *Finding Groups in Data: An Introduction to Cluster Analysis*. Hoboken, NJ: John Wiley & Sons, Inc., 1990.

[2] Rouseeuw, P. J. "Silhouettes: a graphical aid to the interpretation and validation of cluster analysis." *Journal of Computational and Applied Mathematics*. Vol. 20, No. 1, 1987, pp. 53–65.

See Also

`clustering.evaluation.CalinskiHarabaszEvaluation` | `clustering.evaluation.DaviesBouldinEvaluation` | `clustering.evaluation.GapEvaluation` | `evalclusters` | `silhouette`

More About

- Class Attributes
- Property Attributes

single

Class: dataset

Convert dataset variables to single array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
B = single(A)
B = single(A,vars)
```

Description

`B = single(A)` returns the contents of the dataset `A`, converted to one single array. The classes of the variables in the dataset must support the conversion.

`B = single(A,vars)` returns the contents of the dataset variables specified by `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector.

See Also

`dataset` | `double` | `replacedata`

size

Class: dataset

Size of dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
D = SIZE(A)
[NOBS,NVARS] = SIZE(A)
[M1,M2,M3,...,MN] = SIZE(A)
M = size(A,dim)
```

Description

`D = SIZE(A)` returns the two-element row vector `D = [NOBS,NVARS]` containing the number of observations and number of variables in the dataset `A`. A dataset array always has two dimensions.

`[NOBS,NVARS] = SIZE(A)` returns the numbers of observations and variables in the dataset `A` as separate output variables.

`[M1,M2,M3,...,MN] = SIZE(A)`, for `N > 2`, returns `M1 = NOBS`, `M2 = NVARS`, and `M3,..,MN = 1`.

`M = size(A,dim)` returns the length of the dimension specified by the scalar `dim`:

- `M = size(A,1)` returns `NOBS`
- `M = size(A,2)` returns `NVARS`
- `M = size(A,k)` returns `1` for `k > 2`

See Also

`length` | `numel` | `ndims`

size

Class: qrandset

Number of dimensions in matrix

Syntax

```
d = size(p)
[m,n] = size(p)
m = size(p,dim)
```

Description

`d = size(p)` returns the two-element row vector `d = [m,n]` containing the number of points in the point set and the number of dimensions the points are in, for the point set `p`. These correspond to the number of rows and columns in the matrix that would be produced by the expression `p(:,:)`.

`[m,n] = size(p)` returns the number of points and dimensions for `p` as separate output variables.

`m = size(p,dim)` returns the length of the dimension specified by the scalar `dim`. For example, `size(p,1)` returns the number of rows (points in the point set). If `dim` is greater than 2, `m` will be 1.

Examples

The commands

```
P = sobolset(12);
d = size(P)
```

return

```
d = [9.0072e+015 12]
```

The command

```
[m,n] = size(P)
```

returns

```
m = 9.0072e+015
n = 12
```

The command

```
m2 = size(P, 2)
```

returns

```
 m2 = 12
```

See Also

`length` | `ndims` | `qrandset`

slicesample

Slice sampler

Syntax

```
rnd = slicesample(initial,nsamples,'pdf',pdf)
rnd = slicesample(initial,nsamples,'logpdf',logpdf)
[rnd,neval] = slicesample(initial,...)
[rnd,neval] = slicesample(initial,...,Name,Value)
```

Description

`rnd = slicesample(initial,nsamples,'pdf',pdf)` generates `nsamples` random samples using the slice sampling method (see "Algorithms" on page 22-4483). `pdf` gives the target probability density function (pdf). `initial` is a row vector or scalar containing the initial value of the random sample sequences.

`rnd = slicesample(initial,nsamples,'logpdf',logpdf)` generates samples using the logarithm of the pdf.

`[rnd,neval] = slicesample(initial,...)` returns the average number of function evaluations that occurred in the slice sampling.

`[rnd,neval] = slicesample(initial,...,Name,Value)` generates random samples with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`initial`

Initial point, a scalar or row vector. Set `initial` so `pdf(initial)` is a strictly positive scalar. `length(initial)` is the number of dimensions of each sample.

`nsamples`

Positive integer, the number of samples that `slicesample` generates.

`pdf`

Handle to a function that generates the probability density function, specified with `@`. `pdf` can be unnormalized, meaning it need not integrate to `1`.

`logpdf`

Handle to a function that generates the logarithm of the probability density function, specified with `@`. `logpdf` can be the logarithm of an unnormalized pdf.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'burnin'`

Nonnegative integer, the number of samples to generate and discard before generating the samples to return. The slice sampling algorithm is a Markov chain whose stationary distribution is proportional to that of the `pdf` argument. Set `burnin` to a high enough value that you believe the Markov chain approximately reaches stationarity after `burnin` samples.

Default: `0`

`'thin'`

Positive integer, where `slicesample` discards every `thin - 1` samples and returns the next. The slice sampling algorithm is a Markov chain, so the samples are serially correlated. To reduce the serial correlation, choose a larger value of `thin`.

Default: `1`

`'width'`

Width of the interval around the current sample, a scalar or vector of positive values. `slicesample` begins with this interval and searches for an appropriate region containing the points of `pdf` that evaluate to a large enough value.

- If `width` is a scalar and the samples have multiple dimensions, `slicesample` uses `width` for each dimension.
- If `width` is a vector, it should have the same length as `initial`.

Default: 10

Output Arguments

`rnd`

`nsamples`-by-`length(initial)` matrix, where each row is one sample.

`neval`

Scalar, the mean number of function evaluations per sample. `neval` includes the `burnin` and `thin` evaluations, not just the evaluations of samples returned in `rnd`. Therefore the total number of function evaluations is `neval*(nsamples*thin + burnin)`.

Examples

Generate Random Samples From a Multimodal Density

This example shows how to generate random samples from a multimodal density using `slicesample`.

Define a function proportional to a multimodal density.

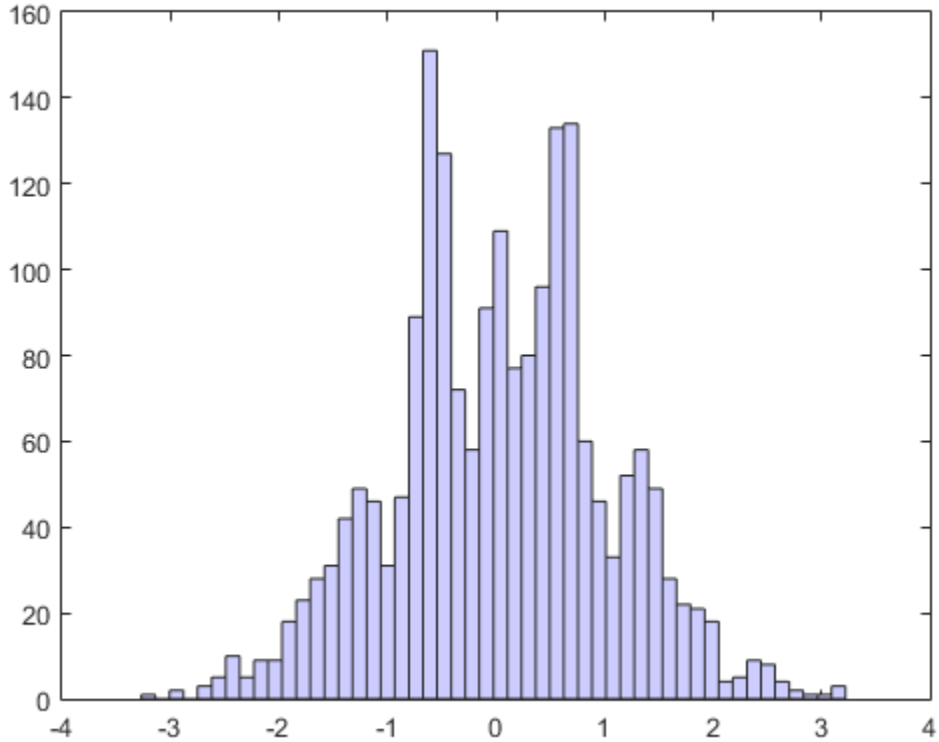
```
rng default  % For reproducibility
f = @(x) exp(-x.^2/2).*(1 + (sin(3*x)).^2).*...
    (1 + (cos(5*x).^2));
area = integral(f,-5,5);
```

Generate 2000 samples from the density, using a burn-in period of 1000, and keeping one in five samples.

```
N = 2000;
x = slicesample(1,N,'pdf',f,'thin',5,'burnin',1000);
```

Plot a histogram of the sample.

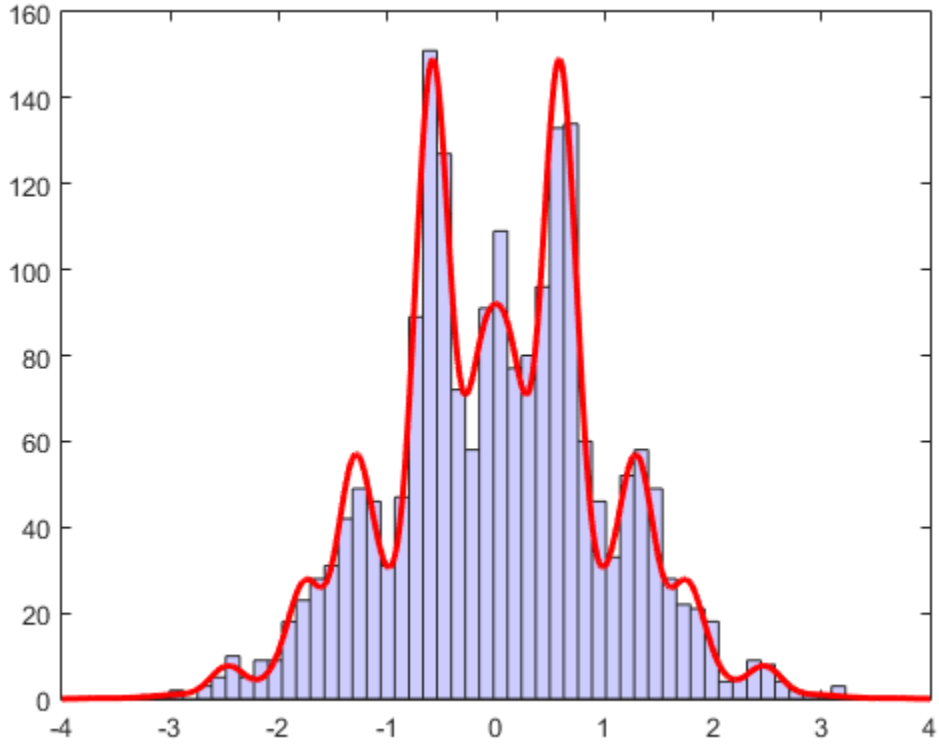
```
[binheight,bincenter] = hist(x,50);
h = bar(bincenter,binheight,'hist');
h.FaceColor = [.8 .8 1];
```



Scale the density to have the same area as the histogram, and superimpose it on the histogram.

```
hold on
h = gca;
xd = h.XLim;
xgrid = linspace(xd(1),xd(2),1000);
binwidth = (bincenter(2)-bincenter(1));
y = (N*binwidth/area) * f(xgrid);
plot(xgrid,y,'r','LineWidth',2)
```

```
hold off
```



The samples seem to fit the theoretical distribution well, so the `burnin` value seems adequate.

More About

Tips

- There are no definitive suggestions for choosing appropriate values for `burnin`, `thin`, or `width`. Choose starting values of `burnin` and `thin`, and increase them, if

necessary, to give the requisite independence and marginal distributions. See Neal [1] for details of the effect of adjusting `width`.

Algorithms

At each point in the sequence of random samples, `slicesample` selects the next point by "slicing" the density to form a neighborhood around the previous point where the density is above some value. Consequently, the sample points are not independent. Nearby points in the sequence tend to be closer together than they would be from a sample of independent values. For many purposes, the entire set of points can be used as a sample from the target distribution. However, when this type of serial correlation is a problem, the `burnin` and `thin` parameters can help reduce that correlation.

`slicesample` uses the slice sampling algorithm of Neal [1]. For numerical stability, it converts a `pdf` function into a `logpdf` function. The algorithm to resize the support region for each level, called "stepping-out" and "stepping-in," was suggested by Neal.

References

[1] Neal, Radford M. *Slice Sampling*. Ann. Stat. Vol. 31, No. 3, pp. 705–767, 2003. Available at Project Euclid.

See Also

`mhsample` | `rand` | `randsample`

skewness

Skewness

Syntax

```
y = skewness(X)
y = skewness(X,flag)
y = skewness(X,flag,dim)
```

Description

`y = skewness(X)` returns the sample skewness of `X`. For vectors, `skewness(x)` is the skewness of the elements of `x`. For matrices, `skewness(X)` is a row vector containing the sample skewness of each column. For N-dimensional arrays, `skewness` operates along the first nonsingleton dimension of `X`.

`y = skewness(X,flag)` specifies whether to correct for bias (`flag = 0`) or not (`flag = 1`, the default). When `X` represents a sample from a population, the skewness of `X` is biased; that is, it will tend to differ from the population skewness by a systematic amount that depends on the size of the sample. You can set `flag = 0` to correct for this systematic bias.

`y = skewness(X,flag,dim)` takes the skewness along dimension `dim` of `X`.

`skewness` treats `NaN`s as missing values and removes them.

Examples

```
X = randn([5 4])
X =
  1.1650  1.6961 -1.4462 -0.3600
  0.6268  0.0591 -0.7012 -0.1356
  0.0751  1.7971  1.2460 -1.3493
  0.3516  0.2641 -0.6390 -1.2704
 -0.6965  0.8717  0.5774  0.9846
```

```
y = skewness(X)
y =
   -0.2933   0.0482   0.2735   0.4641
```

More About

Algorithms

Skewness is a measure of the asymmetry of the data around the sample mean. If skewness is negative, the data are spread out more to the left of the mean than to the right. If skewness is positive, the data are spread out more to the right. The skewness of the normal distribution (or any perfectly symmetric distribution) is zero.

The skewness of a distribution is defined as

$$s = \frac{E(x-\mu)^3}{\sigma^3}$$

where μ is the mean of x, σ is the standard deviation of x, and $E(t)$ represents the expected value of the quantity t. `skewness` computes a sample version of this population value.

When you set `flag` to 1, the following equation applies:

$$s_1 = \frac{\frac{1}{n}\sum_{i=1}^{n}(x_i-\bar{x})^3}{\left(\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_i-\bar{x})^2}\right)^3}$$

When you set `flag` to 0, the following equation applies:

$$s_0 = \frac{\sqrt{n(n-1)}}{n-2}s_1$$

This bias-corrected formula requires that `X` contain at least three elements.

See Also

`kurtosis` | `mean` | `moment` | `std` | `var`

Skip property

Class: qrandset

Number of initial points to omit from sequence

Description

The `Skip` property of a point set contains a positive integer which specifies the number of initial points in the sequence to omit from the point set. The default `Skip` value is 0.

Initial points of a sequence sometimes exhibit undesirable properties, for example the first point is often `(0,0,0,...)` and this may "unbalance" the sequence since its counterpart, `(1,1,1,...)`, never appears. Another common reason is that initial points often exhibit correlations among different dimensions which disappear later in the sequence.

Examples

Examine the difference between skipping and not skipping points:

```
% No skipping produces the standard Sobol sequence.
P = sobolset(5);
P(1:3,:)

% Skip the first point of the sequence.  The point set now
% starts at the second point of the basic Sobol sequence.
P.Skip = 1;
P(1:3,:)
```

See Also

`Leap` | `subsref` | `net` | `qrandset`

sobolset class

Superclasses: qrandset

Sobol quasi-random point sets

Description

`sobolset` is a quasi-random point set class that produces points from the Sobol sequence. The Sobol sequence is a base-2 digital sequence that fills space in a highly uniform manner.

Construction

.sobolset	Construct Sobol quasi-random point set

Methods

Inherited Methods

Methods in the following table are inherited from `qrandset`.

disp	Display qrandset object
end	Last index in indexing expression for point set
length	Length of point set
ndims	Number of dimensions in matrix
net	Generate quasi-random point set

scramble	Scramble quasi-random point set
size	Number of dimensions in matrix
subsref	Subscripted reference for qrandset

Properties

PointOrder	Point generation method

Inherited Properties

Properties in the following table are inherited from `qrandset`.

Dimensions	Number of dimensions
Leap	Interval between points
ScrambleMethod	Settings that control scrambling
Skip	Number of initial points to omit from sequence
Type	Name of sequence on which point set `P` is based

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

References

[1] Bratley, P., and B. L. Fox, "ALGORITHM 659 Implementing Sobol's Quasirandom Sequence Generator," ACM Transactions on Mathematical Software, Vol. 14, No. 1, pp. 88-100, 1988.

[2] Joe, S., and F. Y. Kuo, "Remark on Algorithm 659: Implementing Sobol's Quasirandom Sequence Generator," ACM Transactions on Mathematical Software, Vol. 29, No. 1, pp. 49-57, 2003.

[3] Hong, H. S., and F. J. Hickernell, "ALGORITHM 823: Implementing Scrambled Digital Sequences," ACM Transactions on Mathematical Software, Vol. 29, No. 2, pp. 95-109, 2003.

[4] Matousek, J., "On the L2-discrepancy for anchored boxes," Journal of Complexity, Vol. 14, pp. 527-556, 1998.

See Also

`haltonset`

How To

- “Quasi-Random Point Sets” on page 6-17

sobolset

Class: sobolset

Construct Sobol quasi-random point set

Syntax

```
p = sobolset(d)
p = sobolset(d,prop1,val1,prop2,val2,...)
```

Description

`p = sobolset(d)` constructs a `d`-dimensional point set `p` of the `sobolset` class, with default property settings.

`p = sobolset(d,prop1,val1,prop2,val2,...)` specifies property name/value pairs used to construct `p`.

The object `p` returned by `sobolset` encapsulates properties of a specified quasi-random sequence. The point set is finite, with a length determined by the `Skip` and `Leap` properties and by limits on the size of point set indices (maximum value of 2^{53}). Values of the point set are not generated and stored in memory until you access `p` using `net` or parenthesis indexing.

Examples

Generate a 3-D Sobol point set, skip the first 1000 values, and then retain every 101st point:

```
p = sobolset(3,'Skip',1e3,'Leap',1e2)
p =
    Sobol point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : none
        PointOrder : standard
```

Use `scramble` to apply a random linear scramble combined with a random digital shift:

```
p = scramble(p,'MatousekAffineOwen')
p =
    Sobol point set in 3 dimensions (8.918019e+013 points)
    Properties:
              Skip : 1000
              Leap : 100
    ScrambleMethod : MatousekAffineOwen
        PointOrder : standard
```

Use `net` to generate the first four points:

```
X0 = net(p,4)
X0 =
    0.7601    0.5919    0.9529
    0.1795    0.0856    0.0491
    0.5488    0.0785    0.8483
    0.3882    0.8771    0.8755
```

Use parenthesis indexing to generate every third point, up to the 11th point:

```
X = p(1:3:11,:)
X =
    0.7601    0.5919    0.9529
    0.3882    0.8771    0.8755
    0.6905    0.4951    0.8464
    0.1955    0.5679    0.3192
```

References

[1] Bratley, P., and B. L. Fox. “Algorithm 659 Implementing Sobol's Quasirandom Sequence Generator.” *ACM Transactions on Mathematical Software*. Vol. 14, No. 1, 1988, pp. 88–100.

[2] Joe, S., and F. Y. Kuo. “Remark on Algorithm 659: Implementing Sobol's Quasirandom Sequence Generator.” *ACM Transactions on Mathematical Software*. Vol. 29, No. 1, 2003, pp. 49–57.

[3] Hong, H. S., and F. J. Hickernell. “Algorithm 823: Implementing Scrambled Digital Sequences.” *ACM Transactions on Mathematical Software*. Vol. 29, No. 2, 2003, pp. 95–109.

[4] Matousek, J. “On the L2-Discrepancy for Anchored Boxes.” *Journal of Complexity*. Vol. 14, No. 4, 1998, pp. 527–556.

See Also

`haltonset` | `scramble` | `net`

sortrows

Class: dataset

Sort rows of dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
B = sortrows(A)
B = sortrows(A,vars)
B = sortrows(A,'obsnames')
B = sortrows(A,vars,mode)
[B,idx] = sortrows(A)
```

Description

`B = sortrows(A)` returns a copy of the dataset array `A`, with the observations sorted in ascending order by all of the variables in `A`. The observations in `B` are sorted first by the first variable, next by the second variable, and so on. Each variable in `A` must be a valid input to `sort`, or, if a variable has multiple columns, to the MATLAB `sortrows` function or to its own`sortrows` method.

`B = sortrows(A,vars)` sorts the observations in `A` by the variables specified by `vars`. `vars` is a positive integer, a vector of positive integers, variable names, a cell array containing one or more variable names, or a logical vector.

`B = sortrows(A,'obsnames')` sorts the observations in `A` by observation name.

`B = sortrows(A,vars,mode)` sorts in the direction specified by `mode`. When `mode` is the single string `'ascend'` (the default) or `'descend'`, `sortrows` sorts `A` by the

variables specified by `vars` in ascending or descending order, respectively. `mode` can also be a cell array containing the strings `'ascend'` or `'descend'`, to specify a different sorting direction for each variable in `vars`. Specify `[]` for `vars` to sort using all variables.

`[B,idx] = sortrows(A)` also returns an index vector `idx` such that `B = A(idx,:)`.

Examples

Sort the data in `hospital.mat` by age and then by last name:

```
load hospital
hospital(1:5,1:3)
ans =
            LastName       Sex       Age
 YPL-320    'SMITH'        Male      38
 GLI-532    'JOHNSON'      Male      43
 PNI-258    'WILLIAMS'     Female    38
 MIJ-579    'JONES'        Female    40
 XLK-030    'BROWN'        Female    49

hospital = sortrows(hospital,{'Age','LastName'});
hospital(1:5,1:3)
ans =
            LastName       Sex       Age
 REV-997    'ALEXANDER'    Male      25
 FZR-250    'HALL'         Male      25
 LIM-480    'HILL'         Female    25
 XUE-826    'JACKSON'      Male      25
 SCQ-914    'JAMES'        Male      25
```

Sort the data in `hospital` by gender in ascending order, and age in descending order.

```
hospital = sortrows(hospital,{'Sex','Age'},{'ascend','descend'});
hospital(1:5,1:3)
ans =

               LastName        Sex       Age
    XLK-030    'BROWN'         Female    49
    GGU-691    'HUGHES'        Female    49
    KKL-155    'ADAMS'         Female    48
    HQO-561    'BRYANT'        Female    48
    BKD-785    'CLARK'         Female    48
```

```
hospital(end-4:end,1:3)
ans =

               LastName           Sex     Age
    VNL-702    'MOORE'            Male    28
    REV-997    'ALEXANDER'        Male    25
    FZR-250    'HALL'             Male    25
    XUE-826    'JACKSON'          Male    25
    SCQ-914    'JAMES'            Male    25
```

See Also

`dataset` | `unique`

More About

- “Dataset Arrays” on page 2-132

squareform

Format distance matrix

Syntax

```
Z = squareform(y)
y = squareform(Z)
Z = squareform(y,'tovector')
Y = squareform(Z,'tomatrix')
```

Description

`Z = squareform(y)`, where `y` is a vector as created by the `pdist` function, converts `y` into a square, symmetric format `Z`, in which `Z(i,j)` denotes the distance between the `i`th and `j`th objects in the original data.

`y = squareform(Z)`, where `Z` is a square, symmetric matrix with zeros along the diagonal, creates a vector `y` containing the `Z` elements below the diagonal. `y` has the same format as the output from the `pdist` function.

`Z = squareform(y,'tovector')` forces `squareform` to treat `y` as a vector.

`Y = squareform(Z,'tomatrix')` forces `squareform` to treat `Z` as a matrix.

The last two formats are useful if the input has a single element, so that it is ambiguous whether the input is a vector or square matrix.

Examples

```
y = 1:6
y =
   1   2   3   4   5   6

X = [0 1 2 3; 1 0 4 5; 2 4 0 6; 3 5 6 0]
X =
   0   1   2   3
```

```
   1   0   4   5
   2   4   0   6
   3   5   6   0
```

Then `squareform(y) = X` and `squareform(X) = y`.

See Also

`pdist`

stack

Class: dataset

Stack data from multiple variables into single variable

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
tall = stack(wide,datavars)
[tall,iwide] = stack(wide,datavars)
tall = stack(wide,datavars,Parameter,value)
```

Description

`tall = stack(wide,datavars)` converts a wide-format dataset array into a tall-format array, by stacking multiple variables in `wide` into a single variable in `tall`. In general, `tall` contains fewer variables but more observations than `wide`.

`datavars` specifies a group of `m` data variables in `wide`. `stack` creates a single data variable in `tall` by interleaving their values, and if `wide` has `n` observations, then `tall` has `m`-by-`n` observations. In other words, `stack` takes the `m` data values from each observation in `wide` and stacks them up to create `m` observations in `tall`. `datavars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. `stack` also creates a grouping variable in `tall` to indicate which of the `m` data variables in `wide` each observation in `tall` corresponds to.

`stack` assigns values for the "per-variable properties (e.g., `Units` and `VarDescription`) for the new data variable in `tall` from the corresponding property values for the first variable listed in `datavars`.

`stack` copies the remaining variables from `wide` to `tall` without stacking, by replicating each of their values `m` times. These variables are typically grouping variables. Because their values are constant across each group of `m` observations in `tall`, they identify which observation in `wide` an observation in `tall` came from.

`[tall,iwide] = stack(wide,datavars)` returns an index vector `iwide` indicating the correspondence between observations in `tall` and those in `wide`. `stack` creates `tall(j,:)` using `wide(iwide(j),datavarss)`.

For more information on grouping variables, see "Grouping Variables" on page 2-52.

Input Arguments

`tall = stack(wide,datavars,`*`Parameter`*`,`*`value`*`)` uses the following parameter name/value pairs to control how `stack` converts variables in `wide` to variables in `tall`:

`'ConstVars'`	Variables in `wide` to copy to `tall` without stacking. `ConstVars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. The default is all variables in `wide` not specified in `datavars`.
`'NewDataVarName'`	A name for the data variable to be created in `tall`. The default is a concatenation of the names of the `m` variables that are stacked up.
`'IndVarName'`	A name for the grouping variable to create in `tall` to indicate the source of each value in the new data variable. The default is based on the `'NewDataVarName'` parameter.

You can also specify multiple groups of data variables in `wide`, each of which becomes a variable in `tall`. All groups must contain the same number of variables. Use a cell array to contain multiple parameter values for `datavars`, and a cell array of strings to contain multiple `'NewDataVarName'`.

Examples

Convert a wide format data set to tall format, and then back to a different wide format:

```
load flu

% FLU has a 'Date' variable, and 10 variables for estimated
% influenza rates (in 9 different regions, estimated from
% Google searches, plus a nationwide estimate from the
% CDC). Combine those 10 variables into a "tall" array that
% has a single data variable, 'FluRate', and an indicator
% variable, 'Region', that says which region each estimate
% is from.
[flu2,iflu] = stack(flu, 2:11, 'NewDataVarName','FluRate', ...
    'IndVarName','Region')

% The second observation in FLU is for 10/16/2005.  Find the
% observations in FLU2 that correspond to that date.
flu(2,:)
flu2(iflu==2,:)

% Use the 'Date' variable from that tall array to split
% 'FluRate' into 52 separate variables, each containing the
% estimated influenza rates for each unique date.  The new
% "wide" array has one observation for each region.  In
% effect, this is the original array FLU "on its side".
dateNames = cellstr(datestr(flu.Date,'mmm_DD_YYYY'));
[flu3,iflu2] = unstack(flu2, 'FluRate', 'Date', ...
    'NewDataVarNames',dateNames)

% Since observations in FLU3 represent regions, IFLU2
% indicates the first occurrence in FLU2 of each region.
flu2(iflu2,:)
```

See Also

`dataset.unstack` | `dataset.join`

How To

- “Grouping Variables” on page 2-52

State property

Class: qrandstream

Current state of the stream

Description

The `State` property of a quasi-random stream contains the index into the associated point set of the next point to draw in the stream. Getting and resetting the `State` property allows you to return a stream to a previous state. The initial value of `State` is `1`.

Examples

```
Q = qrandstream('sobol', 5);
s = Q.State;
u1 = qrand(Q, 10)
Q.State = s;
u2 = qrand(Q, 10) % contains exactly the same values as u1
```

See Also

`qrand`

statget

Access values in statistics options structure

Syntax

```
val = statget(options,param)
val = statget(options,param,default)
```

Description

`val = statget(options,param)` returns the value of the parameter specified by the string `param` in the statistics options structure `options`. If the parameter is undefined in `options`, `statget` returns `[]`. You need to type only enough leading characters to define the parameter name uniquely. `statget` ignores case for parameter names. For available `options`, see Inputs.

`val = statget(options,param,default)` returns `default` if the specified parameter is undefined in the optimization options structure `options`.

Input Arguments

`DerivStep`

Relative difference used in finite difference derivative calculations. A positive scalar, or a vector of positive scalars the same size as the vector of parameters estimated by the Statistics and Machine Learning Toolbox function using the options structure.

`Display`

Amount of information displayed by the algorithm.

- `'off'` — Displays no information.
- `'final'` — Displays the final output.
- `'iter'` — Displays iterative output to the command window for some functions; otherwise displays the final output.

FunValCheck

Check for invalid values, such as `NaN` or `Inf`, from the objective function.

- `'off'`
- `'on'`

GradObj

Flags whether the objective function returns a gradient vector as a second output.

- `'off'`
- `'on'`

Jacobian

Flags whether the objective function returns a Jacobian as a second output.

- `'off'`
- `'on'`

MaxFunEvals

Maximum number of objective function evaluations allowed. Positive integer.

MaxIter

Maximum number of iterations allowed. Positive integer.

OutputFcn

The solver calls all output functions after each iteration.

- Function handle specified using @
- a cell array with function handles
- an empty array (default)

Robust

Invoke robust fitting option.

- `'off'`

- `'on'`

`RobustWgtFun`

A weight function for robust fitting. Valid only when `Robust` is `'on'`. Can also be a function handle that accepts a normalized residual as input and returns the robust weights as output.

- `'bisquare'`
- `'andrews'`
- `'cauchy'`
- `'fair'`
- `'huber'`
- `'logistic'`
- `'talwar'`
- `'welsch'`

`Streams`

A single instance of the `RandStream` class, or a cell array of `RandStream` instances. The Streams option is accepted by some functions to govern what stream(s) to use in generating random numbers within the function. If `'UseSubstreams'` is `true`, the Streams value must be a scalar, or must be empty. If `'UseParallel'` is `true` and `'UseSubstreams'` is `false`, then the Streams argument must either be empty, or its length must match the number of processors used in the computation: equal to the *parpool* size if a *parpool* is open, a scalar otherwise.

`TolBnd`

Parameter bound tolerance. Positive scalar.

`TolFun`

Termination tolerance for the objective function value. Positive scalar.

`TolTypeFun`

Use `TolFun` for absolute or relative objective function tolerances.

- `'abs'`

- `'rel'`

`TolTypeX`

Use `TolX` for absolute or relative parameter tolerances.

- `'abs'`
- `'rel'`

`TolX`

Termination tolerance for the parameters. Positive scalar.

`Tune`

The tuning constant used in robust fitting to normalize the residuals before applying the weight function. The default value depends upon the weight function. This parameter is necessary if you specify the weight function as a function handle. Positive scalar.

`UseParallel`

Flag indicating whether eligible functions should use capabilities of the Parallel Computing Toolbox (PCT), if the capabilities are available. That is, if the PCT is installed, and a PCT parpool is in effect. Valid values are `false` (the default), for serial computation, and `true`, for parallel computation.

`UseSubstreams`

Flag indicating whether the random number generator in eligible functions should use `Substream` property of the `RandStream` class. `false` (default) or `true`. When `true`, high level iterations within the function will set the `Substream` property to the value of the iteration. This behavior helps to generate reproducible random number streams in parallel and/or serial mode computation.

`WgtFun`

A weight function for robust fitting. Valid only when `Robust` is `'on'`. Can also be a function handle that accepts a normalized residual as input and returns the robust weights as output.

- `'bisquare'`
- `'andrews'`

- `'cauchy'`
- `'fair'`
- `'huber'`
- `'logistic'`
- `'talwar'`
- `'welsch'`

Examples

This statement returns the value of the `Display` statistics options parameter from the structure called `my_options`.

```
val = statget(my_options,'Display')
```

Return the value of the `Display` statistics options parameter from the structure called `my_options` (as in the previous example). If the `Display` parameter is undefined, `statget` returns the value `'final'`.

```
optnew = statget(my_options,'Display','final');
```

See Also

`statset`

statset

Create statistics options structure

Syntax

```
statset
statset(statfun)
options = statset(...)
options = statset(fieldname1,val1,fieldname2,val2,...)
options = statset(oldopts,fieldname1,val1,fieldname2,val2,...)
options = statset(oldopts,newopts)
```

Description

`statset` with no input arguments and no output arguments displays all fields of a statistics options structure and their possible values.

`statset(statfun)` displays fields and default values used by the Statistics and Machine Learning Toolbox function `statfun`. Specify `statfun` using a string name or a function handle.

`options = statset(...)` creates a statistics options structure `options`. With no input arguments, all fields of the options structure are an empty array (`[]`). With a specified `statfun`, function-specific fields are default values and the remaining fields are `[]`. Function-specific fields set to `[]` indicate that the function is to use its default value for that parameter. For available `options`, see Inputs.

`options = statset(fieldname1,val1,fieldname2,val2,...)` creates an options structure in which the named fields have the specified values. Any unspecified values are `[]`. Use strings for field names. For fields that are string-valued, you must input the complete string for the value. If you provide an invalid string for a value, `statset` uses the default.

`options = statset(oldopts,fieldname1,val1,fieldname2,val2,...)` creates a copy of `oldopts` with the named parameters changed to the specified values.

`options = statset(oldopts,newopts)` combines an existing options structure, `oldopts`, with a new options structure, `newopts`. Any parameters in `newopts` with nonempty values overwrite corresponding parameters in `oldopts`.

Input Arguments

`DerivStep`

Relative difference used in finite difference derivative calculations. A positive scalar, or a vector of positive scalars the same size as the vector of parameters estimated by the Statistics and Machine Learning Toolbox function using the options structure.

`Display`

Amount of information displayed by the algorithm.

- `'off'` — Displays no information.
- `'final'` — Displays the final output.
- `'iter'` — Displays iterative output to the command window for some functions; otherwise displays the final output.

`FunValCheck`

Check for invalid values, such as `NaN` or `Inf`, from the objective function.

- `'off'`
- `'on'`

`GradObj`

Flags whether the objective function returns a gradient vector as a second output.

- `'off'`
- `'on'`

`Jacobian`

Flags whether the objective function returns a Jacobian as a second output.

- `'off'`

- `'on'`

`MaxFunEvals`

Maximum number of objective function evaluations allowed. Positive integer.

`MaxIter`

Maximum number of iterations allowed. Positive integer.

`OutputFcn`

The solver calls all output functions after each iteration.

- Function handle specified using @
- a cell array with function handles
- an empty array (default)

`Robust`

Invoke robust fitting option.

- `'off'`
- `'on'`

`Robust` will be removed in a future software release. Use `RobustWgtFun` for robust fitting.

`RobustWgtFun`

Weight function for robust fitting. Can also be a function handle that accepts a normalized residual as input and returns the robust weights as output. If you use a function handle, give a `Tune` constant. See “Robust Options” on page 22-4513.

`Streams`

A single instance of the `RandStream` class, or a cell array of `RandStream` instances. The Streams option is accepted by some functions to govern what stream(s) to use in generating random numbers within the function. If `'UseSubstreams'` is `true`, the Streams value must be a scalar, or must be empty. If `'UseParallel'` is `true` and `'UseSubstreams'` is `false`, then the Streams argument must either be empty, or

its length must match the number of processors used in the computation: equal to the *parpool* size if a *parpool* is open, a scalar otherwise.

`TolBnd`

Parameter bound tolerance. Positive scalar.

`TolFun`

Termination tolerance for the objective function value. Positive scalar.

`TolTypeFun`

Use `TolFun` for absolute or relative objective function tolerances.

- `'abs'`
- `'rel'`

`TolTypeX`

Use `TolX` for absolute or relative parameter tolerances.

- `'abs'`
- `'rel'`

`TolX`

Termination tolerance for the parameters. Positive scalar.

`Tune`

Tuning constant used in robust fitting to normalize the residuals before applying the weight function. The default value depends upon the weight function. This parameter is necessary if you specify the weight function as a function handle. Positive scalar. See "Robust Options" on page 22-4513.

`UseParallel`

Flag indicating whether eligible functions should use capabilities of the Parallel Computing Toolbox (PCT), if the capabilities are available. That is, if the PCT is installed, and a PCT parpool is in effect. Valid values are `false` (the default), for serial computation, and `true`, for parallel computation.

`UseSubstreams`

Flag indicating whether the random number generator in eligible functions should use `Substream` property of the `RandStream` class. `false` (default) or `true`. When `true`, high level iterations within the function will set the `Substream` property to the value of the iteration. This behavior helps to generate reproducible random number streams in parallel and/or serial mode computation.

`WgtFun`

Weight function for robust fitting. Valid only when `Robust` is `'on'`. Can also be a function handle that accepts a normalized residual as input and returns the robust weights as output. See “Robust Options” on page 22-4513.

`WgtFun` will be removed in a future software release. Use `RobustWgtFun` instead.

Examples

Suppose you want to change the default parameter values for the function `evfit`, which fits an extreme value distribution to data. The defaults parameter values are:

```
statset('evfit')
ans =
          Display: 'off'
      MaxFunEvals: []
          MaxIter: []
           TolBnd: []
           TolFun: []
        TolTypeFun: []
              TolX: 1.0000e-06
         TolTypeX: []
          GradObj: []
         Jacobian: []
        DerivStep: []
      FunValCheck: []
           Robust: []
     RobustWgtFun: []
           WgtFun: []
             Tune: []
      UseParallel: []
    UseSubstreams: []
          Streams: []
```

```
        OutputFcn: []
```

The only parameters that `evfit` uses are `Display` and `TolX`. To create an options structure with the value of `TolX` set to `1e-8`, enter:

```
options = statset('TolX',1e-8)
% Pass options to evfit:
mu = 1;
sigma = 1;
data = evrnd(mu,sigma,1,100);

paramhat = evfit(data,[],[],[],options)
```

More About

Robust Options

Weight Function	Equation	Default Tuning Constant
`'andrews'`	`w = (abs(r)<pi) .* sin(r) ./ r`	1.339
`'bisquare'` (default)	`w = (abs(r)<1) .* (1 - r.^2).^2`	4.685
`'cauchy'`	`w = 1 ./ (1 + r.^2)`	2.385
`'fair'`	`w = 1 ./ (1 + abs(r))`	1.400
`'huber'`	`w = 1 ./ max(1, abs(r))`	1.345
`'logistic'`	`w = tanh(r) ./ r`	1.205
`'talwar'`	`w = 1 * (abs(r)<1)`	2.795
`'welsch'`	`w = exp(-(r.^2))`	2.985
`[]`	No robust fitting	—

See Also

`statget`

std

Standard deviation of probability distribution

Syntax

```
s = std(pd)
```

Description

`s = std(pd)` returns the standard deviation s of the probability distribution pd.

Examples

Standard Deviation of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the standard deviation of the fitted distribution.

```
s = std(pd)
```

```
s =
```

```
   8.7202
```

For a normal distribution, the standard deviation is equal to the parameter `sigma`.

Standard Deviation of a Skewed Distribution

Create a Weibull probability distribution object

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Compute the standard deviation of the distribution.

```
s = std(pd)
```

```
s =
    2.3163
```

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`s` — Standard deviation

nonnegative scalar value

Standard deviation of the probability distribution, returned as a nonnegative scalar value.

See Also

`dfittool` | `fitdist` | `makedist`

std

Class: prob.KernelDistribution
Package: prob

Standard deviation of probability distribution object

Syntax

```
s = std(pd)
```

Description

`s = std(pd)` returns the standard deviation s of the probability distribution pd.

Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Fit a probability distribution object to data using `fitdist` or the Distribution Fitting app.

Output Arguments

s — Standard deviation

nonnegative scalar value

Standard deviation of the probability distribution, returned as a nonnegative scalar value.

Examples

Standard Deviation of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Create a probability distribution object by fitting a kernel distribution to the data.

```
pd = fitdist(x,'Kernel')
```

```
pd =

  KernelDistribution

    Kernel = normal
    Bandwidth = 3.61677
    Support = unbounded
```

Compute the standard deviation of the fitted distribution.

```
s = std(pd)
```

```
s =

    9.4069
```

See Also

`dfittool` | `fitdist`

std

Class: ProbDistUnivParam

Return standard deviation of ProbDistUnivParam object

Syntax

```
S = std(PD)
```

Description

`S = std(PD)` returns *S*, the standard deviation of the ProbDistUnivParam object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

S	The standard deviation of the ProbDistUnivParam object *PD*.

See Also

`std`

std

Class: prob.ParametricTruncatableDistribution
Package: prob

Standard deviation of probability distribution object

Syntax

```
s = std(pd)
```

Description

`s = std(pd)` returns the standard deviation s of the probability distribution pd.

Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`.

Output Arguments

s — Standard deviation

nonnegative scalar value

Standard deviation of the probability distribution, returned as a nonnegative scalar value.

Examples

Standard Deviation of a Triangular Distribution

Create a triangular distribution object.

```
pd = makedist('Triangular','a',-3,'b',1,'c',3)
```

```
pd =

  TriangularDistribution

A = -3, B = 1, C = 3
```

Compute the standard deviation of the distribution.

```
s = std(pd)
```

```
s =

    1.2472
```

See Also

`makedist`

std

Class: prob.ToolboxFittableParametricDistribution
Package: prob

Standard deviation of probability distribution object

Syntax

```
s = std(pd)
```

Description

`s = std(pd)` returns the standard deviation s of the probability distribution pd.

Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

s — Standard deviation

nonnegative scalar value

Standard deviation of the probability distribution, returned as a nonnegative scalar value.

Examples

Standard Deviation of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the standard deviation of the fitted distribution.

```
s = std(pd)
```

```
s =

   8.7202
```

For a normal distribution, the standard deviation is equal to the parameter `sigma`.

Standard Deviation of a Skewed Distribution

Create a Weibull probability distribution object

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Compute the standard deviation of the distribution.

```
s = std(pd)
```

```
s =
    2.3163
```

See Also

`dfittool` | `fitdist` | `makedist`

step

Class: GeneralizedLinearModel

Improve generalized linear regression model by adding or removing terms

Syntax

```
mdl1 = step(mdl)
mdl1 = step(mdl,Name,Value)
```

Description

`mdl1 = step(mdl)` returns an improved generalized linear model based on `mdl`, with one predictor added or removed.

`mdl1 = step(mdl,Name,Value)` improves a generalized linear model with additional options specified by one or more Name,Value pair arguments.

Tips

- Use `addTerms` or `removeTerms` to control exactly which terms enter or leave the model.

Input Arguments

`mdl` — Generalized linear model

`GeneralizedLinearModel` object

Generalized linear model representing a least-squares fit of the link of the response to the data, returned as a `GeneralizedLinearModel` object.

For properties and methods of the generalized linear model object, `mdl`, see the `GeneralizedLinearModel` class page.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Criterion'` — Criterion to add or remove terms

`'sse'` (default) | `'aic'` | `'bic'` | `'rsquared'` | `'adjrsquared'`

Criterion to add or remove terms, specified as the comma-separated pair consisting of `'Criterion'` and one of the following:

- `'sse'` — Default for `stepwiselm`. p-value for an F-test of the change in the sum of squared error by adding or removing the term.
- `'aic'` — Change in the value of Akaike information criterion (AIC).
- `'bic'` — Change in the value of Bayesian information criterion (BIC).
- `'rsquared'` — Increase in the value of R^2.
- `'adjrsquared'` — Increase in the value of adjusted R^2.

Example: `'Criterion','bic'`

`'Lower'` — Model specification describing terms that cannot be removed from model

`'constant'` (default)

Model specification describing terms that cannot be removed from the model, specified as the comma-separated pair consisting of `'Lower'` and one of the string options for modelspec naming the model.

Example: `'Lower','linear'`

`'NSteps'` — Number of steps to take

1 (default) | positive integer

Number of steps to take, specified as the comma-separated pair consisting of `'NSteps'` and a positive integer.

Data Types: `single` | `double`

`'PEnter'` — Improvement measure for adding term

scalar value

Improvement measure for adding a term, specified as the comma-separated pair consisting of `'PEnter'` and a scalar value. The default values are below.

Criterion	Default value	Decision
`'Deviance'`	0.05	If the p-value of F or chi-squared statistic is smaller than `PEnter`, add the term to the model.
`'SSE'`	0.05	If the SSE of the model is smaller than `PEnter`, add the term to the model.
`'AIC'`	0	If the change in the AIC of the model is smaller than `PEnter`, add the term to the model.
`'BIC'`	0	If the change in the BIC of the model is smaller than `PEnter`, add the term to the model.
`'Rsquared'`	0.1	If the increase in the R-squared of the model is larger than `PEnter`, add the term to the model.
`'AdjRsquared'`	0	If the increase in the adjusted R-squared of the model is larger than `PEnter`, add the term to the model.

For more information on the criteria, see Criterion name-value pair argument.

Example: `'PEnter',0.075`

`'PRemove'` — Improvement measure for removing term

scalar value

Improvement measure for removing a term, specified as the comma-separated pair consisting of `'PRemove'` and a scalar value.

Criterion	Default value	Decision
'Deviance'	0.10	If the *p*-value of *F* or chi-squared statistic is larger than PRemove, remove the term from the model.
'SSE'	0.10	If the *p*-value of the F statistic is larger than PRemove, remove the term from the model.
'AIC'	0.01	If the change in the AIC of the model is larger than PRemove, remove the term from the model.
'BIC'	0.01	If the change in the BIC of the model is larger than PRemove, remove the term from the model.
'Rsquared'	0.05	If the increase in the R-squared value of the model is smaller than PRemove, remove the term from the model.
'AdjRsquared'	-0.05	If the increase in the adjusted R-squared value of the model is smaller than PRemove, remove the term from the model.

At each step, stepwise algorithm also checks whether any term is redundant (linearly dependent) with other terms in the current model. When any term is linearly dependent with other terms in the current model, it is removed, regardless of the criterion value.

For more information on the criteria, see Criterion name-value pair argument.

Example: 'PRemove',0.05

'Upper' — Model specification describing largest set of terms in fit

'interaction' (default) | string

Model specification describing the largest set of terms in the fit, specified as the comma-separated pair consisting of `'Upper'` and one of the string options for modelspec naming the model.

Example: `'Upper','quadratic'`

`'Verbose'` — Control for display of information

1 (default) | 0 | 2

Control for display of information, specified as the comma-separated pair consisting of `'Verbose'` and one of the following:

- `0` — Suppress all display.
- `1` — Display the action taken at each step.
- `2` — Also display the actions evaluated at each step.

Example: `'Verbose',2`

Output Arguments

`mdl1`

Linear model, the same as `mdl` but with additional terms given in `terms`. You can set `mdl1` equal to `mdl` to overwrite `mdl`.

Examples

Add Predictors One at a Time

Fit a Poisson regression model using random data and a single predictor, then step in other predictors.

Generate artificial data with 20 predictors, using three of the predictors for the responses.

```
rng('default') % for reproducibility
X = randn(100,20);
mu = exp(X(:,[5 10 15])*[.4;.2;.3] + 1);
```

```
y = poissrnd(mu);
```

Construct a generalized linear model using `X(:,1)` as the only predictor.

```
mdl = fitglm(X,y,...
    'y ~ x1','Distribution','poisson')

mdl =

Generalized Linear regression model:
    log(y) ~ 1 + x1
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)      1.1278    0.057487    19.618    1.0904e-85
    x1             0.061287     0.04848    1.2642       0.20617

100 observations, 98 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 1.59, p-value = 0.208
```

Add a variable to the model using `step`.

```
mdl1 = step(mdl)

1. Adding x5, Deviance = 134.2976, Chi2Stat = 50.80176, PValue = 1.021821e-12

mdl1 =

Generalized Linear regression model:
    log(y) ~ 1 + x1 + x5
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat      pValue
    (Intercept)      1.0418    0.062341     16.712      1.07e-62
    x1             0.018803    0.049916    0.37671       0.70639
    x5              0.47881    0.067875     7.0542    1.7357e-12

100 observations, 97 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 52.4, p-value = 4.21e-12
```

Add another variable to the model using `step`.

```
mdl1 = step(mdl1)

2. Adding x15, Deviance = 105.9973, Chi2Stat = 28.30027, PValue = 1.038814e-07

mdl1 =
```

```
Generalized Linear regression model:
    log(y) ~ 1 + x1 + x5 + x15
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat      pValue
    (Intercept)      1.0459      0.0627     16.681    1.7975e-62
    x1             0.026907     0.05003    0.53782        0.5907
    x5               0.3983    0.068376     5.8251    5.7073e-09
    x15              0.28949    0.053992     5.3618    8.2375e-08

100 observations, 96 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 80.7, p-value = 2.18e-17
```

- “Plots to Understand Predictor Effects and How to Modify a Model” on page 10-30

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a linear or generalized linear model based on their statistical significance in explaining the response variable. The method begins with an initial model, specified using `modelspec`, and then compares the explanatory power of incrementally larger and smaller models.

MATLAB uses forward and backward stepwise regression to determine a final model. At each step, the method searches for terms to add to or remove from the model based on the value of the `'Criterion'` argument. The default value of `'Criterion'` is `'sse'`, and in this case, `stepwiselm` uses the p-value of an F-statistic to test models with and without a potential term at each step. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model.

Here is how stepwise proceeds when `'Criterion'` is `'sse'`:

1. Fit the initial model.
2. If any terms not in the model have p-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest p-value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have p-values greater than an exit tolerance (that is, the hypothesis of a zero coefficient can be rejected), remove the one with the largest p-value and go to step 2; otherwise, end.

The default for `stepwiseglm` is `'Deviance'` and it follows a similar procedure for adding or removing terms.

There are several other criteria available, which you can specify using the `'Criterion'` argument. You can use the change in the value of the Akaike information criterion, Bayesian information criterion, R-squared, adjusted R-squared as a criterion to add or remove terms.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method might build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but might not be globally optimal.

Alternatives

Use `stepwiseglm` to select a model from a starting model, continuing until no single step is beneficial.

Use `addTerms` or `removeTerms` to add or remove particular terms.

See Also

`addTerms` | `GeneralizedLinearModel` | `removeTerms` | `stepwiseglm`

More About

- “Generalized Linear Models” on page 10-12

step

Class: LinearModel

Improve linear regression model by adding or removing terms

Syntax

```
mdl1 = step(mdl)
mdl1 = step(mdl,Name,Value)
```

Description

`mdl1 = step(mdl)` returns an improved linear model based on `mdl`, with one predictor added or removed.

Note: You can use `step` only if `mdl.Robust = []`. This holds when you create `mdl` with `fitlm` having the `RobustOpts` name-value pair set to the default `'off'`.

`mdl1 = step(mdl,Name,Value)` improves a linear model with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`mdl`

Linear model, as constructed by `fitlm` or `stepwiselm`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Criterion'` — Criterion for selecting terms to add or remove

`'SSE'` (default)

Criterion for selecting terms to add or remove, specified as the comma-separated pair consisting of `'Criterion'` and one of the following.

Criterion	PEnter	PRemove	Compared Against
`'SSE'`	`0.05`	`< 0.1`	p-value for F test
`'AIC'`	`0`	`< 0.01`	Change in AIC
`'BIC'`	`0`	`< 0.01`	Change in BIC
`'Rsquared'`	`0.1`	`> 0.05`	Increase in R-squared
`'AdjRsquared'`	`0`	`> -0.05`	Increase in adjusted R-squared

Example: `'Criterion','BIC'`

`'Lower'` — Model specification describing terms that cannot be removed from model

`'constant'` (default)

Model specification describing terms that cannot be removed from the model, specified as the comma-separated pair consisting of `'Lower'` and one of the string options for modelspec naming the model.

Example: `'Lower','linear'`

`'NSteps'` — Number of steps to take

1 (default) | positive integer

Number of steps to take, specified as the comma-separated pair consisting of `'NSteps'` and a positive integer.

Data Types: `single` | `double`

`'PEnter'` — Improvement measure for adding term

scalar value

Improvement measure for adding a term, specified as the comma-separated pair consisting of `'PEnter'` and a scalar value. The default values are below.

Criterion	Default value	Decision
`'Deviance'`	0.05	If the p-value of F or chi-squared statistic is smaller

Criterion	Default value	Decision
		than `PEnter`, add the term to the model.
`'SSE'`	0.05	If the SSE of the model is smaller than `PEnter`, add the term to the model.
`'AIC'`	0	If the change in the AIC of the model is smaller than `PEnter`, add the term to the model.
`'BIC'`	0	If the change in the BIC of the model is smaller than `PEnter`, add the term to the model.
`'Rsquared'`	0.1	If the increase in the R-squared of the model is larger than `PEnter`, add the term to the model.
`'AdjRsquared'`	0	If the increase in the adjusted R-squared of the model is larger than `PEnter`, add the term to the model.

For more information on the criteria, see Criterion name-value pair argument.

Example: `'PEnter',0.075`

`'PRemove'` — Improvement measure for removing term

scalar value

Improvement measure for removing a term, specified as the comma-separated pair consisting of `'PRemove'` and a scalar value.

Criterion	Default value	Decision
`'Deviance'`	0.10	If the p-value of F or chi-squared statistic is larger than `PRemove`, remove the term from the model.

Criterion	Default value	Decision
'SSE'	0.10	If the *p*-value of the F statistic is larger than PRemove, remove the term from the model.
'AIC'	0.01	If the change in the AIC of the model is larger than PRemove, remove the term from the model.
'BIC'	0.01	If the change in the BIC of the model is larger than PRemove, remove the term from the model.
'Rsquared'	0.05	If the increase in the R-squared value of the model is smaller than PRemove, remove the term from the model.
'AdjRsquared'	-0.05	If the increase in the adjusted R-squared value of the model is smaller than PRemove, remove the term from the model.

At each step, stepwise algorithm also checks whether any term is redundant (linearly dependent) with other terms in the current model. When any term is linearly dependent with other terms in the current model, it is removed, regardless of the criterion value.

For more information on the criteria, see Criterion name-value pair argument.

Example: 'PRemove',0.05

'Upper' — Model specification describing largest set of terms in fit

'interaction' (default) | string

Model specification describing the largest set of terms in the fit, specified as the comma-separated pair consisting of 'Upper' and one of the string options for modelspec naming the model.

Example: 'Upper','quadratic'

`'Verbose'` — Control for display of information

1 (default) | 0 | 2

Control for display of information, specified as the comma-separated pair consisting of `'Verbose'` and one of the following:

- `0` — Suppress all display.
- `1` — Display the action taken at each step.
- `2` — Also display the actions evaluated at each step.

Example: `'Verbose',2`

Output Arguments

`mdl1`

Linear model. Typically you set `mdl1` equal to `mdl`.

Examples

Modify a Linear Model

Fit a linear model to car data. Use `step` to see if a quadratic model would help the fit quality.

Load `carsmall` data, and make a dataset from weight and model year predictors with MPG response.

```
load carsmall
ds = dataset(MPG,Weight);
ds.Year = ordinal(Model_Year);
```

Make a linear model of `MPG` as a function of `Year` and `Weight`.

```
mdl = fitlm(ds,'MPG ~ Year + Weight')
```

```
mdl =

Linear regression model:
    MPG ~ 1 + Weight + Year

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
```

```
    (Intercept)         40.11        1.5418     26.016    1.2024e-43
    Weight         -0.0066475    0.00042802    -15.531    3.3639e-27
    Year_76            1.9291       0.74761     2.5804      0.011488
    Year_82            7.9093       0.84975     9.3078    7.8681e-15

Number of observations: 94, Error degrees of freedom: 90
Root Mean Squared Error: 2.92
R-squared: 0.873,  Adjusted R-Squared 0.868
F-statistic vs. constant model: 206, p-value = 3.83e-40
```

Use `step` to adjust the model to potentially include full quadratic terms.

```
mdl1 = step(mdl,'upper','quadratic')
```

```
1. Adding Weight^2, FStat = 9.9164, pValue = 0.0022303

mdl1 =

Linear regression model:
    MPG ~ 1 + Weight + Year + Weight^2

Estimated Coefficients:
                   Estimate      SE            tStat      pValue
    (Intercept)        54.206        4.7117     11.505    2.6648e-19
    Weight          -0.016404     0.0031249    -5.2493    1.0283e-06
    Year_76            2.0887       0.71491     2.9215     0.0044137
    Year_82            8.1864       0.81531     10.041    2.6364e-16
    Weight^2       1.5573e-06    4.9454e-07      3.149     0.0022303

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 2.78
R-squared: 0.885,  Adjusted R-Squared 0.88
F-statistic vs. constant model: 172, p-value = 5.52e-41
```

- “Linear Regression Workflow” on page 9-41
- “Change Models” on page 9-35

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a linear or generalized linear model based on their statistical significance in explaining the response variable. The method begins with an initial model, specified using `modelspec`, and then compares the explanatory power of incrementally larger and smaller models.

MATLAB uses forward and backward stepwise regression to determine a final model. At each step, the method searches for terms to add to or remove from the model based on the value of the `'Criterion'` argument. The default value of `'Criterion'` is `'sse'`, and in this case, `stepwiselm` uses the p-value of an F-statistic to test models with and without a potential term at each step. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If

there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model.

Here is how stepwise proceeds when `'Criterion'` is `'sse'`:

1. Fit the initial model.
2. If any terms not in the model have *p*-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest *p*-value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have *p*-values greater than an exit tolerance (that is, the hypothesis of a zero coefficient can be rejected), remove the one with the largest *p*-value and go to step 2; otherwise, end.

The default for `stepwiseglm` is `'Deviance'` and it follows a similar procedure for adding or removing terms.

There are several other criteria available, which you can specify using the `'Criterion'` argument. You can use the change in the value of the Akaike information criterion, Bayesian information criterion, R-squared, adjusted R-squared as a criterion to add or remove terms.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method might build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but might not be globally optimal.

Alternatives

Use `stepwiselm` to select a model from a starting model, continuing until no single step is beneficial.

Use `addTerms` or `removeTerms` to add or remove particular terms.

See Also

`addTerms` | `LinearModel` | `removeTerms` | `stepwiselm`

How To

- “Linear Regression” on page 9-11

stepwise

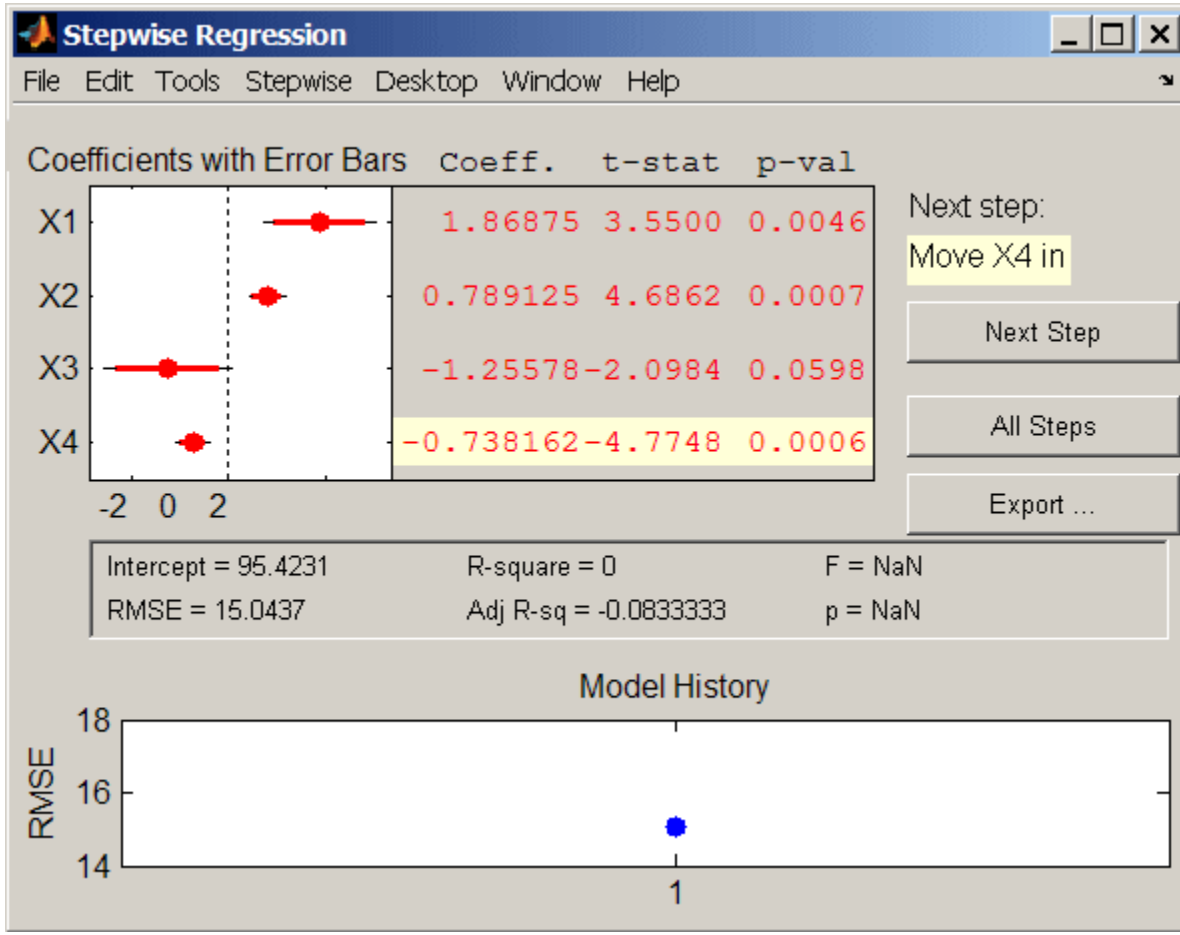
Interactive stepwise regression

Syntax

```
stepwise
stepwise(X,y)
stepwise(X,y,inmodel,penter,premove)
```

Description

`stepwise` uses the sample data in `hald.mat` to display a graphical user interface for performing stepwise regression of the response values in `heat` on the predictive terms in `ingredients`.



The upper left of the interface displays estimates of the coefficients for all potential terms, with horizontal bars indicating 90% (colored) and 95% (grey) confidence intervals. The red color indicates that, initially, the terms are not in the model. Values displayed in the table are those that would result if the terms were added to the model.

The middle portion of the interface displays summary statistics for the entire model. These statistics are updated with each step.

The lower portion of the interface, **Model History**, displays the RMSE for the model. The plot tracks the RMSE from step to step, so you can compare the optimality of

different models. Hover over the blue dots in the history to see which terms were in the model at a particular step. Click on a blue dot in the history to open a copy of the interface initialized with the terms in the model at that step.

Initial models, as well as entrance/exit tolerances for the p-values of F-statistics, are specified using additional input arguments to `stepwise`. Defaults are an initial model with no terms, an entrance tolerance of 0.05, and an exit tolerance of 0.10.

To center and scale the input data (compute z-scores) to improve conditioning of the underlying least-squares problem, select `Scale Inputs` from the **Stepwise** menu.

You proceed through a stepwise regression in one of two ways:

1. Click **Next Step** to select the recommended next step. The recommended next step either adds the most significant term or removes the least significant term. When the regression reaches a local minimum of RMSE, the recommended next step is "Move no terms." You can perform all of the recommended steps at once by clicking **All Steps**.
2. Click a line in the plot or in the table to toggle the state of the corresponding term. Clicking a red line, corresponding to a term not currently in the model, adds the term to the model and changes the line to blue. Clicking a blue line, corresponding to a term currently in the model, removes the term from the model and changes the line to red.

To call `addedvarplot` and produce an added variable plot from the `stepwise` interface, select **Added Variable Plot** from the **Stepwise** menu. A list of terms is displayed. Select the term you want to add, and then click **OK**.

Click **Export** to display a dialog box that allows you to select information from the interface to save to the MATLAB workspace. Check the information you want to export and, optionally, change the names of the workspace variables to be created. Click **OK** to export the information.

`stepwise(X,y)` displays the interface using the p predictive terms in the n-by-p matrix `X` and the response values in the n-by-1 vector `y`. Distinct predictive terms should appear in different columns of `X`.

Note: `stepwise` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`stepwise` treats `NaN` values in either `X` or `y` as missing values, and ignores them.

`stepwise(X,y,inmodel,penter,premove)` additionally specifies the initial model (`inmodel`) and the entrance (`penter`) and exit (`premove`) tolerances for the *p*-values of *F*-statistics. `inmodel` is either a logical vector with length equal to the number of columns of `X`, or a vector of indices, with values ranging from 1 to the number of columns in `X`. The value of `penter` must be less than or equal to the value of `premove`.

More About

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a multilinear model based on their statistical significance in a regression. The method begins with an initial model and then compares the explanatory power of incrementally larger and smaller models. At each step, the *p* value of an *F*-statistic is computed to test models with and without a potential term. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model. The method proceeds as follows:

1. Fit the initial model.
2. If any terms not in the model have *p*-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest *p* value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have *p*-values greater than an exit tolerance (that is, if it is unlikely that the hypothesis of a zero coefficient can be rejected), remove the one with the largest *p* value and go to step 2; otherwise, end.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method may build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but may not be globally optimal.

See Also

`addedvarplot` | `regress` | `stepwisefit`

GeneralizedLinearModel.stepwise

Class: GeneralizedLinearModel

Create generalized linear regression model by stepwise regression

Compatibility

`GeneralizedLinearModel.stepwise` will be removed in a future release. Use `stepwiseglm` instead.

Syntax

```
mdl = GeneralizedLinearModel.stepwise(tbl,modelspec)
mdl = GeneralizedLinearModel.stepwise(X,y,modelspec)
mdl = GeneralizedLinearModel.stepwise(...,modelspec,Name,Value)
```

Description

`mdl = GeneralizedLinearModel.stepwise(tbl,modelspec)` creates a generalized linear model of a table or dataset array `tbl`, using stepwise regression to add or remove predictors. `modelspec` is the starting model for the stepwise procedure.

`mdl = GeneralizedLinearModel.stepwise(X,y,modelspec)` creates a generalized linear model of the responses `y` to a data matrix `X`, using stepwise regression to add or remove predictors.

`mdl = GeneralizedLinearModel.stepwise(...,modelspec,Name,Value)` creates a generalized linear model with additional options specified by one or more Name,Value pair arguments.

Tips

- The generalized linear model `mdl` is a standard linear model unless you specify otherwise with the `Distribution` name-value pair.

- For other methods such as `devianceTest`, or properties of the `GeneralizedLinearModel` object, see `GeneralizedLinearModel`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see "Grouping Variables" on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelspec` — Starting model

string specifying the model | *t*-by-(*p*+1) terms matrix | string of the form `'Y ~ terms'`

Starting model for `stepwiseglm`, specified as one of the following:

- String specifying the type of model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

- *t*-by-(*p*+1) matrix, namely terms matrix, specifying terms to include in model, where *t* is the number of terms and *p* is the number of predictor variables, and plus one is for the response variable.
- String representing a formula in the form
  `'Y ~ terms'`,
  where the `terms` are in "Wilkinson Notation" on page 22-4561.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

'BinomialSize' — Number of trials for binomial distribution

1 (default) | scalar value | vector

Number of trials for binomial distribution, that is the sample size, specified as the comma-separated pair consisting of a scalar value or a vector of the same length as the response. This is the parameter n for the fitted binomial distribution. BinomialSize applies only when the Distribution parameter is 'binomial'.

If BinomialSize is a scalar value, that means all observations have the same number of trials.

As an alternative to BinomialSize, you can specify the response as a two-column vector with counts in column 1 and BinomialSize in column 2.

Data Types: single | double

'CategoricalVars' — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of 'CategoricalVars' and either a cell array of strings of the names of the categorical variables in the table or dataset array tbl, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array tbl, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix X, then the default value of this name-value pair argument is an empty matrix []. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: 'CategoricalVars',[2,3]

Example: 'CategoricalVars',logical([0 1 1 0 0 0])

Data Types: single | double | logical

'Criterion' — Criterion to add or remove terms

'sse' (default) | 'aic' | 'bic' | 'rsquared' | 'adjrsquared'

Criterion to add or remove terms, specified as the comma-separated pair consisting of 'Criterion' and one of the following:

- `'sse'` — Default for `stepwiselm`. p-value for an F-test of the change in the sum of squared error by adding or removing the term.
- `'aic'` — Change in the value of Akaike information criterion (AIC).
- `'bic'` — Change in the value of Bayesian information criterion (BIC).
- `'rsquared'` — Increase in the value of R^2.
- `'adjrsquared'` — Increase in the value of adjusted R^2.

Example: `'Criterion','bic'`

`'DispersionFlag'` — Indicator to compute dispersion parameter

`false` for `'binomial'` and `'poisson'` distributions (default) | `true`

Indicator to compute dispersion parameter for `'binomial'` and `'poisson'` distributions, specified as the comma-separated pair consisting of `'DispersionFlag'` and one of the following.

`true`	Estimate a dispersion parameter when computing standard errors
`false`	Default. Use the theoretical value when computing standard errors

The fitting function always estimates the dispersion for other distributions.

Example: `'DispersionFlag',true`

`'Distribution'` — Distribution of the response variable

`'normal'` (default) | `'binomial'` | `'poisson'` | `'gamma'` | `'inverse gaussian'`

Distribution of the response variable, specified as the comma-separated pair consisting of `'Distribution'` and one of the following.

`'normal'`	Normal distribution
`'binomial'`	Binomial distribution
`'poisson'`	Poisson distribution
`'gamma'`	Gamma distribution
`'inverse gaussian'`	Inverse Gaussian distribution

Example: `'Distribution','gamma'`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Intercept'` — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

`'Link'` — Link function

The canonical link function (default) | scalar value | structure

Link function to use in place of the canonical link function, specified as the comma-separated pair consisting of `'Link'` and one of the following.

Link Function Name	Link Function	Mean (Inverse) Function
`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'probit'`	$f(\mu) = \Phi^{-1}(\mu)$	$\mu = \Phi(Xb)$

Link Function Name	Link Function	Mean (Inverse) Function
`'comploglog'`	$f(\mu) = \log(-\log(1-\mu))$	$\mu = 1 - \exp(-\exp(Xb))$
`'reciprocal'`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`p` (a number)	$f(\mu) = \mu^p$	$\mu = Xb^{1/p}$
`S` (a structure) with three fields. Each field holds a function handle that accepts a vector of inputs and returns a vector of the same size: • `S.Link` — The link function • `S.Inverse` — The inverse link function • `S.Derivative` — The derivative of the link function	$f(\mu)$ = `S.Link`(μ)	μ = `S.Inverse`(Xb)

The link function defines the relationship $f(\mu) = X*b$ between the mean response μ and the linear combination of predictors $X*b$.

For more information on the canonical link functions, see `Definitions`.

Example: `'Link','probit'`

`'Lower'` — Model specification describing terms that cannot be removed from model

`'constant'` (default)

Model specification describing terms that cannot be removed from the model, specified as the comma-separated pair consisting of `'Lower'` and one of the string options for modelspec naming the model.

Example: `'Lower','linear'`

`'Offset'` — Offset variable

[ ] (default) | `vector` | string

Offset variable in the fit, specified as the comma-separated pair consisting of `'Offset'` and a vector or name of a variable with the same length as the response.

`fitglm` and `stepwiseglm` use `Offset` as an additional predictor, with a coefficient value fixed at 1.0. In other words, the formula for fitting is

```
μ ~ Offset + (terms involving real predictors)
```

with the `Offset` predictor having coefficient `1`.

For example, consider a Poisson regression model. Suppose the number of counts is known for theoretical reasons to be proportional to a predictor `A`. By using the log link function and by specifying `log(A)` as an offset, you can force the model to satisfy this theoretical constraint.

Data Types: `single` | `double` | `char`

`'PEnter'` — Improvement measure for adding term

scalar value

Improvement measure for adding a term, specified as the comma-separated pair consisting of `'PEnter'` and a scalar value. The default values are below.

Criterion	Default value	Decision
`'Deviance'`	0.05	If the *p*-value of *F* or chi-squared statistic is smaller than `PEnter`, add the term to the model.
`'SSE'`	0.05	If the SSE of the model is smaller than `PEnter`, add the term to the model.
`'AIC'`	0	If the change in the AIC of the model is smaller than `PEnter`, add the term to the model.
`'BIC'`	0	If the change in the BIC of the model is smaller than `PEnter`, add the term to the model.
`'Rsquared'`	0.1	If the increase in the R-squared of the model is larger than `PEnter`, add the term to the model.

Criterion	Default value	Decision
'AdjRsquared'	0	If the increase in the adjusted R-squared of the model is larger than PEnter, add the term to the model.

For more information on the criteria, see Criterion name-value pair argument.

Example: 'PEnter',0.075

'PredictorVars' — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of 'PredictorVars' and either a cell array of strings of the variable names in the table or dataset array tbl, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in tbl, or the names you specify using the 'VarNames' name-value pair argument.

The default is all variables in X, or all variables in tbl except for ResponseVar.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: 'PredictorVars',[2,3]

Example: 'PredictorVars',logical([0 1 1 0 0 0])

Data Types: single | double | logical | cell

'PRemove' — Improvement measure for removing term

scalar value

Improvement measure for removing a term, specified as the comma-separated pair consisting of 'PRemove' and a scalar value.

Criterion	Default value	Decision
'Deviance'	0.10	If the p-value of F or chi-squared statistic is larger

Criterion	Default value	Decision
		than `PRemove`, remove the term from the model.
`'SSE'`	0.10	If the *p*-value of the F statistic is larger than `PRemove`, remove the term from the model.
`'AIC'`	0.01	If the change in the AIC of the model is larger than `PRemove`, remove the term from the model.
`'BIC'`	0.01	If the change in the BIC of the model is larger than `PRemove`, remove the term from the model.
`'Rsquared'`	0.05	If the increase in the R-squared value of the model is smaller than `PRemove`, remove the term from the model.
`'AdjRsquared'`	-0.05	If the increase in the adjusted R-squared value of the model is smaller than `PRemove`, remove the term from the model.

At each step, stepwise algorithm also checks whether any term is redundant (linearly dependent) with other terms in the current model. When any term is linearly dependent with other terms in the current model, it is removed, regardless of the criterion value.

For more information on the criteria, see Criterion name-value pair argument.

Example: `'PRemove',0.05`

`'ResponseVar'` — Response variable

last column in `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset

array `tbl`, or a logical or numeric index vector indicating which column is the response variable. You typically need to use `'ResponseVar'` when fitting a table or dataset array `tbl`.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

`'Upper'` — Model specification describing largest set of terms in fit

`'interaction'` (default) | string

Model specification describing the largest set of terms in the fit, specified as the comma-separated pair consisting of `'Upper'` and one of the string options for modelspec naming the model.

Example: `'Upper','quadratic'`

`'VarNames'` — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights

`ones(n,1)` (default) | *n*-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an n-by-1 vector of nonnegative scalar values, where n is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Generalized linear model

`GeneralizedLinearModel` object

Generalized linear model representing a least-squares fit of the link of the response to the data, returned as a `GeneralizedLinearModel` object.

For properties and methods of the generalized linear model object, `mdl`, see the `GeneralizedLinearModel` class page.

Definitions

Terms Matrix

A terms matrix is a t-by-(p + 1) matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

  ```
  load hospital
  ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
  ```

```
hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
```

Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

```
T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     1     0     0     0
     0     0     1     0
     0     0     0     1
```

Redefine the dataset array.

```
ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
```

Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

```
T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

  Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes

the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]
```

```
T =

     0     0     0
     1     0     0
     0     1     0
     1     1     0
     0     2     0
```

Fit a linear model.

```
mdl = fitlm(X,MPG,T)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1*x2 + x2^2

Estimated Coefficients:
                   Estimate       SE            tStat      pValue
    (Intercept)         48.906        12.589     3.8847    0.00019665
    x1                 0.54418       0.57125    0.95261       0.34337
    x2                -0.012781     0.0060312    -2.1192      0.036857
    x1:x2          -0.00010892    0.00017925    -0.6076         0.545
    x2^2            9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)
```

```
1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28
```

```
mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *Y* is the response name.
- *terms* contains
  - Variable names
  - `+` means include the next variable
  - `-` means do not include the next variable
  - `:` defines an interaction, a product of terms
  - `*` defines an interaction **and all lower-order terms**
  - `^` raises the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
  - `()` groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

For example,
`'Y ~ A + B + C'` means a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example because `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example because `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Canonical Link Function

The default link function for a generalized linear model is the *canonical link function*.

Canonical Link Functions for Generalized Linear Models

Distribution	Link Function Name	Link Function	Mean (Inverse) Function
`'normal'`	`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'binomial'`	`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'poisson'`	`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'gamma'`	`-1`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`'inverse gaussian'`	`-2`	$f(\mu) = 1/\mu^2$	$\mu = (Xb)^{-1/2}$

Examples

Create a Generalized Linear Model Stepwise

Create response data using just three of 20 predictors, and create a generalized linear model stepwise to see if it uses just the correct predictors.

Create data with 20 predictors, and Poisson response using just three of the predictors, plus a constant.

```
rng('default') % for reproducibility
X = randn(100,20);
mu = exp(X(:,[5 10 15])*[.4;.2;.3] + 1);
y = poissrnd(mu);
```

Fit a generalized linear model using the Poisson distribution.

```
mdl =  stepwiseglm(X,y,...
    'constant','upper','linear','Distribution','poisson')
```

```
1. Adding x5, Deviance = 134.439, Chi2Stat = 52.24814, PValue = 4.891229e-13
2. Adding x15, Deviance = 106.285, Chi2Stat = 28.15393, PValue = 1.1204e-07
3. Adding x10, Deviance = 95.0207, Chi2Stat = 11.2644, PValue = 0.000790094

mdl =


Generalized Linear regression model:
    log(y) ~ 1 + x5 + x10 + x15
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
```

```
    (Intercept)     1.0115     0.064275    15.737    8.4217e-56
    x5             0.39508     0.066665    5.9263    3.0977e-09
    x10            0.18863      0.05534    3.4085     0.0006532
    x15            0.29295     0.053269    5.4995    3.8089e-08

100 observations, 96 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 91.7, p-value = 9.61e-20
```

- “Compare large and small stepwise models” on page 9-124

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a linear or generalized linear model based on their statistical significance in explaining the response variable. The method begins with an initial model, specified using `modelspec`, and then compares the explanatory power of incrementally larger and smaller models.

MATLAB uses forward and backward stepwise regression to determine a final model. At each step, the method searches for terms to add to or remove from the model based on the value of the `'Criterion'` argument. The default value of `'Criterion'` is `'sse'`, and in this case, `stepwiselm` uses the p-value of an F-statistic to test models with and without a potential term at each step. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model.

Here is how stepwise proceeds when `'Criterion'` is `'sse'`:

1. Fit the initial model.
2. If any terms not in the model have p-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest p-value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have p-values greater than an exit tolerance (that is, the hypothesis of a zero coefficient can be rejected), remove the one with the largest p-value and go to step 2; otherwise, end.

The default for `stepwiseglm` is `'Deviance'` and it follows a similar procedure for adding or removing terms.

There are several other criteria available, which you can specify using the `'Criterion'` argument. You can use the change in the value of the Akaike information criterion, Bayesian information criterion, R-squared, adjusted R-squared as a criterion to add or remove terms.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method might build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but might not be globally optimal.

Alternatives

You can also create a stepwise generalized linear model using `stepwiseglm`.

Use `fitglm` to create a model with a fixed specification. Use `step`, `addTerms`, or `removeTerms` to adjust a fitted model.

References

[1] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

[2] Dobson, A. J. *An Introduction to Generalized Linear Models*. New York: Chapman & Hall, 1990.

[3] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

See Also

`fitglm` | `GeneralizedLinearModel` | `stepwiseglm`

More About

- “Generalized Linear Models” on page 10-12

LinearModel.stepwise

Class: LinearModel

Create linear regression model by stepwise regression

Compatibility

`LinearModel.stepwise` will be removed in a future release. Use `stepwiselm` instead.

Syntax

```
mdl = LinearModel.stepwise(tbl,modelspec)
mdl = LinearModel.stepwise(X,y,modelspec)
mdl = LinearModel.stepwise( ___ ,modelspec,Name,Value)
```

Description

`mdl = LinearModel.stepwise(tbl,modelspec)` returns a linear model of a table or dataset array `tbl`, using stepwise regression to add or remove predictors. `modelspec` is the starting model for the stepwise procedure.

`mdl = LinearModel.stepwise(X,y,modelspec)` creates a linear model of the responses `y` to a data matrix `X`, using stepwise regression to add or remove predictors. `modelspec` is the starting model for the stepwise procedure.

`mdl = LinearModel.stepwise( ___ ,modelspec,Name,Value)` creates a linear model for any of the inputs in the previous syntaxes, with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the categorical variables, the smallest or largest set of terms to use in the model, the maximum number of steps to take, or the criterion `LinearModel.stepwise` uses to add or remove terms.

Tips

- You cannot use robust regression with stepwise regression. Check your data for outliers before using `LinearModel.stepwise`.
- For other methods or properties of the `LinearModel` object, see `LinearModel`.

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see "Grouping Variables" on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelspec` — Starting model

string specifying the model | t-by-(p+1) terms matrix | string of the form `'Y ~ terms'`

Starting model for the stepwise regression, specified as one of the following:

- String specifying the type of starting model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

  If you want to specify the smallest or largest set of terms in the model, use the Lower and Upper name-value pair arguments.

- t-by-(p+1) matrix, namely a terms matrix, specifying terms to include in model, where t is the number of terms and p is the number of predictor variables, and plus one is for the response variable.
- String representing a formula in the form
  `'Y ~ terms'`,
  where the `terms` are in "Wilkinson Notation" on page 22-4578.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'CategoricalVars'` — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of `'CategoricalVars'` and either a cell array of strings of the names of the categorical variables in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array `tbl`, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix `X`, then the default value of this name-value pair argument is an empty matrix `[]`. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: `'CategoricalVars',[2,3]`

Example: `'CategoricalVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Criterion'` — Criterion to add or remove terms

`'sse'` (default) | `'aic'` | `'bic'` | `'rsquared'` | `'adjrsquared'`

Criterion to add or remove terms, specified as the comma-separated pair consisting of `'Criterion'` and one of the following:

- `'sse'` — Default for `stepwiselm`. p-value for an F-test of the change in the sum of squared error by adding or removing the term.
- `'aic'` — Change in the value of Akaike information criterion (AIC).
- `'bic'` — Change in the value of Bayesian information criterion (BIC).
- `'rsquared'` — Increase in the value of R^2.

- `'adjrsquared'` — Increase in the value of adjusted R^2.

Example: `'Criterion','bic'`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Intercept'` — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

`'Lower'` — Model specification describing terms that cannot be removed from model

`'constant'` (default)

Model specification describing terms that cannot be removed from the model, specified as the comma-separated pair consisting of `'Lower'` and one of the string options for modelspec naming the model.

Example: `'Lower','linear'`

`'NSteps'` — Number of steps to take

1 (default) | positive integer

Number of steps to take, specified as the comma-separated pair consisting of `'NSteps'` and a positive integer.

Data Types: `single | double`

`'PEnter'` — Improvement measure for adding term

scalar value

Improvement measure for adding a term, specified as the comma-separated pair consisting of `'PEnter'` and a scalar value. The default values are below.

Criterion	Default value	Decision
`'Deviance'`	0.05	If the p-value of F or chi-squared statistic is smaller than `PEnter`, add the term to the model.
`'SSE'`	0.05	If the SSE of the model is smaller than `PEnter`, add the term to the model.
`'AIC'`	0	If the change in the AIC of the model is smaller than `PEnter`, add the term to the model.
`'BIC'`	0	If the change in the BIC of the model is smaller than `PEnter`, add the term to the model.
`'Rsquared'`	0.1	If the increase in the R-squared of the model is larger than `PEnter`, add the term to the model.
`'AdjRsquared'`	0	If the increase in the adjusted R-squared of the model is larger than `PEnter`, add the term to the model.

For more information on the criteria, see Criterion name-value pair argument.

Example: `'PEnter',0.075`

`'PredictorVars'` — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

`'PRemove'` — Improvement measure for removing term

scalar value

Improvement measure for removing a term, specified as the comma-separated pair consisting of `'PRemove'` and a scalar value.

Criterion	Default value	Decision
`'Deviance'`	0.10	If the p-value of F or chi-squared statistic is larger than `PRemove`, remove the term from the model.
`'SSE'`	0.10	If the p-value of the F statistic is larger than `PRemove`, remove the term from the model.
`'AIC'`	0.01	If the change in the AIC of the model is larger than `PRemove`, remove the term from the model.

Criterion	Default value	Decision
'BIC'	0.01	If the change in the BIC of the model is larger than PRemove, remove the term from the model.
'Rsquared'	0.05	If the increase in the R-squared value of the model is smaller than PRemove, remove the term from the model.
'AdjRsquared'	-0.05	If the increase in the adjusted R-squared value of the model is smaller than PRemove, remove the term from the model.

At each step, stepwise algorithm also checks whether any term is redundant (linearly dependent) with other terms in the current model. When any term is linearly dependent with other terms in the current model, it is removed, regardless of the criterion value.

For more information on the criteria, see Criterion name-value pair argument.

Example: 'PRemove',0.05

'ResponseVar' — Response variable

last column in tbl (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of 'ResponseVar' and either a string of the variable name in the table or dataset array tbl, or a logical or numeric index vector indicating which column is the response variable. You typically need to use 'ResponseVar' when fitting a table or dataset array tbl.

For example, you can specify the fourth variable, say yield, as the response out of six variables, in one of the following ways.

Example: 'ResponseVar','yield'

Example: 'ResponseVar',[4]

Example: 'ResponseVar',logical([0 0 0 1 0 0])

Data Types: `single` | `double` | `logical` | `char`

`'Upper'` — Model specification describing largest set of terms in fit

`'interaction'` (default) | string

Model specification describing the largest set of terms in the fit, specified as the comma-separated pair consisting of `'Upper'` and one of the string options for modelspec naming the model.

Example: `'Upper','quadratic'`

`'VarNames'` — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Verbose'` — Control for display of information

`1` (default) | `0` | `2`

Control for display of information, specified as the comma-separated pair consisting of `'Verbose'` and one of the following:

- `0` — Suppress all display.
- `1` — Display the action taken at each step.
- `2` — Also display the actions evaluated at each step.

Example: `'Verbose',2`

`'Weights'` — Observation weights

`ones(n,1)` (default) | *n*-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an n-by-1 vector of nonnegative scalar values, where n is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Linear model
`LinearModel` object

Linear model representing a least-squares fit of the response to the data, returned as a `LinearModel` object.

For the properties and methods of the linear model object, `mdl`, see the `LinearModel` class page.

Definitions

Terms Matrix

A terms matrix is a t-by-(p + 1) matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

  ```
  load hospital
  ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
  ```

```
hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
```

Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

```
T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     1     0     0     0
     0     0     1     0
     0     0     0     1
```

Redefine the dataset array.

```
ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
```

Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

```
T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

  Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes

the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]
```

```
T =

     0     0     0
     1     0     0
     0     1     0
     1     1     0
     0     2     0
```

Fit a linear model.

```
mdl = fitlm(X,MPG,T)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1*x2 + x2^2

Estimated Coefficients:
                   Estimate       SE            tStat      pValue
    (Intercept)         48.906        12.589     3.8847    0.00019665
    x1                 0.54418       0.57125    0.95261       0.34337
    x2                -0.012781     0.0060312    -2.1192      0.036857
    x1:x2           -0.00010892    0.00017925    -0.6076         0.545
    x2^2             9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)
```

```
1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28
```

```
mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *Y* is the response name.
- *terms* contains
  - Variable names
  - `+` means include the next variable
  - `-` means do not include the next variable
  - `:` defines an interaction, a product of terms
  - `*` defines an interaction **and all lower-order terms**
  - `^` raises the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
  - `()` groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

For example,
`'Y ~ A + B + C'` means a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example because `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example because `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Examples

Linear Model from Stepwise Regression

Fit a linear model of the Hald data using stepwise regression.

Load the data.

```
load hald
```

Fit a linear model to the data.

```
 mdl = LinearModel.stepwise(ingredients,heat,'PEnter',0.06)
```

```
1. Adding x4, FStat = 22.7985, pValue = 0.000576232
2. Adding x1, FStat = 108.2239, pValue = 1.105281e-06
3. Adding x2, FStat = 5.0259, pValue = 0.051687
4. Removing x4, FStat = 1.8633, pValue = 0.2054

mdl =


Linear regression model:
    y ~ 1 + x1 + x2

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)     52.577       2.2862    22.998    5.4566e-10
    x1               1.4683      0.1213    12.105    2.6922e-07
    x2              0.66225     0.045855    14.442     5.029e-08


Number of observations: 13, Error degrees of freedom: 10
Root Mean Squared Error: 2.41
R-squared: 0.979,  Adjusted R-Squared 0.974
F-statistic vs. constant model: 230, p-value = 4.41e-09
```

Simultaneously Specify the Variables and Use Formula

Simultaneously identify response and predictor variables and specify the initial model using formula in stepwise regression.

Load sample data.

```
load hospital
```

Fit a linear model to the data.

```
mdl = LinearModel.stepwise(hospital,'Weight~1+Smoker',...
'ResponseVar','Weight','PredictorVars',{'Sex','Age','Smoker'},...
'CategoricalVar',{'Sex','Smoker'})
```

```
1. Adding Sex, FStat = 770.0158, pValue = 6.262758e-48
2. Removing Smoker, FStat = 0.21224, pValue = 0.64605

mdl =

Linear regression model:
    Weight ~ 1 + Sex

Estimated Coefficients:
                   Estimate    SE        tStat     pValue
    (Intercept)    130.47      1.1995    108.77    5.2762e-104
    Sex_Male        50.06      1.7496    28.612     2.2464e-49

Number of observations: 100, Error degrees of freedom: 98
Root Mean Squared Error: 8.73
R-squared: 0.893,  Adjusted R-Squared 0.892
F-statistic vs. constant model: 819, p-value = 2.25e-49
```

The weight of the patients do not seem to differ significantly according to age or the status of smoking, or interaction of these factors with gender. `LinearModel.stepwise` only includes `Sex` in the final linear model.

- “Compare large and small stepwise models” on page 9-124

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a linear or generalized linear model based on their statistical significance in explaining the response variable. The method begins with an initial model, specified using `modelspec`, and then compares the explanatory power of incrementally larger and smaller models.

MATLAB uses forward and backward stepwise regression to determine a final model. At each step, the method searches for terms to add to or remove from the model based on the value of the `'Criterion'` argument. The default value of `'Criterion'` is `'sse'`, and in this case, `stepwiselm` uses the p-value of an F-statistic to test models with and without a potential term at each step. If a term is not currently in the model, the

null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model.

Here is how stepwise proceeds when `'Criterion'` is `'sse'`:

1. Fit the initial model.
2. If any terms not in the model have *p*-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest *p*-value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have *p*-values greater than an exit tolerance (that is, the hypothesis of a zero coefficient can be rejected), remove the one with the largest *p*-value and go to step 2; otherwise, end.

The default for `stepwiseglm` is `'Deviance'` and it follows a similar procedure for adding or removing terms.

There are several other criteria available, which you can specify using the `'Criterion'` argument. You can use the change in the value of the Akaike information criterion, Bayesian information criterion, R-squared, adjusted R-squared as a criterion to add or remove terms.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method might build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but might not be globally optimal.

References

[1] Draper, N. R., and H. Smith. *Applied Regression Analysis*. Hoboken, NJ: Wiley-Interscience, pp. 307–312, 1998.

Alternatives

You can also construct a stepwise linear model using `stepwiselm`.

You can construct a model using `fitlm`, then manually adjust the model using `step`, `addTerms`, or `removeTerms`. Use `fitlm` for robust regression. You cannot use robust regression and stepwise regression together.

See Also

`step` | `LinearModel` | `fitlm`

How To

- "Linear Regression" on page 9-11
- "Stepwise Regression" on page 9-124

stepwiseglm

Create generalized linear regression model by stepwise regression

Syntax

```
mdl = stepwiseglm(tbl,modelspec)
mdl = stepwiseglm(X,y,modelspec)
mdl = stepwiseglm(...,modelspec,Name,Value)
```

Description

`mdl = stepwiseglm(tbl,modelspec)` creates a generalized linear model of a table or dataset array `tbl`, using stepwise regression to add or remove predictors. `modelspec` is the starting model for the stepwise procedure.

`mdl = stepwiseglm(X,y,modelspec)` creates a generalized linear model of the responses `y` to a data matrix `X`, using stepwise regression to add or remove predictors.

`mdl = stepwiseglm(...,modelspec,Name,Value)` creates a generalized linear model with additional options specified by one or more Name,Value pair arguments.

Examples

Generalized Linear Model Using Stepwise Algorithm

Create response data using just three of 20 predictors, and create a generalized linear model using stepwise algorithm to see if it uses just the correct predictors.

Create data with 20 predictors, and Poisson response using just three of the predictors, plus a constant.

```
rng('default') % for reproducibility
X = randn(100,20);
mu = exp(X(:,[5 10 15])*[.4;.2;.3] + 1);
y = poissrnd(mu);
```

Fit a generalized linear model using the Poisson distribution.

```
mdl =  stepwiseglm(X,y,...
    'constant','upper','linear','Distribution','poisson')
```

```
1. Adding x5, Deviance = 134.439, Chi2Stat = 52.24814, PValue = 4.891229e-13
2. Adding x15, Deviance = 106.285, Chi2Stat = 28.15393, PValue = 1.1204e-07
3. Adding x10, Deviance = 95.0207, Chi2Stat = 11.2644, PValue = 0.000790094

mdl =


Generalized Linear regression model:
    log(y) ~ 1 + x5 + x10 + x15
    Distribution = Poisson

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)     1.0115     0.064275    15.737    8.4217e-56
    x5             0.39508     0.066665    5.9263    3.0977e-09
    x10            0.18863      0.05534    3.4085     0.0006532
    x15            0.29295     0.053269    5.4995    3.8089e-08


100 observations, 96 error degrees of freedom
Dispersion: 1
Chi^2-statistic vs. constant model: 91.7, p-value = 9.61e-20
```

The starting model is the constant model. `stepwiseglm` by default uses deviance of the model as the criterion. It first adds `x5` into the model, as the *p*-value for the test statistic, deviance (the differences in the deviances of the two models), is less than the default threshold value 0.05. Then, it adds `x15` because given `x5` is in the model, when `x15` is added, the *p*-value for chi-squared test is smaller than 0.05. It then adds `x10` because given `x5` and `x15` are in the model, when `x10` is added, the *p*-value for the chi-square test statistic is again less than 0.05.

- “Compare large and small stepwise models” on page 9-124

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see “Grouping Variables” on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelspec` — Starting model

string specifying the model | t-by-(p+1) terms matrix | string of the form `'Y ~ terms'`

Starting model for `stepwiseglm`, specified as one of the following:

- String specifying the type of model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.

String	Model Type
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

- *t*-by-(*p*+1) matrix, namely terms matrix, specifying terms to include in model, where *t* is the number of terms and *p* is the number of predictor variables, and plus one is for the response variable.
- String representing a formula in the form
  `'`*`Y ~ terms`*`'`,
  where the `terms` are in "Wilkinson Notation" on page 22-4599.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example:
`'Criterion','aic','Distribution','poisson','Upper','interactions'`
specifies Akaike Information Criterion as the criterion to add or remove variables to the model, Poisson distribution as the distribution of the response variable, and a model with all possible interactions as the largest model to consider as the fit.

`'BinomialSize'` — Number of trials for binomial distribution

1 (default) | scalar value | vector

Number of trials for binomial distribution, that is the sample size, specified as the comma-separated pair consisting of a scalar value or a vector of the same length as the response. This is the parameter `n` for the fitted binomial distribution. `BinomialSize` applies only when the `Distribution` parameter is `'binomial'`.

If `BinomialSize` is a scalar value, that means all observations have the same number of trials.

As an alternative to `BinomialSize`, you can specify the response as a two-column vector with counts in column 1 and `BinomialSize` in column 2.

Data Types: `single` | `double`

`'CategoricalVars'` — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of `'CategoricalVars'` and either a cell array of strings of the names of the categorical variables in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array `tbl`, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix `X`, then the default value of this name-value pair argument is an empty matrix `[]`. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: `'CategoricalVars',[2,3]`

Example: `'CategoricalVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Criterion'` — Criterion to add or remove terms

`'Deviance'` (default) | `'sse'` | `'aic'` | `'bic'` | `'rsquared'` | `'adjrsquared'`

Criterion to add or remove terms, specified as the comma-separated pair consisting of `'Criterion'` and one of the following:

- `'Deviance'` — Default for `stepwiseglm`. p-value for F or chi-squared test of the change in the deviance by adding or removing the term. F-test is for testing a single model. Chi-squared test is for comparing two different models. This option is not valid for `stepwiselm`.
- `'sse'` — Default for `stepwiselm`. p-value for an F-test of the change in the sum of squared error by adding or removing the term.
- `'aic'` — Change in the value of Akaike information criterion (AIC).
- `'bic'` — Change in the value of Bayesian information criterion (BIC).
- `'rsquared'` — Increase in the value of R^2.

- `'adjrsquared'` — Increase in the value of adjusted R^2.

Example: `'Criterion','bic'`

`'DispersionFlag'` — Indicator to compute dispersion parameter

`false` for `'binomial'` and `'poisson'` distributions (default) | `true`

Indicator to compute dispersion parameter for `'binomial'` and `'poisson'` distributions, specified as the comma-separated pair consisting of `'DispersionFlag'` and one of the following.

`true`	Estimate a dispersion parameter when computing standard errors
`false`	Default. Use the theoretical value when computing standard errors

The fitting function always estimates the dispersion for other distributions.

Example: `'DispersionFlag',true`

`'Distribution'` — Distribution of the response variable

`'normal'` (default) | `'binomial'` | `'poisson'` | `'gamma'` | `'inverse gaussian'`

Distribution of the response variable, specified as the comma-separated pair consisting of `'Distribution'` and one of the following.

`'normal'`	Normal distribution
`'binomial'`	Binomial distribution
`'poisson'`	Poisson distribution
`'gamma'`	Gamma distribution
`'inverse gaussian'`	Inverse Gaussian distribution

Example: `'Distribution','gamma'`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Intercept'` — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

`'Link'` — Link function

The canonical link function (default) | scalar value | structure

Link function to use in place of the canonical link function, specified as the comma-separated pair consisting of `'Link'` and one of the following.

Link Function Name	Link Function	Mean (Inverse) Function
`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'probit'`	$f(\mu) = \Phi^{-1}(\mu)$	$\mu = \Phi(Xb)$
`'comploglog'`	$f(\mu) = \log(-\log(1 - \mu))$	$\mu = 1 - \exp(-\exp(Xb))$
`'reciprocal'`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`p` (a number)	$f(\mu) = \mu^p$	$\mu = Xb^{1/p}$
`S` (a structure) with three fields. Each field holds a function handle that accepts a vector of	$f(\mu) =$ `S.Link`(μ)	$\mu =$ `S.Inverse`(Xb)

Link Function Name	Link Function	Mean (Inverse) Function
inputs and returns a vector of the same size: • `S.Link` — The link function • `S.Inverse` — The inverse link function • `S.Derivative` — The derivative of the link function		

The link function defines the relationship $f(\mu) = X*b$ between the mean response μ and the linear combination of predictors $X*b$.

For more information on the canonical link functions, see `Definitions`.

Example: `'Link','probit'`

`'Lower'` — Model specification describing terms that cannot be removed from model
`'constant'` (default)

Model specification describing terms that cannot be removed from the model, specified as the comma-separated pair consisting of `'Lower'` and one of the string options for modelspec naming the model.

Example: `'Lower','linear'`

`'Offset'` — Offset variable
[ ] (default) | `vector` | string

Offset variable in the fit, specified as the comma-separated pair consisting of `'Offset'` and a vector or name of a variable with the same length as the response.

`fitglm` and `stepwiseglm` use `Offset` as an additional predictor, with a coefficient value fixed at 1.0. In other words, the formula for fitting is
`μ ~ Offset + (terms involving real predictors)`

with the `Offset` predictor having coefficient `1`.

For example, consider a Poisson regression model. Suppose the number of counts is known for theoretical reasons to be proportional to a predictor `A`. By using the log link

function and by specifying `log(A)` as an offset, you can force the model to satisfy this theoretical constraint.

Data Types: `single` | `double` | `char`

`'PEnter'` — Improvement measure for adding term

scalar value

Improvement measure for adding a term, specified as the comma-separated pair consisting of `'PEnter'` and a scalar value. The default values are below.

Criterion	Default value	Decision
`'Deviance'`	0.05	If the p-value of F or chi-squared statistic is smaller than `PEnter`, add the term to the model.
`'SSE'`	0.05	If the SSE of the model is smaller than `PEnter`, add the term to the model.
`'AIC'`	0	If the change in the AIC of the model is smaller than `PEnter`, add the term to the model.
`'BIC'`	0	If the change in the BIC of the model is smaller than `PEnter`, add the term to the model.
`'Rsquared'`	0.1	If the increase in the R-squared of the model is larger than `PEnter`, add the term to the model.
`'AdjRsquared'`	0	If the increase in the adjusted R-squared of the model is larger than `PEnter`, add the term to the model.

For more information on the criteria, see Criterion name-value pair argument.

Example: `'PEnter',0.075`

'PredictorVars' — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of 'PredictorVars' and either a cell array of strings of the variable names in the table or dataset array tbl, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in tbl, or the names you specify using the 'VarNames' name-value pair argument.

The default is all variables in X, or all variables in tbl except for ResponseVar.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: 'PredictorVars',[2,3]

Example: 'PredictorVars',logical([0 1 1 0 0 0])

Data Types: single | double | logical | cell

'PRemove' — Improvement measure for removing term

scalar value

Improvement measure for removing a term, specified as the comma-separated pair consisting of 'PRemove' and a scalar value.

Criterion	Default value	Decision
'Deviance'	0.10	If the p-value of F or chi-squared statistic is larger than PRemove, remove the term from the model.
'SSE'	0.10	If the p-value of the F statistic is larger than PRemove, remove the term from the model.
'AIC'	0.01	If the change in the AIC of the model is larger than PRemove, remove the term from the model.

Criterion	Default value	Decision
'BIC'	0.01	If the change in the BIC of the model is larger than PRemove, remove the term from the model.
'Rsquared'	0.05	If the increase in the R-squared value of the model is smaller than PRemove, remove the term from the model.
'AdjRsquared'	-0.05	If the increase in the adjusted R-squared value of the model is smaller than PRemove, remove the term from the model.

At each step, stepwise algorithm also checks whether any term is redundant (linearly dependent) with other terms in the current model. When any term is linearly dependent with other terms in the current model, it is removed, regardless of the criterion value.

For more information on the criteria, see Criterion name-value pair argument.

Example: 'PRemove',0.05

'ResponseVar' — Response variable

last column in tbl (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of 'ResponseVar' and either a string of the variable name in the table or dataset array tbl, or a logical or numeric index vector indicating which column is the response variable. You typically need to use 'ResponseVar' when fitting a table or dataset array tbl.

For example, you can specify the fourth variable, say yield, as the response out of six variables, in one of the following ways.

Example: 'ResponseVar','yield'

Example: 'ResponseVar',[4]

Example: 'ResponseVar',logical([0 0 0 1 0 0])

Data Types: `single` | `double` | `logical` | `char`

`'Upper'` — Model specification describing largest set of terms in fit

`'interaction'` (default) | string

Model specification describing the largest set of terms in the fit, specified as the comma-separated pair consisting of `'Upper'` and one of the string options for modelspec naming the model.

Example: `'Upper','quadratic'`

`'VarNames'` — Names of variables in fit

`{'x1','x2',...,'xn','y'}` (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of `'VarNames'` and a cell array of strings including the names for the columns of `X` first, and the name for the response variable `y` last.

`'VarNames'` is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: `'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}`

Data Types: `cell`

`'Weights'` — Observation weights

`ones(n,1)` (default) | n-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and an n-by-1 vector of nonnegative scalar values, where n is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Generalized linear model

`GeneralizedLinearModel` object

Generalized linear model representing a least-squares fit of the link of the response to the data, returned as a `GeneralizedLinearModel` object.

For properties and methods of the generalized linear model object, `mdl`, see the `GeneralizedLinearModel` class page.

Alternatives

Use `fitglm` to create a model with a fixed specification. Use `step`, `addTerms`, or `removeTerms` to adjust a fitted model.

More About

Terms Matrix

A terms matrix is a t-by-$(p + 1)$ matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

  ```
  load hospital
  ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
  hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
  ```

  Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array,

so there must be a column of 0s for the response variable in the second column of the terms matrix.

```
T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     1     0     0     0
     0     0     1     0
     0     0     0     1
```

Redefine the dataset array.

```
ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
```

Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

```
T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

  Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

  ```
  T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]
  ```

```
T =

     0     0     0
     1     0     0
     0     1     0
     1     1     0
     0     2     0
```

Fit a linear model.

```
mdl = fitlm(X,MPG,T)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1*x2 + x2^2

Estimated Coefficients:
                   Estimate       SE            tStat      pValue
    (Intercept)         48.906        12.589     3.8847    0.00019665
    x1                0.54418       0.57125    0.95261       0.34337
    x2              -0.012781     0.0060312    -2.1192      0.036857
    x1:x2          -0.00010892    0.00017925    -0.6076         0.545
    x2^2            9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)
```

```
1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
```

```
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *`Y`* is the response name.
- *`terms`* contains
  - Variable names
  - `+` means include the next variable
  - `-` means do not include the next variable
  - `:` defines an interaction, a product of terms
  - `*` defines an interaction **and all lower-order terms**
  - `^` raises the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
  - `()` groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

For example,
`'Y ~ A + B + C'` means a three-variable linear model with intercept.

`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example because `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example because `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Canonical Function

The default link function for a generalized linear model is the *canonical link function*.

Canonical Link Functions for Generalized Linear Models

Distribution	Link Function Name	Link Function	Mean (Inverse) Function
`'normal'`	`'identity'`	$f(\mu) = \mu$	$\mu = Xb$
`'binomial'`	`'logit'`	$f(\mu) = \log(\mu/(1-\mu))$	$\mu = \exp(Xb) / (1 + \exp(Xb))$
`'poisson'`	`'log'`	$f(\mu) = \log(\mu)$	$\mu = \exp(Xb)$
`'gamma'`	`-1`	$f(\mu) = 1/\mu$	$\mu = 1/(Xb)$
`'inverse gaussian'`	`-2`	$f(\mu) = 1/\mu^2$	$\mu = (Xb)^{-1/2}$

Tips

- The generalized linear model `mdl` is a standard linear model unless you specify otherwise with the `Distribution` name-value pair.
- For other methods such as `devianceTest`, or properties of the `GeneralizedLinearModel` object, see `GeneralizedLinearModel`.

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a linear or generalized linear model based on their statistical significance in explaining the response variable. The method begins with an initial model, specified using `modelspec`, and then compares the explanatory power of incrementally larger and smaller models.

MATLAB uses forward and backward stepwise regression to determine a final model. At each step, the method searches for terms to add to or remove from the model based on the value of the `'Criterion'` argument. The default value of `'Criterion'` is `'sse'`, and in this case, `stepwiselm` uses the p-value of an F-statistic to test models with and without a potential term at each step. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model.

Here is how stepwise proceeds when `'Criterion'` is `'sse'`:

1. Fit the initial model.
2. If any terms not in the model have p-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest p-value and repeat this step; otherwise, go to step 3.

3 If any terms in the model have *p*-values greater than an exit tolerance (that is, the hypothesis of a zero coefficient can be rejected), remove the one with the largest *p*-value and go to step 2; otherwise, end.

The default for `stepwiseglm` is `'Deviance'` and it follows a similar procedure for adding or removing terms.

There are several other criteria available, which you can specify using the `'Criterion'` argument. You can use the change in the value of the Akaike information criterion, Bayesian information criterion, R-squared, adjusted R-squared as a criterion to add or remove terms.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method might build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but might not be globally optimal.

- "Generalized Linear Models" on page 10-12

References

[1] Collett, D. *Modeling Binary Data*. New York: Chapman & Hall, 2002.

[2] Dobson, A. J. *An Introduction to Generalized Linear Models*. New York: Chapman & Hall, 1990.

[3] McCullagh, P., and J. A. Nelder. *Generalized Linear Models*. New York: Chapman & Hall, 1990.

See Also

`fitglm` | `GeneralizedLinearModel`

stepwiselm

Create linear regression model using stepwise regression

Syntax

```
mdl = stepwiselm(tbl,modelspec)
mdl = stepwiselm(X,y,modelspec)
mdl = stepwiselm(___,Name,Value)
```

Description

`mdl = stepwiselm(tbl,modelspec)` returns a linear model for the variables in the table or dataset array `tbl` using stepwise regression to add or remove predictors. `stepwiselm` uses forward and backward stepwise regression to determine a final model. At each step, the function searches for terms to add to or remove from the model based on the value of the `'Criterion'` argument. `modelspec` is the starting model for the stepwise procedure.

`mdl = stepwiselm(X,y,modelspec)` creates a linear model of the responses `y` to the predictor variables in the data matrix `X`, using stepwise regression to add or remove predictors. `modelspec` is the starting model for the stepwise procedure.

`mdl = stepwiselm(___,Name,Value)` creates a linear model for any of the inputs in the previous syntaxes, with additional options specified by one or more Name,Value pair arguments.

For example, you can specify the categorical variables, the smallest or largest set of terms to use in the model, the maximum number of steps to take, or the criterion `stepwiselm` uses to add or remove terms.

Examples

Linear Model Using Stepwise Regression

Load the sample data.

```
load hald
```

`hald` contains hardening data for 13 different concrete compositions. `heat` is the heat of hardening after 180 days. `ingredients` is the percentage of each different ingredient in the cement sample.

Fit a linear model to the data. Set the criterion value to enter the model as 0.06.

```
 mdl = stepwiselm(ingredients,heat,'PEnter',0.06)
```

```
1. Adding x4, FStat = 22.7985, pValue = 0.000576232
2. Adding x1, FStat = 108.2239, pValue = 1.105281e-06
3. Adding x2, FStat = 5.0259, pValue = 0.051687
4. Removing x4, FStat = 1.8633, pValue = 0.2054

mdl =


Linear regression model:
    y ~ 1 + x1 + x2

Estimated Coefficients:
                   Estimate    SE          tStat     pValue
    (Intercept)     52.577       2.2862    22.998    5.4566e-10
    x1               1.4683      0.1213    12.105    2.6922e-07
    x2              0.66225     0.045855    14.442     5.029e-08


Number of observations: 13, Error degrees of freedom: 10
Root Mean Squared Error: 2.41
R-squared: 0.979,  Adjusted R-Squared 0.974
F-statistic vs. constant model: 230, p-value = 4.41e-09
```

By default, the starting model is the constant model. `stepwiselm` performs forward selection and `x4`, `x1`, and `x2`, respectively, as the corresponding *p*-values are less than the `PEnter` value of 0.06. `stepwiselm` later uses backward elimination and eliminates `x4` from the model. Because, given that `x2` is in the model, the *p*-value of `x4` is higher than the default value of `PRemove`, 0.1.

Specify Model Using Formula and Specify Variables

Perform stepwise regression with variables in a dataset array. Specify the starting model using formula, and identify the response and predictor variables with optional arguments.

Load the sample data.

```
load hospital
```

The hospital dataset array includes the gender, age, weight, and smoking status of patients.

Fit a linear model with a starting model of a constant term and `Smoker` as the predictor variable. Specify the response variable, `Weight`, and categorical predictor variables, `Sex`, `Age`, and `Smoker`.

```
mdl = stepwiselm(hospital,'Weight~1+Smoker',...
'ResponseVar','Weight','PredictorVars',{'Sex','Age','Smoker'},...
'CategoricalVar',{'Sex','Smoker'})
```

```
1. Adding Sex, FStat = 770.0158, pValue = 6.262758e-48
2. Removing Smoker, FStat = 0.21224, pValue = 0.64605

mdl =

Linear regression model:
    Weight ~ 1 + Sex

Estimated Coefficients:
                   Estimate    SE        tStat     pValue
    (Intercept)    130.47      1.1995    108.77    5.2762e-104
    Sex_Male        50.06      1.7496    28.612     2.2464e-49

Number of observations: 100, Error degrees of freedom: 98
Root Mean Squared Error: 8.73
R-squared: 0.893,  Adjusted R-Squared 0.892
F-statistic vs. constant model: 819, p-value = 2.25e-49
```

At each step, `stepwiselm` searches for terms to add and remove. At first step, stepwise algorithm adds `Sex` to the model with a p-value of 6.26e-48. Then, removes Smoker from the model, since given `Sex` in the model, the variable `Smoker` becomes redundant. `stepwiselm` only includes `Sex` in the final linear model. The weight of the patients do not seem to differ significantly according to age or the status of smoking.

- “Compare large and small stepwise models” on page 9-124
- “Linear Regression” on page 9-11

Input Arguments

`tbl` — Input data

table | dataset array

Input data, specified as a table or dataset array. When modelspec is a `formula`, it specifies the variables to be used as the predictors and response. Otherwise, if you do not specify the predictor and response variables, the last variable is the response variable and the others are the predictor variables by default.

Predictor variables can be numeric, or any grouping variable type, such as logical or categorical (see "Grouping Variables" on page 2-52). The response must be numeric or logical.

To set a different column as the response variable, use the ResponseVar name-value pair argument. To use a subset of the columns as predictors, use the PredictorVars name-value pair argument.

Data Types: `single` | `double` | `logical`

`X` — Predictor variables

matrix

Predictor variables, specified as an n-by-p matrix, where n is the number of observations and p is the number of predictor variables. Each column of `X` represents one variable, and each row represents one observation.

By default, there is a constant term in the model, unless you explicitly remove it, so do not include a column of 1s in `X`.

Data Types: `single` | `double` | `logical`

`y` — Response variable

vector

Response variable, specified as an n-by-1 vector, where n is the number of observations. Each entry in `y` is the response for the corresponding row of `X`.

Data Types: `single` | `double`

`modelspec` — Starting model

string specifying the model | t-by-(p+1) terms matrix | string of the form `'Y ~ terms'`

Starting model for the stepwise regression, specified as one of the following:

- String specifying the type of starting model.

String	Model Type
`'constant'`	Model contains only a constant (intercept) term.
`'linear'`	Model contains an intercept and linear terms for each predictor.
`'interactions'`	Model contains an intercept, linear terms, and all products of pairs of distinct predictors (no squared terms).
`'purequadratic'`	Model contains an intercept, linear terms, and squared terms.
`'quadratic'`	Model contains an intercept, linear terms, interactions, and squared terms.
`'poly`*`ijk`*`'`	Model is a polynomial with all terms up to degree *`i`* in the first predictor, degree *`j`* in the second predictor, etc. Use numerals `0` through `9`. For example, `'poly2111'` has a constant plus all linear and product terms, and also contains terms with predictor 1 squared.

  If you want to specify the smallest or largest set of terms in the model, use the Lower and Upper name-value pair arguments.

- *t*-by-(*p*+1) matrix, namely a terms matrix, specifying terms to include in model, where *t* is the number of terms and *p* is the number of predictor variables, and plus one is for the response variable.
- String representing a formula in the form
  `'Y ~ terms'`,
  where the `terms` are in "Wilkinson Notation" on page 22-4617.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Criterion','aic','Upper',interactions,'Verbose',1` instructs `stepwiselm` to use the Akaike information criterion, display the action it takes at each step, and include at most the interaction terms in the model.

`'CategoricalVars'` — Categorical variables

cell array of strings | logical or numeric index vector

Categorical variables in the fit, specified as the comma-separated pair consisting of `'CategoricalVars'` and either a cell array of strings of the names of the categorical variables in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are categorical.

- If data is in a table or dataset array `tbl`, then the default is to treat all categorical or logical variables, character arrays, or cell arrays of strings as categorical variables.
- If data is in matrix `X`, then the default value of this name-value pair argument is an empty matrix `[]`. That is, no variable is categorical unless you specify it.

For example, you can specify the observations 2 and 3 out of 6 as categorical using either of the following examples.

Example: `'CategoricalVars',[2,3]`

Example: `'CategoricalVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Criterion'` — Criterion to add or remove terms

`'sse'` (default) | `'aic'` | `'bic'` | `'rsquared'` | `'adjrsquared'`

Criterion to add or remove terms, specified as the comma-separated pair consisting of `'Criterion'` and one of the following:

- `'sse'` — Default for `stepwiselm`. p-value for an F-test of the change in the sum of squared error by adding or removing the term.
- `'aic'` — Change in the value of Akaike information criterion (AIC).
- `'bic'` — Change in the value of Bayesian information criterion (BIC).
- `'rsquared'` — Increase in the value of R^2.
- `'adjrsquared'` — Increase in the value of adjusted R^2.

Example: `'Criterion','bic'`

`'Exclude'` — Observations to exclude

logical or numeric index vector

Observations to exclude from the fit, specified as the comma-separated pair consisting of `'Exclude'` and a logical or numeric index vector indicating which observations to exclude from the fit.

For example, you can exclude observations 2 and 3 out of 6 using either of the following examples.

Example: `'Exclude',[2,3]`

Example: `'Exclude',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical`

`'Intercept'` — Indicator for constant term

`true` (default) | `false`

Indicator the for constant term (intercept) in the fit, specified as the comma-separated pair consisting of `'Intercept'` and either `true` to include or `false` to remove the constant term from the model.

Use `'Intercept'` only when specifying the model using a string, not a formula or matrix.

Example: `'Intercept',false`

`'Lower'` — Model specification describing terms that cannot be removed from model

`'constant'` (default)

Model specification describing terms that cannot be removed from the model, specified as the comma-separated pair consisting of `'Lower'` and one of the string options for modelspec naming the model.

Example: `'Lower','linear'`

`'NSteps'` — Number of steps to take

1 (default) | positive integer

Number of steps to take, specified as the comma-separated pair consisting of `'NSteps'` and a positive integer.

Data Types: `single` | `double`

`'PEnter'` — Improvement measure for adding term

scalar value

Improvement measure for adding a term, specified as the comma-separated pair consisting of `'PEnter'` and a scalar value. The default values are below.

Criterion	Default value	Decision
`'Deviance'`	0.05	If the p-value of F or chi-squared statistic is smaller than `PEnter`, add the term to the model.
`'SSE'`	0.05	If the SSE of the model is smaller than `PEnter`, add the term to the model.
`'AIC'`	0	If the change in the AIC of the model is smaller than `PEnter`, add the term to the model.
`'BIC'`	0	If the change in the BIC of the model is smaller than `PEnter`, add the term to the model.
`'Rsquared'`	0.1	If the increase in the R-squared of the model is larger than `PEnter`, add the term to the model.
`'AdjRsquared'`	0	If the increase in the adjusted R-squared of the model is larger than `PEnter`, add the term to the model.

For more information on the criteria, see Criterion name-value pair argument.

Example: `'PEnter',0.075`

`'PredictorVars'` — Predictor variables

cell array of strings | logical or numeric index vector

Predictor variables to use in the fit, specified as the comma-separated pair consisting of `'PredictorVars'` and either a cell array of strings of the variable names in the table or dataset array `tbl`, or a logical or numeric index vector indicating which columns are predictor variables.

The strings should be among the names in `tbl`, or the names you specify using the `'VarNames'` name-value pair argument.

The default is all variables in `X`, or all variables in `tbl` except for `ResponseVar`.

For example, you can specify the second and third variables as the predictor variables using either of the following examples.

Example: `'PredictorVars',[2,3]`

Example: `'PredictorVars',logical([0 1 1 0 0 0])`

Data Types: `single` | `double` | `logical` | `cell`

`'PRemove'` — Improvement measure for removing term
scalar value

Improvement measure for removing a term, specified as the comma-separated pair consisting of `'PRemove'` and a scalar value.

Criterion	Default value	Decision
`'Deviance'`	0.10	If the p-value of F or chi-squared statistic is larger than `PRemove`, remove the term from the model.
`'SSE'`	0.10	If the p-value of the F statistic is larger than `PRemove`, remove the term from the model.
`'AIC'`	0.01	If the change in the AIC of the model is larger than `PRemove`, remove the term from the model.
`'BIC'`	0.01	If the change in the BIC of the model is larger than

Criterion	Default value	Decision
		`PRemove`, remove the term from the model.
`'Rsquared'`	0.05	If the increase in the R-squared value of the model is smaller than `PRemove`, remove the term from the model.
`'AdjRsquared'`	-0.05	If the increase in the adjusted R-squared value of the model is smaller than `PRemove`, remove the term from the model.

At each step, stepwise algorithm also checks whether any term is redundant (linearly dependent) with other terms in the current model. When any term is linearly dependent with other terms in the current model, it is removed, regardless of the criterion value.

For more information on the criteria, see Criterion name-value pair argument.

Example: `'PRemove',0.05`

`'ResponseVar'` — Response variable

last column in `tbl` (default) | string for variable name | logical or numeric index vector

Response variable to use in the fit, specified as the comma-separated pair consisting of `'ResponseVar'` and either a string of the variable name in the table or dataset array `tbl`, or a logical or numeric index vector indicating which column is the response variable. You typically need to use `'ResponseVar'` when fitting a table or dataset array `tbl`.

For example, you can specify the fourth variable, say `yield`, as the response out of six variables, in one of the following ways.

Example: `'ResponseVar','yield'`

Example: `'ResponseVar',[4]`

Example: `'ResponseVar',logical([0 0 0 1 0 0])`

Data Types: `single` | `double` | `logical` | `char`

'Upper' — Model specification describing largest set of terms in fit

'interaction' (default) | string

Model specification describing the largest set of terms in the fit, specified as the comma-separated pair consisting of 'Upper' and one of the string options for modelspec naming the model.

Example: 'Upper','quadratic'

'VarNames' — Names of variables in fit

{'x1','x2',...,'xn','y'} (default) | cell array of strings

Names of variables in fit, specified as the comma-separated pair consisting of 'VarNames' and a cell array of strings including the names for the columns of X first, and the name for the response variable y last.

'VarNames' is not applicable to variables in a table or dataset array, because those variables already have names.

For example, if in your data, horsepower, acceleration, and model year of the cars are the predictor variables, and miles per gallon (MPG) is the response variable, then you can name the variables as follows.

Example: 'VarNames',{'Horsepower','Acceleration','Model_Year','MPG'}

Data Types: cell

'Verbose' — Control for display of information

1 (default) | 0 | 2

Control for display of information, specified as the comma-separated pair consisting of 'Verbose' and one of the following:

- 0 — Suppress all display.
- 1 — Display the action taken at each step.
- 2 — Also display the actions evaluated at each step.

Example: 'Verbose',2

'Weights' — Observation weights

ones(n,1) (default) | n-by-1 vector of nonnegative scalar values

Observation weights, specified as the comma-separated pair consisting of 'Weights' and an n-by-1 vector of nonnegative scalar values, where n is the number of observations.

Data Types: `single` | `double`

Output Arguments

`mdl` — Linear model

`LinearModel` object

Linear model representing a least-squares fit of the response to the data, returned as a `LinearModel` object.

For the properties and methods of the linear model object, `mdl`, see the `LinearModel` class page.

Alternative Functionality

You can construct a model using `fitlm`, and then manually adjust the model using `step`, `addTerms`, or `removeTerms`.

More About

Terms Matrix

A terms matrix is a t-by-(p + 1) matrix specifying terms in a model, where t is the number of terms, p is the number of predictor variables, and plus one is for the response variable.

The value of `T(i,j)` is the exponent of variable `j` in term `i`. Suppose there are three predictor variables `A`, `B`, and `C`:

```
[0 0 0 0] % Constant term or intercept
[0 1 0 0] % B; equivalently, A^0 * B^1 * C^0
[1 0 1 0] % A*C
[2 0 0 0] % A^2
[0 1 2 0] % B*(C^2)
```

The `0` at the end of each term represents the response variable. In general,

- If you have the variables in a table or dataset array, then `0` must represent the response variable depending on the position of the response variable. The following example illustrates this.

  Load the sample data and define the dataset array.

```
load hospital
ds = dataset(hospital.Sex,hospital.BloodPressure(:,1),hospital.Age,...
hospital.Smoker,'VarNames',{'Sex','BloodPressure','Age','Smoker'});
```

Represent the linear model `'BloodPressure ~ 1 + Sex + Age + Smoker'` in a terms matrix. The response variable is in the second column of the dataset array, so there must be a column of 0s for the response variable in the second column of the terms matrix.

```
T = [0 0 0 0;1 0 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     1     0     0     0
     0     0     1     0
     0     0     0     1
```

Redefine the dataset array.

```
ds = dataset(hospital.BloodPressure(:,1),hospital.Sex,hospital.Age,...
hospital.Smoker,'VarNames',{'BloodPressure','Sex','Age','Smoker'});
```

Now, the response variable is the first term in the dataset array. Specify the same linear model, `'BloodPressure ~ 1 + Sex + Age + Smoker'`, using a terms matrix.

```
T = [0 0 0 0;0 1 0 0;0 0 1 0;0 0 0 1]
```

```
T =

     0     0     0     0
     0     1     0     0
     0     0     1     0
     0     0     0     1
```

- If you have the predictor and response variables in a matrix and column vector, then you must include `0` for the response variable at the end of each term. The following example illustrates this.

  Load the sample data and define the matrix of predictors.

  ```
  load carsmall
  X = [Acceleration,Weight];
  ```

Specify the model `'MPG ~ Acceleration + Weight + Acceleration:Weight + Weight^2'` using a term matrix and fit the model to the data. This model includes the main effect and two-way interaction terms for the variables, `Acceleration` and `Weight`, and a second-order term for the variable, `Weight`.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0;0 2 0]
```

```
T =

     0     0     0
     1     0     0
     0     1     0
     1     1     0
     0     2     0
```

Fit a linear model.

```
mdl = fitlm(X,MPG,T)
```

```
mdl =

Linear regression model:
    y ~ 1 + x1*x2 + x2^2

Estimated Coefficients:
                   Estimate       SE            tStat      pValue
    (Intercept)          48.906        12.589     3.8847    0.00019665
    x1                 0.54418       0.57125    0.95261       0.34337
    x2                -0.012781     0.0060312    -2.1192      0.036857
    x1:x2           -0.00010892    0.00017925    -0.6076         0.545
    x2^2             9.7518e-07    7.5389e-07     1.2935       0.19917

Number of observations: 94, Error degrees of freedom: 89
Root Mean Squared Error: 4.1
R-squared: 0.751,  Adjusted R-Squared 0.739
F-statistic vs. constant model: 67, p-value = 4.99e-26
```

Only the intercept and `x2` term, which correspond to the `Weight` variable, are significant at the 5% significance level.

Now, perform a stepwise regression with a constant model as the starting model and a linear model with interactions as the upper model.

```
T = [0 0 0;1 0 0;0 1 0;1 1 0];
mdl = stepwiselm(X,MPG,[0 0 0],'upper',T)

1. Adding x2, FStat = 259.3087, pValue = 1.643351e-28

mdl =

Linear regression model:
    y ~ 1 + x2

Estimated Coefficients:
                   Estimate      SE           tStat      pValue
    (Intercept)        49.238       1.6411     30.002    2.7015e-49
    x2             -0.0086119    0.0005348    -16.103    1.6434e-28

Number of observations: 94, Error degrees of freedom: 92
Root Mean Squared Error: 4.13
R-squared: 0.738,  Adjusted R-Squared 0.735
F-statistic vs. constant model: 259, p-value = 1.64e-28
```

The results of the stepwise regression are consistent with the results of `fitlm` in the previous step.

Formula

A formula for model specification is a string of the form `'Y ~ terms'`

where

- *Y* is the response name.
- *terms* contains
  - Variable names
  - `+` means include the next variable
  - `-` means do not include the next variable
  - `:` defines an interaction, a product of terms
  - `*` defines an interaction **and all lower-order terms**
  - `^` raises the predictor to a power, exactly as in `*` repeated, so `^` includes lower order terms as well
  - `()` groups terms

Note: Formulas include a constant (intercept) term by default. To exclude a constant term from the model, include `-1` in the formula.

For example,
`'Y ~ A + B + C'` means a three-variable linear model with intercept.
`'Y ~ A + B + C - 1'` is a three-variable linear model without intercept.
`'Y ~ A + B + C + B^2'` is a three-variable model with intercept and a `B^2` term.
`'Y ~ A + B^2 + C'` is the same as the previous example because `B^2` includes a `B` term.
`'Y ~ A + B + C + A:B'` includes an `A*B` term.
`'Y ~ A*B + C'` is the same as the previous example because `A*B = A + B + A:B`.
`'Y ~ A*B*C - A:B:C'` has all interactions among `A`, `B`, and `C`, except the three-way interaction.
`'Y ~ A*(B + C + D)'` has all linear terms, plus products of `A` with each of the other variables.

Wilkinson Notation

Wilkinson notation describes the factors present in models. The notation relates to factors present in models, not to the multipliers (coefficients) of those factors.

Wilkinson Notation	Factors in Standard Notation
`1`	Constant (intercept) term
`A^k`, where `k` is a positive integer	`A`, A^2, ..., A^k
`A + B`	`A`, `B`
`A*B`	`A`, `B`, `A*B`
`A:B`	`A*B` only
`-B`	Do not include `B`
`A*B + C`	`A`, `B`, `C`, `A*B`
`A + B + C + A:B`	`A`, `B`, `C`, `A*B`
`A*B*C - A:B:C`	`A`, `B`, `C`, `A*B`, `A*C`, `B*C`
`A*(B + C)`	`A`, `B`, `C`, `A*B`, `A*C`

Statistics and Machine Learning Toolbox notation always includes a constant term unless you explicitly remove the term using `-1`.

Tips

- You cannot use robust regression with stepwise regression. Check your data for outliers before using `stepwiselm`.
- For other methods such as `anova`, or properties of the `LinearModel` object, see `LinearModel`.

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a linear or generalized linear model based on their statistical significance in explaining the response variable. The method begins with an initial model, specified using `modelspec`, and then compares the explanatory power of incrementally larger and smaller models.

MATLAB uses forward and backward stepwise regression to determine a final model. At each step, the method searches for terms to add to or remove from the model based on the value of the `'Criterion'` argument. The default value of `'Criterion'` is `'sse'`, and in this case, `stepwiselm` uses the p-value of an F-statistic to test models with and without a potential term at each step. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model.

Here is how stepwise proceeds when `'Criterion'` is `'sse'`:

1. Fit the initial model.
2. If any terms not in the model have p-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest p-value and repeat this step; otherwise, go to step 3.
3. If any terms in the model have p-values greater than an exit tolerance (that is, the hypothesis of a zero coefficient can be rejected), remove the one with the largest p-value and go to step 2; otherwise, end.

The default for `stepwiseglm` is `'Deviance'` and it follows a similar procedure for adding or removing terms.

There are several other criteria available, which you can specify using the `'Criterion'` argument. You can use the change in the value of the Akaike information criterion,

Bayesian information criterion, R-squared, adjusted R-squared as a criterion to add or remove terms.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method might build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but might not be globally optimal.

- "Stepwise Regression" on page 9-124

See Also

`fitlm` | `LinearModel` | `step`

stepwisefit

Stepwise regression

Syntax

```
b = stepwisefit(X,y)
[b,se,pval,inmodel,stats,nextstep,history] = stepwisefit(...)
[...] = stepwisefit(X,y,param1,val1,param2,val2,...)
```

Description

`b = stepwisefit(X,y)` uses a stepwise method to perform a multilinear regression of the response values in the n-by-1 vector `y` on the p predictive terms in the n-by-p matrix `X`. Distinct predictive terms should appear in different columns of `X`.

`b` is a p-by-1 vector of estimated coefficients for all of the terms in `X`. The `stepwisefit` function calculates the coefficient estimate values in `b` as follows:

- If a term is not in the final model, then the corresponding coefficient estimate in `b` results from adding only that term to the predictors in the final model.
- If a term is in the final model, then the coefficient estimate in `b` for that term is a result of the final model, that is `stepwise` does not consider the terms it excluded from the model while computing these values.

Note: `stepwisefit` automatically includes a constant term in all models. Do not enter a column of 1s directly into `X`.

`stepwisefit` treats `NaN` values in either `X` or `y` as missing values, and ignores them.

`[b,se,pval,inmodel,stats,nextstep,history] = stepwisefit(...)` returns the following additional information:

- `se` — A vector of standard errors for `b`
- `pval` — A vector of p-values for testing whether elements of `b` are 0

- `inmodel` — A logical vector, with length equal to the number of columns in `X`, specifying which terms are in the final model
- `stats` — A structure of additional statistics with the following fields. All statistics pertain to the final model except where noted.
  - `source` — The string `'stepwisefit'`
  - `dfe` — Degrees of freedom for error
  - `df0` — Degrees of freedom for the regression
  - `SStotal` — Total sum of squares of the response
  - `SSresid` — Sum of squares of the residuals
  - `fstat` — *F*-statistic for testing the final model vs. no model (mean only)
  - `pval` — *p* value of the *F*-statistic
  - `rmse` — Root mean square error
  - `xr` — Residuals for predictors not in the final model, after removing the part of them explained by predictors in the model
  - `yr` — Residuals for the response using predictors in the final model
  - `B` — Coefficients for terms in final model, with values for a term not in the model set to the value that would be obtained by adding that term to the model
  - `SE` — Standard errors for coefficient estimates
  - `TSTAT` — *t* statistics for coefficient estimates
  - `PVAL` — *p*-values for coefficient estimates
  - `intercept` — Estimated intercept
  - `wasnan` — Indicates which rows in the data contained `NaN` values
- `nextstep` — The recommended next step—either the index of the next term to move in or out of the model, or `0` if no further steps are recommended
- `history` — Structure containing information on steps taken, with the following fields:
  - `B` — Matrix of regression coefficients, where each column is one step, and each row is one coefficient.
  - `rmse` — Root mean square errors for the model at each step.
  - `df0` — Degrees of freedom for the regression at each step.

- `in` — Logical array indicating which predictors are in the model at each step, where each row is one step, and each column is one predictor.

`[...] = stepwisefit(X,y,param1,val1,param2,val2,...)` specifies one or more of the name/value pairs described in the following table.

Parameter	Value
`'inmodel'`	A logical vector specifying terms to include in the initial fit. The default is to specify no terms.
`'penter'`	The maximum p value for a term to be added. The default is `0.05`.
`'premove'`	The minimum p value for a term to be removed. The default is the maximum of the value of `'penter'` and `0.10`.
`'display'`	`'on'` displays information about each step in the command window. This is the default. `'off'` omits the display.
`'maxiter'`	The maximum number of steps in the regression. The default is `Inf`.
`'keep'`	A logical vector specifying terms to keep in their initial state. The default is to specify no terms.
`'scale'`	`'on'` centers and scales each column of `X` (computes z-scores) before fitting. `'off'` does not scale the terms. This is the default.

Examples

Load the data in `hald.mat`, which contains observations of the heat of reaction of various cement mixtures:

```
load hald
whos
  Name          Size    Bytes   Class   Attributes

  Description   22x58   2552    char
  hald          13x5     520    double
  heat          13x1     104    double
  ingredients   13x4     416    double
```

The response (`heat`) depends on the quantities of the four predictors (the columns of `ingredients`).

Use `stepwisefit` to carry out the stepwise regression algorithm, beginning with no terms in the model and using entrance/exit tolerances of 0.05/0.10 on the *p*-values:

```
stepwisefit(ingredients,heat,...
            'penter',0.05,'premove',0.10);
Initial columns included:  none
Step 1, added column 4, p=0.000576232
Step 2, added column 1, p=1.10528e-006
Final columns included:  1 4
    'Coeff'      'Std.Err.'    'Status'    'P'
    [ 1.4400]    [  0.1384]    'In'        [1.1053e-006]
    [ 0.4161]    [  0.1856]    'Out'       [     0.0517]
    [-0.4100]    [  0.1992]    'Out'       [     0.0697]
    [-0.6140]    [  0.0486]    'In'        [1.8149e-007]
```

`stepwisefit` automatically includes an intercept term in the model, so you do not add it explicitly to `ingredients` as you would for `regress`. For terms not in the model, coefficient estimates and their standard errors are those that result by adding the corresponding term to the final model.

The `inmodel` parameter is used to specify terms in an initial model:

```
initialModel = ...
           [false true false false]; % Force in 2nd term
stepwisefit(ingredients,heat,...
            'inmodel',initialModel,...
            'penter',.05,'premove',0.10);
Initial columns included:  2
Step 1, added column 1, p=2.69221e-007
Final columns included:  1 2
    'Coeff'      'Std.Err.'    'Status'    'P'
    [ 1.4683]    [  0.1213]    'In'        [2.6922e-007]
    [ 0.6623]    [  0.0459]    'In'        [5.0290e-008]
    [ 0.2500]    [  0.1847]    'Out'       [     0.2089]
    [-0.2365]    [  0.1733]    'Out'       [     0.2054]
```

The preceding two models, built from different initial models, use different subsets of the predictive terms. Terms 2 and 4, swapped in the two models, are highly correlated:

```
term2 = ingredients(:,2);
term4 = ingredients(:,4);
```

```
R = corrcoef(term2,term4)
R =
    1.0000   -0.9730
   -0.9730    1.0000
```

To compare the models, use the `stats` output of `stepwisefit`:

```
[betahat1,se1,pval1,inmodel1,stats1] = ...
          stepwisefit(ingredients,heat,...
          'penter',.05,'premove',0.10,...
          'display','off');
[betahat2,se2,pval2,inmodel2,stats2] = ...
          stepwisefit(ingredients,heat,...
                      'inmodel',initialModel,...
                      'penter',.05,'premove',0.10,...
                      'display','off');
RMSE1 = stats1.rmse
RMSE1 =
    2.7343
RMSE2 = stats2.rmse
RMSE2 =
    2.4063
```

The second model has a lower Root Mean Square Error (RMSE).

More About

Algorithms

Stepwise regression is a systematic method for adding and removing terms from a multilinear model based on their statistical significance in a regression. The method begins with an initial model and then compares the explanatory power of incrementally larger and smaller models. At each step, the p value of an F-statistic is computed to test models with and without a potential term. If a term is not currently in the model, the null hypothesis is that the term would have a zero coefficient if added to the model. If there is sufficient evidence to reject the null hypothesis, the term is added to the model. Conversely, if a term is currently in the model, the null hypothesis is that the term has a zero coefficient. If there is insufficient evidence to reject the null hypothesis, the term is removed from the model. The method proceeds as follows:

1 Fit the initial model.

2 If any terms not in the model have *p*-values less than an entrance tolerance (that is, if it is unlikely that they would have zero coefficient if added to the model), add the one with the smallest *p* value and repeat this step; otherwise, go to step 3.

3 If any terms in the model have *p*-values greater than an exit tolerance (that is, if it is unlikely that the hypothesis of a zero coefficient can be rejected), remove the one with the largest *p* value and go to step 2; otherwise, end.

Depending on the terms included in the initial model and the order in which terms are moved in and out, the method may build different models from the same set of potential terms. The method terminates when no single step improves the model. There is no guarantee, however, that a different initial model or a different sequence of steps will not lead to a better fit. In this sense, stepwise models are locally optimal, but may not be globally optimal.

References

[1] Draper, N. R., and H. Smith. *Applied Regression Analysis*. Hoboken, NJ: Wiley-Interscience, 1998. pp. 307–312.

See Also

`stepwise` | `addedvarplot` | `regress`

subsasgn

Class: classregtree

Subscripted reference for `classregtree` object

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

Description

Subscript assignment is not allowed for a `classregtree` object.

See Also

`classregtree`

subsasgn

Class: dataset

Subscripted assignment to dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

`A = subsasgn(A,S,B)` is called for the syntax `A(i,j)=B`, `A{i,j}=B`, or `A.var=B` when `A` is a dataset array. `S` is a structure array with the fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

`A(i,j) = B` assigns the contents of the dataset array `B` to a subset of the observations and variables in the dataset array `A`. `i` and `j` are one of the following types:

- positive integers
- vectors of positive integers
- observation/variable names
- cell arrays containing one or more observation/variable names
- logical vectors

The assignment does not use observation names, variable names, or any other properties of `B` to modify properties of `A`; however properties of `A` are extended with default values if the assignment expands the number of observations or variables in `A`. Elements of `B` are assigned into `A` by position, not by matching names.

`A{i,j} = B` assigns the value `B` into an element of the dataset array `A`. `i` and `J` are positive integers, or logical vectors. Cell indexing cannot assign into multiple dataset elements, that is, the subscripts `i` and `j` must each refer to only a single observation or variable. `B` is cast to the type of the target variable if necessary. If the dataset element already exists, `A{i,j}` may also be followed by further subscripting as supported by the variable.

For dataset variables that are cell arrays, assignments such as `A{1,'CellVar'} = B` assign into the contents of the target dataset element in the same way that `{}`-indexing of an ordinary cell array does.

For dataset variables that are `n`-D arrays, i.e., each observation is a matrix or array, an assignment such as `A{1,'ArrayVar'} = B` assigns into the second and following dimensions of the target dataset element, i.e., the assignment adds a leading singleton dimension to `B` to account for the observation dimension of the dataset variable.

`A.var = B or A.(varname) = B` assigns `B` to a dataset variable. `var` is a variable name literal, or `varname` is a character variable containing a variable name. If the dataset variable already exists, the assignment completely replaces that variable. To assign into an element of the variable, `A.var` or `A.(varname)` may be followed by further subscripting as supported by the variable. In particular, `A.var(obsnames,...) = B` and `A.var{obsnames,...} = B` (when supported by `var`) provide assignment into a dataset variable using observation names.

`A.properties.propertyname = P` assigns to a dataset property. `propertyname` is one of the following:

- `'ObsNames'`
- `'VarNames'`
- `'Description'`
- `'Units'`
- `'DimNames'`
- `'UserData'`
- `'VarDescription'`

To assign into an element of the property, `A.properties.propertyname` may also be followed by further subscripting as supported by the property.

You cannot assign multiple values into dataset variables or properties using assignments such as `[A.CellVar{1:2}] = B`, `[A.StructVar(1:2).field] = B`,

or `[A.Properties.ObsNames{1:2}] = B`. Use multiple assignments of the form `A.CellVar{1} = B` instead.

Similarly, if a dataset variable is a cell array with multiple columns or is an `n`-D cell array, then the contents of that variable for a single observation consists of multiple cells, and you cannot assign to all of them using the syntax `A{1,'CellVar'} = B`. Use multiple assignments of the form `[A.CellVar{1,1}] = B` instead.

See Also

`dataset` | `set` | `subsref`

subsasgn

Class: gmdistribution

Subscripted reference for Gaussian mixture distribution object

Description

Subscript assignment is not allowed for `gmdistribution` objects.

See Also

`gmdistribution`

subsasgn

Class: NaiveBayes

Subscripted reference for `NaiveBayes` object

Description

Subscript assignment is not allowed for a `NaiveBayes` object.

subsref

Class: classregtree

Subscripted reference for `classregtree` object

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
B = subsref(T,S)
```

Description

`B = subsref(T,S)` is called for the syntax `T(X)` when `T` is a `classregtree` object. `S` is a structure array with the fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

`[...]=T(...)` invokes the `eval` method for the tree `T`.

See Also

`classregtree` | `eval`

subsref

Class: dataset

Subscripted reference for dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
B = subsref(A,S)
```

Description

`B = subsref(A,S)` is called for the syntax `A(i,j)`, `A{i,j}`, or `A.var` when `A` is a dataset array. `S` is a structure array with the fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

`B = A(i,j)` returns a dataset array that contains a subset of the observations and variables in the dataset array `A`. `i` and `j` are one of the following types:

- positive integers
- vectors of positive integers
- observation/variable names
- cell arrays containing one or more observation/variable names
- logical vectors

`B` contains the same property values as `A`, subsetted for observations or variables where appropriate.

`B = A{i,j}` returns an element of a dataset variable. `i` and `j` are positive integers, or logical vectors. Cell indexing cannot return multiple dataset elements, that is, the subscripts `i` and `j` must each refer to only a single observation or variable. `A{i,j}` may also be followed by further subscripting as supported by the variable.

For dataset variables that are cell arrays, expressions such as `A{1,'CellVar'}` return the contents of the referenced dataset element in the same way that `{}`-indexing on an ordinary cell array does. If the dataset variable is a single column of cells, the contents of a single cell is returned. If the dataset variable has multiple columns or is `n`-D, multiple outputs containing the contents of multiple cells are returned.

For dataset variables that are `n`-D arrays, i.e., each observation is a matrix or an array, expressions such as `A{1,'ArrayVar'}` return `A.ArrayVar(1,:,...)` with the leading singleton dimension squeezed out.

`B = A.var` or `A.(varname)` returns a dataset variable. `var` is a variable name literal, or `varname` is a character variable containing a variable name. `A.var` or `A.(varname)` may also be followed by further subscripting as supported by the variable. In particular, `A.var(obsnames,...)` and `A.var{obsnames,...}` (when supported by `var`) provide subscripting into a dataset variable using observation names.

`P = A.Properties.propertyname` returns a dataset property. `propertyname` is one of the following:

- `'ObsNames'`
- `'VarNames'`
- `'Description'`
- `'Units'`
- `'DimNames'`
- `'UserData'`
- `'VarDescription'`

`A.properties.propertyname` may also be followed by further subscripting as supported by the property.

Limitations

Subscripting expressions such as `A.CellVar{1:2}`, `A.StructVar(1:2).field`, or `A.Properties.ObsNames{1:2}` are valid, but result in `subsref` returning

multiple outputs in the form of a comma-separated list. If you explicitly assign to output arguments on the left-hand side of an assignment, for example, `[cellval1,cellval2] = A.CellVar{1:2}`, those variables will receive the corresponding values. However, if there are no output arguments, only the first output in the comma-separated list is returned.

Similarly, if a dataset variable is a cell array with multiple columns or is an `n`-D cell array, then subscripting expressions such as `A{1,'CellVar'}` result in `subsref` returning the contents of multiple cells. You should explicitly assign to output arguments on the left-hand side of an assignment, for example, `[cellval1,cellval2] = A{1,'CellVar'}`.

See Also

`dataset` | `set` | `subsasgn`

subsref

Class: gmdistribution

Subscripted reference for Gaussian mixture distribution object

Syntax

```
B = subsref(T,S)
```

Description

`B = subsref(T,S)` is called for the syntax `T(X)` when `T` is a `gmdistribution` object. `S` is a structure array with the following fields:

`type`	String containing `'()'`, `'{}'`, or `'.'` specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

See Also

`gmdistribution`

subsref

Class: NaiveBayes

Subscripted reference for `NaiveBayes` object

Syntax

```
b = subsref(nb,s)
```

Description

`b = subsref(nb,s)` is called for the syntax `nb(s)` when `nb` is a `NaiveBayes` object. `S` is a structure array with the fields:

`type`	string containing '()', '{}', or '.' specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

subsref

Class: qrandset

Subscripted reference for qrandset

Syntax

```
x = p(i,j)
x = subsref(p,s)
```

Description

`x = p(i,j)` returns a matrix that contains a subset of the points from the point set `p`. The indices in `i` select points from the set and the indices in `j` select columns from those points. `i` and `j` are vector of positive integers or logical vectors. A colon used as a subscript, as in `p(i,:)`, indicates the entire row (or column).

`x = subsref(p,s)` is called for the syntax `p(i)`, `p{i}`, or `p.i`. `s` is a structure array with the fields:

`type`	string containing '()', '{}', or '.' specifying the subscript type.
`subs`	Cell array or string containing the actual subscripts.

Examples

Command	Returns
`p = sobolset(5);`	The fifth point
`x = p(1:10,:)`	All columns of the first 10 points
`x = p(end,1)`	The first column of the last point
`x = p([1,4,5], :)`	Points 1, 4, and 5

See Also

`qrandset`

summary

Class: dataset

Print summary of dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
summary(A)
s = summary(A)
```

Description

`summary(A)` prints a summary of a dataset array and the variables that it contains.

`s = summary(A)` returns a scalar structure `s` that contains a summary of the dataset `A` and the variables that `A` contains. For more information on the fields in `s`, see Outputs.

Summary information depends on the type of the variables in the data set:

- For numerical variables, `summary` computes a five-number summary of the data, giving the minimum, the first quartile, the median, the third quartile, and the maximum.
- For logical variables, `summary` counts the number of `true`s and `false`s in the data.
- For categorical variables, `summary` counts the number of data at each level.

Output Arguments

The following list describes the fields in the structure `s`:

- `Description` — A character array containing the dataset description.
- `Variables` — A structure array with one element for each dataset variable in A. Each element has the following fields:
  - `Name` — A character string containing the name of the variable.
  - `Description` — A character string containing the variable's description.
  - `Units` — A character string containing the variable's units.
  - `Size` — A numeric vector containing the size of the variable.
  - `Class` — A character string containing the class of the variable.
  - `Data` — A scalar structure containing the following fields.

    For numeric variables:

    - `Probabilities` — A numeric vector containing the probabilities [0.0 .25 .50 .75 1.0] and NaN (if any are present in the corresponding dataset variable).
    - `Quantiles` — A numeric vector containing the values that correspond to 'Probabilities' for the corresponding dataset variable, and a count of NaNs (if any are present).

    For logical variables:

    - `Values` — The logical vector [true false].
    - `Counts` — A numeric vector of counts for each logical value.

    For categorical variables:

    - `Levels` — A cell array containing the labels for each level of the corresponding dataset variable.
    - `Counts` — A numeric vector of counts for each level.

    `'Data'` is empty if variable is not numeric, categorical, or logical. If a dataset variable has more than one column, then the corresponding `'Quantiles'` or `'Counts'` field is a matrix or an array.

Examples

Summarize Fisher's iris data:

```
load fisheriris
species = nominal(species);
data = dataset(species,meas);
summary(data)
species: [150x1 nominal]
  setosa   versicolor   virginica
      50           50          50
meas: [150x4 double]
  min       4.3000         2         1    0.1000
  1st Q     5.1000    2.8000    1.6000    0.3000
  median    5.8000         3    4.3500    1.3000
  3rd Q     6.4000    3.3000    5.1000    1.8000
  max       7.9000    4.4000    6.9000    2.5000
```

Summarize the data in `hospital.mat`:

```
load hospital
summary(hospital)

Dataset array created from the data file hospital.dat.

The first column of the file ("id") is used for observation
names.  Other columns ("sex" and "smoke") have been
converted from their original coded values into categorical
and logical variables.  Two sets of columns ("sys" and
"dia", "trial1" through "trial4") have been combined into
single variables with multivariate observations.  Column
headers have been replaced with more descriptive variable
names.  Units have been added where appropriate.


LastName: [100x1 cell string]
Sex: [100x1 nominal]
     Female      Male
         53        47

Age: [100x1 double, Units = Yrs]
     min      1st Q      median      3rd Q      max
      25         32          39         44       50

Weight: [100x1 double, Units = Lbs]
     min      1st Q         median        3rd Q        max
     111      130.5000      142.5000      180.5000     202

Smoker: [100x1 logical]
```

```
     true      false
       34         66

BloodPressure: [100x2 double, Units = mm Hg]
Systolic/Diastolic
     min              109           68
     1st Q       117.5000      77.5000
     median           122      81.5000
     3rd Q       127.5000           89
     max              138           99

Trials: [100x1 cell, Units = Counts]
From zero to four measurement trials performed
```

See Also

get | set | grpstats

Support property

Class: ProbDist

Read-only structure containing information about support of ProbDist object

Description

`Support` is a read-only property of the `ProbDist` class. `Support` is a structure containing information about the support of a ProbDist object. It includes the following fields:

- `range`
- `closedbound`
- `iscontinuous`

Values

The values for the three fields in the structure are:

- `range` — A two-element vector `[L, U]`, such that all of the probability is contained from `L` to `U`.
- `closedbound` — A two-element logical vector indicating whether the corresponding range endpoint is included. Possible values for each endpoint are `1` (`true`) or `0` (`false`).
- `iscontinuous` — A logical value indicates if the distribution takes values on the entire interval from `L` to `U` (true), or if it takes only integer values within this range (false). Possible values are `1` (`true`) or `0` (`false`).

Use this information to view and compare information about the support of distributions.

struct2dataset

Convert structure array to dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds = struct2dataset(S)
ds = struct2dataset(S,Name,Value)
```

Description

`ds = struct2dataset(S)` converts a structure array to a dataset array.

`ds = struct2dataset(S,Name,Value)` performs the conversion using additional options specified by one or more Name,Value pair arguments.

Examples

Convert Scalar Structure Array to Dataset Array

Convert a scalar structure array to a dataset array using the default options.

Create a structure array to convert.

```
S.Name = {'CLARK';'BROWN';'MARTIN'};
S.Gender = {'M';'F';'M'};
S.SystolicBP = [124;122;130];
S.DiastolicBP = [93;80;92];
```

```
S
```

```
S =

          Name: {3x1 cell}
        Gender: {3x1 cell}
     SystolicBP: [3x1 double]
    DiastolicBP: [3x1 double]
```

The scalar structure array has four fields, each with three rows.

Convert the structure array to a dataset array.

```
ds = struct2dataset(S)
```

```
ds =

    Name            Gender     SystolicBP    DiastolicBP
    'CLARK'         'M'        124           93
    'BROWN'         'F'        122           80
    'MARTIN'        'M'        130           92
```

The structure field names in `S` become the variable names in the output dataset array. The size of `ds` is 3-by-4.

Convert Nonscalar Structure Array to Dataset Array

Convert a nonscalar structure array to a dataset array, using one of the structure fields for observation names.

Create a nonscalar structure array to convert.

```
S(1,1).Name = 'CLARK';
S(1,1).Gender = 'M';
S(1,1).SystolicBP = 124;
S(1,1).DiastolicBP = 93;

S(2,1).Name = 'BROWN';
S(2,1).Gender = 'F';
S(2,1).SystolicBP = 122;
S(2,1).DiastolicBP = 80;

S(3,1).Name = 'MARTIN';
S(3,1).Gender = 'M';
```

```
S(3,1).SystolicBP = 130;
S(3,1).DiastolicBP = 92;

S

S =

3x1 struct array with fields:
    Name
    Gender
    SystolicBP
    DiastolicBP
```

This is a 3-by-1 structure array with 4 fields.

Convert the structure array to a dataset array, using the `Name` field for observation names.

```
ds = struct2dataset(S,'ReadObsNames','Name')

ds =

             Gender     SystolicBP    DiastolicBP
    CLARK    'M'        124           93
    BROWN    'F'        122           80
    MARTIN   'M'        130           92
```

The size of `ds` is 3-by-3 because the structure field `Name` is used for observation names, and not as a dataset array variable.

```
ds.Properties.DimNames

ans =

    'Name'    'Variables'

ds.Properties.ObsNames

ans =

    'CLARK'
    'BROWN'
    'MARTIN'
```

- “Create a Dataset Array from Workspace Variables” on page 2-63

- “Create a Dataset Array from a File” on page 2-69

Input Arguments

S — Input structure array

structure array

Input structure array to convert to a dataset array, specified as a scalar structure array with *N* fields, each with *M* rows, or a nonscalar *M*-by-1 structure array with *N* fields.

Data Types: `struct`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'ReadObsNames','myField'` specifies that the structure field, `myField`, contains observation names.

`'ReadObsNames'` — Name of structure field containing observation names for dataset array

`false` (default) | string

Name of structure field containing observation names for the output dataset array, specified as the comma-separated pair consisting of `'ReadObsNames'` and a string containing a field name from the input structure array, S. When you specify a field name, `struct2dataset` uses that field to create observation names, and sets `ds.Properties.DimNames` equal to `{ReadObsNames,'Variables'}`.

For example, to specify that observation names are in the structure field, `Names`, use

Example: `'ReadObsNames','Names'`

By default, or if `ReadObsNames` is equal to `false`, `struct2dataset` does not create observation names unless you specify names using the name-value pair argument ObsNames.

`'ObsNames'` — Observation names for dataset array

cell array of strings

Observation names for the output dataset array, specified as the comma-separated pair consisting of `'ObsNames'` and a cell array of strings containing observation names. The names do not need to be valid MATLAB identifiers, but they must be unique.

`'AsScalar'` — Indicator for how to treat scalar structure
`false | true`

Indicator for how to treat a scalar input structure array, specified as the comma-separated pair consisting of `'AsScalar'` and either `true` or `false`. The default value is `true` if S is a scalar structure array, and `false` otherwise.

By default, `struct2dataset` converts a scalar structure array with *N* fields, each with *M* rows, into an *M*-by-*N* dataset array.

If instead you set `AsScalar` equal to `false` for a scalar input structure array, then `struct2dataset` converts `S` to a dataset array with *N* observations.

Output Arguments

`ds` — Output dataset array
dataset array

Output dataset array, returned by default with *M* observations and *N* variables.

- If S is a scalar structure array with *N* fields, each with *M* rows, then ds is an *M*-by-*N* dataset array.
- If S is a nonscalar *M*-by-1 structure array with *N* fields, then ds is an *M*-by-*N* dataset array.
- If S is a scalar structure array with *N* fields, each with *M* rows, and AsScalar is set equal to `false`, then ds is a dataset array with *N* observations.

More About

- “Dataset Arrays” on page 2-132

See Also

`cell2dataset | dataset | dataset2struct`

surfht

Interactive contour plot

Syntax

```
surfht(Z)
surfht(x,y,Z)
```

Description

`surfht(Z)` is an interactive contour plot of the matrix `Z` treating the values in `Z` as height above the plane. The *x*-values are the column indices of `Z` while the *y*-values are the row indices of `Z`.

`surfht(x,y,Z)` where `x` and `y` are vectors specify the *x* and *y*-axes on the contour plot. The length of `x` must match the number of columns in `Z`, and the length of `y` must match the number of rows in `Z`.

There are vertical and horizontal reference lines on the plot whose intersection defines the current *x* value and *y* value. You can drag these dotted white reference lines and watch the interpolated *z* value (at the top of the plot) update simultaneously. Alternatively, you can get a specific interpolated *z* value by typing the *x* value and *y* value into editable text fields on the *x*-axis and *y*-axis respectively.

surrcutcategories

Class: classregtree

Categories used for surrogate splits in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
C = surrcutcategories(T)
C = surrcutcategories(T,J)
```

Description

`C = surrcutcategories(T)` returns an *n*-element cell array `C` of the categories used for surrogate splits in the decision tree `T`, where *n* is the number of nodes in the tree. For each node `K`, `C{K}` is a cell array. The length of `C{K}` is equal to the number of surrogate predictors found at this node. Every element of `C{K}` is either an empty string for a continuous surrogate predictor or a two-element cell array with categories for a categorical surrogate predictor. The first element of this two-element cell array lists categories assigned to the left child by this surrogate split and the second element of this two-element cell array lists categories assigned to the right child by this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `C` contains an empty cell.

`C = surrcutcategories(T,J)` takes an array `J` of node numbers and returns the categories for the specified nodes.

See Also

`classregtree` | `surrcuttype` | `surrcutpoint` | `surrcutvar` | `cutcategories`

surrcutflip

Class: classregtree

Numeric cutpoint assignments used for surrogate splits in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
V = surrcutflip(T)
V = surrcutflip(T,J)
```

Description

`V = surrcutflip(T)` returns an *n*-element cell array `V` of the numeric cut assignments used for surrogate splits in the decision tree `T`, where *n* is the number of nodes in the tree. For each node `K`, `V{K}` is a numeric vector. The length of `V{K}` is equal to the number of surrogate predictors found at this node. Every element of `V{K}` is either zero for a categorical surrogate predictor or a numeric cut assignment for a continuous surrogate predictor. The numeric cut assignment can be either -1 or +1. For every surrogate split with a numeric cut *C* based on a continuous predictor variable *Z*, the left child is chosen if *Z*<*C* and the cut assignment for this surrogate split is +1, or if *Z*>=*C* and the cut assignment for this surrogate split is -1. Similarly, the right child is chosen if *Z*>=*C* and the cut assignment for this surrogate split is +1, or if *Z*<*C* and the cut assignment for this surrogate split is -1. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `V` contains an empty array.

`V = surrcutflip(T,J)` takes an array `J` of node numbers and returns the cutpoint assignments for the specified nodes.

See Also

`classregtree` | `surrcuttype` | `surrcutpoint` | `surrcutvar` | `surrcutcategories` | `cutpoint`

surrcutpoint

Class: classregtree

Cutpoints used for surrogate splits in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
V = surrcutpoint(T)
V = surrcutpoint(T,J)
```

Description

`V = surrcutpoint(T)` returns an n-element cell array `V` of the numeric values used for surrogate splits in the decision tree `T`, where n is the number of nodes in the tree. For each node `K`, `V{K}` is a numeric vector. The length of `V{K}` is equal to the number of surrogate predictors found at this node. Every element of `V{K}` is either either `NaN` for a categorical surrogate predictor or a numeric cut for a continuous surrogate predictor. For every surrogate split with a numeric cut C based on a continuous predictor variable Z, the left child is chosen if $Z<C$ and `surrcutflip` for this surrogate split is -1. Similarly, the right child is chosen if $Z>=C$ and `surrcutflip` for this surrogate split is +1, or if $Z<C$ and `surrcutflip` for this surrogate split is -1. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `V` contains an empty cell.

`V = surrcutpoint(T,J)` takes an array `J` of node numbers and returns the cutpoint assignments for the specified nodes.

See Also

`classregtree` | `surrcuttype` | `surrcutflip` | `surrcutvar` | `surrcutcategories` | `cutpoint`

surrcuttype

Class: classregtree

Types of surrogate splits used at branches in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
C = surrcuttype(T)
C = surrcuttype(T,J)
```

Description

`C = surrcuttype(T)` returns an n-element cell array `C` indicating types of surrogate splits at each node in the tree `T`, where n is the number of nodes in the tree. For each node `K`, `C{K}` is a cell array with the types of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `C` contains an empty cell. A surrogate split type can be either `'continuous'` if the cut is defined in the form `Z<V` for a variable `Z` and cutpoint `V` or `'categorical'` if the cut is defined by whether `Z` takes a value in a set of categories.

`C = surrcuttype(T,J)` takes an array `J` of node numbers and returns the cut types for the specified nodes.

See Also

`classregtree` | `cuttype` | `numnodes` | `surrcutvar`

surrcutvar

Class: classregtree

Variables used for surrogate splits in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
V = surrcutvar(T)
V = surrcutvar(T,J)
[V,NUM] = surrcutvar(...)
```

Description

`V = surrcutvar(T)` returns an *n*-element cell array `V` of the names of the variables used for surrogate splits in each node of the tree `T`, where *n* is the number of nodes in the tree. Every element of `V` is a cell array with the names of the surrogate split variables at this node. The variables are sorted by the predictive measure of association with the optimal predictor in the descending order, and only variables with the positive predictive measure are included. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, `V` contains an empty cell.

`V = surrcutvar(T,J)` takes an array `J` of node numbers and returns the cut types for the specified nodes.

`[V,NUM] = surrcutvar(...)` also returns a cell array `NUM` with indices for each variable.

See Also

`classregtree` | `children` | `numnodes` | `cutvar`

surrvarassoc

Class: classregtree

Predictive measure of association for surrogate splits in decision tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
A = surrvarassoc(T)
A = surrvarassoc(T,J)
```

Description

`A = surrvarassoc(T)` returns an n-element cell array `A` of the predictive measures of association for surrogate splits in the decision tree `T`, where n is the number of nodes in the tree. For each node `K`, `A{K}` is a numeric vector. The length of `A{K}` is equal to the number of surrogate predictors found at this node. Every element of `A{K}` gives the predictive measure of association between the optimal split and this surrogate split. The order of the surrogate split variables at each node is matched to the order of variables returned by `surrcutvar`. The optimal-split variable at this node is not included. For non-branch (leaf) nodes, V contains an empty cell.

`A = surrvarassoc(T,J)` takes an array `J` of node numbers and returns the predictive measure of association for the specified nodes.

See Also

`classregtree` | `surrcuttype` | `surrcutflip` | `surrcutvar` | `surrcutcategories` | `surrcutpoint`

svmclassify

Classify using support vector machine (SVM)

Compatibility

`svmclassify` will be removed in a future release. See `fitcsvm`, `ClassificationSVM`, and `CompactClassificationSVM` instead.

Syntax

```
Group = svmclassify(SVMStruct,Sample)
Group = svmclassify(SVMStruct,Sample,'Showplot',true)
```

Description

`Group = svmclassify(SVMStruct,Sample)` classifies each row of the data in `Sample`, a matrix of data, using the information in a support vector machine classifier structure `SVMStruct`, created using the `svmtrain` function. Like the training data used to create `SVMStruct`, `Sample` is a matrix where each row corresponds to an observation or replicate, and each column corresponds to a feature or variable. Therefore, `Sample` must have the same number of columns as the training data. This is because the number of columns defines the number of features. `Group` indicates the group to which each row of `Sample` has been assigned.

`Group = svmclassify(SVMStruct,Sample,'Showplot',true)` plots the *`Sample`* data in the figure created using the `Showplot` property with the `svmtrain` function. This plot appears only when the data is two-dimensional.

Input Arguments

`SVMStruct`

Support vector machine classifier structure created using the `svmtrain` function.

`Sample`

A matrix where each row corresponds to an observation or replicate, and each column corresponds to a feature or variable. Therefore, `Sample` must have the same number of columns as the training data. This is because the number of columns defines the dimensionality of the data space.

`Showplot`

Describes whether to display a plot of the classification. Displays only for 2-D problems. Follow with a Boolean argument: `true` to display the plot, `false` to give no display.

Output Arguments

`Group`

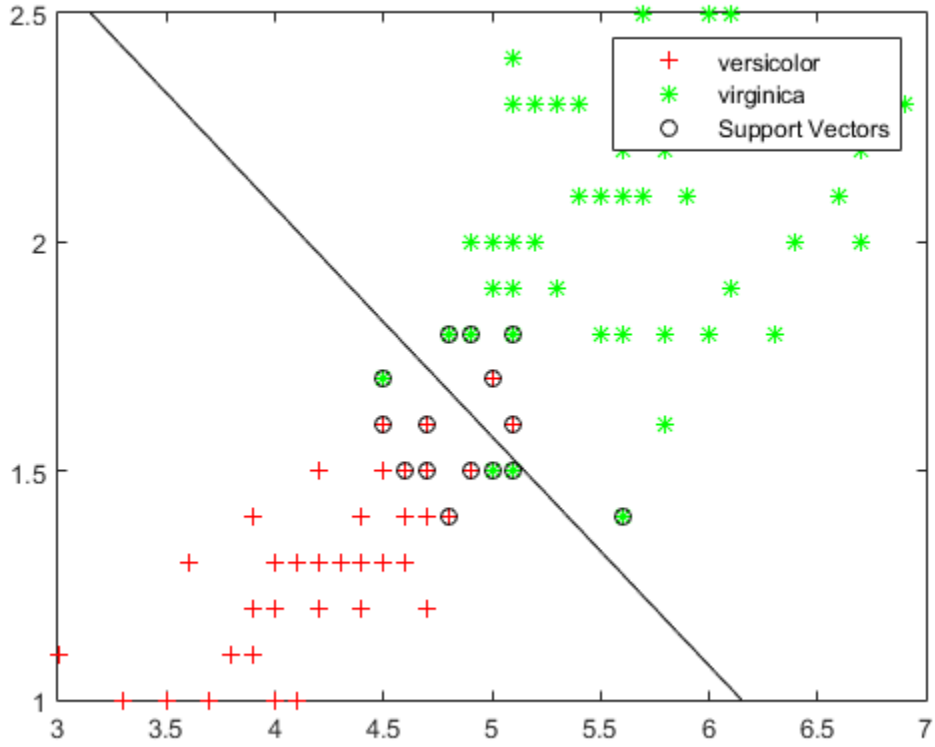
Column vector with the same number of rows as `Sample`. Each entry (row) in `Group` represents the class of the corresponding row of `Sample`.

Examples

Classify an Observation Using a Trained SVM Classifier.

Find a line separating the Fisher iris data on versicolor and virginica species, according to the petal length and petal width measurements. These two species are in rows 51 and higher of the data set, and the petal length and width are the third and fourth columns.

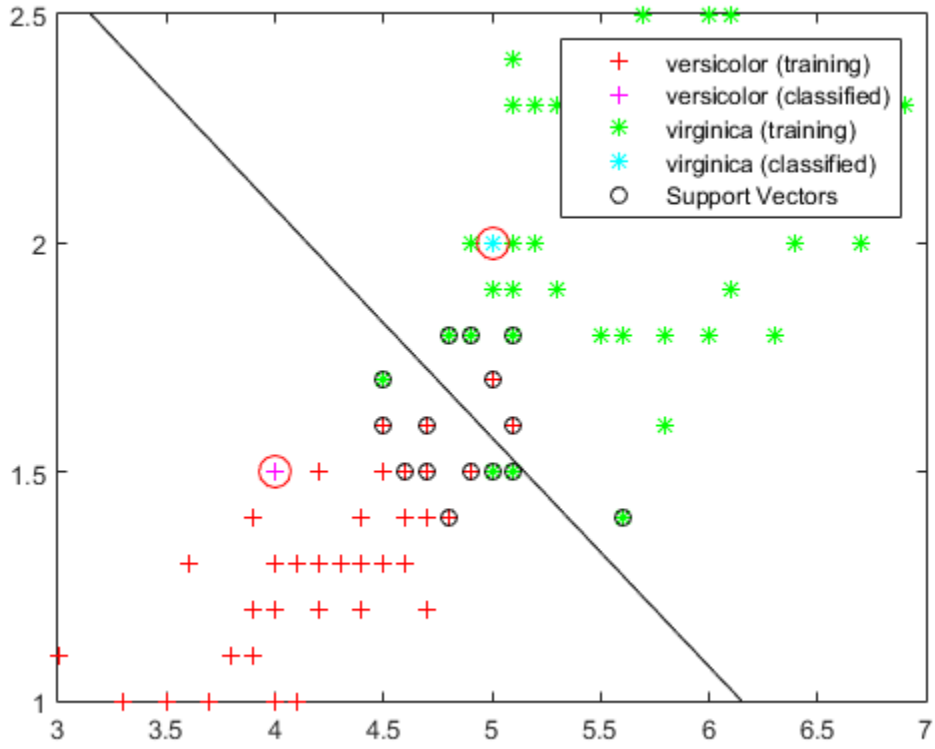
```
load fisheriris
xdata = meas(51:end,3:4);
group = species(51:end);
figure;
svmStruct = svmtrain(xdata,group,'ShowPlot',true);
```



Classify two new flowers, one with petal length 5 and petal width 2 and the other with petal length 4 and petal width 1.5.

```
Xnew = [5 2; 4 1.5];
species = svmclassify(svmStruct,Xnew,'ShowPlot',true)
hold on;
plot(Xnew(:,1),Xnew(:,2),'ro','MarkerSize',12);
hold off
```

```
species =

    'virginica'
    'versicolor'
```



More About

Algorithms

The `svmclassify` function uses results from `svmtrain` to classify vectors x according to the following equation:

$$c = \sum_i \alpha_i k(s_i, x) + b,$$

where s_i are the support vectors, a_i are the weights, b is the bias, and k is a kernel function. In the case of a linear kernel, k is the dot product. If $c \geq 0$, then x is classified as a member of the first group, otherwise it is classified as a member of the second group.

- "Support Vector Machines (SVM)" on page 16-170

References

[1] Kecman, V., Learning and Soft Computing, MIT Press, Cambridge, MA. 2001.

[2] Suykens, J.A.K., Van Gestel, T., De Brabanter, J., De Moor, B., and Vandewalle, J., Least Squares Support Vector Machines, World Scientific, Singapore, 2002.

[3] Scholkopf, B., and Smola, A.J., Learning with Kernels, MIT Press, Cambridge, MA. 2002.

[4] Cristianini, N., and Shawe-Taylor, J. (2000). An Introduction to Support Vector Machines and Other Kernel-based Learning Methods, First Edition (Cambridge: Cambridge University Press). http://www.support-vector.net/

See Also

`svmtrain`

svmtrain

Train support vector machine classifier

Compatibility

`svmtrain` will be removed in a future release. See `fitcsvm`, `ClassificationSVM`, and `CompactClassificationSVM` instead.

Syntax

```
SVMStruct = svmtrain(Training,Group)
SVMStruct = svmtrain(Training,Group,Name,Value)
```

Description

`SVMStruct = svmtrain(Training,Group)` returns a structure, `SVMStruct`, containing information about the trained support vector machine (SVM) classifier.

`SVMStruct = svmtrain(Training,Group,Name,Value)` returns a structure with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`Training`

Matrix of training data, where each row corresponds to an observation or replicate, and each column corresponds to a feature or variable. `svmtrain` treats `NaN`s or empty strings in `Training` as missing values and ignores the corresponding rows of `Group`.

`Group`

Grouping variable, which can be a categorical, numeric, or logical vector, a cell vector of strings, or a character matrix with each row representing a class label. Each element of

`Group` specifies the group of the corresponding row of `Training`. `Group` should divide `Training` into two groups. `Group` has the same number of elements as there are rows in `Training`. `svmtrain` treats each `NaN`, empty string, or `'undefined'` in `Group` as a missing value, and ignores the corresponding row of `Training`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'autoscale'`

Boolean specifying whether `svmtrain` automatically centers the data points at their mean, and scales them to have unit standard deviation, before training.

Default: `true`

`'boxconstraint'`

Value of the box constraint `C` for the soft margin. `C` can be a scalar, or a vector of the same length as the training data.

If `C` is a scalar, it is automatically rescaled by `N/(2*N1)` for the data points of group one and by `N/(2*N2)` for the data points of group two, where `N1` is the number of elements in group one, `N2` is the number of elements in group two, and `N = N1 + N2`. This rescaling is done to take into account unbalanced groups, that is cases where `N1` and `N2` have very different values.

If `C` is an array, then each array element is taken as a box constraint for the data point with the same index.

Default: `1`

`'kernelcachelimit'`

Value that specifies the size of the kernel matrix cache for the SMO training method. The algorithm keeps a matrix with up to `kernelcachelimit` × `kernelcachelimit` double-precision, floating-point numbers in memory.

Default: 5000

`'kernel_function'`

Kernel function `svmtrain` uses to map the training data into kernel space. The default kernel function is the dot product. The kernel function can be one of the following strings or a function handle:

- `'linear'` — Linear kernel, meaning dot product.
- `'quadratic'` — Quadratic kernel.
- `'polynomial'` — Polynomial kernel (default order 3). Specify another order with the `polyorder` name-value pair.
- `'rbf'` — Gaussian Radial Basis Function kernel with a default scaling factor, sigma, of 1. Specify another value for sigma with the `rbf_sigma` name-value pair.
- `'mlp'` — Multilayer Perceptron kernel with default scale `[1 –1]`. Specify another scale with the `mlp_params` name-value pair.
- `@`*`kfun`* — Function handle to a kernel function. A kernel function must be of the form

  ```
  function K = kfun(U, V)
  ```

  The returned value, `K`, is a matrix of size `M`-by-`N`, where `U` and `V` have `M` and `N` rows respectively.

  If `kfun` has extra parameters, include the extra parameters via an anonymous function. For example, suppose that your kernel function is:

  ```
  function k = kfun(u,v,p1,p2)
  k = tanh(p1*(u*v')+p2);
  ```

  Set values for `p1` and `p2`, and then use an anonymous function:

  ```
  @(u,v) kfun(u,v,p1,p2)
  ```

Default: `'linear'`

`'kktviolationlevel'`

Value that specifies the fraction of variables allowed to violate the Karush-Kuhn-Tucker (KKT) conditions for the SMO training method. Set any value in [0,1). For example, if you set `kktviolationlevel` to `0.05`, then 5% of the variables are allowed to violate the KKT conditions.

Tip Set this option to a positive value to help the algorithm converge if it is fluctuating near a good solution.

For more information on KKT conditions, see Cristianini and Shawe-Taylor [4].

Default: `0`

`'method'`

Method used to find the separating hyperplane. Options are:

- `'QP'` — Quadratic programming (requires an Optimization Toolbox license). The classifier is a 2-norm soft-margin support vector machine. Give quadratic programming options with the `options` name-value pair, and create `options` with `optimset`.
- `'SMO'` — Sequential Minimal Optimization. Give SMO options with the `options` name-value pair, and create `options` with `statset`.
- `'LS'` — Least squares.

Default: `SMO`

`'mlp_params'`

Parameters of the Multilayer Perceptron (`mlp`) kernel. The `mlp` kernel requires two parameters, `[P1 P2]`. The kernel `K = tanh(P1*U*V' + P2)`, where `P1 > 0` and `P2 < 0`.

Default: `[1 –1]`

`'options'`

Options structure for training.

- When you set `'method'` to `'SMO'` (default), create the `options` structure using `statset`. Options are:

  `Display` — String that specifies the level of information about the optimization iterations that is displayed as the algorithm runs. Choices are:

  - `off` (default) — Reports nothing.

	• `iter` — Reports every 500 iterations. • `final` — Reports only when the algorithm finishes.
`MaxIter`	Integer that specifies the maximum number of iterations of the main loop. If this limit is exceeded before the algorithm converges, then the algorithm stops and returns an error. Default is `15000`.

The other name-value pairs that relate specifically to the `'SMO'` method are `kernelcachelimit`, `kktviolationlevel`, and `tolkkt`.

- When you set `method` to `'QP'`, create the options structure using `optimset`. For details of applicable option choices, see `quadprog` options. SVM uses a convex quadratic program, so you can choose the `'interior-point-convex'` `quadprog` algorithm. In limited testing, the `'interior-point-convex'` algorithm was the best `quadprog` option for `svmtrain`, in both speed and memory utilization.

`'polyorder'`

Order of the polynomial kernel.

Default: 3

`'rbf_sigma'`

Scaling factor (sigma) in the radial basis function kernel.

Default: 1

`'showplot'`

Boolean indicating whether to plot the grouped data and separating line. Creates a plot only when the data has two columns (features).

Default: `false`

`'tolkkt'`

Value that specifies the tolerance with which the Karush-Kuhn-Tucker (KKT) conditions are checked for the SMO training method. For a definition of KKT conditions, see “Karush-Kuhn-Tucker (KKT) Conditions” on page 22-4669.

Default: `1e-3`

Output Arguments

`SVMStruct`

Structure containing information about the trained SVM classifier in the following fields:

- `SupportVectors` — Matrix of data points with each row corresponding to a support vector in the normalized data space. This matrix is a subset of the *`Training`* input data matrix, after normalization has been applied according to the `'AutoScale'` argument.
- `Alpha` — Vector of weights for the support vectors. The sign of the weight is positive for support vectors belonging to the first group, and negative for the second group.
- `Bias` — Intercept of the hyperplane that separates the two groups in the normalized data space (according to the `'AutoScale'` argument).
- `KernelFunction` — Handle to the function that maps the training data into kernel space.
- `KernelFunctionArgs` — Cell array of any additional arguments required by the kernel function.
- `GroupNames` — Categorical, numeric, or logical vector, a cell vector of strings, or a character matrix with each row representing a class label. Specifies the group identifiers for the support vectors. It has the same number of elements as there are rows in `SupportVectors`. Each element specifies the group to which the corresponding row in `SupportVectors` belongs.
- `SupportVectorIndices` — Vector of indices that specify the rows in `Training`, the training data, that were selected as support vectors after the data was normalized, according to the `AutoScale` argument.
- `ScaleData` — Field containing normalization factors. When `'AutoScale'` is set to `false`, it is empty. When `AutoScale` is set to `true`, it is a structure containing two fields:
  - `shift` — Row vector of values. Each value is the negative of the mean across an observation in *`Training`*, the training data.
  - `scaleFactor` — Row vector of values. Each value is `1` divided by the standard deviation of an observation in *`Training`*, the training data.

Both `svmtrain` and `svmclassify` apply the scaling in `ScaleData`.

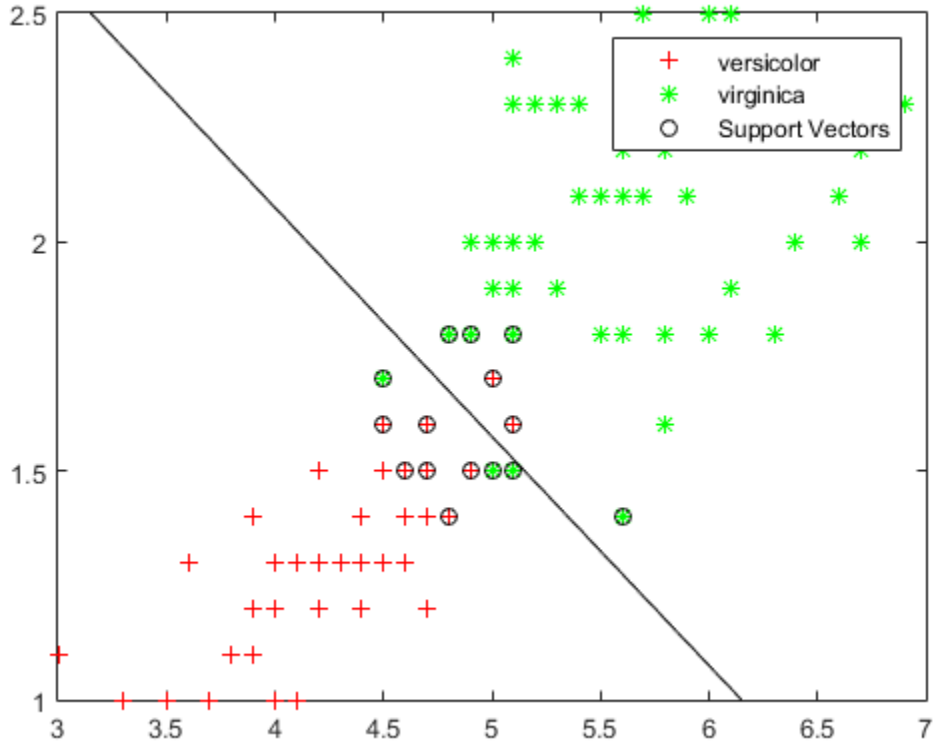
- `FigureHandles` — Vector of figure handles created by `svmtrain` when using the `'Showplot'` argument.

Examples

Train an SVM Classifier

Find a line separating the Fisher iris data on versicolor and virginica species, according to the petal length and petal width measurements. These two species are in rows 51 and higher of the data set, and the petal length and width are the third and fourth columns.

```
load fisheriris
xdata = meas(51:end,3:4);
group = species(51:end);
svmStruct = svmtrain(xdata,group,'ShowPlot',true);
```



More About

Karush-Kuhn-Tucker (KKT) Conditions

The Karush-Kuhn-Tucker (KKT) conditions are analogous to the condition that the gradient must be zero at a minimum, modified to take constraints into account. The difference is that the KKT conditions hold for constrained problems. The KKT conditions use the auxiliary Lagrangian function:

$$L(x,\lambda) = f(x) + \sum \lambda_{g,i} g_i(x) + \sum \lambda_{h,i} h_i(x).$$

Here $f(x)$ is the objective function, $g(x)$ is a vector of constraint functions $g(x) \le 0$, and $h(x)$ is a vector of constraint functions $h(x) = 0$. The vector λ, which is the concatenation of λ_g and λ_h, is the Lagrange multiplier vector. Its length is the total number of constraints.

The KKT conditions are:

$$\begin{aligned} \nabla_x L(x,\lambda) &= 0 \\ \lambda_{g,i} g_i(x) &= 0 \ \forall i \\ g(x) &\le 0 \\ h(x) &= 0 \\ \lambda_{g,i} &\ge 0. \end{aligned}$$

For more information, see Karush-Kuhn-Tucker conditions.

Tips

- To classify new data, use the result of training, `SVMStruct`, with the `svmclassify` function.

Algorithms

The `svmtrain` function uses an optimization method to identify support vectors s_i, weights a_i, and bias b that are used to classify vectors x according to the following equation:

$$c = \sum_i \alpha_i k(s_i, x) + b,$$

where k is a kernel function. In the case of a linear kernel, k is the dot product. If $c \ge 0$, then x is classified as a member of the first group, otherwise it is classified as a member of the second group.

Memory Usage and Out of Memory Error

When you set `'Method'` to `'QP'`, the `svmtrain` function operates on a data set containing `N` elements, and it creates an `(N+1)`-by-`(N+1)` matrix to find the separating hyperplane. This matrix needs at least `8*(n+1)^2` bytes of contiguous memory. If this size of contiguous memory is not available, the software displays an “out of memory” error message.

When you set `'Method'` to `'SMO'` (default), memory consumption is controlled by the `kernelcachelimit` option. The SMO algorithm stores only a submatrix of the kernel matrix, limited by the size specified by the `kernelcachelimit` option. However, if the number of data points exceeds the size specified by the `kernelcachelimit` option, the SMO algorithm slows down because it has to recalculate the kernel matrix elements.

When using `svmtrain` on large data sets, and you run out of memory or the optimization step is very time consuming, try either of the following:

- Use a smaller number of samples and use cross-validation to test the performance of the classifier.
- Set `'Method'` to `'SMO'`, and set the `kernelcachelimit` option as large as your system permits.

- "Support Vector Machines (SVM)" on page 16-170
- "Grouping Variables" on page 2-52

References

[1] Kecman, V., Learning and Soft Computing, MIT Press, Cambridge, MA. 2001.

[2] Suykens, J.A.K., Van Gestel, T., De Brabanter, J., De Moor, B., and Vandewalle, J., Least Squares Support Vector Machines, World Scientific, Singapore, 2002.

[3] Scholkopf, B., and Smola, A.J., Learning with Kernels, MIT Press, Cambridge, MA. 2002.

[4] Cristianini, N., and Shawe-Taylor, J. (2000). An Introduction to Support Vector Machines and Other Kernel-based Learning Methods, First Edition (Cambridge: Cambridge University Press). http://www.support-vector.net/

See Also

`svmclassify` | `classify`

table2dataset

Convert table to dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds = table2dataset(t)
```

Description

`ds = table2dataset(t)` converts a table to a dataset array.

Examples

Convert a Table to a Dataset Array

Load the sample data, which contains nutritional information for 77 cereals.

```
load cereal;
```

Create a table containing the calorie, protein, fat, and name data for the first five cereals. Label the variables.

```
Calories = Calories(1:5);
Protein = Protein(1:5);
Fat = Fat(1:5);
Name = Name(1:5);

cereal = table(Calories,Protein,Fat,'RowNames',Name)
```

```
cereal =
```

```
                            Calories    Protein    Fat
                            --------    -------    ---
    100% Bran                70         4          1
    100% Natural Bran       120         3          5
    All-Bran                 70         4          1
    All-Bran with Extra Fiber 50        4          0
    Almond Delight          110         2          2
```

Convert the table to a dataset array.

```
ds = table2dataset(cereal)
```

```
ds =

                            Calories    Protein    Fat
    100% Bran                70         4          1
    100% Natural Bran       120         3          5
    All-Bran                 70         4          1
    All-Bran with Extra Fiber 50        4          0
    Almond Delight          110         2          2
```

Input Arguments

`t` — Input table

table

Input table to convert to a dataset array, specified as a table. Each variable in t becomes a variable in the output dataset array ds.

Example:

Data Types: `table`

Output Arguments

`ds` — Output dataset array

dataset array

Output dataset array, returned as a dataset array containing the variables from the input table t.

More About

- "Array Dimensions"
- "Dataset Arrays" on page 2-132

See Also

`dataset` | `table`

tabulate

Frequency table

Syntax

```
tbl = tabulate(x)
tabulate(x)
```

Description

`tbl = tabulate(x)` creates a frequency table of data in vector `x`. Information in `tbl` is arranged as follows:

- 1st column — The unique values of `x`
- 2nd column — The number of instances of each value
- 3rd column — The percentage of each value

If `x` is a numeric array, `tbl` is a numeric matrix. If the elements of `x` are nonnegative integers, `tbl` includes 0 counts for integers between `1` and `max(x)` that do not appear in `x`.

If `x` is a categorical variable, character array, or cell array of strings, `tbl` is a cell array.

`tabulate(x)` with no output arguments displays the table in the command window.

Examples

```
tabulate([1 2 4 4 3 4])
  Value  Count  Percent
  1      1      16.67%
  2      1      16.67%
  3      1      16.67%
  4      3      50.00%
```

More About

- “Grouping Variables” on page 2-52

See Also

`pareto`

tblread

Read tabular data from file

Syntax

```
[data,varnames,casenames] = tblread
[data,varnames,casenames] = tblread(filename)
[data,varnames,casenames] = tblread(filename,delimiter)
```

Description

`[data,varnames,casenames] = tblread` displays the File Open dialog box for interactive selection of a tabular data file. The file format has variable names in the first row, case names in the first column and data starting in the (2, 2) position. Outputs are:

- `data` — Numeric matrix with a value for each variable-case pair
- `varnames` — String matrix containing the variable names in the first row of the file
- `casenames` — String matrix containing the names of each case in the first column of the file

`[data,varnames,casenames] = tblread(filename)` allows command line specification of the name of a file in the current folder, or the complete path name of any file, using the string *`filename`*.

`[data,varnames,casenames] = tblread(filename,delimiter)` reads from the file using *`delimiter`* as the delimiting character. Accepted values for *`delimiter`* are:

- `' '` or `'space'`
- `'\t'` or `'tab'`
- `','` or `'comma'`
- `';'` or `'semi'`
- `'|'` or `'bar'`

The default value of *`delimiter`* is `'space'`.

Examples

```
[data,varnames,casenames] = tblread('sat.dat')
data =
  470  530
  520  480

varnames =
Male
Female

casenames =
Verbal
Quantitative
```

See Also

`tblwrite` | `tdfread` | `caseread`

tblwrite

Write tabular data to file

Syntax

```
tblwrite(data,varnames,casenames)
tblwrite(data,varnames,casenames,filename)
tblwrite(data,varnames,casenames,filename,delimiter)
```

Description

`tblwrite(data,varnames,casenames)` displays the **File Open** dialog box for interactive specification of the tabular data output file. The file format has variable names in the first row, case names in the first column and `data` starting in the (2,2) position.

`varnames` is a string matrix containing the variable names. `casenames` is a string matrix containing the names of each case in the first column. `data` is a numeric matrix with a value for each variable-case pair.

`tblwrite(data,varnames,casenames,filename)` specifies a file in the current folder, or the complete path name of any file in the string *`filename`*.

`tblwrite(data,varnames,casenames,filename,delimiter)` writes to the file using *`delimiter`* as the delimiting character. The following table lists the accepted character values for *`delimiter`* and their equivalent string values.

Character	String
`' '`	`'space'`
`'\t'`	`'tab'`
`','`	`'comma'`
`';'`	`'semi'`
`'|'`	`'bar'`

The default value of *`delimiter`* is `'space'`.

Examples

Continuing the example from `tblread`:

```
tblwrite(data,varnames,casenames,'sattest.dat')
type sattest.dat
               Male  Female
Verbal       470  530
Quantitative  520  480
```

See Also

`casewrite` | `tblread`

tcdf

Student's *t* cumulative distribution function

Syntax

```
p = tcdf(x,nu)
p = tcdf(x,nu,'upper')
```

Description

`p = tcdf(x,nu)` returns the cumulative distribution function (cdf) of the Student's *t* distribution at each of the values in `x` using the corresponding degrees of freedom in `nu`. `x` and `nu` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

`p = tcdf(x,nu,'upper')` returns the complement of the Student's *t* cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

Examples

Compute Student's *t* cdf

```
mu = 1;     % Population mean
sigma = 2;  % Population standard deviation
n = 100;    % Sample size

rng default   % For reproducibility
x = normrnd(mu,sigma,n,1);  % Random sample from population

xbar = mean(x);  % Sample mean
s = std(x);      % Sample standard deviation
t = (xbar - mu)/(s/sqrt(n))
```

```
t =

    1.0589

p = 1-tcdf(t,n-1) % Probability of larger t-statistic

p =

    0.1461
```

This probability is the same as the p value returned by a t test of the null hypothesis that the sample comes from a normal population with mean μ

```
[h,ptest] = ttest(x,mu,0.05,'right')

h =

     0

ptest =

    0.1461
```

More About

Student's *t* cdf

The cumulative distribution function (cdf) of Student's t distribution is

$$p = F(x \mid \nu) = \int_{-\infty}^{x} \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{t^2}{\nu}\right)^{\frac{\nu+1}{2}}} dt$$

where ν is the degrees of freedom and $\Gamma(\cdot)$ is the Gamma function. The result p is the probability that a single observation from the t distribution with ν degrees of freedom will fall in the interval $[-\infty, x]$.

- "Student's t Distribution" on page B-146

See Also

`tpdf` | `tinv` | `tstat` | `trnd` | `cdf`

tdfread

Read tab-delimited file

Syntax

```
tdfread
tdfread(filename)
tdfread(filename,delimiter)
s = tdfread(filename,...)
```

Description

`tdfread` displays the **File Open** dialog box for interactive selection of a data file, then reads data from the file. The file should have variable names separated by tabs in the first row, and data values separated by tabs in the remaining rows. `tdfread` creates variables in the workspace, one for each column of the file. The variable names are taken from the first row of the file. If a column of the file contains only numeric data in the second and following rows, `tdfread` creates a `double` variable. Otherwise, `tdfread` creates a `char` variable. After all values are imported, `tdfread` displays information about the imported values using the format of the `tdfread` command.

`tdfread(`*`filename`*`)` allows command line specification of the name of a file in the current folder, or the complete path name of any file, using the string *`filename`*.

`tdfread(`*`filename`*`,`*`delimiter`*`)` indicates that the character specified by *`delimiter`* separates columns in the file. Accepted values for *`delimiter`* are:

- `' '` or `'space'`
- `'\t'` or `'tab'`
- `','` or `'comma'`
- `';'` or `'semi'`
- `'|'` or `'bar'`

The default delimiter is `'tab'`.

`s = tdfread(filename,...)` returns a scalar structure `s` whose fields each contain a variable.

Examples

The following displays the contents of the file `sat2.dat`:

```
type sat2.dat

Test,Gender,Score
Verbal,Male,470
Verbal,Female,530
Quantitative,Male,520
Quantitative,Female,480
```

The following creates the variables `Gender`, `Score`, and `Test` from the file `sat2.dat` and displays the contents of the MATLAB workspace:

```
tdfread('sat2.dat',',')

Name    Size    Bytes    Class    Attributes

Gender  4x6     48       char
Score   4x1     32       double
Test    4x12    96       char
```

See Also

`tblread` | `caseread`

ClassificationDiscriminant.template

Class: ClassificationDiscriminant

Discriminant analysis classifier template for ensemble (to be removed)

Compatibility

`ClassificationDiscriminant.template` will be removed in a future release. Use `templateDiscriminant` instead.

Syntax

```
t = ClassificationDiscriminant.template()
t = ClassificationDiscriminant.template(Name,Value)
```

Description

`t = ClassificationDiscriminant.template()` returns a learner template suitable to use in the `fitensemble` function.

`t = ClassificationDiscriminant.template(Name,Value)` creates a template with additional options specified by one or more Name,Value pair arguments.

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Delta'` — Linear coefficient threshold
0 (default) | nonnegative scalar value

Linear coefficient threshold, specified as the comma-separated pair consisting of `'Delta'` and a nonnegative scalar value. If a coefficient of `obj` has magnitude smaller than `Delta`, `obj` sets this coefficient to `0`, and you can eliminate the corresponding predictor from the model. Set `Delta` to a higher value to eliminate more predictors.

`Delta` must be `0` for quadratic discriminant models.

Data Types: `single` | `double`

`'DiscrimType'` — Discriminant type
`'linear'` (default) | `'quadratic'` | `'diagLinear'` | `'diagQuadratic'` | `'pseudoLinear'` | `'pseudoQuadratic'`

Discriminant type, specified as the comma-separated pair consisting of `'DiscrimType'` and one of the following:

- `'linear'`
- `'quadratic'`
- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

Example: `'DiscrimType','quadratic'`

`'FillCoeffs'` — `Coeffs` property flag
`'on'` | `'off'`

`Coeffs` property flag, specified as the comma-separated pair consisting of `'FillCoeffs'` and `'on'` or `'off'`. Setting the flag to `'on'` populates the `Coeffs` property in the classifier object. This can be computationally intensive, especially when cross validating. The default is `'on'`, unless you specify a cross validation name-value pair, in which case the flag is set to `'off'` by default.

Example: `'FillCoeffs','off'`

`'Gamma'` — Regularization parameter
scalar value in the range `[0,1]`

Parameter for regularizing the correlation matrix of predictors, specified as the comma-separated pair consisting of `'Gamma'` and a scalar value in the range `[0,1]`.

- Linear discriminant — Scalar value in the range `[0,1]`.
  - If you pass a value strictly between `0` and `1`, `fitcdiscr` sets the discriminant type to `'Linear'`.
  - If you pass `0` for `Gamma` and `'Linear'` for `DiscrimType`, and if the correlation matrix is singular, `fitcdiscr` sets `Gamma` to the minimal value required for inverting the covariance matrix.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagLinear'`.
- Quadratic discriminant — Either `0` or `1`.
  - If you pass `0` for `Gamma` and `'Quadratic'` for `DiscrimType`, and if one of the classes has a singular covariance matrix, `fitcdiscr` errors.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagQuadratic'`.
  - If you set Gamma to a value between `0` and `1` for a quadratic discriminant, `fitcdiscr` errors.

Example: `'Gamma',1`

Data Types: `single | double`

`'SaveMemory'` — Flag to save covariance matrix
`'off'` (default) | `'on'`

Flag to save covariance matrix, specified as the comma-separated pair consisting of `'SaveMemory'` and either `'on'` or `'off'`. If you specify `'on'`, then `fitcdiscr` does not store the full covariance matrix, but instead stores enough information to compute the matrix. The `predict` method computes the full covariance matrix for prediction, and does not store the matrix. If you specify `'off'`, then `fitcdiscr` computes and stores the full covariance matrix in `obj`.

Specify `SaveMemory` as `'on'` when the input matrix contains thousands of predictors.

Example: `'SaveMemory','on'`

Output Arguments

`t` — Discriminant analysis classification template
classification template object

Discriminant analysis classification template suitable to use in the `fitensemble` function, returned as a classification template object. In an ensemble, `t` specifies how to create the discriminant analysis classifier.

Examples

Discriminant Analysis Template for Nondefault Options

Create a nondefault discriminant analysis template for use in `fitensemble`.

Create a template for pseudolinear discriminant analysis.

```
t = ClassificationDiscriminant.template('discrimType','pseudoLinear')
```

```
t =

Fit template for classification Discriminant.

    DiscrimType: 'pseudoLinear'
          Gamma: []
          Delta: []
     FillCoeffs: []
     SaveMemory: []
         Method: 'Discriminant'
           Type: 'classification'
```

You can use `t` for ensemble learning.

See Also

`ClassificationDiscriminant` | `fitensemble` | `templateDiscriminant`

ClassificationKNN.template

Class: ClassificationKNN

k-nearest neighbor classifier template for ensemble (to be removed)

Compatibility

`ClassificationKNN.template` will be removed in a future release. Use `templateKNN` instead.

Syntax

```
t = ClassificationKNN.template()
t = ClassificationKNN.template(Name,Value)
```

Description

`t = ClassificationKNN.template()` returns a learner template suitable to use in the `fitensemble` function.

`t = ClassificationKNN.template(Name,Value)` creates a template with additional options specified by one or more Name,Value pair arguments.

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'BreakTies'` — Tie-breaking algorithm
`'smallest'` (default) | `'nearest'` | `'random'`

Tie-breaking algorithm used by the `predict` method if multiple classes have the same smallest cost, specified as the comma-separated pair consisting of `'BreakTies'` and one of the following:

- `'smallest'` — Use the smallest index among tied groups.
- `'nearest'` — Use the class with the nearest neighbor among tied groups.
- `'random'` — Use a random tiebreaker among tied groups.

By default, ties occur when multiple classes have the same number of nearest points among the `K` nearest neighbors.

Example: `'BreakTies','nearest'`

`'BucketSize'` — Maximum data points in node

`50` (default) | positive integer value

Maximum number of data points in the leaf node of the *k*d-tree, specified as the comma-separated pair consisting of `'BucketSize'` and a positive integer value. This argument is meaningful only when `NSMethod` is `'kdtree'`.

Example: `'BucketSize',40`

Data Types: `single` | `double`

`'Cov'` — Covariance matrix

`nancov(X)` (default) | positive definite matrix of scalar values

Covariance matrix, specified as the comma-separated pair consisting of `'Cov'` and a positive definite matrix of scalar values representing the covariance matrix when computing the Mahalanobis distance. This argument is only valid when `'Distance'` is `'mahalanobis'`.

You cannot simultaneously specify `'Standardize'` and either of `'Scale'` or `'Cov'`.

Data Types: `single` | `double`

`'Distance'` — Distance metric

valid distance metric string | function handle

Distance metric, specified as the comma-separated pair consisting of `'Distance'` and a valid distance metric string or function handle. The allowable strings depend on the `NSMethod` parameter, which you set in `fitcknn`, and which exists as a field in

`ModelParameters`. If you specify `CategoricalPredictors` as `'all'`, then the default distance metric is `'hamming'`. Otherwise, the default distance metric is `'euclidean'`.

NSMethod	Distance Metric Names
`exhaustive`	Any distance metric of `ExhaustiveSearcher`
`kdtree`	`'cityblock'`, `'chebychev'`, `'euclidean'`, or `'minkowski'`

For definitions, see “Distance Metrics”.

This table includes valid distance metrics of `ExhaustiveSearcher`.

Value	Description
`'cityblock'`	City block distance.
`'chebychev'`	Chebychev distance (maximum coordinate difference).
`'correlation'`	One minus the sample linear correlation between observations (treated as sequences of values).
`'cosine'`	One minus the cosine of the included angle between observations (treated as vectors).
`'euclidean'`	Euclidean distance.
`'hamming'`	Hamming distance, percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of X, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair argument.
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'Exponent'` name-value pair argument.
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between X and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from X, `S = nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair argument.

Value	Description
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@distfun`	Distance function handle. *`distfun`* has the form
	`function D2 = DISTFUN(ZI,ZJ)`
	`% calculation of  distance`
	`...`
	where
	• `ZI` is a 1-by-N vector containing one row of X or y.
	• `ZJ` is an M2-by-N matrix containing multiple rows of X or y.
	• `D2` is an M2-by-1 vector of distances, and `D2(k)` is the distance between observations `ZI` and `ZJ(J,:)`.

Example: `'Distance','minkowski'`

Data Types: `function_handle`

`'DistanceWeight'` — Distance weighting function

`'equal'` (default) | `'inverse'` | `'squaredinverse'` | function handle

Distance weighting function, specified as the comma-separated pair consisting of `'DistanceWeight'` and either a function handle or one of the following strings specifying the distance weighting function.

DistanceWeight	Meaning
`'equal'`	No weighting
`'inverse'`	Weight is 1/distance
`'squaredinverse'`	Weight is $1/\text{distance}^2$
`@fcn`	*`fcn`* is a function that accepts a matrix of nonnegative distances, and returns a matrix the same size containing nonnegative distance weights. For example, `'squaredinverse'` is equivalent to `@(d)d.^(-2)`.

Example: `'DistanceWeight','inverse'`

Data Types: `function_handle`

'Exponent' — Minkowski distance exponent

2 (default) | positive scalar value

Minkowski distance exponent, specified as the comma-separated pair consisting of 'Exponent' and a positive scalar value. This argument is only valid when 'Distance' is 'minkowski'.

Example: 'Exponent',3

Data Types: single | double

'IncludeTies' — Tie inclusion flag

false (default) | true

Tie inclusion flag, specified as the comma-separated pair consisting of 'IncludeTies' and a logical value indicating whether predict includes all the neighbors whose distance values are equal to the Kth smallest distance. If IncludeTies is true, predict includes all these neighbors. Otherwise, predict uses exactly K neighbors.

Example: 'IncludeTies',true

Data Types: logical

'NSMethod' — Nearest neighbor search method

'kdtree' | 'exhaustive'

Nearest neighbor search method, specified as the comma-separated pair consisting of 'NSMethod' and 'kdtree' or 'exhaustive'.

- 'kdtree' — Create and use a *k*d-tree to find nearest neighbors. 'kdtree' is valid when the distance metric is one of the following:
  - 'euclidean'
  - 'cityblock'
  - 'minkowski'
  - 'chebyshev'
- 'exhaustive' — Use the exhaustive search algorithm. The distance values from all points in X to each point in y are computed to find nearest neighbors.

The default is 'kdtree' when X has 10 or fewer columns, X is not sparse, and the distance metric is a 'kdtree' type; otherwise, 'exhaustive'.

Example: 'NSMethod','exhaustive'

`'NumNeighbors'` — Number of nearest neighbors to find

`1` (default) | positive integer value

Number of nearest neighbors in X to find for classifying each point when predicting, specified as the comma-separated pair consisting of `'NumNeighbors'` and a positive integer value.

Example: `'NumNeighbors',3`

Data Types: `single` | `double`

`'Scale'` — Distance scale

`nanstd(X)` (default) | vector of nonnegative scalar values

Distance scale, specified as the comma-separated pair consisting of `'Scale'` and a vector containing nonnegative scalar values with length equal to the number of columns in X. Each coordinate difference between X and a query point is scaled by the corresponding element of `Scale`. This argument is only valid when `'Distance'` is `'seuclidean'`.

You cannot simultaneously specify `'Standardize'` and either of `'Scale'` or `'Cov'`.

Data Types: `single` | `double`

Output Arguments

`t` — Classification template

classification template object

K-nearest neighbor classification template suitable to use in the `fitensemble` function. In an ensemble, `t` specifies how to create the KNN classifier.

Examples

KNN template for nondefault options

Create a nondefault *k*-nearest neighbor template for use in `fitensemble`.

Create a template for 5-nearest neighbor search.

```
t = ClassificationKNN.template('NumNeighbors',5)
```

```
t =

Fit template for classification KNN.

      NumNeighbors: 5
          NSMethod: ''
          Distance: ''
        BucketSize: []
       IncludeTies: ''
    DistanceWeight: []
         BreakTies: []
          Exponent: []
               Cov: []
             Scale: []
            Method: 'KNN'
              Type: 'classification'
```

You can use `t` for ensemble learning.

- "Random Subspace Classification" on page 16-124

See Also

`ClassificationKNN` | `fitensemble`

ClassificationTree.template

Class: ClassificationTree

Create classification template (to be removed)

Compatibility

`ClassificationTree.template` will be removed in a future release. Use `templateTree` instead.

Syntax

```
t = ClassificationTree.template
t = ClassificationTree.template(Name,Value)
```

Description

`t = ClassificationTree.template` returns a learner template suitable to use in the `fitensemble` function.

`t = ClassificationTree.template(Name,Value)` creates a template with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

'AlgorithmForCategorical'

Algorithm to find the best split on a categorical predictor for data with $K = 3$ or more classes. The available algorithms are:

'Exact'	For a categorical predictor with C categories, consider all $2^{C-1} - 1$ combinations.
'PullLeft'	Start with all C categories on the right branch. Consider moving each category to the left branch as it achieves the minimum impurity for the K classes among the remaining categories. Out of this sequence, choose the split that has the lowest impurity.
'PCA'	Compute a score for each category using the inner product between the first principal component of a weighted covariance matrix (of the centered class probability matrix) and the vector of class probabilities for that category. Sort the scores in ascending order, and consider all $C - 1$ splits.
'OVAbyClass'	Start with all C categories on the right branch. For each class, order the categories based on their probability for that class. For the first class, consider moving each category to the left branch in order, recording the impurity criterion at each move. Repeat for the remaining classes. Out of this sequence, choose the split that has the minimum impurity.

Default: `ClassificationTree` selects the optimal subset of algorithms for each split using the known number of classes and levels of a categorical predictor. For two classes, `ClassificationTree` always performs the exact search.

`'MaxCat'`

`ClassificationTree` splits a categorical predictor using the exact search algorithm if the predictor has at most `MaxCat` levels in the split node. Otherwise, `ClassificationTree` finds the best categorical split using one of the inexact algorithms.

Specify `MaxCat` as a numeric nonnegative scalar value. Passing a small value can lead to long computation time and memory overload.

Default: `10`

`'MergeLeaves'`

String that specifies whether to merge leaves after the tree is grown. Values are `'on'` or `'off'`.

When `'on'`, `ClassificationTree` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `ClassificationTree` does not merge leaves.

Default: `'off'`

`'MinLeaf'`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Half the number of training observations for boosting, `1` for bagging

`'MinParent'`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `ClassificationTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Number of training observations for boosting, `2` for bagging

`'NVarToSample'`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'` for boosting, square root of number of predictors for bagging

`'Prune'`

When `'on'`, `ClassificationTree` grows the classification tree and computes the optimal sequence of pruned subtrees. When `'off'` `ClassificationTree` grows the tree without pruning.

Default: `'off'`

`'PruneCriterion'`

String with the pruning criterion, either `'error'` or `'impurity'`.

Default: `'error'`

`'SplitCriterion'`

Criterion for choosing a split. One of `'gdi'` (Gini's diversity index), `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction (also known as cross entropy).

Default: `'gdi'`

`'Surrogate'`

String describing whether to find surrogate decision splits at each branch node. Specify as `'on'`, `'off'`, `'all'`, or a positive scalar value.

- When `'on'`, `ClassificationTree` finds at most 10 surrogate splits at each branch node.
- When set to a positive integer value, `ClassificationTree` finds at most the specified number of surrogate splits at each branch node.
- When set to `'all'`, `ClassificationTree` finds all surrogate splits at each branch node. The `'all'` setting can use much time and memory.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also enables you to compute measures of predictive association between predictors.

Default: `'off'`

Output Arguments

`t`

Classification tree template suitable to use in the `fitensemble` function. In an ensemble, `t` specifies how to grow the classification trees.

Examples

Construct a Classification Template with Surrogate Splits

Create a classification template with surrogate splits, and train an ensemble for the Fisher iris model with the template.

```
t = ClassificationTree.template('surrogate','on');
load fisheriris
ens = fitensemble(meas,species,'AdaBoostM2',100,t);
```

References

[1] Coppersmith, D., S. J. Hong, and J. R. M. Hosking. “Partitioning Nominal Attributes in Decision Trees.” *Data Mining and Knowledge Discovery*, Vol. 3, 1999, pp. 197–217.

See Also

`ClassificationTree` | `fitctree` | `templateTree` | `fitensemble`

RegressionTree.template

Class: RegressionTree

Create regression template (to be removed)

Compatibility

`RegressionTree.template` will be removed in a future release. Use `templateTree` instead.

Syntax

```
t = RegressionTree.template
t = RegressionTree.template(Name,Value)
```

Description

`t = RegressionTree.template` returns a learner template suitable to use in the `fitensemble` function.

`t = RegressionTree.template(Name,Value)` creates a template with additional options specified by one or more Name,Value pair arguments. You can specify several name-value pair arguments in any order as `Name1,Value1,…,NameN,ValueN`.

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'MergeLeaves'`

String that specifies whether to merge leaves after the tree is grown. Values are `'on'` or `'off'`.

When `'on'`, `RegressionTree` merges leaves that originate from the same parent node, and that give a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, `RegressionTree` does not merge leaves.

Default: `'off'`

`'MinLeaf'`

Each leaf has at least `MinLeaf` observations per tree leaf. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Half the number of training observations for boosting, `5` for bagging

`'MinParent'`

Each branch node in the tree has at least `MinParent` observations. If you supply both `MinParent` and `MinLeaf`, `RegressionTree` uses the setting that gives larger leaves: `MinParent=max(MinParent,2*MinLeaf)`.

Default: Number of training observations for boosting, `10` for bagging

`'NVarToSample'`

Number of predictors to select at random for each split. Can be a positive integer or `'all'`, which means use all available predictors.

Default: `'all'` for boosting, one third of the number of predictors for bagging

`'Prune'`

When `'on'`, `RegressionTree` grows the regression tree and computes the optimal sequence of pruned subtrees. When `'off' RegressionTree` grows the tree without pruning.

Default: `'off'`

`'Surrogate'`

String describing whether to find surrogate decision splits at each branch node. Specify as `'on'`, `'off'`, `'all'`, or a positive scalar value.

- When `'on'`, `RegressionTree` finds at most 10 surrogate splits at each branch node.
- When set to a positive integer value, `RegressionTree` finds at most the specified number of surrogate splits at each branch node.
- When set to `'all'`, `RegressionTree` finds all surrogate splits at each branch node. The `'all'` setting can use much time and memory.

Use surrogate splits to improve the accuracy of predictions for data with missing values. The setting also enables you to compute measures of predictive association between predictors.

Default: `'off'`

Output Arguments

`t`

Regression tree template suitable to use in the `fitensemble` function. In an ensemble, `t` specifies how to grow the regression trees.

Examples

Create a regression template with surrogate splits, and train an ensemble for the `carsmall` data with the template:

```
t = RegressionTree.template('surrogate','on');
load carsmall
X = [Acceleration Displacement Horsepower Weight];
ens = fitensemble(X,MPG,'LSBoost',100,t);
```

See Also

`RegressionTree` | `fitrtree` | `fitensemble`

templateDiscriminant

Discriminant analysis classifier template

Syntax

```
t = templateDiscriminant()
t = templateDiscriminant(Name,Value)
```

Description

`t = templateDiscriminant()` returns a discriminant analysis learner template suitable for training ensembles or error-correcting output code (ECOC) multiclass models.

If you specify a default template, then the software uses default values for all input arguments during training.

Specify `t` as a learner in `fitensemble` or `fitcecoc`.

`t = templateDiscriminant(Name,Value)` creates a template with additional options specified by one or more name-value pair arguments.

For example, you can specify the discriminant type or the regularization parameter.

If you display `t` in the Command Window, then all options appear empty (`[ ]`), except those that you specify using name-value pair arguments. During training, the software uses default values for empty options.

Examples

Create a Discriminant Analysis Template for Ensemble Learning

Create a nondefault discriminant analysis template for use in fitensemble.

Load Fisher's iris data set.

```
load fisheriris
```

Create a template for pseudolinear discriminant analysis.

```
t = templateDiscriminant('DiscrimType','pseudoLinear')
```

```
t =

Fit template for classification Discriminant.

    DiscrimType: 'pseudoLinear'
          Gamma: []
          Delta: []
     FillCoeffs: []
     SaveMemory: []
         Method: 'Discriminant'
           Type: 'classification'
```

All properties of the template object are empty except for `DiscrimType`, `Method`, and `Type`. When trained on, the software fills in the empty properties with their respective default values.

Specify `t` as a weak learner for a classification ensemble.

```
Mdl = fitensemble(meas,species,'Subspace',100,t);
```

Display the in-sample (resubstitution) misclassification error.

```
L = resubLoss(Mdl)
```

```
L =

    0.0400
```

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'DiscrimType','pseudoLinear','SaveMemory','on'` specifies a template for pseudolinear discriminant analysis that does not store the full covariance matrix.

`'Delta'` — Linear coefficient threshold

`0` (default) | nonnegative scalar value

Linear coefficient threshold, specified as the comma-separated pair consisting of `'Delta'` and a nonnegative scalar value. If a coefficient of `obj` has magnitude smaller than `Delta`, `obj` sets this coefficient to `0`, and you can eliminate the corresponding predictor from the model. Set `Delta` to a higher value to eliminate more predictors.

`Delta` must be `0` for quadratic discriminant models.

Data Types: `single` | `double`

`'DiscrimType'` — Discriminant type

`'linear'` (default) | `'quadratic'` | `'diagLinear'` | `'diagQuadratic'` | `'pseudoLinear'` | `'pseudoQuadratic'`

Discriminant type, specified as the comma-separated pair consisting of `'DiscrimType'` and one of the following:

- `'linear'`
- `'quadratic'`
- `'diagLinear'`
- `'diagQuadratic'`
- `'pseudoLinear'`
- `'pseudoQuadratic'`

Example: `'DiscrimType','quadratic'`

`'FillCoeffs'` — `Coeffs` property flag

`'on'` | `'off'`

`Coeffs` property flag, specified as the comma-separated pair consisting of `'FillCoeffs'` and `'on'` or `'off'`. Setting the flag to `'on'` populates the `Coeffs` property in the classifier object. This can be computationally intensive, especially when

cross validating. The default is `'on'`, unless you specify a cross validation name-value pair, in which case the flag is set to `'off'` by default.

Example: `'FillCoeffs','off'`

`'Gamma'` — Regularization parameter

scalar value in the range `[0,1]`

Parameter for regularizing the correlation matrix of predictors, specified as the comma-separated pair consisting of `'Gamma'` and a scalar value in the range `[0,1]`.

- Linear discriminant — Scalar value in the range `[0,1]`.
  - If you pass a value strictly between `0` and `1`, `fitcdiscr` sets the discriminant type to `'Linear'`.
  - If you pass `0` for `Gamma` and `'Linear'` for `DiscrimType`, and if the correlation matrix is singular, `fitcdiscr` sets `Gamma` to the minimal value required for inverting the covariance matrix.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagLinear'`.
- Quadratic discriminant — Either `0` or `1`.
  - If you pass `0` for `Gamma` and `'Quadratic'` for `DiscrimType`, and if one of the classes has a singular covariance matrix, `fitcdiscr` errors.
  - If you set `Gamma` to `1`, `fitcdiscr` sets the discriminant type to `'DiagQuadratic'`.
  - If you set Gamma to a value between `0` and `1` for a quadratic discriminant, `fitcdiscr` errors.

Example: `'Gamma',1`

Data Types: `single` | `double`

`'SaveMemory'` — Flag to save covariance matrix

`'off'` (default) | `'on'`

Flag to save covariance matrix, specified as the comma-separated pair consisting of `'SaveMemory'` and either `'on'` or `'off'`. If you specify `'on'`, then `fitcdiscr` does not store the full covariance matrix, but instead stores enough information to compute the matrix. The `predict` method computes the full covariance matrix for prediction, and does not store the matrix. If you specify `'off'`, then `fitcdiscr` computes and stores the full covariance matrix in `obj`.

Specify `SaveMemory` as `'on'` when the input matrix contains thousands of predictors.

Example: `'SaveMemory','on'`

Output Arguments

`t` — Discriminant analysis classification template

template object

Discriminant analysis classification template suitable for training ensembles or error-correcting output code (ECOC) multiclass models, returned as a template object. Pass `t` to `fitensemble` or `fitcecoc` to specify how to create the discriminant analysis classifier for the ensemble or ECOC model, respectively.

If you display `t` to the Command Window, then all unspecified options appear empty (`[ ]`). However, the software replaces empty options with their corresponding default values during training.

See Also

`ClassificationDiscriminant` | `fitcecoc` | `fitensemble` | `predict`

templateECOC

Error-correcting output codes learner template

Syntax

```
t = templateECOC()
t = templateECOC(Name,Value)
```

Description

`t = templateECOC()` returns an error-correcting output codes (ECOC) classification learner template.

If you specify a default template, then the software uses default values for all input arguments during training.

`t = templateECOC(Name,Value)` returns a template with additional options specified by one or more name-value pair arguments.

For example, you can specify a coding design, whether to fit posterior probabilities, or the types of binary learners.

If you display `t` in the Command Window, then all options appear empty (`[ ]`), except those that you specify using name-value pair arguments. During training, the software uses default values for empty options.

Examples

Create a Default ECOC Classification Learner Template

Use `templateECOC` to create a default ECOC template.

```
t = templateECOC()
```

```
t =

Fit template for classification ECOC.

    BinaryLearners: ''
            Coding: ''
      FitPosterior: []
           Options: []
    VerbosityLevel: []
            Method: 'ECOC'
              Type: 'classification'
```

All properties of the template object are empty except for `Method` and `Type`. When you pass `t` to testckfold, the software fills in the empty properties with their respective default values. For example, the software fills the `BinaryLearners` property with `'SVM'`. For details on other default values, see fitcecoc.

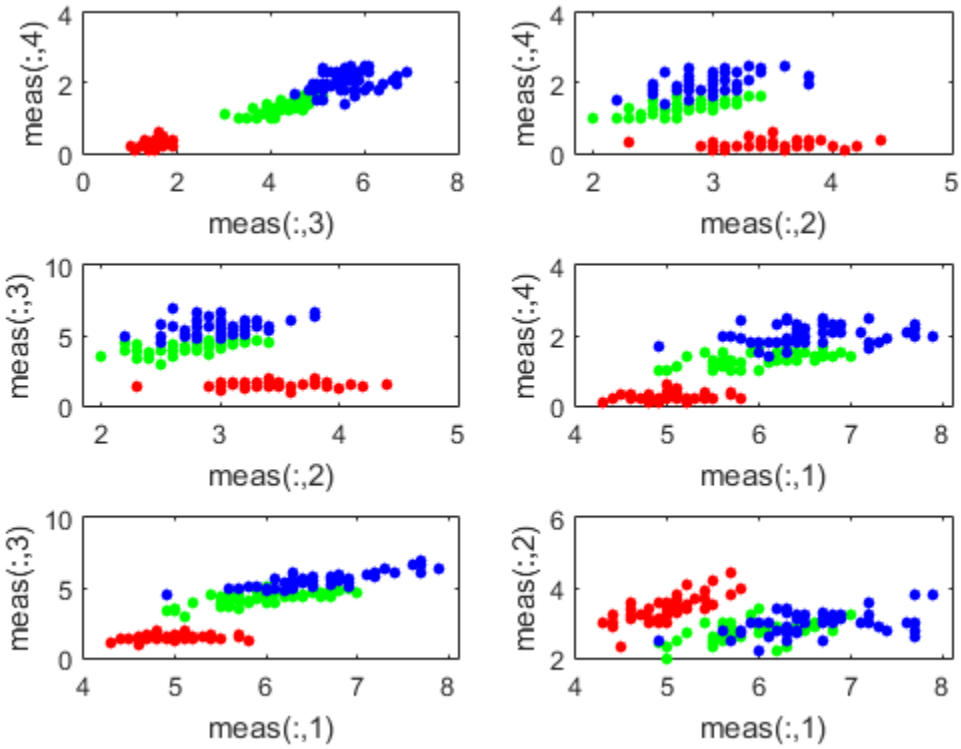
`t` is a plan for an ECOC learner. When you create it, no computation occurs. You can pass `t` to `testckfold` to specify a plan for an ECOC classification model to statistically compare with another model.

Statistically Compare Performance of Two ECOC Classification Models

One way to select predictors or features is to train two models where one that uses a subset of the predictors that trained the other. Statistically compare the predictive performances of the models. If there is sufficient evidence that model trained on fewer predictors performs better than the model trained using more of the predictors, then you can proceed with a more efficient model.

Load Fisher's iris data set. Plot all 2-dimensional combinations of predictors.

```
load fisheriris
d = size(meas,2); % Number of predictors
pairs = combnk(1:d,2);

figure;
for j = 1:size(pairs,1);
    subplot(3,2,j);
    gscatter(meas(:,pairs(j,1)),meas(:,pairs(j,2)),species);
    xlabel(sprintf('meas(:,%d)',pairs(j,1)));
    ylabel(sprintf('meas(:,%d)',pairs(j,2)));
    legend off;
end
```



Based on the scatterplot, `meas(:,3)` and `meas(:,4)` seem like they separate the groups well.

Create an ECOC template. Specify to use a one-versus-all coding design.

```
t = templateECOC('Coding','onevsall');
```

By default, the ECOC model uses linear SVM binary learners. You can choose other, supported algorithms by specifying them using the `'Learners'` name-value pair argument.

Test whether an ECOC model that is just trained using predictors 3 and 4 performs at most as well as an ECOC model that is trained using all predictors. Rejecting this null hypothesis means that the ECOC model trained using predictors 3 and 4 performs

better than the ECOC model trained using all predictors. Suppose C_1 represents the classification error of the ECOC model trained using predictors 3 and 4 and C_2 represents the classification error of the ECOC model trained using all predictors, then the test is:

$$H_0 : C_1 \geq C_2$$
$$H_1 : C_1 < C_2$$

By default, `testckfold` conducts a 5-by-2 k-fold F test, which is not appropriate as a one-tailed test. Specify to conduct a 5-by-2 k-fold t test.

```
rng(1); % For reproducibility
[h,pValue] = testckfold(t,t,meas(:,pairs(1,:)),meas,species,...
    'Alternative','greater','Test','5x2t')
```

```
h =

     0


pValue =

    0.8940
```

The `h = 0` indicates that there is not enough evidence to suggest that the model trained using predictors 3 and 4 is more accurate than the model trained using all predictors.

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example:
`'Coding','ternarycomplete','FitPosterior',true,'Learners','tree'`

specifies a ternary complete coding design, to transform scores to posterior probabilities, and to grow classification trees for all binary learners.

`'Coding'` — Coding design
`'onevsall'` (default) | `'allpairs'` | `'binarycomplete'` | `'denserandom'` | `'onevsone'` | `'ordinal'` | `'sparserandom'` | `'ternarycomplete'` | numeric matrix

Coding design name, specified as the comma-separated pair consisting of `'Coding'` and a numeric matrix or string.

This table summarizes the available, built-in coding designs.

Value	Number of Binary Learners	Description
`'allpairs'` and `'onevsone'`	$K(K-1)/2$	For each binary learner, one class is positive, another is negative, and the software ignores the rest. This design exhausts all combinations of class pair assignments.
`'binarycomplete'`	$2^{(K-1)}-1$	This design partitions the classes into all binary combinations, and does not ignore any classes. For each binary learner, all class assignments are `-1` and `1` with at least one positive and negative class in the assignment.
`'denserandom'`	Random, but approximately $10\log_2 K$	For each binary learner, the software randomly assigns classes into positive or negative classes, with at least one of each type. For more details, see "Random Coding Design Matrices" on page 22-1542.
`'onevsall'`	K	For each binary learner, one class is positive and the rest are negative. This design

Value	Number of Binary Learners	Description
		exhausts all combinations of positive class assignments.
`'ordinal'`	$K-1$	For the first binary learner, the first class is negative, and the rest positive. For the second binary learner, the first two classes are negative, the rest positive, and so on.
`'sparserandom'`	Random, but approximately $15\log_2 K$	For each binary learner, the software randomly assigns classes as positive or negative with probability 0.25 for each, and ignores classes with probability 0.5. For more details, see "Random Coding Design Matrices" on page 22-1542.
`'ternarycomplete'`	$\left(3^K-2^{(K+1)}+1\right)/2$	This design partitions the classes into all ternary combinations. All class assignments are `0`, `-1`, and `1` with at least one positive and one negative class in the assignment.

You can also specify a coding design using a custom coding matrix. The custom coding matrix is a K-by-L matrix. Each row corresponds to a class and each column corresponds to a binary learner. The class order (rows) corresponds to the order in `ClassNames`. Compose the matrix by following these guidelines:

- Every element of the custom coding matrix must be `-1`, `0`, or `1`, and the value must correspond to a dichotomous class assignment. This table describes the meaning of `Coding(i,j)`, that is, the class that learner `j` assigns to observations in class `i`.

Value	Dichotomous Class Assignment
`-1`	Negative class

Value	Dichotomous Class Assignment
0	Before training, learner `j` removes observations in class `i` from the data set.
1	Positive class

- Every column must contain at least one `-1` or `1`.
- For all column indices `i`,`j` such that $i \neq j$, `Coding(:,i)` cannot equal `Coding(:,j)` and `Coding(:,i)` cannot equal `-Coding(:,j)`.
- All rows of the custom coding matrix must be different.

For more details on the form of custom coding design matrices, see "Custom Coding Design Matrices" on page 22-1540.

Example: `'Coding','ternarycomplete'`

Data Types: `char` | `double` | `single` | `int16` | `int32` | `int64` | `int8`

`'FitPosterior'` — Flag indicating whether to transform scores to posterior probabilities
`false` or `0` (default) | `true` or `1`

Flag indicating whether to transform scores to posterior probabilities, specified as the comma-separated pair consisting of `'FitPosterior'` and a `true` (`1`) or `false` (`0`).

If `FitPosterior` is `true`, then the software transforms binary-learner classification scores to posterior probabilities. You can obtain posterior probabilities by using `kfoldPredict`, `predict`, or `resubPredict`.

Ensemble methods that do not fit posterior probabilities are `AdaBoostM2`, `LPBoost`, `RUSBoost`, `RobustBoost`, and `TotalBoost`. Therefore, if any binary learner is an ensemble that uses any of these methods, then the software generates an error.

Example: `'FitPosterior',true`

Data Types: `logical`

`'Learners'` — Binary learner templates
`'svm'` (default) | `'discriminant'` | `'knn'` | `'tree'` | template object | cell vector of template objects

Binary learner templates, specified as the comma-separated pair consisting of `'Learners'` and a string, template object, or cell vector of template objects.

Specifically, you can specify binary classifiers such as SVM, and the ensembles that use `GentleBoost`, `LogitBoost`, and `RobustBoost`, to solve multiclass problems. However, `fitcecoc` also supports multiclass models as binary classifiers.

- If `Learners` is a string, then the software trains each binary learner using the default values of the algorithm corresponding to the string. This table summarizes the available strings.

Value	Description
`'discriminant'`	Discriminant analysis. For default options, see `templateDiscriminant`.
`'knn'`	*k*-nearest neighbors. For default options, see `templateKNN`.
`'naivebayes'`	Naive Bayes. For default options, see `templateNaiveBayes`.
`'svm'`	SVM. For default options, see `templateSVM`.
`'tree'`	Classification trees. For default options, see `templateTree`.

- If `Learners` is a template object, then each binary learner trains according to the stored options. You can create a template object using:
  - `templateDiscriminant`, for discriminant analysis.
  - `templateEnsemble`, for ensemble learning. You must at least specify the learning method (`Method`), the number of learners (`NLearn`), and the type of learner (`Learners`). You cannot use the `AdaBoostM2` ensemble method for binary learning.
  - `templateKNN`, for *k*-nearest neighbors.
  - `templateNaiveBayes`, for naive Bayes.
  - `templateSVM`, for SVM.
  - `templateTree`, for classification trees.
- If `Learners` is cell vector of template objects, then:
  - Cell *j* corresponds to binary learner *j* (in other words, column *j* of the coding design matrix), and the cell vector must have length *L*. *L* is the number of columns in the coding design matrix. For details, see Coding.

- To use one of the built-in loss functions for prediction, then all binary learners must return a score in the same range. For example, you cannot include default SVM binary learners with default naive Bayes binary learners. The former returns a score in the range (-∞,∞), and the latter returns a posterior probability as a score. Otherwise, you must provide a custom loss as a function handle to functions such as `predict` and `loss`.

By default, the software trains learners using default SVM templates.

Example: `'Learners','tree'`

Output Arguments

`t` — ECOC classification template

template object

ECOC classification template, returned as a template object. Pass `t` to `testckfold` to specify how to create an ECOC classifier whose predictive performance you want to compare with another classifier.

If you display `t` to the Command Window, then all, unspecified options appear empty ([ ]). However, the software replaces empty options with their corresponding default values during training.

See Also

`ClassificationECOC` | `designecoc` | `fitcecoc` | `predict` | `templateDiscriminant` | `templateEnsemble` | `templateKNN` | `templateSVM` | `templateTree` | `testckfold`

Introduced in R2015a

templateEnsemble

Ensemble learning template

Syntax

```
t = templateEnsemble(Method,NLearn,Learners)
t = templateNaiveBayes(Method,NLearn,Learners,Name,Value)
```

Description

`t = templateEnsemble(Method,NLearn,Learners)` returns an ensemble learning template suitable for training error-correcting output code (ECOC) multiclass models, which uses the method `Method`, `NLearn` learning cycles, and the weak learners (`Leaners`).

All other options of the template (`t`) specific to ensemble learning appear empty, but the software uses their corresponding default values during training.

Specify `t` as a binary learner, or one in a set of binary learners, in `fitcecoc` to train an ECOC multiclass classifer.

`t = templateNaiveBayes(Method,NLearn,Learners,Name,Value)` returns a template with additional options specified by one or more name-value pair arguments.

For example, you can specify the number of predictors in each random subspace learner, learning rate for shrinkage, or the target classification error for `RobustBoost`.

If you display `t` in the Command Window, then all options appear empty (`[ ]`), except those that you specify using name-value pair arguments. During training, the software uses default values for empty options.

Input Arguments

`Method`

Case-insensitive string consisting of one of the following.

- For classification with two classes:
  - `'AdaBoostM1'`
  - `'LogitBoost'`
  - `'GentleBoost'`
  - `'RobustBoost'` (requires an Optimization Toolbox license)
  - `'LPBoost'` (requires an Optimization Toolbox license)
  - `'TotalBoost'` (requires an Optimization Toolbox license)
  - `'RUSBoost'`
  - `'Subspace'`
  - `'Bag'`
- For classification with three or more classes:
  - `'AdaBoostM2'`
  - `'LPBoost'` (requires an Optimization Toolbox license)
  - `'TotalBoost'` (requires an Optimization Toolbox license)
  - `'RUSBoost'`
  - `'Subspace'`
  - `'Bag'`
- For regression:
  - `'LSBoost'`
  - `'Bag'`

`'Bag'` applies to all methods. So when you use `'Bag'`, indicate whether you want a classifier or regressor with the `type` name-value pair set to `'classification'` or `'regression'`.

`NLearn`

Number of ensemble learning cycles, a positive integer (or the string `'AllPredictorCombinations'`, see the next paragraph). At every training cycle, `fitensemble` loops over all learner templates in `Learners` and trains one weak learner for every template. The total number of trained learners in Ensemble is `NLearn*numel(Learners)`.

If you set `Method` to `'Subspace'`, you can set `NLearn` to `'AllPredictorCombinations'`. With this setting, `fitensemble` constructs learners for all possible combinations of predictors taken `NPredToSample` at a time. This gives a total of `nchoosek(size(X,2),NPredToSample)` learners in the ensemble. You can use only one learner template for this setting.

`NLearn` for ensembles can vary from a few dozen to a few thousand. Usually, an ensemble with a good predictive power needs from a few hundred to a few thousand weak learners. You do not have to train an ensemble for that many cycles at once. You can start by growing a few dozen learners, inspect the ensemble performance and, if necessary, train more weak learners using the `resume` method of the ensemble.

`Learners`

One of the following:

- A string with the name of a weak learner:
  - `'Discriminant'` (recommended for `'Subspace'`)
  - `'KNN'` (applies only to `'Subspace'`)
  - `'Tree'` (applies to all methods except `'Subspace'`)
- A single weak learner template you create with `templateTree`, `templateKNN`, or `templateDiscriminant`.
- A cell array of weak learner templates. Usually you should supply only one weak learner template.

Ensemble performance depends on the parameters of the weak learners, and you can get poor performance using weak learners with default parameters. Specify the parameters for the weak learners in the template.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

All Ensembles

`'FResample'`

Fraction of the training set to be selected by resampling for every weak learner. A numeric scalar from `0` through `1`. This parameter has no effect unless you grow an ensemble by bagging or set `'Resample'` to `'on'`. The default setting is the one used most often for an ensemble grown by resampling.

Default: `1`

`'NPredToSample'`

Number of predictors in each random subspace learner, a positive integer from 1 to the number of predictors.

Default: `1`

`'NPrint'`

Printout frequency, a positive integer scalar. Set to `'Off'` for no printout. Use this parameter to track how many weak learners have been trained so far. This is useful when you train ensembles with many learners on large data sets. If you use one of the cross-validation options, this parameter defines the printout frequency per number of cross-validation folds.

Default: `'Off'`

`'Replace'`

`'On'` or `'Off'`. If `'On'`, sample with replacement. If `'Off'`, sample without replacement. This parameter has no effect unless you grow an ensemble by bagging or set `Resample` to `'On'`. If you set `Resample` to `'On'` and `Replace` to `'Off'`, `fitensemble` samples training observations assuming uniform weights, and boosts by reweighting observations.

Default: `'On'`

`'Resample'`

`'On'` or `'Off'`. If `'On'`, grow an ensemble by resampling, with the resampling fraction given by `FResample`, and sampling with or without replacement given by `Replace`.

- Boosting — When `'Off'`, the boosting algorithm reweights observations at every learning iteration. When `'On'`, the algorithm samples training observations using updated weights as the multinomial sampling probabilities.
- Bagging — You can use only the default value of this parameter (`'On'`).

Default: `'Off'` for boosting, `'On'` for bagging

AdaBoostM1, AdaBoostM2, LogitBoost, GentleBoost, RUSBoost, and LSBoost:

`'LearnRate'`

Learning rate for shrinkage, a numeric scalar from `0` to `1`. If you set the learning rate to less than `1`, the ensemble requires more learning iterations but often achieves a better accuracy. `0.1` is a popular choice for an ensemble grown with shrinkage.

Default: `1`

RUSBoost

`'RatioToSmallest'`

Either a numeric scalar or vector with `K` elements when there are `K` classes. Every element of this vector is the sampling proportion for this class with respect to the class with fewest observations in `Y`. If you pass a scalar, the software uses this sampling proportion for all classes. For example, suppose you have class `A` with 100 observations and class `B` with 10 observations. If you pass `[2 1]` for `'RatioToSmallest'`, every learner in the ensemble is trained on 20 observations of class `A` and 10 observations of class `B`. If you pass `2` or `[2 2]`, every learner is trained on 20 observations of class `A` and 20 observations of class `B`. If you specify class names by using the `ClassNames` name-value pair argument of the fitting function, then the software matches elements in the array of class names to elements in this vector.

Default: `ones(K,1)`

LPBoost and TotalBoost

`'MarginPrecision'`

Margin precision, a numeric scalar between `0` and `1`. `MarginPrecision` affects the number of boosting iterations required for conversion. Use a small value to grow an ensemble with many learners, and use a large value to grow an ensemble with few learners.

Default: `0.01`

RobustBoost

`'RobustErrorGoal'`

Target classification error for `RobustBoost`, a numeric scalar from `0` through `1`. Usually there is an optimal range for this parameter for your training data. If you set the error goal too low or too high, `RobustBoost` can produce a model with poor classification accuracy.

Default: `0.1`

`'RobustMarginSigma'`

Spread of the distribution of classification margins over the training set for `RobustBoost`, a numeric positive scalar. You should consult literature on `RobustBoost` before setting this parameter

Default: `0.1`

`'RobustMaxMargin'`

Maximal classification margin for `RobustBoost` in the training set, a nonnegative numeric scalar. `RobustBoost` minimizes the number of observations in the training set with classification margins below `RobustMaxMargin`.

Default: `0`

Output Arguments

`t` — Classification template for ensemble learning

classification template object

Classification template for ensemble learning suitable for training error-correcting output code (ECOC) multiclass models, returned as a template object. Pass `t` to `fitcecoc` to specify how to create the ensemble learning classifier for the ECOC model.

If you display `t` in the Command Window, then all, unspecified options appear empty ([ ]). However, the software replaces empty options with their corresponding default values during training.

Examples

Create an Ensemble Learning Template

Use `templateEnsemble` to specify an ensemble learning template. You must specify the ensemble method, the number of learning cycles, and the type of weak learners. For this example, specify the AdaBoostM1 method, 100 learners, and classification tree weak learners.

```
t = templateEnsemble('AdaBoostM1',100,'tree')
```

```
t =

Fit template for classification AdaBoostM1.

               Type: 'classification'
             Method: 'AdaBoostM1'
    LearnerTemplates: 'Tree'
             NLearn: 100
          LearnRate: []
```

All properties of the template object are empty except for `Method`, `Type`, `LearnerTemplates`, and `NLearn`. When trained on, the software fills in the empty properties with their respective default values. For example, the software fills the `LearnRate` property with `1`.

`t` is a plan for an ensemble learner, and no computation takes place when you specify it. You can pass `t` to fitcecoc to specify ensemble binary learners for ECOC multiclass learning.

Create an Ensemble Template for ECOC Multiclass Learning

Create an ensemble template for use in fitcecoc.

Load the arrhythmia data set.

```
load arrhythmia
tabulate(categorical(Y));
rng(1); % For reproducibility
```

```
  Value    Count   Percent
      1      245     54.20%
      2       44      9.73%
      3       15      3.32%
      4       15      3.32%
      5       13      2.88%
      6       25      5.53%
      7        3      0.66%
      8        2      0.44%
      9        9      1.99%
     10       50     11.06%
     14        4      0.88%
     15        5      1.11%
     16       22      4.87%
```

Some classes have small relative frequencies in the data.

Create a template for a GentleBoost ensemble of classification trees, and specify to use a 100 learners and a shrinkage of 0.1. By default, boosting grows stumps (i.e., one node having a set of leaves). Since there are classes with small frequencies, the trees must be leafy enough to be sensitive to the minority classes. Specify the minimum number of leaf node observations to 3.

```
tTree = templateTree('MinLeaf',20);
t = templateEnsemble('AdaBoostM1',100,tTree,'LearnRate',0.1);
```

All properties of the template objects are empty except for `Method` and `Type`, and the corresponding properties of the name-value pair argument values in the function calls. When you pass `t` to the training function, the software fills in the empty properties with their respective default values.

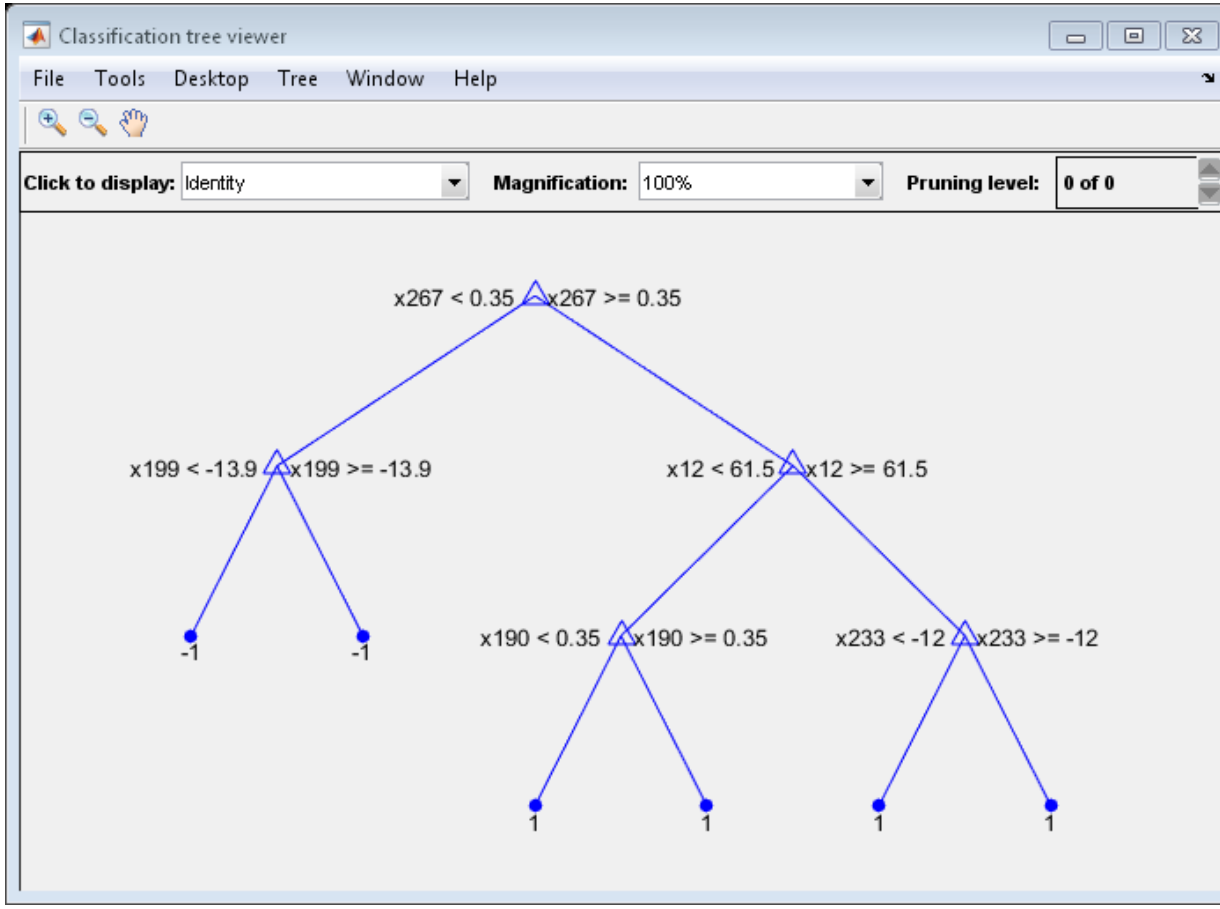
Specify `t` as a binary learner for an ECOC multiclass model. Train using the default one-versus-one coding design.

```
Mdl = fitcecoc(X,Y,'Learners',t);
```

- `Mdl` is a `ClassificationECOC` multiclass model.
- `Mdl.BinaryLearners` is a 78-by-1 cell array of `CompactClassificationEnsemble` models.
- `Mdl.BinaryLearners{j}.Trained` is a 100-by-1 cell array of `CompactClassificationTree` models, for `j` = 1,...,78.

You can verify that one of the binary learners contains a weak learner that isn't a stump by using `view`.

```
view(Mdl.BinaryLearners{1}.Trained{1},'Mode','graph')
```



Display the in-sample (resubstitution) misclassification error.

```
L = resubLoss(Mdl,'LossFun','classiferror')
```

```
L =

    0.0597
```

More About

Algorithms

By default, if you specify `Method` to be a boosting algorithm and `Learners` to be decision trees, then the software grows *stumps* (i.e., one root node connected to two terminal, leaf nodes). You can adjust this by specifying values for the `MinLeaf` or `MinParent` name-value pair arguments using `templateTree`.

See Also

`ClassificationECOC` | `ClassificationEnsemble` | `fitcecoc` | `fitensemble` | `templateDiscriminant` | `templateKNN` | `templateTree`

templateKNN

k-nearest neighbor classifier template

Syntax

```
t = templateKNN()
t = templateKNN(Name,Value)
```

Description

`t = templateKNN()` returns a *k*-nearest neighbor (KNN) learner template suitable for training ensembles or error-correcting output code (ECOC) multiclass models.

If you specify a default template, then the software uses default values for all input arguments during training.

Specify `t` as a learner in `fitensemble` or `fitcecoc`.

`t = templateKNN(Name,Value)` creates a template with additional options specified by one or more name-value pair arguments.

For example, you can specify the nearest neighbor search method, the number of nearest neighbors to find, or the distance metric.

If you display `t` in the Command Window, then all options appear empty (`[ ]`), except those that you specify using name-value pair arguments. During training, the software uses default values for empty options.

Examples

Create a *k*-Nearest Neighbors Template for Ensemble

Create a nondefault *k*-nearest neighbor template for use in `fitensemble`.

Load Fisher's iris data set.

```
load fisheriris
```

Create a template for a 5-nearest neighbor search, and specify to standardize the predictors.

```
t = templateKNN('NumNeighbors',5,'Standardize',1)
```

```
t =

Fit template for classification KNN.

       NumNeighbors: 5
           NSMethod: ''
           Distance: ''
         BucketSize: ''
        IncludeTies: []
     DistanceWeight: []
          BreakTies: []
           Exponent: []
                Cov: []
              Scale: []
    StandardizeData: 1
             Method: 'KNN'
               Type: 'classification'
```

All properties of the template object are empty except for `NumNeighbors`, `Method`, `StandardizeData`, and `Type`. When you specify `t` as a learner, the software fills in the empty properties with their respective default values.

Specify `t` as a weak learner for a classification ensemble.

```
Mdl = fitensemble(meas,species,'Subspace',100,t);
```

Display the in-sample (resubstitution) misclassification error.

```
L = resubLoss(Mdl)
```

```
L =

    0.0600
```

Create a *k*-Nearest Neighbors Template for ECOC Multiclass Learning

Create a nondefault *k*-nearest neighbor template for use in `fitcecoc`.

Load Fisher's iris data set.

```
load fisheriris
```

Create a template for a 5-nearest neighbor search, and specify to standardize the predictors.

```
t = templateKNN('NumNeighbors',5,'Standardize',1)
```

```
t =

Fit template for classification KNN.

       NumNeighbors: 5
           NSMethod: ''
           Distance: ''
         BucketSize: ''
        IncludeTies: []
     DistanceWeight: []
          BreakTies: []
           Exponent: []
                Cov: []
              Scale: []
    StandardizeData: 1
             Method: 'KNN'
               Type: 'classification'
```

All properties of the template object are empty except for `NumNeighbors`, `Method`, `StandardizeData`, and `Type`. When you specify `t` as a learner, the software fills in the empty properties with their respective default values.

Specify `t` as a binary learner for an ECOC multiclass model.

```
Mdl = fitcecoc(meas,species,'Learners',t);
```

By default, the software trains `Mdl` using the one-versus-one coding design.

Display the in-sample (resubstitution) misclassification error.

```
L = resubLoss(Mdl,'LossFun','classiferror')
```

```
L =
```

```
0.0467
```

- “Random Subspace Classification” on page 16-124

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'NumNeighbors',4,'Distance','minkowski'` specifies a 4-nearest neighbor classifier template using the Minkowski distance measure.

`'BreakTies'` — Tie-breaking algorithm

`'smallest'` (default) | `'nearest'` | `'random'`

Tie-breaking algorithm used by the `predict` method if multiple classes have the same smallest cost, specified as the comma-separated pair consisting of `'BreakTies'` and one of the following:

- `'smallest'` — Use the smallest index among tied groups.
- `'nearest'` — Use the class with the nearest neighbor among tied groups.
- `'random'` — Use a random tiebreaker among tied groups.

By default, ties occur when multiple classes have the same number of nearest points among the `K` nearest neighbors.

Example: `'BreakTies','nearest'`

`'BucketSize'` — Maximum data points in node

50 (default) | positive integer value

Maximum number of data points in the leaf node of the *k*d-tree, specified as the comma-separated pair consisting of `'BucketSize'` and a positive integer value. This argument is meaningful only when `NSMethod` is `'kdtree'`.

Example: 'BucketSize',40

Data Types: single | double

'Cov' — Covariance matrix
nancov(X) (default) | positive definite matrix of scalar values

Covariance matrix, specified as the comma-separated pair consisting of 'Cov' and a positive definite matrix of scalar values representing the covariance matrix when computing the Mahalanobis distance. This argument is only valid when 'Distance' is 'mahalanobis'.

You cannot simultaneously specify 'Standardize' and either of 'Scale' or 'Cov'.

Data Types: single | double

'Distance' — Distance metric
valid distance metric string | function handle

Distance metric, specified as the comma-separated pair consisting of 'Distance' and a valid distance metric string or function handle. The allowable strings depend on the NSMethod parameter, which you set in fitcknn, and which exists as a field in ModelParameters. If you specify CategoricalPredictors as 'all', then the default distance metric is 'hamming'. Otherwise, the default distance metric is 'euclidean'.

NSMethod	Distance Metric Names
exhaustive	Any distance metric of ExhaustiveSearcher
kdtree	'cityblock', 'chebychev', 'euclidean', or 'minkowski'

For definitions, see "Distance Metrics".

This table includes valid distance metrics of ExhaustiveSearcher.

Value	Description
'cityblock'	City block distance.
'chebychev'	Chebychev distance (maximum coordinate difference).
'correlation'	One minus the sample linear correlation between observations (treated as sequences of values).
'cosine'	One minus the cosine of the included angle between observations (treated as vectors).

Value	Description
`'euclidean'`	Euclidean distance.
`'hamming'`	Hamming distance, percentage of coordinates that differ.
`'jaccard'`	One minus the Jaccard coefficient, the percentage of nonzero coordinates that differ.
`'mahalanobis'`	Mahalanobis distance, computed using a positive definite covariance matrix `C`. The default value of `C` is the sample covariance matrix of X, as computed by `nancov(X)`. To specify a different value for `C`, use the `'Cov'` name-value pair argument.
`'minkowski'`	Minkowski distance. The default exponent is `2`. To specify a different exponent, use the `'Exponent'` name-value pair argument.
`'seuclidean'`	Standardized Euclidean distance. Each coordinate difference between X and a query point is scaled, meaning divided by a scale value `S`. The default value of `S` is the standard deviation computed from X, `S = nanstd(X)`. To specify another value for `S`, use the `Scale` name-value pair argument.
`'spearman'`	One minus the sample Spearman's rank correlation between observations (treated as sequences of values).

`@`*`distfun`*	Distance function handle. *`distfun`* has the form
	`function D2 = DISTFUN(ZI,ZJ)`
	`% calculation of  distance`
	`...`
	where
	• `ZI` is a `1`-by-`N` vector containing one row of X or y.
	• `ZJ` is an `M2`-by-`N` matrix containing multiple rows of X or y.
	• `D2` is an `M2`-by-`1` vector of distances, and `D2(k)` is the distance between observations `ZI` and `ZJ(J,:)`.

Example: `'Distance','minkowski'`

Data Types: `function_handle`

'DistanceWeight' — Distance weighting function

'equal' (default) | 'inverse' | 'squaredinverse' | function handle

Distance weighting function, specified as the comma-separated pair consisting of 'DistanceWeight' and either a function handle or one of the following strings specifying the distance weighting function.

DistanceWeight	Meaning
'equal'	No weighting
'inverse'	Weight is 1/distance
'squaredinverse'	Weight is 1/distance^2
@*fcn*	*fcn* is a function that accepts a matrix of nonnegative distances, and returns a matrix the same size containing nonnegative distance weights. For example, 'squaredinverse' is equivalent to @(d)d.^(-2).

Example: 'DistanceWeight','inverse'

Data Types: function_handle

'Exponent' — Minkowski distance exponent

2 (default) | positive scalar value

Minkowski distance exponent, specified as the comma-separated pair consisting of 'Exponent' and a positive scalar value. This argument is only valid when 'Distance' is 'minkowski'.

Example: 'Exponent',3

Data Types: single | double

'IncludeTies' — Tie inclusion flag

false (default) | true

Tie inclusion flag, specified as the comma-separated pair consisting of 'IncludeTies' and a logical value indicating whether predict includes all the neighbors whose distance values are equal to the Kth smallest distance. If IncludeTies is true, predict includes all these neighbors. Otherwise, predict uses exactly K neighbors.

Example: 'IncludeTies',true

Data Types: logical

`'NSMethod'` — Nearest neighbor search method

`'kdtree' | 'exhaustive'`

Nearest neighbor search method, specified as the comma-separated pair consisting of `'NSMethod'` and `'kdtree'` or `'exhaustive'`.

- `'kdtree'` — Create and use a *k*d-tree to find nearest neighbors. `'kdtree'` is valid when the distance metric is one of the following:
  - `'euclidean'`
  - `'cityblock'`
  - `'minkowski'`
  - `'chebyshev'`
- `'exhaustive'` — Use the exhaustive search algorithm. The distance values from all points in X to each point in y are computed to find nearest neighbors.

The default is `'kdtree'` when X has `10` or fewer columns, X is not sparse, and the distance metric is a `'kdtree'` type; otherwise, `'exhaustive'`.

Example: `'NSMethod','exhaustive'`

`'NumNeighbors'` — Number of nearest neighbors to find

`1` (default) | positive integer value

Number of nearest neighbors in X to find for classifying each point when predicting, specified as the comma-separated pair consisting of `'NumNeighbors'` and a positive integer value.

Example: `'NumNeighbors',3`

Data Types: `single` | `double`

`'Scale'` — Distance scale

`nanstd(X)` (default) | vector of nonnegative scalar values

Distance scale, specified as the comma-separated pair consisting of `'Scale'` and a vector containing nonnegative scalar values with length equal to the number of columns in X. Each coordinate difference between X and a query point is scaled by the corresponding element of `Scale`. This argument is only valid when `'Distance'` is `'seuclidean'`.

You cannot simultaneously specify `'Standardize'` and either of `'Scale'` or `'Cov'`.

Data Types: `single` | `double`

`'Standardize'` — Flag to standardize predictors

`false` (default) | `true`

Flag to standardize the predictors, specified as the comma-separated pair consisting of `'Standardize'` and `true` (`1`) or `false` (`0`).

If you set `'Standardize',true`, then the software centers and scales each column of the predictor data (X) by the column mean and standard deviation, respectively.

The software does not standardize categorical predictors, and throws an error if all predictors are categorical.

You cannot simultaneously specify `'Standardize',1` and either of `'Scale'` or `'Cov'`.

It is good practice to standardize the predictor data.

Example: `'Standardize',true`

Data Types: `logical`

Output Arguments

`t` — *k*NN classification template

template object

*k*NN classification template suitable for training ensembles or error-correcting output code (ECOC) multiclass models, returned as a template object. Pass `t` to `fitensemble` or `fitcecoc` to specify how to create the KNN classifier for the ensemble or ECOC model, respectively.

If you display `t` to the Command Window, then all, unspecified options appear empty ([ ]). However, the software replaces empty options with their corresponding default values during training.

See Also

`ClassificationKNN` | `ExhaustiveSearcher` | `fitcecoc` | `fitensemble`

templateNaiveBayes

Naive Bayes classifier template

Syntax

```
t = templateNaiveBayes()
t = templateNaiveBayes(Name,Value)
```

Description

`t = templateNaiveBayes()` returns a naive Bayes template suitable for training error-correcting output code (ECOC) multiclass models.

If you specify a default template, then the software uses default values for all input arguments during training.

Specify `t` as a learner in `fitcecoc`.

`t = templateNaiveBayes(Name,Value)` returns a template with additional options specified by one or more name-value pair arguments. All properties of `t` are empty, except those you specify using `Name,Value` pair arguments.

For example, you can specify distributions for the predictors.

If you display `t` in the Command Window, then all options appear empty (`[ ]`), except those that you specify using name-value pair arguments. During training, the software uses default values for empty options.

Examples

Create a Default Naive Bayes Template

Use `templateNaiveBayes` to specify a default naive Bayes template.

```
t = templateNaiveBayes()
```

```
t =

Fit template for classification NaiveBayes.

    DistributionNames: [1x0 double]
               Kernel: []
              Support: []
                Width: []
               Method: 'NaiveBayes'
                 Type: 'classification'
```

All properties of the template object are empty except for `Method` and `Type`. When you pass `t` to the training function, the software fills in the empty properties with their respective default values. For example, the software fills the `DistributionNames` property with a 1-by- `D` cell array of strings with `'normal'` in each cell, where `D` is the number of predictors. For details on other default values, see fitcnb.

`t` is a plan for a naive Bayes learner, and no computation occurs when you specify it. You can pass `t` to fitcecoc to specify naive Bayes binary learners for ECOC multiclass learning.

Create a Naive Bayes Template for ECOC Multiclass Learning

Create a nondefault naive Bayes template for use in fitcecoc.

Load Fisher's iris data set.

```
load fisheriris
```

Create a template for naive Bayes binary classifiers, and specify kernel distributions for all predictors.

```
t = templateNaiveBayes('DistributionNames','kernel')
```

```
t =

Fit template for classification NaiveBayes.

    DistributionNames: 'kernel'
               Kernel: []
              Support: []
                Width: []
               Method: 'NaiveBayes'
```

```
                Type: 'classification'
```

All properties of the template object are empty except for `DistributionNames`, `Method`, and `Type`. When you pass `t` to the training function, the software fills in the empty properties with their respective default values.

Specify `t` as a binary learner for an ECOC multiclass model.

```
Mdl = fitcecoc(meas,species,'Learners',t);
```

By default, the software trains `Mdl` using the one-versus-one coding design.

Display the in-sample (resubstitution) misclassification error.

```
L = resubLoss(Mdl,'LossFun','classiferror')
```

```
L =

    0.0333
```

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'DistributionNames','mn'` specifies to treat all predictors as token counts for a multinomial model.

`'DistributionNames'` — Data distributions

`'kernel'` | `'mn'` | `'mvmn'` | `'normal'` | cell array of strings

Data distributions `fitcnb` uses to model the data, specified as the comma-separated pair consisting of `'DistributionNames'` and a string or cell array of strings.

This table summarizes the available distributions.

Value	Description
`'kernel'`	Kernel smoothing density estimate.
`'mn'`	Multinomial distribution. If you specify `mn`, then all features are components of a multinomial distribution. Therefore, you cannot include `'mn'` as an element of a cell array of strings. For details, see "Algorithms".
`'mvmn'`	Multivariate multinomial distribution. For details, see "Algorithms".
`'normal'`	Normal (Gaussian) distribution.

If you specify a string, then the software models all the features using that distribution. If you specify a 1-by-P cell array of strings, then the software models feature j using the distribution in element j of the cell array.

By default, the software sets all predictors specified as categorical predictors (using the CategoricalPredictors name-value pair argument) to `'mvmn'`. Otherwise, the default distribution is `'normal'`.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'Distribution','mn'`

Data Types: `cell` | `char`

`'Kernel'` — Kernel smoother type

`'normal'` (default) | `'box'` | `'epanechnikov'` | `'triangle'` | cell array of strings

Kernel smoother type, specified as the comma-separated pair consisting of `'Kernel'` and a string or cell array of strings.

This table summarizes the available options for setting the kernel smoothing density region. Let $I\{u\}$ denote the indictor function.

Value	Kernel	Formula
`'box'`	Box (uniform)	$f(x) = 0.5I\{\lvert x\rvert \le 1\}$

Value	Kernel	Formula
`'epanechni`	Epanechnikov	$f(x) = 0.75\left(1 - x^2\right) I\left\{\lvert x\rvert \le 1\right\}$
`'normal'`	Gaussian	$f(x) = \frac{1}{\sqrt{2\pi}} \exp\left(-0.5x^2\right)$
`'triangle'`	Triangular	$f(x) = \left(1 - \lvert x\rvert\right) I\left\{\lvert x\rvert \le 1\right\}$

If you specify a 1-by-*P* cell array, with each cell containing any value in the table, then the software trains the classifier using the kernel smoother type in cell *j* for feature *j* in X. The software ignores cells of `Kernel` not corresponding to a predictor whose distribution is `'kernel'`.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'Kernel',{'epanechnikov','normal'}`

Data Types: `cell` | `char`

`'Support'` — Kernel smoothing density support

`'unbounded'` (default) | `'positive'` | cell array | numeric row vector

Kernel smoothing density support, specified as the comma-separated pair consisting of `'Support'` and `'positive'`, `'unbounded'`, a cell array, or a numeric row vector. The software applies the kernel smoothing density to the specified region.

This table summarizes the available options for setting the kernel smoothing density region.

Value	Description
1-by-2 numeric row vector	For example, `[L,U]`, where `L` and `U` are the finite lower and upper bounds, respectively, for the density support.
`'positive'`	The density support is all positive real values.
`'unbounded'`	The density support is all real values.

If you specify a 1-by-*P* cell array, with each cell containing any value in the table, then the software trains the classifier using the kernel support in cell *j* for feature *j* in X. The

software ignores cells of `Kernel` not corresponding to a predictor whose distribution is `'kernel'`.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'KSSupport',{[-10,20],'unbounded'}`

Data Types: `cell` | `char` | `double`

`'Width'` — Kernel smoothing window width

matrix of numeric values | numeric column vector | numeric row vector | scalar

Kernel smoothing window width, specified as the comma-separated pair consisting of `'Width'` and a matrix of numeric values, numeric column vector, numeric row vector, or scalar.

Suppose there are K class levels and P predictors. This table summarizes the available options for setting the kernel smoothing window width.

Value	Description
K-by-P matrix of numeric values	Element (k,j) specifies the width for predictor j in class k.
K-by-1 numeric column vector	Element k specifies the width for all predictors in class k.
1-by-P numeric row vector	Element j specifies the width in all class levels for predictor j.
scalar	Specifies the bandwidth for all features in all classes.

By default, the software selects a default width automatically for each combination of predictor and class by using a value that is optimal for a Gaussian distribution. If you specify `Width` and it contains `NaN`s, then the software selects widths for the elements containing `NaN`s.

You must specify that at least one predictor has distribution `'kernel'` to additionally specify Kernel, Support, or Width.

Example: `'Width',[NaN NaN]`

Data Types: `double` | `struct`

Output Arguments

`t` — Naive Bayes classification template

template object

Naive Bayes classification template suitable for training error-correcting output code (ECOC) multiclass models, returned as a template object. Pass `t` to `fitcecoc` to specify how to create the naive Bayes classifier for the ECOC model.

If you display `t` to the Command Window, then all, unspecified options appear empty ([ ]). However, the software replaces empty options with their corresponding default values during training.

More About

Naive Bayes

Naive Bayes is a classification algorithm that applies density estimation to the data.

The algorithm leverages Bayes theorem, and (naively) assumes that the predictors are conditionally independent, given the class. Though the assumption is usually violated in practice, naive Bayes classifiers tend to yield posterior distributions that are robust to biased class density estimates, particularly where the posterior is 0.5 (the decision boundary) [1].

Naive Bayes classifiers assign observations to the most probable class (in other words, the *maximum a posteriori* decision rule). Explicitly, the algorithm:

1. Estimates the densities of the predictors within each class.
2. Models posterior probabilities according to Bayes rule. That is, for all $k = 1,...,K$,

$$\hat{P}\left(Y = k \mid X_1,..,X_P\right) = \frac{\pi\left(Y = k\right)\prod_{j=1}^{P} P\left(X_j \mid Y = k\right)}{\sum_{k=1}^{K}\pi\left(Y = k\right)\prod_{j=1}^{P} P\left(X_j \mid Y = k\right)},$$

where:

- Y is the random variable corresponding to the class index of an observation.
- $X_1,...,X_P$ are the random predictors of an observation.
- $\pi(Y = k)$ is the prior probability that a class index is k.

3 Classifies an observation by estimating the posterior probability for each class, and then assigns the observation to the class yielding the maximum posterior probability.

If the predictors compose a multinomial distribution, then the posterior probability $\hat{P}(Y = k \mid X_1,..,X_P) \propto \pi(Y = k)P_{mn}(X_1,...,X_P \mid Y = k)$, where $P_{mn}(X_1,...,X_P \mid Y = k)$ is the probability mass function of a multinomial distribution.

Algorithms

- If you specify `'Distribution','mn'` when training Mdl using `fitcnb`, then the software fits a multinomial distribution using the bag-of-tokens model. The software stores the probability that token j appears in class k in the property `DistributionParameters{`k`,`j`}`. Using additive smoothing [2], the estimated probability is

$$P(\text{token } j \mid \text{class } k) = \frac{1 + c_{j|k}}{P + c_k},$$

where:

- $c_{j|k} = n_k \dfrac{\sum_{i:y_i \in \text{class } k} x_{ij} w_i}{\sum_{i:y_i \in \text{class } k} w_i}$; which is the weighted number of occurrences of token j in class k.
- n_k is the number of observations in class k.
- w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.

- $c_k = \sum_{j=1}^{P} c_{j|k}$; which is the total weighted number of occurrences of all tokens in class k.

- If you specify `'Distribution','mvmn'` when training Mdl using `fitcnb`, then:

  1. For each predictor, the software collects a list of the unique levels, stores the sorted list in `CategoricalLevels`, and considers each level a bin. Each predictor/class combination is a separate, independent multinomial random variable.
  2. For predictor j in class k, the software counts instances of each categorical level using the list stored in `CategoricalLevels{`j`}`.
  3. The software stores the probability that predictor j, in class k, has level L in the property `DistributionParameters{`k`,`j`}`, for all levels in `CategoricalLevels{`j`}`. Using additive smoothing [2], the estimated probability is

$$P(\text{predictor } j = L \mid \text{class } k) = \frac{1 + m_{j|k}(L)}{m_j + m_k},$$

     where:

     - $m_{j|k}(L) = n_k \frac{\sum_{i:y_i \in \text{ class } k} I\{x_{ij} = L\} w_i}{\sum_{i:y_i \in \text{ class } k} w_i}$; which is the weighted number of observations for which predictor j equals L in class k.
     - n_k is the number of observations in class k.
     - $I\{x_{ij} = L\} = 1$ if $x_{ij} = L$, 0 otherwise.
     - w_i is the weight for observation i. The software normalizes weights within a class such that they sum to the prior probability for that class.
     - m_j is the number of distinct levels in predictor j.

- m_k is the weighted number of observations in class k.

References

[1] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[2] Manning, C. D., P. Raghavan, and M. Schütze. *Introduction to Information Retrieval*, NY: Cambridge University Press, 2008.

See Also

`ClassificationECOC` | `ClassificationNaiveBayes` | `fitcecoc` | `fitcnb`

templateSVM

Support vector machine template

Syntax

```
t = templateSVM()
t = templateSVM(Name,Value)
```

Description

`t = templateSVM()` returns a support vector machine (SVM) learner template suitable for training error-correcting output code (ECOC) multiclass models.

If you specify a default template, then the software uses default values for all input arguments during training.

Specify `t` as a binary learner, or one in a set of binary learners, in `fitcecoc` to train an ECOC multiclass classifer.

`t = templateSVM(Name,Value)` returns a template with additional options specified by one or more name-value pair arguments.

For example, you can specify the box constraint, the kernel function, or whether to standardize the predictors.

If you display `t` in the Command Window, then all options appear empty (`[ ]`), except those that you specify using name-value pair arguments. During training, the software uses default values for empty options.

Examples

Create a Default Support Vector Machine Template

Use `templateSVM` to specify a default SVM template.

```
t = templateSVM()
```

```
t =

Fit template for classification SVM.

                    Alpha: [0x1 double]
          BoxConstraint: []
              CacheSize: []
          CachingMethod: ''
    DeltaGradientTolerance: []
           GapTolerance: []
           KKTTolerance: []
         IterationLimit: []
         KernelFunction: ''
            KernelScale: []
           KernelOffset: []
     KernelPolynomialOrder: []
                NumPrint: []
                      Nu: []
        OutlierFraction: []
        ShrinkagePeriod: []
                  Solver: ''
        StandardizeData: []
      SaveSupportVectors: []
          VerbosityLevel: []
                  Method: 'SVM'
                    Type: 'classification'
```

All properties of the template object are empty except for `Method` and `Type`. When you pass `t` to the training function, the software fills in the empty properties with their respective default values. For example, the software fills the `KernelFunction` property with `'linear'`. For details on other default values, see fitcsvm.

`t` is a plan for an SVM learner, and no computation occurs when you specify it. You can pass `t` to fitcecoc to specify SVM binary learners for ECOC multiclass learning. However, by default, `fitcecoc` uses default SVM binary learners.

Create an SVM Template for ECOC Multiclass Learning

Create a nondefault SVM template for use in fitcecoc.

Load Fisher's iris data set.

```
load fisheriris
```

Create a template for SVM binary classifiers, and specify to use a Gaussian kernel function.

```
t = templateSVM('KernelFunction','gaussian')
```

```
t =

Fit template for classification SVM.

                    Alpha: [0x1 double]
          BoxConstraint: []
              CacheSize: []
          CachingMethod: ''
    DeltaGradientTolerance: []
           GapTolerance: []
           KKTTolerance: []
         IterationLimit: []
         KernelFunction: 'gaussian'
            KernelScale: []
           KernelOffset: []
     KernelPolynomialOrder: []
                NumPrint: []
                      Nu: []
        OutlierFraction: []
        ShrinkagePeriod: []
                 Solver: ''
        StandardizeData: []
      SaveSupportVectors: []
          VerbosityLevel: []
                  Method: 'SVM'
                    Type: 'classification'
```

All properties of the template object are empty except for `DistributionNames`, `Method`, and `Type`. When trained on, the software fills in the empty properties with their respective default values.

Specify `t` as a binary learner for an ECOC multiclass model.

```
Mdl = fitcecoc(meas,species,'Learners',t);
```

`Mdl` is a `ClassificationECOC` multiclass classifier. By default, the software trains `Mdl` using the one-versus-one coding design.

Display the in-sample (resubstitution) misclassification error.

```
L = resubLoss(Mdl,'LossFun','classiferror')
```

```
L =

    0.0200
```

Retain and Discard Support Vectors of SVM Binary Learners

By default, `fitcecoc` empties the `Alpha`, `SupportVectorLabels`, and `SupportVectors` properties of the linear, SVM binary learners stored in the `BinaryLearners` property of the trained ECOC model. You can retain the support vectors and related values, and then discard them from the model.

Load Fisher's iris data set.

```
load fisheriris
rng(1); % For reproducibility
```

Train an ECOC model using the entire data set. Specify retaining the support vectors by passing in the appropriate SVM template.

```
t = templateSVM('SaveSupportVectors',true);
MdlSV = fitcecoc(meas,species,'Learners',t);
```

`Mdl` is a trained `ClassificationECOC` model. By default, `fitcecoc` uses linear, SVM binary learners. It implements a one-versus-one coding design, which requires three binary learners for three-class learning.

Access the estimated α values using dot notation.

```
alpha = cell(3,1);
alpha{1} = MdlSV.BinaryLearners{1}.Alpha;
alpha{2} = MdlSV.BinaryLearners{2}.Alpha;
alpha{3} = MdlSV.BinaryLearners{3}.Alpha;
alpha
```

```
alpha =

    [ 3x1 double]
    [ 3x1 double]
```

```
    [23x1 double]
```

`alpha` is a 3-by-1 cell array that stores the estimated values of α.

Discard the support vectors and related values from the ECOC model.

```
Mdl = discardSupportVectors(MdlSV);
```

`Mdl` is similar to `MdlSV`, except that the `Alpha`, `SupportVectorLabels`, and `SupportVectors` of all linear SVM binary learners are empty (`[ ]`).

```
areAllEmpty = @(x)isempty([x.Alpha x.SupportVectors x.SupportVectorLabels]);
cellfun(areAllEmpty,Mdl.BinaryLearners)
```

```
ans =

     1
     1
     1
```

Compare the sizes of the two ECOC models.

```
vars = whos('MdlSV','Mdl');
100*(1 - vars(1).bytes/vars(2).bytes)
```

```
ans =

    5.3485
```

`Mdl` is about 5% smaller than `MdlSV`.

Reduce your memory footprint by compacting `Mdl`, and then clearing `MdlSV` and `Mdl` from the workspace.

```
CMdl = compact(Mdl);
clear MdlSV Mdl;
```

Predict the label for a random row of the training data using the more efficient SVM model.

```
idx = randsample(size(meas,1),1)
```

```
predictedLabel = predict(CMdl,meas(idx,:))
trueLabel = species(idx)

idx =

    63

predictedLabel =

    'versicolor'

trueLabel =

    'versicolor'
```

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'BoxConstraint',0.1,'KernelFunction','gaussian','Standardize',1` specifies a box constraint of `0.1`, to use the Gaussian (RBF) kernel, and to standardize the predictors.

`'BoxConstraint'` — Box constraint

1 (default) | positive scalar

Box constraint, specified as the comma-separated pair consisting of `'BoxConstraint'` and a positive scalar.

For one-class learning, the software always sets the box constraint to `1`.

Example: `'BoxConstraint',100`

Data Types: `double` | `single`

`'CacheSize'` — Cache size

`1000` (default) | `'maximal'` | positive scalar

Cache size, specified as the comma-separated pair consisting of `'CacheSize'` and `'maximal'` or a positive scalar.

If `CacheSize` is `'maximal'`, then the software reserves enough disk space to hold the entire n-by-n Gram matrix.

If `CacheSize` is a positive scalar, then the software reserves `CacheSize` megabytes of disk space for training the classifier.

Example: `'CacheSize','maximal'`

Data Types: `double` | `char` | `single`

`'DeltaGradientTolerance'` — Tolerance for gradient difference

nonnegative scalar

Tolerance for the gradient difference between upper and lower violators obtained by Sequential Minimal Optimization (SMO) or Iterative Single Data Algorithm (ISDA), specified as the comma-separated pair consisting of `'DeltaGradientTolerance'` and a nonnegative scalar.

If `DeltaGradientTolerance` is `0`, then the software does not use the tolerance for the gradient difference to check for optimization convergence.

The defaults are:

- `1e-3` if the solver is SMO (for example, you set `'Solver','SMO'`)
- `0` if the solver is ISDA (for example, you set `'Solver','ISDA'`)

Example: `'DeltaGapTolerance',1e-2`

Data Types: `double` | `single`

`'GapTolerance'` — Feasibility gap tolerance

`0` (default) | nonnegative scalar

Feasibility gap tolerance obtained by SMO or ISDA, specified as the comma-separated pair consisting of `'GapTolerance'` and a nonnegative scalar.

If `GapTolerance` is `0`, then the software does not use the feasibility gap tolerance to check for optimization convergence.

Example: `'GapTolerance',1e-2`

Data Types: `double` | `single`

`'IterationLimit'` — Maximal number of numerical optimization iterations

`1e6` (default) | positive integer

Maximal number of numerical optimization iterations, specified as the comma-separated pair consisting of `'IterationLimit'` and a positive integer.

The software returns a trained classifier regardless of whether the optimization routine successfully converges.

Example: `'IterationLimit',1e8`

Data Types: `double` | `single`

`'KernelFunction'` — Kernel function

string

Kernel function used to compute the Gram matrix, specified as the comma-separated pair consisting of `'KernelFunction'` and a string.

This table summarizes the available options for setting a kernel function.

Value	Description	Formula
`'gaussian'` or `'rbf'`	Gaussian or Radial Basis Function (RBF) kernel, default for one-class learning	$G(x_1,x_2) = \exp\left(-\|x_1 - x_2\|^2\right)$
`'linear'`	Linear kernel, default for two-class learning	$G(x_1,x_2) = x_1'x_2$
`'polynomial'`	Polynomial kernel. Use `'PolynomialOrder',polyO` to specify a polynomial kernel of order `polyOrder`.	$G(x_1,x_2) = (1 + x_1'x_2)^p$

You can set your own kernel function, for example, `kernel`, by setting `'KernelFunction','kernel'`. `kernel` must have the following form:

```
function G = kernel(U,V)
```
where:

- `U` is an m-by-p matrix.
- `V` is an n-by-p matrix.
- `G` is an m-by-n Gram matrix of the rows of `U` and `V`.

And `kernel.m` must be on the MATLAB path.

It is good practice to avoid using generic names for kernel functions. For example, call a sigmoid kernel function `'mysigmoid'` rather than `'sigmoid'`.

Example: `'KernelFunction','gaussian'`

Data Types: `char`

`'KernelOffset'` — Kernel offset parameter
nonnegative scalar

Kernel offset parameter, specified as the comma-separated pair consisting of `'KernelOffset'` and a nonnegative scalar.

The software adds `KernelOffset` to each element of the Gram matrix.

The defaults are:

- `0` if the solver is SMO (for example, you set `'Solver','SMO'`)
- `0.1` if the solver is ISDA (for example, you set `'Solver','ISDA'`)

Example: `'KernelOffset',0`

Data Types: `double | single`

`'KernelScale'` — Kernel scale parameter
`1` (default) | `'auto'` | positive scalar

Kernel scale parameter, specified as the comma-separated pair consisting of `'KernelScale'` and `'auto'` or a positive scalar.

- If `KernelFunction` is `'gaussian'` (`'rbf'`), `'linear'`, or `'polymonial'`, then the software divides all elements of the predictor matrix X by the value of `KernelScale`. Then, the software applies the appropriate kernel norm to compute the Gram matrix.

- If you specify `'auto'`, then the software uses a heuristic procedure to select the scale value. The heuristic procedure uses subsampling. Therefore, to reproduce results, set a random number seed using `rng` before training the classifier.
- If you specify `KernelScale` and your own kernel function, for example, `kernel`, using `'KernelFunction','kernel'`, then the software displays an error. You must apply scaling within `kernel`.

Example: `'KernelScale',''auto'`

Data Types: `double | single | char`

`'KKTTolerance'` — Karush-Kuhn-Tucker complementarity conditions violation tolerance
nonnegative scalar

Karush-Kuhn-Tucker (KKT) complementarity conditions violation tolerance, specified as the comma-separated pair consisting of `'KKTTolerance'` and a nonnegative scalar.

If `KKTTolerance` is `0`, then the software does not use the KKT complementarity conditions violation tolerance to check for optimization convergence.

The defaults are:

- `0` if the solver is SMO (for example, you set `'Solver','SMO'`)
- `1e-3` if the solver is ISDA (for example, you set `'Solver','ISDA'`)

Example: `'KKTTolerance',1e-2`

Data Types: `double | single`

`'Nu'` — ν parameter for one-class learning
`0.5` (default) | positive scalar

ν parameter for one-class learning, specified as the comma-separated pair consisting of `'Nu'` and a positive scalar. `Nu` must be greater than `0` and at most `1`.

Set `Nu` to control the tradeoff between ensuring most training examples are in the positive class and minimizing the weights in the score function.

Example: `'Nu',0.25`

Data Types: `double | single`

`'NumPrint'` — Number of iterations between optimization diagnostic message output
1000 (default) | nonnegative integer

Number of iterations between optimization diagnostic message output, specified as the comma-separated pair consisting of `'NumPrint'` and a nonnegative integer.

If you use `'Verbose',1` and `'NumPrint',numprint`, then the software displays all optimization diagnostic messages from SMO and ISDA every `numprint` iterations in the Command Window.

Example: `'NumPrint',500`

Data Types: `double | single`

`'OutlierFraction'` — Expected proportion of outliers in training data

`0` (default) | nonnegative scalar

Expected proportion of outliers in the training data, specified as the comma-separated pair consisting of `'OutlierFraction'` and a nonnegative scalar. `OutlierFraction` must be at least `0` and less than `1`.

If you set `'OutlierFraction',outlierfraction`, where `outlierfraction` is a value greater than 0, then:

- For two-class learning, the software implements *robust learning*. In other words, the software attempts to remove 100*`outlierfraction`% of the observations when the optimization algorithm converges. The removed observations correspond to gradients that are large in magnitude.
- For one-class learning, the software finds an appropriate bias term such that `outlierfraction` of the observations in the training set have negative scores.

Example: `'OutlierFraction',0.01`

Data Types: `double | single`

`'PolynomialOrder'` — Polynomial kernel function order

`3` (default) | positive integer

Polynomial kernel function order, specified as the comma-separated pair consisting of `'PolynomialOrder'` and a positive integer.

If you set `'PolynomialOrder'` and `KernelFunction` is not `'polynomial'`, then the software displays an error.

Example: `'PolynomialOrder',2`

Data Types: `double | single`

'SaveSupportVectors' — Store support vectors, their labels, and the estimated α coefficients
`true | false`

Store support vectors, their labels, and the estimated α coefficients as properties of the resulting model, specified as the comma-separated pair consisting of `'SaveSupportVectors'` and `true` or `false`.

If `SaveSupportVectors` is `true`, the resulting model stores the support vectors in the `SupportVectors` property, their labels in the `SupportVectorLabels` property, and the estimated α coefficients in the `Alpha` property of the compact, SVM learners.

If `SaveSupportVectors` is `false` and `KernelFunction` is `'linear'`, the resulting model does not store the support vectors and the related estimates.

To reduce memory consumption by compact SVM models, specify `SaveSupportVectors`.

For linear, SVM binary learners in an ECOC model, the default value is `false`. Otherwise, the default value is `true`.

Example: `'SaveSupportVectors',true`

Data Types: `logical`

'ShrinkagePeriod' — Number of iterations between movement of observations from active to inactive set
`0` (default) | nonnegative integer

Number of iterations between the movement of observations from the active to inactive set, specified as the comma-separated pair consisting of `'ShrinkagePeriod'` and a nonnegative integer.

If you set `'ShrinkagePeriod',0`, then the software does not shrink the active set.

Example: `'ShrinkagePeriod',1000`

Data Types: `double | single`

'Solver' — Optimization routine
`'ISDA' | 'L1QP' | 'SMO'`

Optimization routine, specified as a string.

This table summarizes the available optimization routine options.

Value	Description
`'ISDA'`	Iterative Single Data Algorithm (see [4])
`'L1QP'`	Uses `quadprog` to implement $L1$ soft-margin minimization by quadratic programming. This option requires an Optimization Toolbox license. For more details, see "Quadratic Programming Definition".
`'SMO'`	Sequential Minimal Optimization (see [2])

The defaults are:

- `'ISDA'` if you set `'OutlierFraction'` to a positive value and for two-class learning
- `'SMO'` otherwise

Example: `'Solver','ISDA'`

Data Types: `char`

`'Standardize'` — Flag to standardize predictors

`false` (default) | `true`

Flag to standardize the predictors, specified as the comma-separated pair consisting of `'Standardize'` and `true` (`1`) or `false` (`0`).

If you set `'Standardize',true`, then the software centers and scales each column of the predictor data (X) by the column mean and standard deviation, respectively. It is good practice to standardize the predictor data.

Example: `'Standardize',true`

Data Types: `logical`

`'Verbose'` — Verbosity level

`0` (default) | `1` | `2`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and either `0`, `1`, or `2`. `Verbose` controls the amount of optimization information that the software displays in the Command Window and saves as a structure to `SVMModel.ConvergenceInfo.History`.

This table summarizes the available verbosity level options.

Value	Description
0	The software does not display or save convergence information.
1	The software displays diagnostic messages and saves convergence criteria every `numprint` iterations, where `numprint` is the value of the name-value pair argument `'NumPrint'`.
2	The software displays diagnostic messages and saves convergence criteria at every iteration.

Example: `'Verbose',1`

Data Types: `double | single`

Output Arguments

`t` — SVM classification template

template object

SVM classification template suitable for training error-correcting output code (ECOC) multiclass models, returned as a template object. Pass `t` to `fitcecoc` to specify how to create the SVM classifier for the ECOC model.

If you display `t` to the Command Window, then all, unspecified options appear empty ([ ]). However, the software replaces empty options with their corresponding default values during training.

More About

Tips

For linear, SVM binary learners, and for efficiency, `fitcecoc` empties the properties `Alpha`, `SupportVectorLabels`, and `SupportVectors`. `fitcecoc` lists `Beta`, rather than `Alpha`, in the model display.

To store `Alpha`, `SupportVectorLabels`, and `SupportVectors`, pass a linear, SVM template that specifies storing support vectors to `fitcecoc`. For example, enter:

```
t = templateSVM('SaveSupportVectors','on')
Mdl = fitcecoc(X,Y,'Learners',t);
```

You can subsequently remove the support vectors and related values by passing the resulting `ClassificationECOC` model to `discardSupportVectors`.

References

[1] Christianini, N., and J. C. Shawe-Taylor. *An Introduction to Support Vector Machines and Other Kernel-Based Learning Methods*. Cambridge, UK: Cambridge University Press, 2000.

[2] Fan, R.-E., P.-H. Chen, and C.-J. Lin. "Working set selection using second order information for training support vector machines." *Journal of Machine Learning Research*, Vol 6, 2005, pp. 1889–1918.

[3] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, Second Edition. NY: Springer, 2008.

[4] Kecman V., T. -M. Huang, and M. Vogt. "Iterative Single Data Algorithm for Training Kernel Machines from Huge Data Sets: Theory and Performance." In *Support Vector Machines: Theory and Applications*. Edited by Lipo Wang, 255–274. Berlin: Springer-Verlag, 2005.

[5] Scholkopf, B., J. C. Platt, J. C. Shawe-Taylor, A. J. Smola, and R. C. Williamson. "Estimating the Support of a High-Dimensional Distribution." *Neural Comput.*, Vol. 13, Number 7, 2001, pp. 1443–1471.

[6] Scholkopf, B., and A. Smola. *Learning with Kernels: Support Vector Machines, Regularization, Optimization and Beyond, Adaptive Computation and Machine Learning*. Cambridge, MA: The MIT Press, 2002.

See Also

`ClassificationECOC` | `ClassificationSVM` | `fitcecoc` | `fitcsvm`

Introduced in R2014b

templateTree

Create decision tree template

Syntax

```
t = templateTree
t = templateTree(Name,Value)
```

Description

`t = templateTree` returns a default decision tree learner template suitable for training ensembles or error-correcting output code (ECOC) multiclass models. Specify `t` as a learner using:

- `fitensemble` for classification or regression ensembles
- `fitcecoc` for ECOC model classification

If you specify a default decision tree template, then the software uses default values for all input arguments during training. It is good practice to specify the type of decision tree, e.g., for a classification tree template, specify `'Type','classification'`. If you specify the type of decision tree and display `t` in the Command Window, then all options except `Type` appear empty (`[]`).

`t = templateTree(Name,Value)` creates a template with additional options specified by one or more name-value pair arguments.

For example, you can specify the algorithm used to find the best split on a categorical predictor, the split criterion, or the number of predictors selected for each split.

If you display `t` in the Command Window, then all options appear empty (`[]`), except those that you specify using name-value pair arguments. During training, the software uses default values for empty options.

Examples

Create a Classification Template with Surrogate Splits

Create a decision tree template with surrogate splits, and use the template to train an ensemble using sample data.

Load Fisher's iris data set.

```
load fisheriris
```

Create a decision tree template with surrogate splits.

```
t = templateTree('Surrogate','on')
```

```
t =

Fit template for Tree.
    Surrogate: 'on'
```

All options of the template object are empty except for `Surrogate`. When you pass `t` to the training function, the software fills in the empty options with their respective default values.

Specify `t` as a weak learner for a classification ensemble.

```
Mdl = fitensemble(meas,species,'AdaBoostM2',100,t)
```

```
Mdl =

  classreg.learning.classif.ClassificationEnsemble
         PredictorNames: {'x1'  'x2'  'x3'  'x4'}
           ResponseName: 'Y'
             ClassNames: {'setosa'  'versicolor'  'virginica'}
         ScoreTransform: 'none'
        NumObservations: 150
             NumTrained: 100
                 Method: 'AdaBoostM2'
          LearnerNames: {'Tree'}
    ReasonForTermination: 'Terminated normally after completing the reques...'
                FitInfo: [100x1 double]
     FitInfoDescription: {2x1 cell}
```

Display the in-sample (resubstitution) misclassification error.

```
L = resubLoss(Mdl)
```

```
L =

    0.0333
```

Train a Regression Ensemble

Use a trained, boosted regression tree ensemble to predict the fuel economy of a car. Choose the number of cylinders, volume displaced by the cylinders, horsepower, and weight as predictors.

Load the `carsmall` data set. Set the predictors to `X`.

```
load carsmall
X = [Cylinders,Displacement,Horsepower,Weight];
xnames = {'Cylinders','Displacement','Horsepower','Weight'};
```

Specify a regression tree template that uses surrogate splits to impove predictive accuracy in the presence of `NaN` values.

```
RegTreeTemp = templateTree('Surrogate','On');
```

Train the regression tree ensemble using LSBoost and 100 learning cycles.

```
RegTreeEns = fitensemble(X,MPG,'LSBoost',100,RegTreeTemp,...
    'PredictorNames',xnames);
```

`RegTreeEns` is a trained `RegressionEnsemble` regression ensemble.

Use the trained regression ensemble to predict the fuel economy for a four-cylinder car with a 200-cubic inch displacement, 150 horsepower, and weighing 3000 lbs.

```
predMPG = predict(RegTreeEns,[4 200 150 3000])
```

```
predMPG =

   22.6290
```

The average fuel economy of a car with these specifications is 21.78 mpg.

Find the Optimal Number of Splits and Trees for an Ensemble

You can control the depth of the trees in an ensemble of decision trees. You can also control the tree depth in an ECOC model containing decision tree binary learners using the `MaxNumSplits`, `MinLeafSize`, or `MinParentSize` name-value pair parameters.

- When bagging decision trees, `fitensemble` grows deep decision trees by default. You can grow shallower trees to reduce model complexity or computation time.
- When boosting decision trees, fitensemble grows stumps (a tree with one split) by default. You can grow deeper trees for better accuracy.

Load the `carsmall` data set. Specify the variables `Acceleration`, `Displacement`, `Horsepower`, and `Weight` as predictors, and `MPG` as the response.

```
load carsmall
X = [Acceleration Displacement Horsepower Weight];
Y = MPG;
```

The default values of the tree depth controllers for boosting regression trees are:

- `1` for `MaxNumSplits`. This option grows stumps.
- `5` for `MinLeafSize`
- `10` for `MinParentSize`

To search for the optimal number of splits:

1. Train a set of ensembles. Exponentially increase the maximum number of splits for subsequent ensembles from stump to at most n - 1 splits. Also, decrease the learning rate for each ensemble from 1 to 0.1.
2. Cross validate the ensembles.
3. Estimate the cross-validated mean-squared error (MSE) for each ensemble.
4. Compare the cross-validated MSEs. The ensemble with the lowest one performs the best, and indicates the optimal maximum number of splits, number of trees, and learning rate for the data set.

Grow and cross validate a deep classification tree and a stump. Specify to use surrogate splits because the data contain missing values. These serve as benchmarks.

```
MdlDeep = fitrtree(X,Y,'CrossVal','on','MergeLeaves','off',...
    'MinParentSize',1,'Surrogate','on');
```

```
MdlStump = fitrtree(X,Y,'MaxNumSplits',1,'CrossVal','on','Surrogate','on');
```

Train the boosting ensembles using 200 regression trees. Cross validate the ensemble using 10-fold cross validation. Vary the maximum number of splits using the values in the sequence $\{2^0, 2^1, ..., 2^m\}$, where m is such that 2^m is no greater than n - 1. For each variant, adjust the learning rate to each value in the set {0.1, 0.25, 0.5, 1};

```
n = size(X,1);
m = floor(log2(n - 1));
lr = [0.1 0.25 0.5 1];
maxNumSplits = 2.^(0:m);
numTrees = 250;
Mdl = cell(numel(maxNumSplits),numel(lr));
rng(1); % For reproducibility
for k = 1:numel(lr);
    for j = 1:numel(maxNumSplits);
        t = templateTree('MaxNumSplits',maxNumSplits(j),'Surrogate','on');
        Mdl{j,k} = fitensemble(X,Y,'LSBoost',numTrees,t,...
            'Type','regression','CrossVal','on','LearnRate',lr(k));
    end;
end;
```

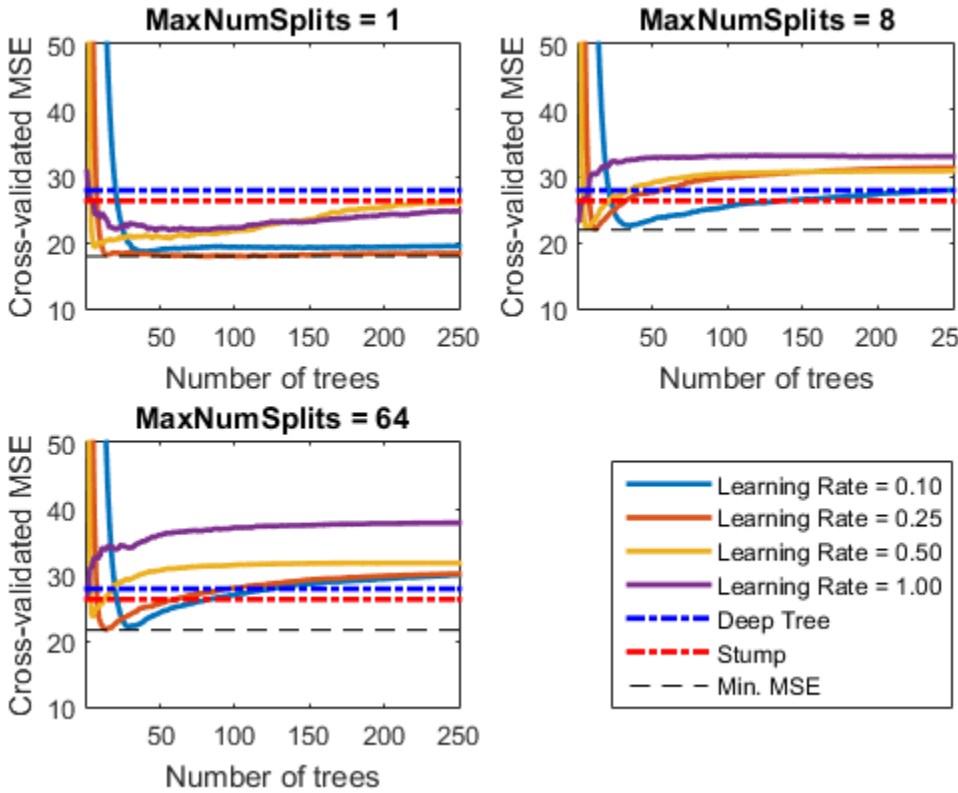
Compute the cross-validated MSE for each ensemble.

```
kflAll = @(x)kfoldLoss(x,'Mode','cumulative');
errorCell = cellfun(kflAll,Mdl,'Uniform',false);
error = reshape(cell2mat(errorCell),[numTrees numel(maxNumSplits) numel(lr)]);
errorDeep = kfoldLoss(MdlDeep);
errorStump = kfoldLoss(MdlStump);
```

Plot how the cross-validated classification error behaves as the number of trees in the ensemble increases for a few of the ensembles, the deep tree, and the stump. Plot the curves with respect to learning rate in the same plot, and plot separate plots for varying tree complexities. Choose a subset of tree complexity levels.

```
mnsPlot = [1 round(numel(maxNumSplits)/2) numel(maxNumSplits)];
figure;
for k = 1:3;
    subplot(2,2,k);
    plot(squeeze(error(:,mnsPlot(k),:)),'LineWidth',2);
    axis tight;
    hold on;
    h = gca;
    plot(h.XLim,[errorDeep errorDeep],'-.b','LineWidth',2);
```

```
    plot(h.XLim,[errorStump errorStump],'-.r','LineWidth',2);
    plot(h.XLim,min(min(error(:,mnsPlot(k),:))).*[1 1],'--k');
    h.YLim = [10 50];
    xlabel 'Number of trees';
    ylabel 'Cross-validated MSE';
    title(sprintf('MaxNumSplits = %0.3g', maxNumSplits(mnsPlot(k))));
    hold off;
end;
hL = legend([cellstr(num2str(lr','Learning Rate = %0.2f'));...
        'Deep Tree';'Stump';'Min. MSE']);
hL.Position(1) = 0.6;
```



Each curve contains a minimum cross-validated MSE occuring at the optimal number of trees in the ensemble.

Identify the maximum number of splits, number of trees, and learning rate that yields the lowest MSE overall.

```
[minErr minErrIdxLin] = min(error(:));
[idxNumTrees idxMNS idxLR] = ind2sub(size(error),minErrIdxLin);

fprintf('\nMin. MSE = %0.5f',minErr)
fprintf('\nOptimal Parameter Values:\nNum. Trees = %d',idxNumTrees);
fprintf('\nMaxNumSplits = %d\nLearning Rate = %0.2f\n',...
    maxNumSplits(idxMNS),lr(idxLR))
```

```
Min. MSE = 17.87423
Optimal Parameter Values:
Num. Trees = 79
MaxNumSplits = 1
Learning Rate = 0.25
```

Input Arguments

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Surrogate','on','NVarToSample','all'` specifies a template with surrogate splits, and uses all available predictors at each split.

For Classification Trees and Regression Trees

`'MaxNumSplits'` — Maximal number of decision splits

positive integer

Maximal number of decision splits (or branch nodes) per tree, specified as the comma-separated pair consisting of `'MaxNumSplits'` and a positive integer. `templateTree` splits `MaxNumSplits` or fewer branch nodes. For more details on splitting behavior, see “Algorithms” on page 22-4776.

For bagged decision trees and decision tree binary learners in ECOC models, the default is `size(X,1) - 1`. For boosted decision trees, the default is `1`.

Example: `'MaxNumSplits',5`

Data Types: `single | double`

`'MergeLeaves'` — Leaf merge flag

`'off' | 'on'`

Leaf merge flag, specified as the comma-separated pair consisting of `'MergeLeaves'` and either `'on'` or `'off'`.

When `'on'`, the decision tree merges leaves that originate from the same parent node, and that provide a sum of risk values greater or equal to the risk associated with the parent node. When `'off'`, the decision tree does not merge leaves.

For ensembles models, the default is `'off'`. For decision tree binary learners in ECOC models, the default is `'on'`.

Example: `'MergeLeaves','on'`

`'MinLeafSize'` — Minimum observations per leaf

positive integer value

Minimum observations per leaf, specified as the comma-separated pair consisting of `'MinLeafSize'` and a positive integer value. Each leaf has at least `MinLeafSize` observations per tree leaf. If you supply both `MinParentSize` and `MinLeafSize`, the decision tree uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

For boosted and bagged decision trees, the defaults are `1` for classification and `5` for regression. For decision tree binary learners in ECOC models, the default is `1`.

Example: `'MinLeafSize',2`

`'MinParentSize'` — Minimum observations per branch node

positive integer value

Minimum observations per branch node, specified as the comma-separated pair consisting of `'MinParentSize'` and a positive integer value. Each branch node in the tree has at least `MinParentSize` observations. If you supply both `MinParentSize` and `MinLeafSize`, the decision tree uses the setting that gives larger leaves: `MinParentSize = max(MinParentSize,2*MinLeafSize)`.

For boosted and bagged decision trees, the defaults are 2 for classification and 10 for regression. For decision tree binary learners in ECOC models, the default is 10.

Example: 'MinParentSize',4

'NumVariablesToSample' — Number of predictors to select at random for each split
positive integer value | 'all'

Number of predictors to select at random for each split, specified as the comma-separated pair consisting of 'NumVariablesToSample' and a positive integer value. Alternatively, you can specify 'all' to use all available predictors.

For boosted decision trees and decision tree binary learners in ECOC models models, the default is 'all'. The default for bagged decision trees is the square root of the number of predictors for classification, or one third of predictors for regression.

Example: 'NumVariablesToSample',3

'Prune' — Flag to estimate optimal sequence of pruned subtrees
'off' (default) | 'on'

Flag to estimate the optimal sequence of pruned subtrees, specified as the comma-separated pair consisting of 'Prune' and 'on' or 'off'.

If Prune is 'on', then the software trains the classification tree learners without pruning them, but estimates the optimal sequence of pruned subtrees for each learner in the ensemble or decision tree binary learner in ECOC models. Otherwise, the software trains the classification tree learners without estimating the optimal sequence of pruned subtrees.

For ensembles, the default is 'off'.

For decision tree binary learners in ECOC models, then the default is 'on'.

Example: 'Prune','on'

'PruneCriterion' — Pruning criterion
'error' | 'impurity' | 'mse'

Pruning criterion, specified as the comma-separated pair consisting of 'PruneCriterion' and a pruning criterion string valid for the tree type.

- For classification trees, you can specify 'error' (default) or 'impurity'.
- For regression, you can only specify 'mse'(default).

Example: `'PruneCriterion','impurity'`

`'SplitCriterion'` — Split criterion

`'gdi'` | `'twoing'` | `'deviance'` | `'mse'`

Split criterion, specified as the comma-separated pair consisting of `'SplitCriterion'` and a split criterion string valid for the tree type.

- For classification trees:
  - `'gdi'` for Gini's diversity index (default)
  - `'twoing'` for the twoing rule
  - `'deviance'` for maximum deviance reduction (also known as cross entropy)
- For regression trees:
  - `'mse'` for mean squared error (default)

Example: `'SplitCriterion','deviance'`

`'Surrogate'` — Surrogate decision splits

`'off'` (default) | `'on'` | `'all'` | positive integer value

Surrogate decision splits flag, specified as the comma-separated pair consisting of `'Surrogate'` and one of `'off'`, `'on'`, `'all'`, or a positive integer value.

- When `'off'`, the decision tree does not find surrogate splits at the branch nodes.
- When `'on'`, the decision tree finds at most 10 surrogate splits at each branch node.
- When set to `'all'`, the decision tree finds all surrogate splits at each branch node. The `'all'` setting can consume considerable time and memory.
- When set to a positive integer value, the decision tree finds at most the specified number of surrogate splits at each branch node.

Use surrogate splits to improve the accuracy of predictions for data with missing values. This setting also lets you compute measures of predictive association between predictors.

Example: `'Surrogate','on'`

For Classification Trees Only

`'AlgorithmForCategorical'` — Algorithm for best categorical predictor split

`'Exact'` | `'PullLeft'` | `'PCA'` | `'OVAbyClass'`

Algorithm to find the best split on a categorical predictor for data with C categories for data and $K \geq 3$ classes, specified as the comma-separated pair consisting of `'AlgorithmForCategorical'` and one of the following.

`'Exact'`	Consider all $2^{C-1} - 1$ combinations.
`'PullLeft'`	Start with all C categories on the right branch. Consider moving each category to the left branch as it achieves the minimum impurity for the K classes among the remaining categories. From this sequence, choose the split that has the lowest impurity.
`'PCA'`	Compute a score for each category using the inner product between the first principal component of a weighted covariance matrix (of the centered class probability matrix) and the vector of class probabilities for that category. Sort the scores in ascending order, and consider all C — 1 splits.
`'OVAbyClass'`	Start with all C categories on the right branch. For each class, order the categories based on their probability for that class. For the first class, consider moving each category to the left branch in order, recording the impurity criterion at each move. Repeat for the remaining classes. From this sequence, choose the split that has the minimum impurity.

`ClassificationTree` selects the optimal subset of algorithms for each split using the known number of classes and levels of a categorical predictor. For two classes, `ClassificationTree` always performs the exact search. Use the `'AlgorithmForCategorical'` name-value pair argument to specify a particular algorithm.

Example: `'AlgorithmForCategorical','PCA'`

`'MaxNumCategories'` — Maximum category levels in split node

10 (default) | nonnegative scalar value

Maximum category levels in the split node, specified as the comma-separated pair consisting of `'MaxNumCategories'` and a nonnegative scalar value. `ClassificationTree` splits a categorical predictor using the exact search algorithm if the predictor has at most `MaxNumCategories` levels in the split node. Otherwise, `ClassificationTree` finds the best categorical split using one of the inexact algorithms. Note that passing a small value can increase computation time and memory overload.

Example: `'MaxNumCategories',8`

For Regression Trees Only

`'QuadraticErrorTolerance'` — Quadratic error tolerance

`1e-6` (default) | nonnegative scalar value

Quadratic error tolerance per node, specified as the comma —separated pair consisting of `'QuadraticErrorTolerance'` and a nonnegative scalar value. `RegressionTree` stops splitting nodes when the quadratic error per node drops below `QuadraticErrorTolerance*QED`, where `QED` is the quadratic error for the entire data computed before the decision tree is grown. `QED = NORM(Y - YBAR)`, where `YBAR` is estimated as the average of the input array `Y`.

Example: `'QuadraticErrorTolerance',1e-4`

Output Arguments

`t` — Decision tree template for classification or regression

template object

Decision tree template for classification or regression suitable for training ensembles or error-correcting output code (ECOC) multiclass models, returned as a template object. Pass `t` to `fitensemble` or `fitcecoc` to specify how to create the decision tree for the ensemble or ECOC model, respectively.

If you display `t` in the Command Window, then all unspecified options appear empty (`[ ]`). However, the software replaces empty options with their corresponding default values during training.

More About

Algorithms

- To accommodate `MaxNumSplits`, the software splits all nodes in the current *layer*, and then counts the number of branch nodes. A layer is the set of nodes that are equidistant from the root node. If the number of branch nodes exceeds `MaxNumSplits`, then the software follows this procedure.

  1. Determine how many branch nodes in the current layer need to be unsplit so that there would be at most `MaxNumSplits` branch nodes.
  2. Sort the branch nodes by their impurity gains.
  3. Unsplit the desired number of least successful branches.
  4. Return the decision tree grown so far.

  This procedure aims at producing maximally balanced trees.
- The software splits branch nodes layer by layer until at least one of these events occurs.

  - There are MaxNumSplits + 1 branch nodes.
  - A proposed split causes the number of observations in at least one branch node to be fewer than MinParentSize.
  - A proposed split causes the number of observations in at least one leaf node to be fewer than MinLeafSize.
  - The algorithm cannot find a good split within a layer (i.e., the pruning criterion (see PruneCriterion), does not improve for all proposed splits in a layer). A special case of this event is when all nodes are pure (i.e., all observations in the node have the same class).

  `MaxNumSplits` and `MinLeafSize` do not affect splitting at their default values. Therefore, if you set `'MaxNumSplits'`, then splitting might stop due to the value of `MinParentSize` before `MaxNumSplits` splits occur.

References

[1] Coppersmith, D., S. J. Hong, and J. R. M. Hosking. “Partitioning Nominal Attributes in Decision Trees.” *Data Mining and Knowledge Discovery*, Vol. 3, 1999, pp. 197–217.

See Also

`RegressionTree` | `ClassificationTree` | `fitcecoc` | `fitctree` | `fitensemble`

test

Class: classregtree

Error rate

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
cost = test(t,'resubstitution')
cost = test(t,'test',X,y)
cost = test(t,'crossvalidate',X,y)
[cost,secost,ntnodes,bestlevel] = test(...)
[...] = test(...,param1,val1,param2,val2,...)
```

Description

`cost = test(t,'resubstitution')` computes the cost of the tree `t` using a resubstitution method. `t` is a decision tree as created by `classregtree`. The cost of the tree is the sum over all terminal nodes of the estimated probability of a node times the cost of a node. If `t` is a classification tree, the cost of a node is the sum of the misclassification costs of the observations in that node. If `t` is a regression tree, the cost of a node is the average squared error over the observations in that node. `cost` is a vector of cost values for each subtree in the optimal pruning sequence for `t`. The resubstitution cost is based on the same sample that was used to create the original tree, so it under estimates the likely cost of applying the tree to new data.

`cost = test(t,'test',X,y)` uses the matrix of predictors `X` and the response vector `y` as a test sample, applies the decision tree `t` to that sample, and returns a vector `cost` of cost values computed for the test sample. `X` and `y` should not be the same as the learning sample, that is, the sample that was used to fit the tree `t`.

`cost = test(t,'crossvalidate',X,y)` uses 10-fold cross-validation to compute the cost vector. `X` and `y` should be the learning sample, that is, the sample that was used to fit the tree `t`. The function partitions the sample into 10 subsamples, chosen randomly but with roughly equal size. For classification trees, the subsamples also have roughly the same class proportions. For each subsample, `test` fits a tree to the remaining data and uses it to predict the subsample. It pools the information from all subsamples to compute the cost for the whole sample.

`[cost,secost,ntnodes,bestlevel] = test(...)` also returns the vector `secost` containing the standard error of each `cost` value, the vector `ntnodes` containing the number of terminal nodes for each subtree, and the scalar `bestlevel` containing the estimated best level of pruning. A `bestlevel` of `0` means no pruning. The best level is the one that produces the smallest tree that is within one standard error of the minimum-cost subtree.

`[...] = test(...,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs for methods other than `'resubstitution'`, chosen from the following:

- `'weights'` — Observation weights.
- `'nsamples'` — The number of cross-validation samples (default is `10`).
- `'treesize'` — Either `'se'` (default) to choose the smallest tree whose cost is within one standard error of the minimum cost, or `'min'` to choose the minimal cost tree.

Examples

Compute the Cost of a Decision Tree

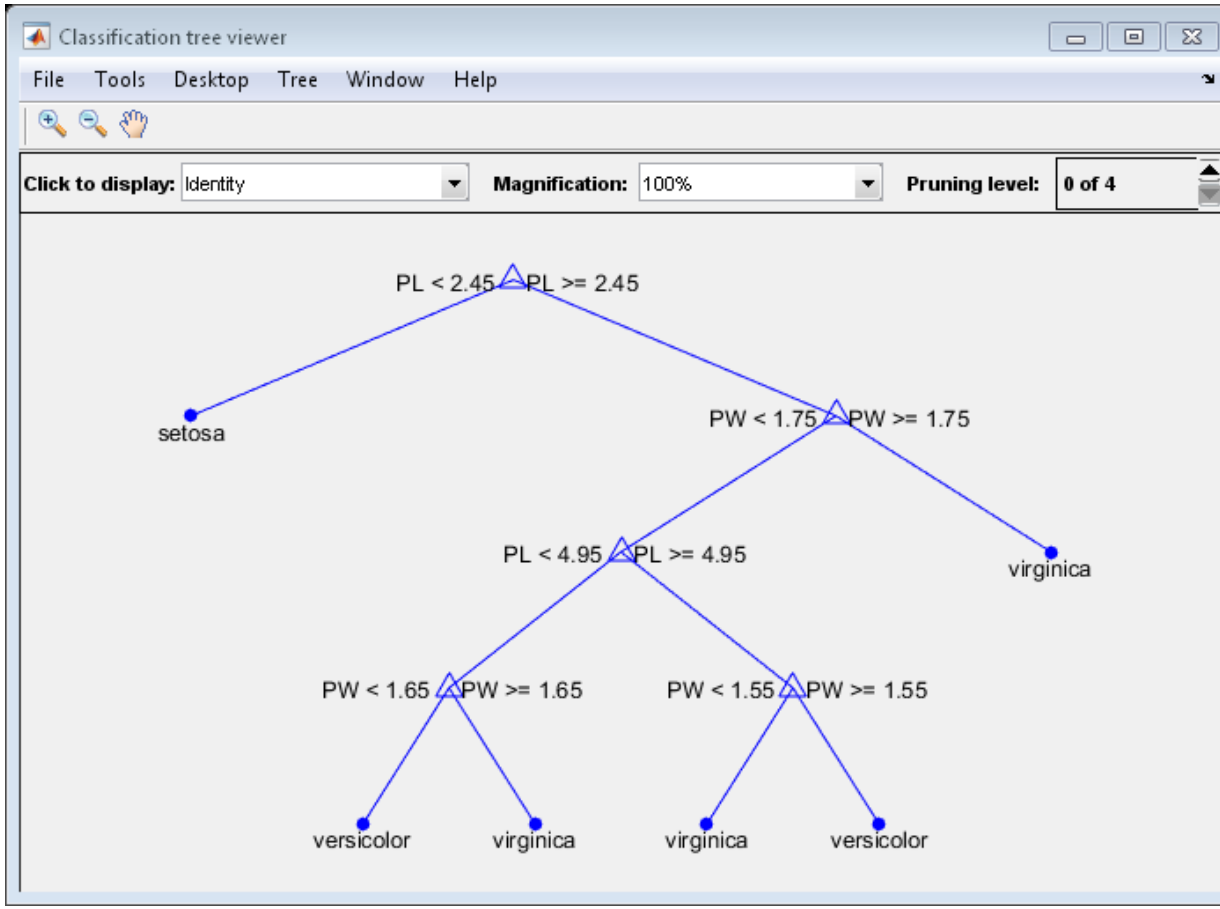
Find the best tree for Fisher's iris data using cross-validation.

Grow a large tree:

```
load fisheriris;
t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'},...
                 'minparent',5)
view(t)
```

```
t =

Decision tree for classification
```

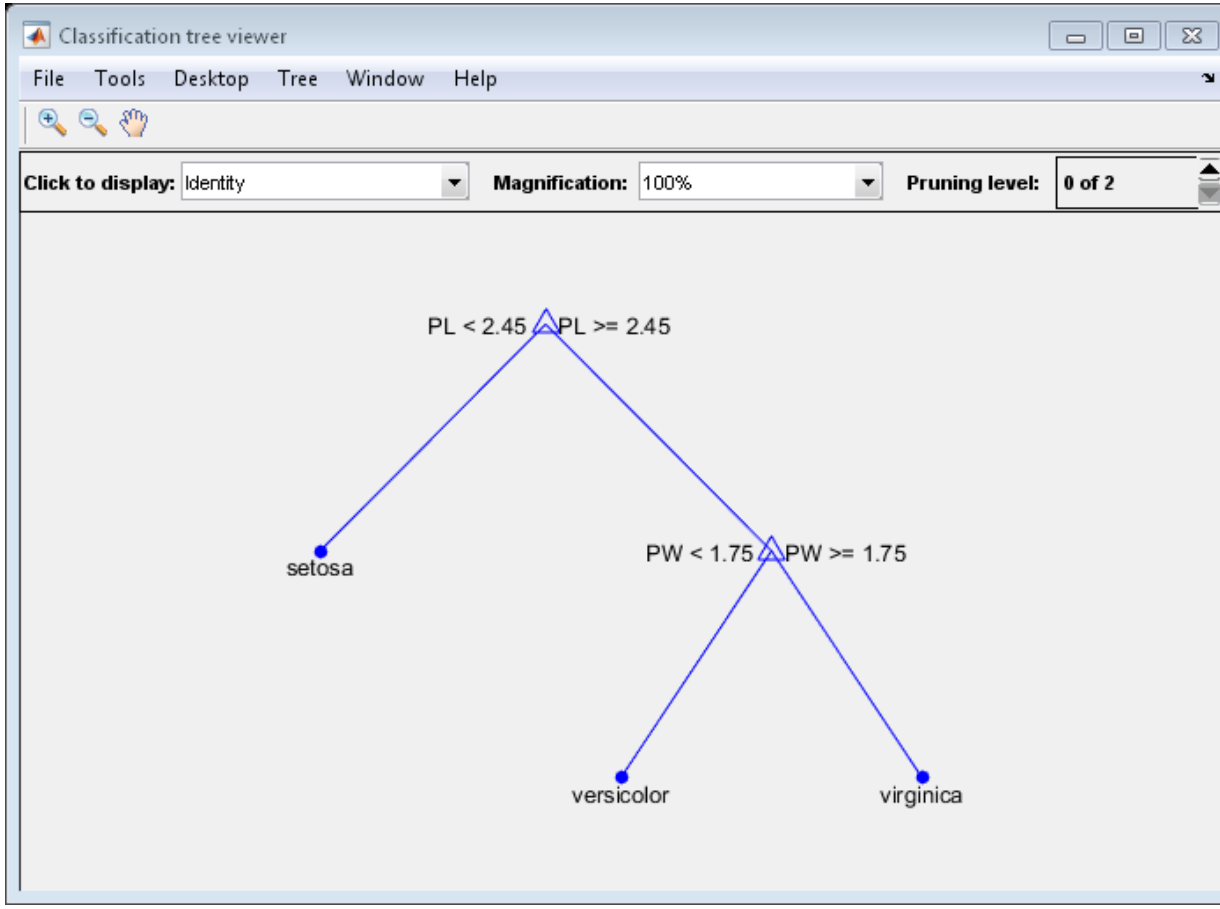
```
 1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
 2  class = setosa
 3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
 4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
 5  class = virginica
 6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
 7  if PW<1.55 then node 10 elseif PW>=1.55 then node 11 else virginica
 8  class = versicolor
 9  class = virginica
10  class = virginica
11  class = versicolor
```



Find the minimum-cost tree:

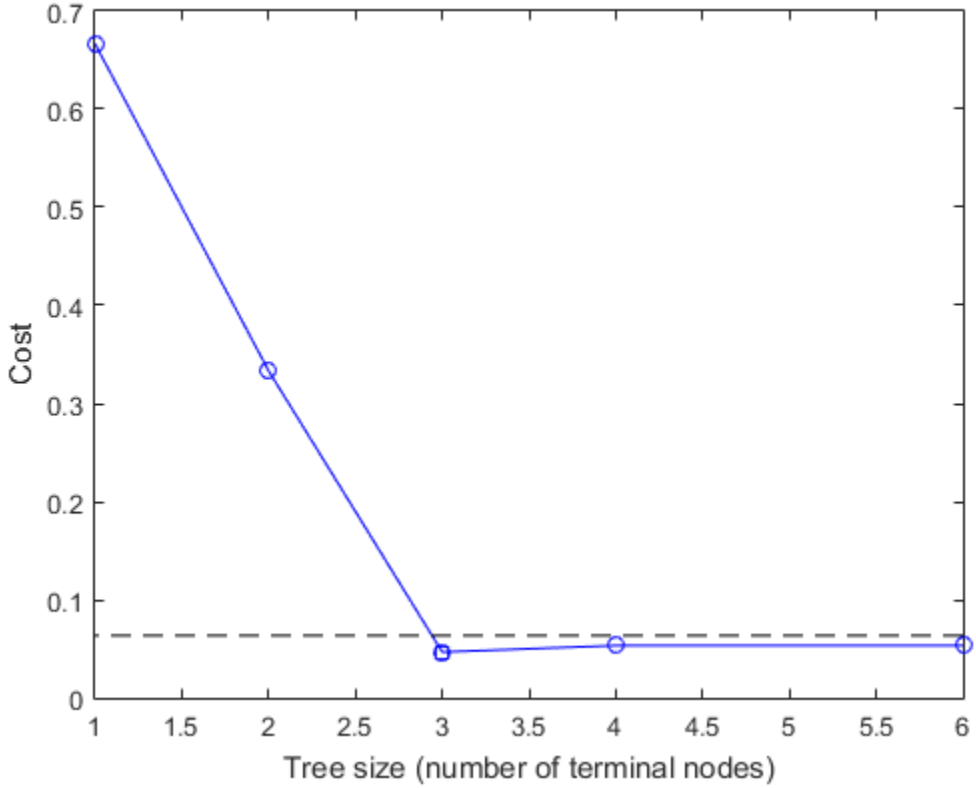
```
rng(1); % For reproducibility
[c,s,n,best] = test(t,'crossvalidate',meas,species);
tmin = prune(t,'level',best)
view(tmin)
```

```
tmin =

Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  class = versicolor
5  class = virginica
```



Plot the smallest tree within one standard error of the minimum cost tree:

```
[mincost,minloc] = min(c);
plot(n,c,'b-o',...
     n(best+1),c(best+1),'bs',...
     n,(mincost+s(minloc))*ones(size(n)),'k--')
xlabel('Tree size (number of terminal nodes)')
ylabel('Cost')
```



The solid line shows the estimated cost for each tree size, the dashed line marks one standard error above the minimum, and the square marks the smallest tree under the dashed line.

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `view` | `eval` | `prune`

test

Class: cvpartition

Test indices for cross-validation

Syntax

```
idx = test(c)
idx = test(c,i)
```

Description

`idx = test(c)` returns the logical vector `idx` of test indices for an object `c` of the `cvpartition` class of type `'holdout'` or `'resubstitution'`.

If `c.Type` is `'holdout'`, `idx` specifies the observations in the test set.

If `c.Type` is `'resubstitution'`, `idx` specifies all observations.

`idx = test(c,i)` returns the logical vector `idx` of test indices for repetition `i` of an object `c` of the `cvpartition` class of type `'kfold'` or `'leaveout'`.

If `c.Type` is `'kfold'`, `idx` specifies the observations in the test set in fold `i`.

If `c.Type` is `'leaveout'`, `idx` specifies the observation left out at repetition `i`.

Examples

Identify the test indices in the first fold of a partition of 10 observations for 3-fold cross-validation:

```
c = cvpartition(10,'kfold',3)
c =
K-fold cross validation partition
             N: 10
   NumTestSets: 3
```

```
     TrainSize: 7  6  7
      TestSize: 3  4  3

test(c,1)
ans =
     1
     1
     0
     0
     0
     0
     0
     0
     1
     0
```

See Also

cvpartition | training

testcholdout

Compare predictive accuracies of two classification models

`testcholdout` statistically assesses the accuracies of two classification models. The function first compares their predicted labels against the true labels, and then it detects whether the difference between the misclassification rates is statistically significant.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. `testcholdout` can conduct several McNemar test variations, including the asymptotic test, the exact-conditional test, and the mid-*p*-value test. For cost-sensitive assessment, available tests include a chi-square test (requires an Optimization Toolbox license) and a likelihood ratio test.

Syntax

```
h = testcholdout(YHat1,YHat2,Y)
h = testcholdout(YHat1,YHat2,Y,Name,Value)
[h,p,e1,e2] = testcholdout( ___ )
```

Description

`h = testcholdout(YHat1,YHat2,Y)` returns the test decision, by conducting the mid-*p*-value McNemar test, from testing the null hypothesis that the predicted class labels `YHat1` and `YHat2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at 5% level.

`h = testcholdout(YHat1,YHat2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, specify the type of test, or supply a cost matrix.

`[h,p,e1,e2] = testcholdout( ___ )` returns the *p*-value for the hypothesis test (`p`) and the respective classification loss of each set of predicted class labels (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Examples

Compare Accuracies of Two Different Classification Models

Train two classification models using different algorithms. Conduct a statistical test comparing the misclassification rates of the two models on a held-out set.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train an SVM model and an ensemble of 100 bagged classification trees. For the SVM model, specify to use the radial basis function kernel and a heuristic procedure to determine the kernel scale. It is a good practice to standardize the predictor data for SVM.

```
MdlSVM = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF','KernelScale','auto');
MdlBag = fitensemble(X(idxTrain,:),Y(idxTrain),'Bag',100,'Tree',...
    'Type','classification');
```

`MdlSVM` is a trained `ClassificationSVM` model. `MdlBag` is a trained `ClassificationBaggedEnsemble` model.

Label the test-set observations using the trained models.

```
YhatSVM = predict(MdlSVM,X(idxTest,:));
YhatBag = predict(MdlBag,X(idxTest,:));
```

`YhatSVM` and `YhatBag` are vectors continuing the predicted class labels of the respective models.

Test whether the two models have equal predictive accuracies.

```
h = testcholdout(YhatSVM,YhatBag,Y(idxTest))
```

```
h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Train two classification models using the same algorithm, but adjust a hyperparameter to make the algorithm more complex. Conduct a statistical test to assess whether the simpler model has better accuracy in held-out data than the more complex model.

Load the `ionosphere` data set.

```
load ionosphere;
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Train two SVM models: one that uses a linear kernel (the default for binary classification) and one that uses the radial basis function kernel. Use the default kernel scale of 1. It is a good practice to standardize the predictor data for SVM.

```
MdlLinear = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true);
MdlRBF = fitcsvm(X(idxTrain,:),Y(idxTrain),'Standardize',true,...
    'KernelFunction','RBF');
```

`MdlLinear` and `MdlRBF` are trained `ClassificationSVM` models.

Label the test-set observations using the trained models.

```
YhatLinear = predict(MdlLinear,X(idxTest,:));
YhatRBF = predict(MdlRBF,X(idxTest,:));
```

`YhatLinear` and `YhatRBF` are vectors continuing the predicted class labels of the respective models.

Test the null hypothesis that the simpler model (`MdlLinear`) is at most as accurate as the more complex model (`MdlRBF`). Because the test-set size is large, conduct the asymptotic McNemar test, and compare the results with the mid- *p*-value test (the cost-insensitive testing default). Request to return *p*-values and misclassification rates.

```
Asymp = zeros(4,1); % Preallocation
MidP = zeros(4,1);

[Asymp(1),Asymp(2),Asymp(3),Asymp(4)] = testcholdout(YhatLinear,YhatRBF,Y(idxTest),...
    'Alternative','greater','Test','asymptotic');
[MidP(1),MidP(2),MidP(3),MidP(4)] = testcholdout(YhatLinear,YhatRBF,Y(idxTest),...
    'Alternative','greater');
table(Asymp,MidP,'RowNames',{'h' 'p' 'e1' 'e2'})
```

```
ans =

            Asymp          MidP
          _________    _________

    h           1              1
    p    7.2801e-09    2.7649e-10
    e1      0.13714       0.13714
    e2      0.33143       0.33143
```

The *p*-value is close to zero for both tests, which indicates strong evidence to reject the null hypothesis that the simpler model is less accurate than the more complex model. No matter what test you specify, `testcholdout` returns the same type of misclassification measure for both models.

Conduct a Cost-Sensitive Comparison of Two Classification Models

For data sets with imbalanced class representations, or if the false-positive and false-negative costs are imbalanced, you can statistically compare the predictive performances of two classification models by including a cost matrix in the analysis.

Load the `arrhythmia` data set. Determine the class representations in the data.

```
load arrhythmia;
Y = categorical(Y);
tabulate(Y);
```

```
  Value    Count   Percent
      1      245     54.20%
```

```
     2        44       9.73%
     3        15       3.32%
     4        15       3.32%
     5        13       2.88%
     6        25       5.53%
     7         3       0.66%
     8         2       0.44%
     9         9       1.99%
    10        50      11.06%
    14         4       0.88%
    15         5       1.11%
    16        22       4.87%
```

There are 16 classes, however some are not represented in the data set. Most observations are classified as not having arrhythmia (class 1). To summarize, the data set is highly discrete with imbalanced classes.

Combine all observations with arrhythmia (classes 2 through 15) into one class. Remove those observations with unknown arrhythmia status from the data set.

```
Y = Y(Y ~= '16');
Y(Y ~= '1') = '2';
X = X(Y ~= '16',:);
```

Create a partition that evenly splits the data into training and testing sets.

```
rng(1);                              % For reproducibility
CVP = cvpartition(Y,'holdout',0.5);
idxTrain = training(CVP);            % Training-set indices
idxTest = test(CVP);                 % Test-set indices
```

`CVP` is a cross-validation partition object that specifies the training and test sets.

Create a cost matrix such that misclassifiying an arrhythmatic patient into the no arrhythmia class is five times worse that misclassifying a patient without arrhythmia into the arrhythmia class. Classifying correctly incurs no cost. The rows indicate the true class and the columns indicate predicted class. When conducting a cost-sensitive analysis, it is a good practice to specify the order of the classes.

```
Cost = [0 1;5 0];
ClassNames = categorical([2 1]);
```

Train two boosting ensembles of 50 classification trees, one that uses AdaBoostM1 and the other that uses LogitBoost. Because there are missing values, specify to use surrogate splits. Train the models using the cost matrix.

```
t = templateTree('Surrogate','on');
numTrees = 50;
MdlAda = fitensemble(X(idxTrain,:),Y(idxTrain),'AdaBoostM1',numTrees,t,...
    'Cost',Cost,'ClassNames',ClassNames);
MdlLogit = fitensemble(X(idxTrain,:),Y(idxTrain),'LogitBoost',numTrees,t,...
    'Cost',Cost,'ClassNames',ClassNames);
```

`MdlAda` and `MdlLogit` are trained `ClassificationEnsemble` models.

Label the test-set observations using the trained models.

```
YhatAda = predict(MdlAda,X(idxTest,:));
YhatLogit = predict(MdlLogit,X(idxTest,:));
```

`YhatLinear` and `YhatRBF` are vectors containing the predicted class labels of the respective models.

Test whether the AdaBoostM1 ensemble (`MdlAda`) and the LogitBoost ensemble (`MdlLogit`) have equal predictive accuracy. Supply the cost matrix. Conduct the asymptotic, likelihood ratio, cost-sensitive test (the default when you pass in a cost matrix). Request to return *p*-values and misclassification costs.

```
[h,p,e1,e2] = testcholdout(YhatAda,YhatLogit,Y(idxTest),'Cost',Cost)
```

```
h =

     0


p =

    0.2300


e1 =

    2.0837


e2 =

    1.9581
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Input Arguments

`YHat1` — Predicted class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Predicted class labels of the first classification model, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `YHat1` is a character array, then each element must correspond to one row of the array.

`YHat1`, YHat2, and Y must have equal lengths.

It is a best practice for `YHat1`, `YHat2`, and `Y` to share the same data type.

`YHat2` — Predicted class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Predicted class labels of the second classification model, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `YHat2` is a character array, then each element must correspond to one row of the array.

YHat1, `YHat2`, and Y must have equal lengths.

It is a best practice for `YHat1`, `YHat2`, and `Y` to share the same data type.

`Y` — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, logical or numeric vector, or cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

YHat1, YHat2, and `Y` must have equal lengths.

It is a best practice for `YHat1`, `YHat2`, and `Y` to share the same data type.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','asymptotic','Cost',[0 2;1 0]` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the asymptotic McNemar test, and to penalize misclassifying observations with the true label `ClassNames{1}` twice as much as for misclassifying observations with the true label `ClassNames{2}`.

`'Alpha'` — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

`'Alternative'` — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of the values listed in the table.

Value	Alternative hypothesis
`'unequal'` (default)	For predicting Y, YHat1 and YHat2 have unequal accuracies.
`'greater'`	For predicting Y, YHat1 is more accurate than YHat2.
`'less'`	For predicting Y, YHat1 is less accurate than YHat2.

Example: `'Alternative','greater'`

Data Types: `char`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical | char | logical | single | double | cell`

`'Cost'` — Misclassification cost

square matrix | structure array

Misclassification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array. If you specify:

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.
- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

If you specify `Cost`, then `testcholdout` cannot conduct one-sided, exact, or mid-*p* tests. You must also specify `'Alternative','unequal','Test','asymptotic'`. For cost-sensitive testing options, see the CostTest name-value pair argument.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double | single | struct`

`'CostTest'` — Cost-sensitive test type

`'likelihood'` (default) | `'chisquare'`

Cost-sensitive test type, specified as the comma-separated pair consisting of `'CostTest'` and `'chisquare'` or `'likelihood'`. Unless you specify a cost matrix using the Cost name-value pair argument, `testcholdout` ignores `CostTest`.

This table summarizes the available options for cost-sensitive testing.

Value	Asymptotic test type	Requirements
`'chisquare'`	Chi-square test	Optimization Toolbox license to implement `quadprog`
`'likelihood'`	Likelihood ratio test	None

For more details, see “Cost-Sensitive Testing” on page 22-4797.

Example: `'CostTest','chisquare'`

Data Types: `char`

`'Test'` — Test to conduct

`'asymptotic' | 'exact' | 'midp'`

Test to conduct, specified as the comma-separated pair consisting of `'Test'` and `'asymptotic'`, `'exact'`, and `'midp'`. This table summarizes the available options for cost-insensitive testing.

Value	Description
`'asymptotic'`	Asymptotic McNemar test
`'exact'`	Exact-conditional McNemar test
`'midp'` (default)	Mid-*p*-value McNemar test

For more details, see “McNemar Tests” on page 22-4799.

For cost-sensitive testing, `Test` must be `'asymptotic'`. When you specify the Cost name-value pair argument, and choose a cost-sensitive test using the CostTest name-value pair argument, `'asymptotic'` is the default.

Example: `'Test','asymptotic'`

Data Types: `char`

Note: `NaN`s, `<undefined>` values, and empty strings (`''`) indicate missing values. `testcholdout`:

- Treats missing values in YHat1 and YHat2 as misclassified observations.
- Removes missing values in Y and the corresponding values of YHat1 and YHat2

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

`h = 1` indicates the rejection of the null hypothesis at the Alpha significance level.

`h = 0` indicates failure to reject the null hypothesis at the `Alpha` significance level.

p — *p*-value

scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. `p` is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

`testcholdout` estimates `p` using the distribution of the test statistic, which varies with the type of test. For details on test statistics derived from the available variants of the McNemar test, see "McNemar Tests" on page 22-4799. For details on test statistics derived from cost-sensitive tests, see "Cost-Sensitive Testing" on page 22-4797.

e1 — Classification loss

scalar

Classification loss that summarizes the accuracy of the first set of class labels (YHat1) predicting the true class labels (Y), returned as a scalar.

For cost-insensitive testing, `e1` is the misclassification rate. That is, `e1` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e1` is the misclassification cost. That is, `e1` is the weighted average of the misclassification costs, in which the weights are the respective estimated proportions of misclassified observations.

e2 — Classification loss

scalar

Classification loss that summarizes the accuracy of the second set of class labels (YHat2) predicting the true class labels (Y), returned as a scalar.

For cost-insensitive testing, `e2` is the misclassification rate. That is, `e2` is the proportion of misclassified observations, which is a scalar in the interval [0,1].

For cost-sensitive testing, `e2` is the misclassification cost. That is, `e2` is the weighted average of the costs of misclassification, in which the weights are the respective estimated proportions of misclassified observations.

More About

Cost-Sensitive Testing

Conduct *cost-sensitive testing* when the cost of misclassification is imbalanced. When conducting a cost-sensitive analysis, you can account for the cost imbalance in training the classification models, and then in statistically comparing them.

If the cost of misclassification is imbalanced, then the misclassification rate tends to be a poorly performing classification loss. Use misclassification cost instead to compare classification models.

Misclassification costs are often unbalanced in applications. For example, consider classifying subjects based on a set of predictors into two categories: healthy and sick. Misclassifying a sick subject as healthy poses a danger to the subject's life. However, misclassifying a healthy subject as sick can cause some inconvenience, but does not pose any danger. In this situation, you assign misclassification costs such that misclassifying a sick subject as healthy is more costly than misclassifying a healthy subject as sick.

The definitions that follow summarize the cost-sensitive tests. In the definitions:

- n_{ijk} and $\hat{\pi}_{ijk}$ are the number and estimated proportion of test-sample observations with true class k that the first classification model assigns label i. The second

classification model assigns label j. The unknown, true value of $\hat{\pi}_{ijk}$ is π_{ijk}. The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. $\sum_{i,j,k} \pi_{ijk} = \sum_{i,j,k} \pi_{ijk} = 1$. .

- c_{ij} is the relative cost of assigning label j to an observation with true class i. $c_{ii} = 0$, $c_{ij} \geq 0$, and, for at least one (i,j) pair, $c_{ij} > 0$.
- All subscripts take on integer values from 1 through K, which is the number of classes.
- The expected difference in the misclassification costs of the two classification models is

$$\delta = \sum_{i=1}^{K} \sum_{j=1}^{K} \sum_{k=1}^{K} \left(c_{ki} - c_{kj} \right) \pi_{ijk}.$$

- The hypothesis test is

$$\begin{aligned} H_0 &: \delta = 0 \\ H_1 &: \delta \neq 0 \end{aligned}.$$

The available cost-sensitive tests are appropriate for two-tailed testing.

Available, asymptotic tests that address imbalanced costs are a *chi-square test* and a *likelihood ratio test*.

- Chi-square test — The chi-square test statistic is based on the Pearson and Neyman chi-square test statistics, but with a Laplace correction factor to account for any $n_{ijk} = 0$. The test statistic is

$$t^*_{\chi^2} = \sum_{i \neq j} \sum_{k} \frac{\left(n_{ijk} + 1 - \left(n_{test} + K^3 \right) \hat{\pi}^{(1)}_{ijk} \right)^2}{n_{ijk} + 1}.$$

If $1 - F_{\chi^2}\left(t^*_{\chi^2}; 1 \right) < \alpha$, then reject H_0.

- $\hat{\pi}^{(1)}_{ijk}$ are estimated by minimizing $t^*_{\chi^2}$ under the constraint that $\delta = 0$.

- $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

- Likelihood ratio test — The likelihood ratio test is based on N_{ijk}, which are binomial random variables having sample size n_{test} and success probability π_{ijk}. They represent the random number of observations with true class k that the first classification model assigns label i. The second classification model assigns label j. Jointly, their distribution is multinomial.

  The test statistic is

$$t^*_{LRT} = 2\log\left[\frac{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(2)}_{ijk}\right)}{P\left(\bigcap_{i,j,k} N_{ijk} = n_{ijk}; n_{test}, \pi_{ijk} = \pi^{(3)}_{ijk}\right)}\right].$$

  If $1 - F_{\chi^2}\left(t^*_{LRT};1\right) < \alpha,$, then reject H_0.

  - $\hat{\pi}^{(2)}_{ijk} = \dfrac{n_{ijk}}{n_{test}}$ is the unrestricted MLE of π_{ijk}.

  - $\hat{\pi}^{(3)}_{ijk} = \dfrac{n_{ijk}}{n_{test} + \lambda(c_{ki} - c_{kj})}$ is the MLE under the null hypothesis that $\delta = 0$. λ is the solution to

$$\sum_{i,j,k} \frac{n_{ijk}(c_{ki} - c_{kj})}{n_{test} + \lambda(c_{ki} - c_{kj})} = 0.$$

  - $F_{\chi^2}(x;1)$ is the χ^2 C.D.F. with one degree of freedom evaluated at x.

McNemar Tests

McNemar Tests are hypothesis tests that compare two population proportions while addressing the issues resulting from two dependent, matched-pair samples.

One way to compare the predictive accuracies of two classification models is:

1. Partition the data into training and test sets.
2. Train both classification models using the training set.
3. Predict class labels using the test set.
4. Summarize the results in a two-by-two table resembling this figure.

		Model 2: Correct	Model 2: Incorrect	
Model 1	Correct	n_{11}	n_{12}	$n_{1\bullet}$
	Incorrect	n_{21}	n_{22}	$n_{2\bullet}$
		$n_{\bullet 1}$	$n_{\bullet 2}$	n_{test}

n_{ii} are the number of concordant pairs, that is, the number of observations that both models classify the same way (correctly or incorrectly). n_{ij}, $i \neq j$, are the number of discordant pairs, that is, the number of observations that models classify differently (correctly or incorrectly).

The misclassification rates for Models 1 and 2 are

$$\hat{\pi}_{2\bullet} = n_{2\bullet} / n$$

and $\hat{\pi}_{\bullet 2} = n_{\bullet 2} / n$, respectively. A two-sided test for comparing the accuracy of the two models is

$$\begin{aligned} H_0 &: \pi_{\bullet 2} = \pi_{2\bullet} \\ H_1 &: \pi_{\bullet 2} \neq \pi_{2\bullet} \end{aligned}.$$

The null hypothesis suggests that the population exhibits marginal homogeneity, which reduces the null hypothesis to $H_0 : \pi_{12} = \pi_{21}$. Also, under the null hypothesis, N_{12} ~ Binomial($n_{12} + n_{21}$,0.5) [1].

These facts are the basis for these, available McNemar test variants: the *asymptotic*, *exact-conditional* and *mid-p-value* McNemar tests. The definitions that follow summarize the available variants.

- Asymptotic — The asymptotic McNemar test statistics and rejection regions (for significance-level α) are:

  - For one-sided tests, the test statistic

    $$t_{a1}^{*} = \frac{n_{12} - n_{21}}{\sqrt{n_{12} + n_{21}}}.$$

    If $1 - \Phi\left(\left|t_1^{*}\right|\right) < \alpha,$, where Φ is the standard Gaussian C.D.F., then reject H_0.

  - For two-sided tests, the test statistic

    $$t_{a2}^{*} = \frac{\left(n_{12} - n_{21}\right)^2}{n_{12} + n_{21}}.$$

    If $1 - F_{\chi^2}\left(t_2^{*}; m\right) < \alpha$, where $F_{\chi^2}(x; m)$ is the ${\chi_m}^2$ C.D.F. evaluated at x, then reject H_0.

  This variant requires large-sample theory, specifically, the Gaussian approximation to the binomial distribution. Therefore:

  - The total number of discordant pairs, $n_d = n_{12} + n_{21}$ must be greater than 10 ([1], Ch. 10.1.4).
  - In general, asymptotic tests do not guarantee nominal coverage. The observed probability of falsely rejecting the null hypothesis can exceed α. Simulation studies in [14] suggest this, but the asymptotic McNemar test performs well in terms of statistical power.

- Exact Conditional — The exact-conditional McNemar test statistics and rejection regions (for significance-level α) are ([24], [25]):

  - For one-sided tests, the test statistic

    $$t_1^* = n_{12}$$

    If $F_{\text{Bin}}\left(t_1^*; n_d, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ is the binomial C.D.F. with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

    $$t_2^* = \min(n_{12}, n_{21})$$

    If $F_{\text{Bin}}\left(t_2^*; n_d, 0.5\right) < \alpha / 2$, then reject H_0.

  The exact conditional test always attains nominal coverage. Simulation studies in [14] suggest that the test is conservative, and then show that the test lacks statistical power compared to other variants. For small or highly discrete test samples, consider using the mid-p-value test ([1], Ch. 3.6.3). For details, see Test and "McNemar Tests" on page 22-4799.

- Mid-p-value test — The mid-p-value McNemar test statistics and rejection regions (for significance-level α) are ([23]):

  - For one-sided tests, the test statistic

    $$t_1^* = n_{12}$$

    If $F_{\text{Bin}}\left(t_1^* - 1; n_{12} + n_{21}, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_1^*; n_{12} + n_{21}, 0.5\right) < \alpha$, where $F_{\text{Bin}}\left(x; n, p\right)$ and $f_{\text{Bin}}\left(x; n, p\right)$ are the binomial C.D.F. and P.D.F, respectively, with sample size n and success probability p evaluated at x, then reject H_0.

  - For two-sided tests, the test statistic

    $$t_2^* = \min(n_{12}, n_{21})$$

If $F_{\text{Bin}}\left(t_2^* - 1; n_{12} + n_{21} - 1, 0.5\right) + 0.5 f_{\text{Bin}}\left(t_2^*; n_{12} + n_{21}, 0.5\right) < \alpha / 2$, then reject H_0.

The mid-*p*-value test addresses the over-conservative behavior of the exact conditional test. The simulation studies in [14] demonstrate that this test attains nominal coverage, and has good statistical power.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. Two classification losses are misclassification rate and cost.

`testcholdout` returns the classification losses (see e1 and e2) under the alternative hypothesis (i.e., the unrestricted classification losses). n_{ijk} is the number of test-sample observations with true class k that the first classification model assigns label i and the second classification model assigns label j, and the corresponding estimated proportion is $\hat{\pi}_{ijk} = \frac{n_{ijk}}{n_{test}}$. . The test-set sample size is $\sum_{i,j,k} n_{ijk} = n_{test}$. The indices are taken from 1 through K, the number of classes.

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk}.$$

  For the misclassification rate of the second classification model (e_2), switch the indices i and j in the formula.

  Classification accuracy decreases as the misclassification rate increases to 1.

- *Misclassification cost* is a nonnegative scalar and is a measure of classification quality relative to the values the specified cost matrix elements. Its interpretation depends on the specified costs of misclassification. Misclassification cost is the weighted average of the costs of misclassification (specified in a cost matrix, C) in which the weights are the respective, estimated proportions of misclassified observations. The misclassification cost for the first classification model is

$$e_1 = \sum_{j=1}^{K} \sum_{k=1}^{K} \sum_{i \neq k} \hat{\pi}_{ijk} c_{ki},$$

where c_{kj} is the cost of classifying an observation into class j if its true class is k. For the misclassification cost of the second classification model (e_2), switch the indices i and j in the formula.

In general, for a fixed cost matrix, classification accuracy decreases as misclassification cost increases.

Tips

- It is a good practice to obtain predicted class labels by passing any trained classification model and new predictor data to the `predict` method. For example, for predicted labels from an SVM model, see `predict`.
- Cost-sensitive tests perform numerical optimization, which requires additional computational resources. The likelihood ratio test conducts numerical optimization indirectly by finding the root of a Lagrange multiplier in an interval. For some data sets, if the root lies close to the boundaries of the interval, then the method can fail. Therefore, if you have an Optimization Toolbox license, consider conducting the cost-sensitive chi-square test instead. For more details, see CostTest and "Cost-Sensitive Testing" on page 22-4797.
- "Hypothesis Tests"

References

[1] Agresti, A. *Categorical Data Analysis*, 2nd Ed. John Wiley & Sons, Inc.: Hoboken, NJ, 2002.

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[3] Lancaster, H.O. "Significance Tests in Discrete Distributions." *JASA*, Vol. 56, Number 294, 1961, pp. 223–234.

[4] McNemar, Q. “Note on the Sampling Error of the Difference Between Correlated Proportions or Percentages.” *Psychometrika*, Vol. 12, Number 2, 1947, pp. 153–157.

[5] Mosteller, F. “Some Statistical Problems in Measuring the Subjective Response to Drugs.” *Biometrics*, Vol. 8, Number 3, 1952, pp. 220–226.

See Also

`testckfold`

Introduced in R2015a

testckfold

Compare accuracies of two classification models by repeated cross validation

`testckfold` statistically assesses the accuracies of two classification models by repeatedly cross validating the two models, determining the differences in the classification loss, and then formulating the test statistic by combining the classification loss differences. This type of test is particularly appropriate when sample size is limited.

You can assess whether the accuracies of the classification models are different, or whether one classification model performs better than another. Available tests include a 5-by-2 paired *t* test, a 5-by-2 paired *F* test, and a 10-by-10 repeated cross-validation *t* test. For more details, see "Repeated Cross-Validation Tests" on page 22-4826. To speed up computations, `testckfold` supports parallel computing (requires a Parallel Computing Toolbox license).

Syntax

```
h = testckfold(C1,C2,X1,X2,Y)
h = testckfold(C1,C2,X1,X2,Y,Name,Value)
[h,p,e1,e2] = testckfold( ___ )
```

Description

`h = testckfold(C1,C2,X1,X2,Y)` returns the decision that results from testing the null hypothesis that classification models `C1` and `C2` have equal accuracy for predicting the true class labels `Y`. The alternative hypothesis is that the labels have unequal accuracy.

The first classification model, `C1`, uses predictor data `X1`. The second classification model, `C2`, uses `X2`. `testckfold` conducts a 5-by-2 paired *F* test (see "Repeated Cross-Validation Tests" on page 22-4826).

`h = 1` indicates to reject the null hypothesis at the 5% significance level. `h = 0` indicates to not reject the null hypothesis at the 5% level.

Examples of tests you can conduct include:

- Compare the accuracies of a simple classification model and a more complex model by passing the same set of predictor data (that is, `X1 = X2`).
- Compare the accuracies of two different models using two different sets of predictors.
- Perform various types of feature selection. For example, you can compare the accuracy of a model trained using a set of predictors to the accuracy of one trained on a subset or different set of those predictors. You can arbitrarily choose the set of predictors, or use a feature selection technique like PCA or sequential feature selection (see `pca` and `sequentialfs`).

`h = testckfold(C1,C2,X1,X2,Y,Name,Value)` returns the result of the hypothesis test with additional options specified by one or more `Name,Value` pair arguments. For example, you can specify the type of alternative hypothesis, the type of test, or the use of parallel computing.

`[h,p,e1,e2] = testckfold( ___ )` additionally returns the *p*-value for the hypothesis test (`p`) and the respective classification losses for each cross-validation run and fold (`e1` and `e2`) using any of the input arguments in the previous syntaxes.

Examples

Compare Accuracies of Two Different Classification Models

Conduct a statistical test comparing the misclassification rates of the two models using a 5-by-2 paired *F* test.

Load Fisher's iris data set.

```
load fisheriris;
```

Create a naive Bayes template and a classification tree template using default options.

```
C1 = templateNaiveBayes;
C2 = templateTree;
```

`C1` and `C2` are template objects corresponding to the naive Bayes and classification tree algorithms, respectively.

Test whether the two models have equal predictive accuracies. Use the same predictor data for each model. `testckfold` conducts a 5-by-2, two-sided, paired *F* test by default.

```
rng(1); % For reproducibility
```

```
h = testckfold(C1,C2,meas,meas,species)

h =

     0
```

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies.

Assess Whether One Classification Model Classifies Better Than Another

Conduct a statistical test to assess whether a simpler model has better accuracy than a more complex model using a 10-by-10 repeated cross-validation *t* test.

Load Fisher's iris data set. Create a cost matrix that penalizes misclassifying a setosa iris twice as much as misclassifying a virginica iris as a versicolor.

```
load fisheriris;
tabulate(species)
Cost = [0 2 2;2 0 1;2 1 0];
ClassNames  = {'setosa' 'versicolor' 'virginica'};...
    % Specifies the order of the rows and columns in Cost
```

```
       Value    Count   Percent
      setosa       50     33.33%
  versicolor       50     33.33%
   virginica       50     33.33%
```

The empirical distribution of the classes is uniform, and the classification cost is slightly imbalanced.

Create two ECOC templates: one that uses linear SVM binary learners and one that uses SVM binary learners equipped with the RBF kernel. It is a good practice to standardize the predictor data when using SVM.

```
tSVMLinear = templateSVM('Standardize',true); % Linear SVM by default
tSVMRBF = templateSVM('KernelFunction','RBF','Standardize',true);
C1 = templateECOC('Learners',tSVMLinear);
C2 = templateECOC('Learners',tSVMRBF);
```

`C1` and `C2` are ECOC template objects. `C1` is prepared for linear SVM. `C2` is prepared for SVM with an RBF kernel training.

Test the null hypothesis that the simpler model (`C1`) is at most as accurate as the more complex model (`C2`) in terms of classification costs. Conduct the 10-by-10 repeated cross-validation test. Request to return *p*-values and misclassification costs.

```
rng(1); % For reproducibility
[h,p,e1,e2] = testckfold(C1,C2,meas,meas,species,...
    'Alternative','greater','Test','10x10t','Cost',Cost,...
    'ClassNames',ClassNames)
```

```
h =

     0


p =

    0.1077


e1 =

  Columns 1 through 7

         0         0         0    0.0667         0    0.0667    0.1333
    0.0667    0.0667         0         0         0         0    0.0667
         0         0         0         0         0    0.0667    0.0667
    0.0667    0.0667         0    0.0667         0    0.0667         0
    0.0667    0.0667    0.0667         0    0.0667    0.0667         0
         0         0    0.1333         0         0    0.0667         0
    0.0667    0.0667         0         0    0.0667         0         0
    0.0667         0    0.0667    0.0667         0    0.1333         0
         0    0.0667    0.1333    0.0667    0.0667         0         0
         0    0.0667    0.0667    0.0667    0.0667         0         0

  Columns 8 through 10

         0    0.1333         0
         0    0.0667    0.0667
    0.0667    0.0667    0.0667
         0    0.0667         0
         0         0         0
         0    0.0667    0.0667
    0.0667         0    0.0667
```

```
    0.0667         0         0
         0         0         0
    0.0667         0         0


e2 =

  Columns 1 through 7

         0         0         0    0.1333         0    0.0667    0.1333
    0.0667    0.0667         0    0.1333         0         0         0
    0.1333    0.1333         0         0         0    0.0667         0
         0    0.1333         0    0.0667    0.1333    0.1333         0
    0.0667    0.0667    0.0667         0    0.0667    0.1333    0.1333
    0.0667         0    0.0667    0.0667         0    0.0667    0.1333
    0.2000    0.0667         0         0    0.0667         0         0
    0.2000         0         0    0.1333         0    0.1333         0
         0    0.0667    0.0667    0.0667    0.1333         0    0.2000
    0.0667    0.0667         0    0.0667    0.1333         0         0

  Columns 8 through 10

         0    0.2667         0
    0.1333    0.1333    0.0667
    0.0667    0.0667    0.0667
         0    0.0667         0
         0         0    0.0667
         0    0.0667    0.0667
    0.1333         0    0.0667
    0.0667         0         0
         0         0         0
    0.0667    0.1333    0.0667
```

The *p*-value is slightly greater than 0.10, which indicates to retain the null hypothesis that the simpler model is at most as accurate as the more complex model. This result is consistent for any significance level (`Alpha`) that is at most 0.10.

`e1` and `e2` are 10-by-10 matrices containing misclassification costs. Row *r* corresponds to run *r* of the repeated cross validation. Column *k* corresponds to test-set fold *k* within a particular cross-validation run. For example, element (2,4) of `e2` is 0.1333. This value

means that in cross-validation run 2, when the test set is fold 4, the estimated test-set misclassification cost is 0.1333.

Select Features Using Statistical Accuracy Comparison

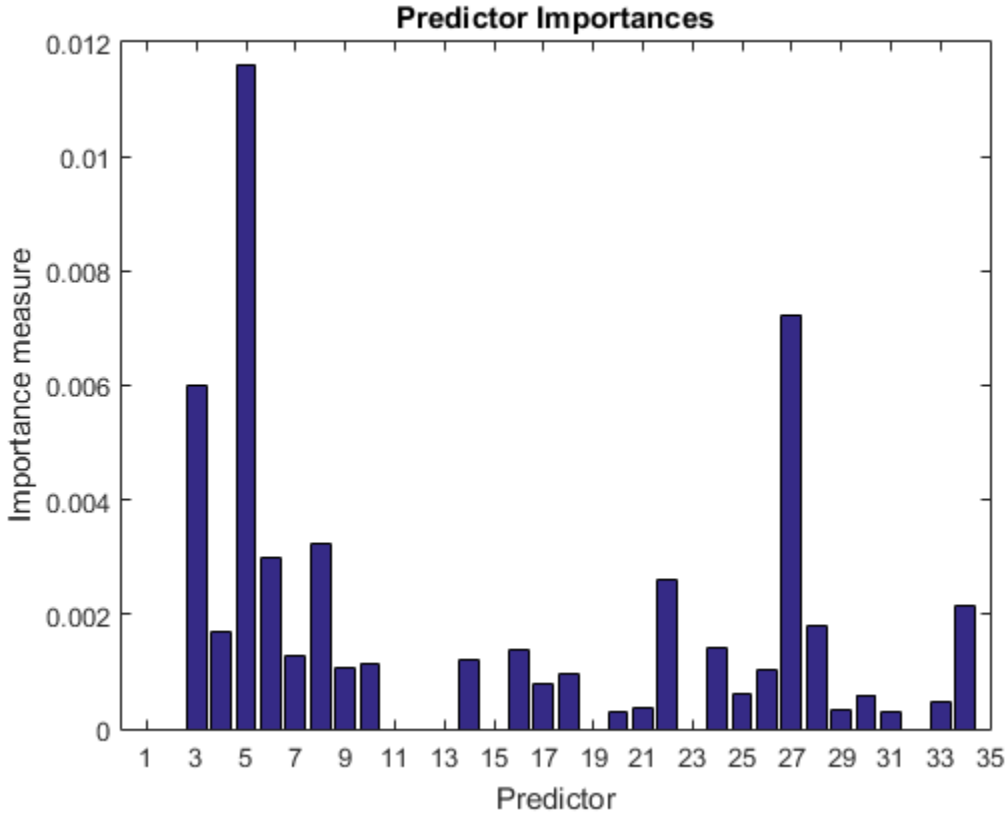
Reduce classification model complexity by selecting a subset of predictor variables (features) from a larger set. Then, statistically compare the accuracy between the two models.

Load the `ionosphere` data set.

```
load ionosphere;
```

Train an ensemble of 100 boosted classification trees using AdaBoostM1 and the entire set of predictors. Inspect the importance measure for each predictor.

```
nTrees = 100;
C = fitensemble(X,Y,'AdaBoostM1',nTrees,'Tree');
predImp = predictorImportance(C);

figure;
bar(predImp);
h = gca;
h.XTick = 1:2:h.XLim(2);
title('Predictor Importances');
xlabel('Predictor');
ylabel('Importance measure');
```



Identify the top five predictors in terms of their importance.

```
[~,idxSort] = sort(predImp,'descend');
idx5 = idxSort(1:5);
```

Test whether the two models have equal predictive accuracies. Specify the reduced data set and then the full predictor data. Use parallel computing to speed up computations.

```
Options = statset('UseParallel',true);
[h,p,e1,e2] = testckfold(C,C,X(:,idx5),X,Y,'Options',Options)
```

```
h =

     0
```

```
p =

    0.3318


e1 =

    0.0800    0.0739
    0.0629    0.0966
    0.0629    0.0625
    0.0629    0.0909
    0.0800    0.1080


e2 =

    0.0914    0.0852
    0.0800    0.0852
    0.0857    0.0739
    0.1086    0.1023
    0.0857    0.0966
```

`testckfold` treats trained classification models as templates, and so it ignores all fitted parameters in `C`. That is, `testckfold` cross validates `C` using only the specified options and the predictor data to estimate the out-of-fold classification losses.

`h = 0` indicates to not reject the null hypothesis that the two models have equal predictive accuracies. This result favors the simpler ensemble. Your results can vary.

Input Arguments

`C1` — Classification model template or trained classification model

Classification model template object | Trained classification model object

Classification model template or trained classification model, specified as any classification model template object or trained classification model object described in these tables.

Template Type	Returned By
Classification tree	`templateTree`

Template Type	Returned By
Discriminant analysis	`templateDiscriminant`
Ensemble (boosting, bagging, and random subspace)	`templateEnsemble`
Error-correcting output codes (ECOC), multiclass classification model	`templateECOC`
*k*NN	`templateKNN`
Naive Bayes	`templateNaiveBayes`
Support Vector Machine (SVM)	`templateSVM`

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
ECOC model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
SVM	`ClassificationSVM`	`fitcsvm`

For efficiency, supply a classification model template object instead of a trained classification model object.

`C2` — Classification model template or trained model

Classification model template object | Trained classification model object

Classification model template or trained classification model, specified as any classification model template object or trained classification model object described in these tables.

Template Type	Returned By
Classification tree	`templateTree`

Template Type	Returned By
Discriminant analysis	`templateDiscriminant`
Ensemble (boosting, bagging, and random subspace)	`templateEnsemble`
Error-correcting output codes (ECOC), multiclass classification model	`templateECOC`
*k*NN	`templateKNN`
Naive Bayes	`templateNaiveBayes`
Support Vector Machine (SVM)	`templateSVM`

Trained Model Type	Model Object	Returned By
Classification tree	`ClassificationTree`	`fitctree`
Discriminant analysis	`ClassificationDiscriminant`	`fitcdiscr`
Ensemble of bagged classification models	`ClassificationBaggedEnsemble`	`fitensemble`
Ensemble of classification models	`ClassificationEnsemble`	`fitensemble`
ECOC model	`ClassificationECOC`	`fitcecoc`
*k*NN	`ClassificationKNN`	`fitcknn`
Naive Bayes	`ClassificationNaiveBayes`	`fitcnb`
SVM	`ClassificationSVM`	`fitcsvm`

For efficiency, supply a classification model template object instead of a trained classification model object.

`X1` — Predictor data for first classification model

numeric matrix

Predictor data for the first classification model, C1, specified as a numeric matrix.

Each row of `X1` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C1` must compose `X1`.

The number of rows in `X1` and X2 must equal the length of Y.

Data Types: `double` | `single`

`X2` — Predictor data for second classification model

numeric matrix

Predictor data for the second classification model, C2, specified as a numeric matrix.

Each row of `X2` corresponds to one observation (also known as an instance or example), and each column corresponds to one variable (also known as a predictor or feature). The variables used to train `C2` must compose `X2`.

The number of rows in `X2` and X1 must equal the length of Y.

Data Types: `double` | `single`

`Y` — True class labels

categorical array | character array | logical vector | vector of numeric values | cell array of strings

True class labels, specified as a categorical or character array, a logical or numeric vector, or a cell array of strings.

If `Y` is a character array, then each element must correspond to one row of the array.

The number of rows in X1 and X2 must equal the length of Y.

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Alternative','greater','Test','10x10t','Options',statsset('UseParallel',true)` specifies to test whether the first set of first predicted class labels is more accurate than the second set, to conduct the 10-by-10 t test, and to use parallel computing for cross validation.

`'Alpha'` — Hypothesis test significance level

`0.05` (default) | scalar value in the interval (0,1)

Hypothesis test significance level, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the interval (0,1).

Example: `'Alpha',0.1`

Data Types: `single` | `double`

`'Alternative'` — Alternative hypothesis to assess

`'unequal'` (default) | `'greater'` | `'less'`

Alternative hypothesis to assess, specified as the comma-separated pair consisting of `'Alternative'` and one of the values listed in the table.

Value	Alternative Hypothesis Description	Supported Tests
`'unequal'` (default)	For predicting Y, the set of predictions resulting from C1 applied to X1 and C2 applied to X2 have unequal accuracies.	`'5x2F'`, `'5x2t'`, and `'10x10t'`
`'greater'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is more accurate than C2 applied to X2.	`'5x2t'` and `'10x10t'`
`'less'`	For predicting Y, the set of predictions resulting from C1 applied to X1 is less accurate than C2 applied to X2.	`'5x2t'` and `'10x10t'`

For details on supported tests, see Test.

Example: `'Alternative','greater'`

Data Types: `char`

`'X1CategoricalPredictors'` — Flag identifying categorical predictors

`[ ]` (default) | logical vector | numeric vector | `'all'`

Flag identifying categorical predictors in the first test-set predictor data (X1), specified as the comma-separated pair consisting of `'X1CategoricalPredictors'` and one of the following:

- A numeric vector with indices from `1` through `p`, where `p` is the number of columns of X1.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of X1 is a categorical variable.

- `'all'`, meaning all predictors are categorical.

Specification of `X1CategoricalPredictors` is appropriate if:

- At least one predictor is categorical and C1 is a classification tree, an ensemble of classification trees, an ECOC model, or a naive Bayes classification model.
- All predictors are categorical and C1 is a *k*NN classification model.

If you specify `X1CategoricalPredictors` for any other case, then `testckfold` throws an error. For example, the function cannot train SVM learners using categorical predictors.

The default is `[]`, which indicates that there are no categorical predictors.

Example: `'X1CategoricalPredictors','all'`

Data Types: `single` | `double`

`'X2CategoricalPredictors'` — Flag identifying categorical predictors

`[]` (default) | logical vector | numeric vector | `'all'`

Flag identifying categorical predictors in the second test-set predictor data (X2), specified as the comma-separated pair consisting of `'X2CategoricalPredictors'` and one of the following:

- A numeric vector with indices from `1` through `p`, where `p` is the number of columns of X2.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of X2 is a categorical variable.
- `'all'`, meaning all predictors are categorical.

Specification of `X2CategoricalPredictors` is appropriate if:

- At least one predictor is categorical and C2 is a classification tree, an ensemble of classification trees, an ECOC model, or a naive Bayes classification model.
- All predictors are categorical and C2 is a *k*NN classification model.

If you specify `X2CategoricalPredictors` for any other case, then `testckfold` throws an error. For example, the function cannot train SVM learners using categorical predictors.

The default is `[]`, which indicates that there are no categorical predictors.

Example: `'X2CategoricalPredictors','all'`

Data Types: `single` | `double`

`'ClassNames'` — Class names

categorical array | character array | logical vector | vector of numeric values | cell array of strings

Class names, specified as the comma-separated pair consisting of `'ClassNames'` and a categorical or character array, logical or numeric vector, or cell array of strings. You must set `ClassNames` using the data type of Y.

If `ClassNames` is a character array, then each element must correspond to one *row* of the array.

Use `ClassNames` to order the classes or to select a subset of classes for testing.

When supplying a cost matrix using the Cost name-value pair argument, it is a good practice to specify the class order.

The default is the distinct class names in `Y`.

Example: `'ClassNames',{'virginica','versicolor'}`

Data Types: `categorical` | `char` | `logical` | `single` | `double` | `cell`

`'Cost'` — Classification cost

square matrix | structure array

Classification cost, specified as the comma-separated pair consisting of `'Cost'` and a square matrix or structure array.

- If you specify the square matrix `Cost`, then `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. That is, the rows correspond to the true class and the columns correspond to the predicted class. To specify the class order for the corresponding rows and columns of `Cost`, additionally specify the ClassNames name-value pair argument.
- If you specify the structure `S`, then `S` must have two fields:
  - `S.ClassNames`, which contains the class names as a variable of the same data type as Y. You can use this field to specify the order of the classes.
  - `S.ClassificationCosts`, which contains the cost matrix, with rows and columns ordered as in `S.ClassNames`

For cost-sensitive testing use, `testcholdout`.

It is a best practice to supply the same cost matrix used to train the classification models.

The default is `Cost(i,j) = 1` if `i ~= j`, and `Cost(i,j) = 0` if `i = j`.

Example: `'Cost',[0 1 2 ; 1 0 2; 2 2 0]`

Data Types: `double` | `single` | `struct`

`'LossFun'` — Loss function
`'classiferror'` (default) | `'binodeviance'` | `'exponential'` | `'hinge'` | function handle

Loss function, specified as the comma-separated pair consisting of `'LossFun'` and a function handle or string.

- The following lists available loss functions. Specify one using its corresponding string.

Value	Loss Function
`'binodeviance'`	Binomial deviance
`'classiferror'`	Classification error
`'exponential'`	Exponential loss
`'hinge'`	Hinge loss

- Specify your own function using function handle notation.

  Suppose that `n = size(X,1)` is the sample size and there are `K` unique classes. Your function must have the signature `lossvalue = lossfun(C,S,W,Cost)`, where:

  - The output argument `lossvalue` is a scalar.
  - *`lossfun`* is the name of your function.
  - `C` is an `n`-by-`K` logical matrix with rows indicating which class the corresponding observation belongs to. The column order corresponds to the class order in the ClassNames name-value pair argument.

    Construct `C` by setting `C(p,q) = 1` if observation `p` is in class `q`, for each row. Set all other elements of row `p` to `0`.
  - `S` is an `n`-by-`K` numeric matrix of classification scores. The column order corresponds to the class order in the ClassNames name-value pair argument. `S` is a matrix of classification scores.

- `W` is an `n`-by-1 numeric vector of observation weights. If you pass `W`, the software normalizes the weights to sum to `1`.
- `Cost` is a `K`-by-`K` numeric matrix of classification costs. For example, `Cost = ones(K) - eye(K)` specifies a cost of `0` for correct classification and a cost of `1` for misclassification.

Specify your function using `'LossFun',@lossfun`.

Data Types: `char` | `function_handle`

`'Options'` — Parallel computing options

`[ ]` (default) | structure array returned by `statset`

Parallel computing options, specified as the comma-separated pair consisting of `'Options'` and a structure array returned by `statset`. These options require Parallel Computing Toolbox. `testckfold` uses `'Streams'`, `'UseParallel'`, and `'UseSubstreams'` fields.

This table summarizes the available options.

Option	Description
`'Streams'`	A `RandStream` object or cell array of such objects. If you do not specify `Streams`, the software uses the default stream or streams. If you specify `Streams`, use a single object except when the following are true: • You have an open parallel pool. • `UseParallel` is `true`. • `UseSubstreams` is `false`. In that case, use a cell array of the same size as the parallel pool. If a parallel pool is not open, then the software tries to open one (depending on your preferences), and `Streams` must supply a single random number stream.

Option	Description
`'UseParallel'`	If you have Parallel Computing Toolbox, then you can invoke a pool of workers by setting `'UseParallel',1`.
`'UseSubstreams'`	Set to `true` to compute in parallel using the stream specified by `'Streams'`. Default is `false`. For example, set `Streams` to a type allowing substreams, such as `'mlfg6331_64'` or `'mrg32k3a'`.

A best practice to ensure more predictable results is to use `parpool` and explicitly create a parallel pool before you invoke parallel computing using `testckfold`.

Example: `'Options',statset('UseParallel',1)`

`'Prior'` — Prior probabilities

`'empirical'` (default) | `'uniform'` | numeric vector | structure

Prior probabilities for each class, specified as the comma-separated pair consisting of `'Prior'` and a string, numeric vector, or a structure.

This table summarizes the available options for setting prior probabilities.

Value	Description
`'empirical'`	The class prior probabilities are the class relative frequencies in Y.
`'uniform'`	All class prior probabilities are equal to $1/K$, where K is the number of classes.
numeric vector	Each element is a class prior probability. Specify the order using the ClassNames name-value pair argument. The software normalizes the elements such that they sum to 1.
structure	A structure `S` with two fields: • `S.ClassNames` contains the class names as a variable of the same type as Y.

Value	Description
	• `S.ClassProbs` contains a vector of corresponding prior probabilities. The software normalizes the elements such that they sum to `1`.

Example: `'Prior',struct('ClassNames',{{'setosa','versicolor'}},'ClassProbs',[1,2])`

`'Test'` — Test to conduct

`'5x2F'` (default) | `'5x2t'` | `'10x10t'`

Test to conduct, specified as the comma-separated pair consisting of `'Test'` and one of he following: `'5x2F'`, `'5x2t'`, `'10x10t'`.

Value	Description	Supported Alternative Hypothesis
`'5x2F'` (default)	5-by-2 paired F test. Appropriate for two-sided testing only.	`'unequal'`
`'5x2t'`	5-by-2 paired t test	`'unequal'`, `'less'`, `'greater'`
`'10x10t'`	10-by-10 repeated cross validation t test	`'unequal'`, `'less'`, `'greater'`

For details on the available tests, see “Repeated Cross-Validation Tests” on page 22-4826. For details on supported alternative hypotheses, see Alternative.

Example: `'Test','10x10t'`

`'Verbose'` — Verbosity level

`0` (default) | `1` | `2`

Verbosity level, specified as the comma-separated pair consisting of `'Verbose'` and `0`, `1`, or `2`. `Verbose` controls the amount of diagnostic information that the software displays in the Command Window during training of each cross-validation fold.

This table summarizes the available verbosity level options.

Value	Description
0	The software does not display diagnostic information.
1	The software displays diagnostic messages every time it implements a new cross validation run.
2	The software displays diagnostic messages every time it implements a new cross validation run, and every time it trains on a particular fold.

Example: `'Verbose',1`

Data Types: `double | single`

`'Weights'` — Observation weights

`ones(size(X,1),1)` (default) | numeric vector

Observation weights, specified as the comma-separated pair consisting of `'Weights'` and a numeric vector.

The size of `Weights` must equal the number of rows of X1. The software weighs the observations in each row of `X` with the corresponding weight in `Weights`.

The software normalizes `Weights` to sum up to the value of the prior probability in the respective class.

Data Types: `double | single`

Notes:

- `testckfold` treats trained classification models as templates. Therefore, it ignores all fitted parameters in the model. That is, `testckfold` cross validates using only the options specified in the model and the predictor data.
- The repeated cross-validation tests depend on the assumption that the test statistics are asymptotically normal under the null hypothesis. Highly imbalanced cost matrices (for example, `Cost = [0 100;1 0]`) and highly discrete response distributions (that is, most of the observations are in a small number of classes) might violate the asymptotic normality assumption. For cost-sensitive testing, use `testcholdout`.

- NaNs, <undefined> values, and empty strings ('') indicate missing values.
  - For the treatment of missing values in X1 and X2, see the appropriate classification model training function reference page: fitctree, fitcdiscr, fitensemble, fitensemble, fitcecoc, fitcknn, fitcnb, or fitcsvm.
  - testckfold removes missing values in Y and the corresponding rows of X1 and X2.

Output Arguments

h — Hypothesis test result

1 | 0

Hypothesis test result, returned as a logical value.

h = 1 indicates the rejection of the null hypothesis at the Alpha significance level.

h = 0 indicates failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar in the interval [0,1]

p-value of the test, returned as a scalar in the interval [0,1]. p is the probability that a random test statistic is at least as extreme as the observed test statistic, given that the null hypothesis is true.

testckfold estimates p using the distribution of the test statistic, which varies with the type of test. For details on test statistics, see "Repeated Cross-Validation Tests" on page 22-4826.

e1 — Classification losses

numeric matrix

Classification losses, returned as a numeric matrix. The rows of e1 correspond to the cross-validation run and the columns correspond to the test fold.

testckfold applies the first test-set predictor data (X1) to the first classification model (C1) to estimate the first set of class labels.

`e1` summarizes the accuracy of the first set of class labels predicting the true class labels (Y) for each cross-validation run and fold. The meaning of the elements of `e1` depends on the type of classification loss.

`e2` — Classification losses

numeric matrix

Classification losses, returned as a numeric matrix. The rows of `e2` correspond to the cross-validation run and the columns correspond to the test fold.

`testckfold` applies the first test-set predictor data (X2) to the first classification model (C2) to estimate the first set of class labels.

`e2` summarizes the accuracy of the first set of class labels predicting the true class labels (Y) for each cross-validation run and fold. The meaning of the elements of `e2` depends on the type of classification loss.

Alternatives

Use `testcholdout`:

- For test sets with larger sample sizes
- To implement variants of the McNemar test to compare two classification model accuracies
- For cost-sensitive testing using a chi-square or likelihood ratio test. The chi-square test uses `quadprog`, which requires an Optimization Toolbox license.

More About

Repeated Cross-Validation Tests

Repeated cross-validation tests form the test statistic for comparing the accuracies of two classification models by combining the classification loss differences resulting from repeatedly cross validating the data. Repeated cross-validation tests are useful when sample size is limited.

To conduct an R-by-K test:

1. Randomly divide (stratified by class) the predictor data sets and true class labels into K sets, R times. Each division is called a *run* and each set within a run is called a *fold*. Each run contains the complete, but divided, data sets.
2. For runs $r = 1$ through R, repeat these steps for $k = 1$ through K:
   a. Reserve fold k as a test set, and train the two classification models using their respective predictor data sets on the remaining $K - 1$ folds.
   b. Predict class labels using the trained models and their respective fold k predictor data sets.
   c. Estimate the classification loss by comparing the two sets of estimated labels to the true labels. Denote e_{crk} as the classification loss when the test set is fold k in run r of classification model c.
   d. Compute the difference between the classification losses of the two models:

$$\hat{\delta}_{rk} = e_{1rk} - e_{2rk}.$$

   At the end of a run, there are K classification losses per classification model.
3. Combine the results of step 2. For each $r = 1$ through R:
   - Estimate the within-fold averages of the differences and their average:

$$\bar{\delta}_r = \frac{1}{K}\sum_{k=1}^{K}\hat{\delta}_{kr}.$$

   - Estimate the overall average of the differences: $\bar{\delta} = \frac{1}{KR}\sum_{r=1}^{R}\sum_{k=1}^{K}\hat{\delta}_{rk}$.
   - Estimate the within-fold variances of the differences: $s_r^2 = \frac{1}{K}\sum_{k=1}^{K}\left(\hat{\delta}_{rk} - \bar{\delta}_r\right)^2$.
   - Estimate the average of the within-fold differences: $\bar{s}^2 = \frac{1}{R}\sum_{r=1}^{R}s_r^2$.
   - Estimate the overall sample variance of the differences:

$$S^2 = \frac{1}{KR-1}\sum_{r=1}^{R}\sum_{k=1}^{K}\left(\hat{\delta}_{rk} - \bar{\delta}\right)^2.$$

Compute the test statistic. All supported tests described here assume that, under H_0, the estimated differences are independent and approximately normally distributed, with mean 0 and a finite, common standard deviation. However, these tests violate the independence assumption, and so the test-statistic distributions are approximate.

- For $R = 2$, the test is a paired test. The two supported tests are a paired t and F test.

  - The test statistic for the paired t test is

$$t^*_{paired} = \frac{\hat{\delta}_{11}}{\sqrt{\bar{s}^2}}.$$

    t^*_{paired} has a t-distribution with R degrees of freedom under the null hypothesis.

    To reduce the effects of correlation between the estimated differences, the quantity $\hat{\delta}_{11}$ occupies the numerator rather than $\bar{\delta}$.

    5-by-2 paired t tests can be slightly conservative [4].

  - The test statistic for the paired F test is

$$F^*_{paired} = \frac{\frac{1}{RK}\sum_{r=1}^{R}\sum_{k=1}^{K}\left(\hat{\delta}_{rk}\right)^2}{\bar{s}^2}.$$

    F^*_{paired} has an F distribution with RK and R degrees of freedom.

    A 5-by-2 paired F test has comparable power to the 5-by-2 t test, but is more conservative [1].

- For $R > 2$, the test is a repeated cross-validation test. The test statistic is

$$t_{CV}^{*} = \frac{\bar{\delta}}{S/\sqrt{\nu+1}}.$$

t_{CV}^{*} has a t distribution with ν degress of freedom. If the differences were truly independent, then $\nu = RK - 1$. In this case, the degrees of freedom parameter must be optimized.

For a 10-by-10 repeated cross-validation t test, the optimal degrees of freedom between 8 and 11 ([2] and [3]). `testckfold` uses $\nu = 10$.

The advantage of repeated cross validation tests over paired tests is that the results are more repeatable [3]. The disadvantage is that they require high computational resources.

Classification Loss

Classification losses indicate the accuracy of a classification model or set of predicted labels. In general, for a fixed cost matrix, classification accuracy decreases as classification loss increases.

`testckfold` returns the classification losses (see e1 and e2) under the alternative hypothesis (that is, the unrestricted classification losses). In the definitions that follow:

- The classification losses focus on the first classification model. The classification losses for the second model are similar.
- n_{test} is the test-set sample size.
- $I(x)$ is the indicator function. If x is a true statement, then $I(x) = 1$. Otherwise, $I(x) = 0$.
- $\hat{p}_{1j}$ is the predicted class assignment of classification model 1 for observation j.
- y_j is the true class label of observation j.
- *Binomial deviance* has the form

$$e_1 = \frac{\sum_{j=1}^{n_{test}} w_j \log\left(1+\exp\left(-2y_j' f(X_j)\right)\right)}{\sum_{j=1}^{n_{test}} w_j}$$

where:

- $y_j = 1$ for the positive class and -1 for the negative class.
- $f(X_j)$ is the classification score.

The binomial deviance has connections to the maximization of the binomial likelihood function. For details on binomial deviance, see [5].

- *Exponential loss* is similar to binomial deviance and has the form

$$e_1 = \frac{\sum_{j=1}^{n_{test}} w_j \exp\left(-y_j f(X_j)\right)}{\sum_{j=1}^{n_{test}} w_j}.$$

y_j and $f(X_j)$ take the same forms here as in the binomial deviance formula.

- *Hinge loss* has the form

$$e_1 = \frac{\sum_{j=1}^{n} w_j \max\left\{0, 1 - y_j' f\left(X_j\right)\right\}}{\sum_{j=1}^{n} w_j},$$

y_j and $f(X_j)$ take the same forms here as in the binomial deviance formula.

Hinge loss linearly penalizes for misclassified observations and is related to the SVM objective function used for optimization. For more details on hinge loss, see [5].

- *Misclassification rate*, or classification error, is a scalar in the interval [0,1] representing the proportion of misclassified observations. That is, the misclassification rate for the first classification model is

$$e_1 = \frac{\sum_{j=1}^{n_{test}} w_j I(p_{1j} \neq y_j)}{\sum_{j=1}^{n_{test}} w_j}.$$

Tips

- One way to perform cost-insensitive feature selection is:

  1. Create a classification model template that characterizes the first classification model (C1).
  2. Create a classification model template that characterizes the second classification model (C2).
  3. Specify two predictor data sets. For example, specify `X1` as the full predictor set and `X2` as a reduced set.
  4. Enter `testckfold(C1,C2,X1,X2,'Alternative','less')`. If `testckfold` returns `1`, then there is enough evidence to suggest that the classification model that uses fewer predictors performs better than the model that uses the full predictor set.

  Alternatively, you can assess whether there is a significant difference between the accuracies of the two models. To perform this assessment, remove the `'Alternative','less'` specification in step 4.`testckfold` conducts a two-sided test, and `h = 0` indicates that there is not enough evidence to suggest a difference in the accuracy of the two models.
- The tests are appropriate for the misclassification rate classification loss, but you can specify other loss functions (see LossFun). The key assumptions are that the estimated classification losses are independent and normally distributed with mean 0 and finite common variance under the two-sided null hypothesis. Classification losses other than the misclassification rate might violate this assumption.
- Highly discrete data, imbalanced classes, and highly imbalanced cost matrices can violate the normality assumption of classification loss differences.

Algorithms

If you specify to conduct the 10-by-10 repeated cross-validation t test using `'Test','10x10t'`, then `testckfold` uses 10 degrees of freedom for the t distribution to find the critical region and estimate the p-value. For more details, see [2] and [3].

- "Hypothesis Tests"

References

[1] Alpaydin, E. "Combined 5 x 2 CV F Test for Comparing Supervised Classification Learning Algorithms." *Neural Computation*, Vol. 11, No. 8, 1999, pp. 1885–1992.

[2] Bouckaert. R. "Choosing Between Two Learning Algorithms Based on Calibrated Tests." *International Conference on Machine Learning*, 2003, pp. 51–58.

[3] Bouckaert, R., and E. Frank. "Evaluating the Replicability of Significance Tests for Comparing Learning Algorithms." *Advances in Knowledge Discovery and Data Mining, 8th Pacific-Asia Conference*, 2004, pp. 3–12.

[4] Dietterich, T. "Approximate statistical tests for comparing supervised classification learning algorithms." *Neural Computation*, Vol. 10, No. 7, 1998, pp. 1895–1923.

[5] Hastie, T., R. Tibshirani, and J. Friedman. *The Elements of Statistical Learning*, 2nd Ed. New York: Springer, 2008.

See Also

`templateDiscriminant` | `templateECOC` | `templateEnsemble` | `templateKNN` | `templateNaiveBayes` | `templateSVM` | `templateTree` | `testcholdout`

Introduced in R2015a

TestSize property

Class: cvpartition

Size of each test set

Description

Value is a vector in partitions of type `'kfold'` and `'leaveout'`.
Value is a scalar in partitions of type `'holdout'` and `'resubstitution'`.

tiedrank

Rank adjusted for ties

Syntax

```
[R,TIEADJ] = tiedrank(X)
[R,TIEADJ] = tiedrank(X,1)
[R,TIEADJ] = tiedrank(X,0,1)
```

Description

`[R,TIEADJ] = tiedrank(X)` computes the ranks of the values in the vector `X`. If any `X` values are tied, `tiedrank` computes their average rank. The return value `TIEADJ` is an adjustment for ties required by the nonparametric tests `signrank` and `ranksum`, and for the computation of Spearman's rank correlation.

`[R,TIEADJ] = tiedrank(X,1)` computes the ranks of the values in the vector `X`. `TIEADJ` is a vector of three adjustments for ties required in the computation of Kendall's tau. `tiedrank(X,0)` is the same as `tiedrank(X)`.

`[R,TIEADJ] = tiedrank(X,0,1)` computes the ranks from each end, so that the smallest and largest values get rank 1, the next smallest and largest get rank 2, etc. These ranks are used in the Ansari-Bradley test.

Examples

Counting from smallest to largest, the two 20 values are 2nd and 3rd, so they both get rank 2.5 (average of 2 and 3):

```
tiedrank([10 20 30 40 20])
ans =
    1.0000    2.5000    4.0000    5.0000    2.5000
```

See Also

`ansaribradley` | `ranksum` | `signrank` | `corr` | `partialcorr`

tinv

Student's t inverse cumulative distribution function

Syntax

```
x = tinv(p,nu)
```

Description

`x = tinv(p,nu)` returns the inverse of Student's t cdf using the degrees of freedom in `nu` for the corresponding probabilities in `p`. `p` and `nu` can be vectors, matrices, or multidimensional arrays that are the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The values in `p` must lie on the interval [0 1].

The t inverse function in terms of the t cdf is

$$x = F^{-1}(p \mid \nu) = \{x : F(x \mid \nu) = p\}$$

where

$$p = F(x \mid \nu) = \int_{-\infty}^{x} \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{t^2}{\nu}\right)^{\frac{\nu+1}{2}}} dt$$

The result, x, is the solution of the cdf integral with parameter ν, where you supply the desired probability p.

Examples

Compute Student's *t* icdf

What is the 99th percentile of the Student's t distribution for one to six degrees of freedom?

```
percentile = tinv(0.99,1:6)

percentile =

   31.8205    6.9646    4.5407    3.7469    3.3649    3.1427
```

More About

- "Student's t Distribution" on page B-146

See Also

`tcdf` | `tpdf` | `tstat` | `trnd` | `icdf`

prob.tLocationScaleDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

t Location-Scale probability distribution object

Description

`prob.tLocationScaleDistribution` is an object consisting of parameters, a model description, and sample data for a *t* location-scale probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('tLocationScale')` creates a *t* location-scale probability distribution object using the default parameter values.

`pd = makedist('tLocationScale','mu',mu,'sigma',sigma,'nu',nu)` creates a *t* location-scale probability distribution object using the specified parameter values.

Input Arguments

`mu` — Location parameter

0 (default) | scalar value

Location parameter for the *t* location-scale distribution, specified as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

1 (default) | positive scalar value

Scale parameter for the *t* location-scale distribution, specified as a positive scalar value.

Data Types: `single` | `double`

`nu` — Degrees of freedom

5 (default) | positive scalar value

Degrees of freedom for the *t* location-scale distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

`mu` — Location parameter

scalar value

Location parameter of the *t* location-scale distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

positive scalar value

Scale parameter of the *t* location-scale distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`nu` — Degrees of freedom

positive scalar value

Degrees of freedom of the *t* location-scale distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.

- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object

iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

t Location-Scale Distribution

The *t* location-scale distribution is useful for modeling data distributions with heavier tails (more prone to outliers) than the normal distribution. It approaches the normal distribution as ν approaches infinity, and smaller values of ν yield heavier tails.

The *t* location-scale distribution uses the following parameters.

Parameter	Description	Support
`mu`	Location parameter	$-\infty < \mu < \infty$
`sigma`	Scale parameter	$\sigma > 0$
`nu`	Shape parameter	$\nu > 0$

The probability density function (pdf) is

$$f(x \mid \mu,\sigma,\nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\sigma\sqrt{\nu\pi}\,\Gamma\left(\frac{\nu}{2}\right)}\left[\frac{\nu + \left(\frac{x-\mu}{\sigma}\right)^2}{\nu}\right]^{-\left(\frac{\nu+1}{2}\right)} \quad ; \quad -\infty < x < \infty,$$

where $\Gamma(\cdot)$ is the Gamma function.

Examples

Create a *t* Location-Scale Distribution Object Using Default Parameters

Create a *t* location scale distribution object using the default parameter values.

```
pd = makedist('tLocationScale')
```

```
pd =
```

```
  tLocationScaleDistribution

  t Location-Scale distribution
       mu = 0
    sigma = 1
       nu = 5
```

Create a *t* Location-Scale Distribution Object Using Specified Parameters

Create a *t* location-scale distribution object by specifying the parameter values.

```
pd = makedist('tLocationScale','mu',-2,'sigma',1,'nu',20)
```

```
pd =

  tLocationScaleDistribution

  t Location-Scale distribution
       mu = -2
    sigma =  1
       nu = 20
```

Compute the interquartile range of the distribution.

```
r = iqr(pd)
```

```
r =

    1.3739
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "t Location-Scale Distribution"
- Class Attributes
- Property Attributes

prob.ToolboxFittableParametricDistribution class

Package: prob
Superclasses: prob.TruncatableDistribution

Toolbox-integrated fittable parametric probability distribution object

Description

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Methods

mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Inherited Methods

cdf	Cumulative distribution function of probability distribution object

icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object

See Also

`dfittool` | `fitdist` | `makedist`

More About

- Class Attributes
- Property Attributes

tpdf

Student's t probability density function

Syntax

```
y = tpdf(x,nu)
```

Description

`y = tpdf(x,nu)` returns the probability density function (pdf) of the Student's t distribution at each of the values in `x` using the corresponding degrees of freedom in `nu`. `x` and `nu` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

Examples

Compute Student's *t* pdf

The mode of the Student's t distribution is at $x = 0$. This example shows that the value of the function at the mode is an increasing function of the degrees of freedom.

```
tpdf(0,1:6)
```

```
ans =

    0.3183    0.3536    0.3676    0.3750    0.3796    0.3827
```

The t distribution converges to the standard normal distribution as the degrees of freedom approaches infinity. How good is the approximation for ν equal to 30?

```
difference = tpdf(-2.5:2.5,30)-normpdf(-2.5:2.5)
```

```
difference =
```

```
    0.0035   -0.0006   -0.0042   -0.0042   -0.0006    0.0035
```

More About

Student's *t* pdf

The probability density function (pdf) of the Student's t distribution is

$$y = f(x \mid \nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{x^2}{\nu}\right)^{\frac{\nu+1}{2}}}$$

where ν is the degrees of freedom and $\Gamma(\cdot)$ is the Gamma function. The result y is the probability of observing a particular value of x from a Student's t distribution with ν degrees of freedom.

- "Student's t Distribution" on page B-146

See Also

`tcdf` | `tinv` | `tstat` | `trnd` | `pdf`

training

Class: cvpartition

Training indices for cross-validation

Syntax

```
idx = training(c)
idx = training(c,i)
```

Description

`idx = training(c)` returns the logical vector `idx` of training indices for an object `c` of the `cvpartition` class of type `'holdout'` or `'resubstitution'`.

If `c.Type` is `'holdout'`, `idx` specifies the observations in the training set.

If `c.Type` is `'resubstitution'`, `idx` specifies all observations.

`idx = training(c,i)` returns the logical vector `idx` of training indices for repetition `i` of an object `c` of the `cvpartition` class of type `'kfold'` or `'leaveout'`.

If `c.Type` is `'kfold'`, `idx` specifies the observations in the training set in fold `i`.

If `c.Type` is `'leaveout'`, `idx` specifies the observations left in at repetition `i`.

Examples

Identify the training indices in the first fold of a partition of 10 observations for 3-fold cross-validation:

```
c = cvpartition(10,'kfold',3)
c =
K-fold cross validation partition
             N: 10
   NumTestSets: 3
```

```
     TrainSize: 7  6  7
      TestSize: 3  4  3

training(c,1)
ans =
     0
     0
     1
     1
     1
     1
     1
     1
     0
     1
```

See Also

cvpartition | test

TrainSize property

Class: cvpartition

Size of each training set

Description

Value is a vector in partitions of type `'kfold'` and `'leaveout'`.
Value is a scalar in partitions of type `'holdout'` and `'resubstitution'`.

See Also

`type`

TreeArgs property

Class: TreeBagger

Cell array of arguments for `fitctree` or `fitrtree`

Description

The `TreeArgs` property is a cell array of arguments for `fitctree` or `fitrtree`. `TreeBagger` uses these arguments in growing new trees for the ensemble.

See Also

`ClassificationTree` | `RegressionTree` | `TreeBagger` | `fitctree` | `fitrtree`

TreeBagger class

Bootstrap aggregation for ensemble of decision trees

Description

`TreeBagger` bags an ensemble of decision trees for either classification or regression. Bagging stands for bootstrap aggregation. Every tree in the ensemble is grown on an independently drawn bootstrap replica of input data. Observations not included in this replica are "out of bag" for this tree. To compute prediction of an ensemble of trees for unseen data, `TreeBagger` takes an average of predictions from individual trees. To estimate the prediction error of the bagged ensemble, you can compute predictions for each tree on its out-of-bag observations, average these predictions over the entire ensemble for each observation and then compare the predicted out-of-bag response with the true value at this observation.

`TreeBagger` relies on the `ClassificationTree` and `RegressionTree` functionality for growing individual trees. In particular, `ClassificationTree` and `RegressionTree` accepts the number of features selected at random for each decision split as an optional input argument.

The `compact` method returns an object of another class, `CompactTreeBagger`, with sufficient information to make predictions using new data. This information includes the tree ensemble, variable names, and class names (for classification). `CompactTreeBagger` requires less memory than `TreeBagger`, but only `TreeBagger` has methods for growing more trees for the ensemble. Once you grow an ensemble of trees using `TreeBagger` and no longer need access to the training data, you can opt to work with the compact version of the trained ensemble from then on.

Construction

.TreeBagger

Create ensemble of bagged decision trees

Methods

append	Append new trees to ensemble
compact	Compact ensemble of decision trees
error	Error (misclassification probability or MSE)
fillProximities	Proximity matrix for training data
growTrees	Train additional trees and add to ensemble
margin	Classification margin
mdsProx	Multidimensional scaling of proximity matrix
meanMargin	Mean classification margin
oobError	Out-of-bag error
oobMargin	Out-of-bag margins
oobMeanMargin	Out-of-bag mean margins
oobPredict	Ensemble predictions for out-of-bag observations
predict	Predict response

Properties

ClassNames

A cell array containing the class names for the response variable `Y`. This property is empty for regression trees.

ComputeOOBPrediction

A logical flag specifying whether out-of-bag predictions for training observations should be computed. The default is `false`.

If this flag is true, the following properties are available:

- `OOBIndices`
- `OOBInstanceWeight`

If this flag is true, the following methods can be called:

- `oobError`
- `oobMargin`
- `oobMeanMargin`

See also `oobError`, `OOBIndices`, `OOBInstanceWeight`, `oobMargin`, `oobMeanMargin`.

ComputeOOBVarImp

A logical flag specifying whether out-of-bag estimates of variable importance should be computed. The default is `false`. If this flag is `true`, then `ComputeOOBPrediction` is true as well.

If this flag is `true`, the following properties are available:

- `OOBPermutedVarDeltaError`
- `OOBPermutedVarDeltaMeanMargin`
- `OOBPermutedVarCountRaiseMargin`

Cost

Square matrix, where `Cost(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the

predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in ClassNames. The number of rows and columns in `Cost` is the number of unique classes in the response.

This property is:

- read-only
- empty (`[ ]`) for ensembles of regression trees

`DefaultYfit`

Default value returned by `predict` and `oobPredict`. The `DefaultYfit` property controls what predicted value is returned when no prediction is possible. For example, when `oobPredict` needs to predict for an observation that is in-bag for all trees in the ensemble.

- For classification, you can set this property to either `''` or `'MostPopular'`. If you choose `'MostPopular'` (the default), the property value becomes the name of the most probably class in the training data. If you choose `''`, the in-bag observations are excluded from computation of the out-of-bag error and margin.
- For regression, you can set this property to any numeric scalar. The default value is the mean of the response for the training data. If you set this property to `NaN`, the in-bag observations are excluded from computation of the out-of-bag error and margin.

`DeltaCritDecisionSplit`

A numeric array of size 1-by-*Nvars* of changes in the split criterion summed over splits on each variable, averaged across the entire ensemble of grown trees.

See also `ClassificationTree.predictorImportance` and `RegressionTree.predictorImportance`.

`FBoot`

Fraction of observations that are randomly selected with replacement for each bootstrap replica. The size of each replica is *Nobs*×`FBoot`, where *Nobs* is the number of observations in the training set. The default value is 1.

`MergeLeaves`

A logical flag specifying whether decision tree leaves with the same parent are merged for splits that do not decrease the total risk. The default value is `false`.

Method

Method used by trees. The possible values are `'classification'` for classification ensembles, and `'regression'` for regression ensembles.

MinLeaf

Minimum number of observations per tree leaf. By default, `MinLeaf` is 1 for classification and 5 for regression. For decision tree training, the `MinParent` value is set equal to `2*MinLeaf`.

NTrees

Scalar value equal to the number of decision trees in the ensemble.

NVarSplit

A numeric array of size 1-by-*Nvars*, where every element gives a number of splits on this predictor summed over all trees.

NVarToSample

Number of predictor or feature variables to select at random for each decision split. By default, `NVarToSample` is equal to the square root of the total number of variables for classification, and one third of the total number of variables for regression.

OOBIndices

Logical array of size *Nobs*-by-*NTrees*, where *Nobs* is the number of observations in the training data and *NTrees* is the number of trees in the ensemble. A `true` value for the (*i*,*j*) element indicates that observation *i* is out-of-bag for tree *j*. In other words, observation *i* was not selected for the training data used to grow tree *j*.

OOBInstanceWeight

Numeric array of size *Nobs*-by-1 containing the number of trees used for computing the out-of-bag response for each observation. *Nobs* is the number of observations in the training data used to create the ensemble.

OOBPermutedVarCountRaiseMargin

A numeric array of size 1-by-*Nvars* containing a measure of variable importance for each predictor variable (feature). For any variable, the measure is the difference between

the number of raised margins and the number of lowered margins if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble. This property is empty for regression trees.

`OOBPermutedVarDeltaError`

A numeric array of size 1-by-*Nvars* containing a measure of importance for each predictor variable (feature). For any variable, the measure is the increase in prediction error if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble.

`OOBPermutedVarDeltaMeanMargin`

A numeric array of size 1-by-*Nvars* containing a measure of importance for each predictor variable (feature). For any variable, the measure is the decrease in the classification margin if the values of that variable are permuted across the out-of-bag observations. This measure is computed for every tree, then averaged over the entire ensemble and divided by the standard deviation over the entire ensemble. This property is empty for regression trees.

`OutlierMeasure`

A numeric array of size *Nobs*-by-1, where *Nobs* is the number of observations in the training data, containing outlier measures for each observation.

See also `CompactTreeBagger.OutlierMeasure`.

`Prior`

Numeric vector of prior probabilities for each class. The order of the elements of `Prior` corresponds to the order of the classes in ClassNames.

This property is:

- read-only
- empty ([ ]) for ensembles of regression trees

`Proximity`

A numeric matrix of size *Nobs*-by-*Nobs*, where *Nobs* is the number of observations in the training data, containing measures of the proximity between observations. For

any two observations, their proximity is defined as the fraction of trees for which these observations land on the same leaf. This is a symmetric matrix with 1s on the diagonal and off-diagonal elements ranging from 0 to 1.

See also `CompactTreeBagger.proximity`.

`Prune`

The `Prune` property is true if decision trees are pruned and false if they are not. Pruning decision trees is not recommended for ensembles. The default value is false.

See also `ClassificationTree.prune` and `RegressionTree.prune`.

`SampleWithReplacement`

A logical flag specifying if data are sampled for each decision tree with replacement. True if `TreeBagger` samples data with replacement and false otherwise. True by default.

`TreeArgs`

Cell array of arguments for `fitctree` or `fitrtree`. These arguments are used by `TreeBagger` when growing new trees for the ensemble.

`Trees`

A cell array of size *NTrees*-by-1 containing the trees in the ensemble.

See also `NTrees`.

`VarAssoc`

A matrix of size *Nvars*-by-*Nvars* with predictive measures of variable association, averaged across the entire ensemble of grown trees. If you grew the ensemble setting `'surrogate'` to `'on'`, this matrix for each tree is filled with predictive measures of association averaged over the surrogate splits. If you grew the ensemble setting `'surrogate'` to `'off'` (default), `VarAssoc` is diagonal.

`VarNames`

A cell array containing the names of the predictor variables (features). `TreeBagger` takes these names from the optional `'names'` parameter. The default names are `'x1'`, `'x2'`, etc.

W

Numeric vector of weights of length *Nobs*, where *Nobs* is the number of observations (rows) in the training data. `TreeBagger` uses these weights for growing every decision tree in the ensemble. The default `W` is `ones(Nobs,1)`.

X

A numeric matrix of size *Nobs*-by-*Nvars*, where *Nobs* is the number of observations (rows) and *Nvars* is the number of variables (columns) in the training data. This matrix contains the predictor (or feature) values.

Y

An array of true class labels for classification, or response values for regression. `Y` can be a numeric column vector, a character matrix, or a cell array of strings.

Copy Semantics

Value. To learn how this affects your use of the class, see Comparing Handle and Value Classes in the MATLAB Object-Oriented Programming documentation.

How To

- “Ensemble Methods” on page 16-68
- “Classification Trees and Regression Trees” on page 16-33
- “Grouping Variables” on page 2-52

TreeBagger

Class: TreeBagger

Create ensemble of bagged decision trees

Syntax

```
B = TreeBagger(NTrees,X,Y)
B = TreeBagger(NTrees,X,Y,'param1',val1,'param2',val2,...)
```

Description

`B = TreeBagger(NTrees,X,Y)` creates an ensemble `B` of `NTrees` decision trees for predicting response `Y` as a function of predictors `X`. By default `TreeBagger` builds an ensemble of classification trees. The function can build an ensemble of regression trees by setting the optional input argument `'method'` to `'regression'`.

`X` is a numeric matrix of training data. Each row represents an observation and each column represents a predictor or feature. `Y` is an array of true class labels for classification or numeric function values for regression. True class labels can be a numeric vector, character matrix, vector cell array of strings or categorical vector. `TreeBagger` converts labels to a cell array of strings for classification.

For more information on grouping variables, see “Grouping Variables” on page 2-52.

`B = TreeBagger(NTrees,X,Y,'param1',val1,'param2',val2,...)` specifies optional parameter name/value pairs:

`'FBoot'`	Fraction of input data to sample with replacement from the input data for growing each new tree. Default value is 1.
`'Cost'`	Square matrix `C`, where `C(i,j)` is the cost of classifying a point into class `j` if its true class is `i` (i.e., the rows correspond to the true class and the columns correspond to the predicted class). The order of the rows and columns of `Cost` corresponds to the order of the classes in the ClassNames property of the trained `TreeBagger` model `B`.

Alternatively, `cost` can be a structure `S` having two fields:

- `S.ClassNames` containing the group names as a categorical variable, character array, or cell array of strings
- `S.ClassificationCosts` containing the cost matrix `C`

The default value is `C(i,j) = 1` if `i ~= j`, and `C(i,j) = 0` if `i = j`.

If `Cost` is highly skewed, then, for in-bag samples, the software oversamples unique observations from the class that has a large penalty. For smaller sample sizes, this might cause a very low relative frequency of out-of-bag observations from the class that has a large penalty. Therefore, the estimated out-of-bag error is highly variable, and might be difficult to interpret.

`'SampleWithReplacement'` `'on'` to sample with replacement or `'off'` to sample without replacement. If you sample without replacement, you need to set `'FBoot'` to a value less than one. Default is `'on'`.

`'OOBPred'` `'on'` to store info on what observations are out of bag for each tree. This info can be used by `oobPredict` to compute the predicted class probabilities for each tree in the ensemble. Default is `'off'`.

`'OOBVarImp'` `'on'` to store out-of-bag estimates of feature importance in the ensemble. Default is `'off'`. Specifying `'on'` also sets the `'OOBPred'` value to `'on'`.

`'Method'` Either `'classification'` or `'regression'`. Regression requires a numeric `Y`.

`'NVarToSample'` Number of variables to select at random for each decision split. Default is the square root of the number of variables for classification and one third of the number of variables for regression. Valid values are `'all'` or a positive integer. Setting this argument to any valid value but `'all'` invokes Breiman's 'random forest' algorithm.

`'NPrint'` Number of training cycles (grown trees) after which `TreeBagger` displays a diagnostic message showing training progress. Default is no diagnostic messages.

`'MinLeaf'` Minimum number of observations per tree leaf. Default is 1 for classification and 5 for regression.

`'Options'` A structure that specifies options that govern the computation when growing the ensemble of decision trees. One option requests that the computation of decision trees on multiple bootstrap replicates uses multiple processors, if the Parallel Computing Toolbox is available. Two options specify the random number streams to use in selecting bootstrap replicates. You can create this argument with a call to `statset`. You can retrieve values of the individual fields with a call to `statget`. Applicable `statset` parameters are:

- `'UseParallel'` — If `true` and if a `parpool` of the Parallel Computing Toolbox is open, compute decision trees drawn on separate boostrap replicates in parallel. If the Parallel Computing Toolbox is not installed, or a `parpool` is not open, computation occurs in serial mode. Default is `false`, or serial computation.
- `'UseSubstreams'` — If `true` select each bootstrap replicate using a separate Substream of the random number generator (aka Stream). This option is available only with `RandStream` types that support Substreams: `'mlfg6331_64'` or `'mrg32k3a'`. Default is `false`, do not use a different Substream to compute each bootstrap replicate.
- `Streams` — A `RandStream` object or cell array of such objects. If you do not specify `Streams`, `TreeBagger` uses the default stream or streams. If you choose to specify `Streams`, use a single object except in the case

  - You have an open Parallel pool
  - `UseParallel` is `true`
  - `UseSubstreams` is `false`

  In that case, use a cell array the same size as the Parallel pool.

`'Prior'` Prior probabilities for each class. Specify as one of:

- A string:
  - `'Empirical'` determines class probabilities from class frequencies in `Y`. If you pass observation weights, they are used to compute the class probabilities. This is the default.
  - `'Uniform'` sets all class probabilities equal.
- A vector (one scalar value for each class). The order of the elements `Prior` corresponds to the order of the classes in the ClassNames property of the trained `TreeBagger` model `B`.
- A structure `S` with two fields:
  - `S.ClassNames` containing the class names as a categorical variable, character array, or cell array of strings
  - `S.ClassProbs` containing a vector of corresponding probabilities

If you set values for both `Weights` and `Prior`, the weights are renormalized to add up to the value of the prior probability in the respective class.

If `Prior` is highly skewed, then, for in-bag samples, the software oversamples unique observations from the class that has a large prior probability. For smaller sample sizes, this might cause a very low relative frequency of out-of-bag observations from the class that has a large prior probability. Therefore, the estimated out-of-bag error is highly variable, and might be difficult to interpret.

`'CategoricalPredictors'` Categorical predictors list, specified as the comma-separated pair consisting of `'CategoricalPredictors'` and one of the following.

- A numeric vector with indices from `1` to `p`, where `p` is the number of columns of X.
- A logical vector of length `p`, where a `true` entry means that the corresponding column of X is a categorical variable.
- A cell array of strings, where each element in the array is the name of a predictor variable. The names must match entries in `PredictorNames` values.
- A character matrix, where each row of the matrix is a name of a predictor variable. The names must match entries in `PredictorNames` values. Pad the names with extra blanks so each row of the character matrix has the same length.
- `'all'`, meaning all predictors are categorical.

In addition to the optional arguments above, this method accepts all optional `fitctree` and `fitrtree` arguments with the exception of `'minparent'`. Refer to the documentation for `fitctree` and `fitrtree` for more detail.

Examples

Train a Bagged Ensemble of Classification Trees

Load Fisher's iris data set.

```
load fisheriris
```

Train a bagged ensemble of classification trees using the data and specifying 50 weak learners. Store which observations are out of bag for each tree.

```
rng(1); % For reproducibility
BaggedEnsemble = TreeBagger(50,meas,species,'OOBPred','On')
```

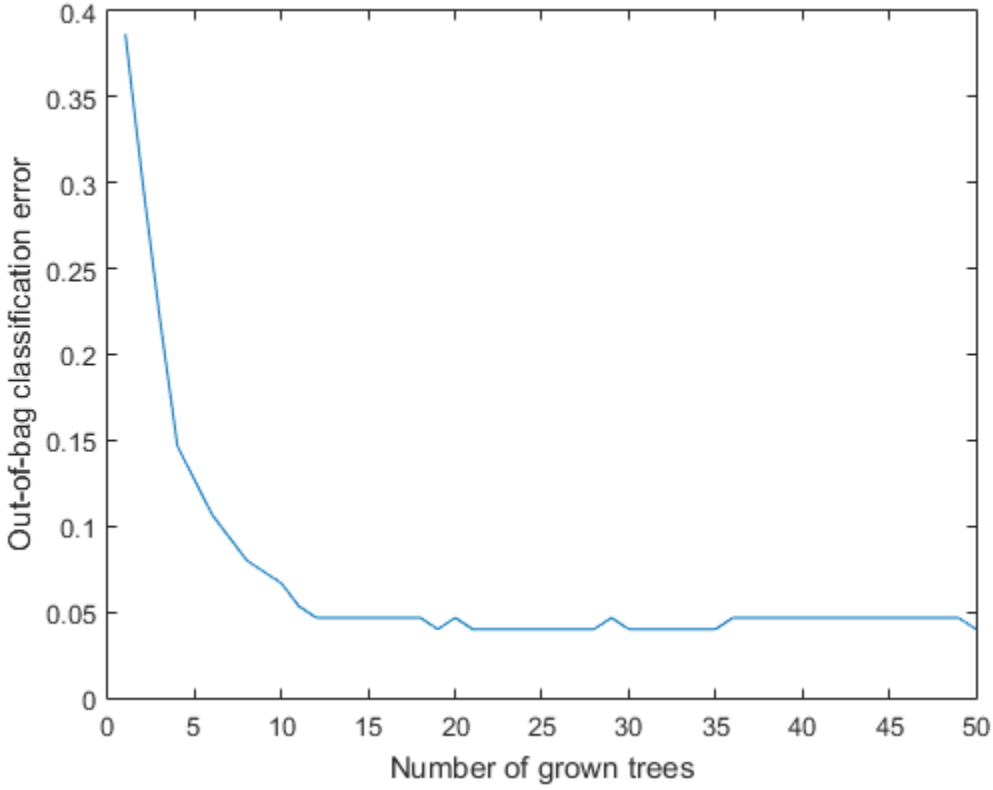
```
BaggedEnsemble =
```

```
  TreeBagger
Ensemble with 50 bagged decision trees:
               Training X:              [150x4]
               Training Y:              [150x1]
                   Method:       classification
                    Nvars:                    4
             NVarToSample:                    2
                 MinLeaf:                     1
                   FBoot:                     1
    SampleWithReplacement:                    1
     ComputeOOBPrediction:                    1
         ComputeOOBVarImp:                    0
                Proximity:                   []
               ClassNames:        'setosa'    'versicolor'     'virginica'
```

`BaggedEnsemble` is a `TreeBagger` ensemble. `BaggedEnsemble.OOBIndices` stores the out-of-bag indices as a matrix of logical values.

Plot the out-of-bag error over the number of grown classification trees.

```
oobErrorBaggedEnsemble = oobError(BaggedEnsemble);
plot(oobErrorBaggedEnsemble)
xlabel 'Number of grown trees';
ylabel 'Out-of-bag classification error';
```



The out-of-bag error decreases with the number of grown trees.

To label out-of-bag observations, pass `BaggedEnsemble` to `oobPredict`.

Algorithms

`TreeBagger` generates in-bag samples by oversampling classes with large misclassification costs and undersampling classes with small misclassification costs. Consequently, out-of-bag samples have fewer observations from classes with large misclassification costs and more observations from classes with small misclassification costs. If you train a classification ensemble using a small data set and a highly skewed

cost matrix, then the number of out-of-bag observations per class might be very low. Therefore, the estimated out-of-bag error might have a large variance and might be difficult to interpret. The same phenomenon can occur for classes with large prior probabilities.

Tips

Avoid large estimated out-of-bag error variances by setting a more balanced misclassification cost matrix or a less skewed prior probability vector.

See Also

`TreeBagger` | `statset` | `fitctree` | `fitrtree` | `CompactTreeBagger`

How To

- “Ensemble Methods” on page 16-68
- “Grouping Variables” on page 2-52

treedisp

Plot tree

Compatibility

`treedisp` will be removed in a future release. Use `fitctree` or `fitrtree` to grow a tree. Then use `view` (`ClassificationTree`) or `view` (`RegressionTree`) instead of `treedisp`.

Syntax

```
treedisp(t)
treedisp(t,param1,val1,param2,val2,...)
```

Description

`treedisp(t)` takes as input a decision tree `t` as computed by the `treefit` function, and displays it in a figure window. Each branch in the tree is labeled with its decision rule, and each terminal node is labeled with the predicted value for that node.

For each branch node, the left child node corresponds to the points that satisfy the condition, and the right child node corresponds to the points that do not satisfy the condition.

The **Click to display** pop-up menu at the top of the figure enables you to display more information about each node, as described in the following table.

Menu Choice	Displays
`Identity`	The node number, whether the node is a branch or a leaf, and the rule that governs the node
`Variable ranges`	The range of each of the predictor variables for that node
`Node statistics`	Descriptive statistics for the observations falling into this node

After you select the type of information you want, click any node to display the information for that node.

The **Pruning level** button displays the number of levels that have been cut from the tree and the number of levels in the unpruned tree. For example, `1 of 6` indicates that the unpruned tree has six levels, and that one level has been cut from the tree. Use the spin button to change the pruning level.

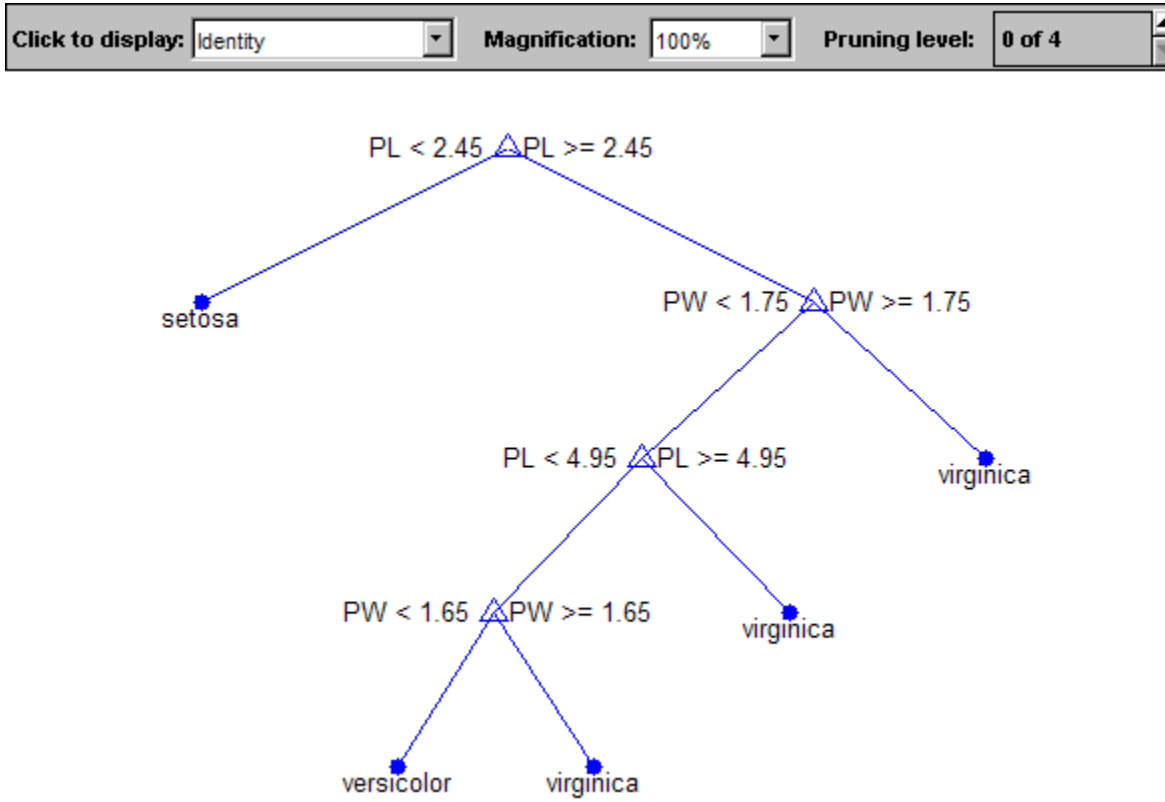
`treedisp(t,`*`param1`*`,`*`val1`*`,`*`param2`*`,`*`val2`*`,...)` specifies optional parameter name-value pairs, listed in the following table.

Parameter	Value
`'names'`	A cell array of names for the predictor variables, in the order in which they appear in the `X` matrix from which the tree was created (see `treefit`)
`'prunelevel'`	Initial pruning level to display

Examples

Create and graph classification tree for Fisher's iris data. The names in this example are abbreviations for the column contents (sepal length, sepal width, petal length, and petal width).

```
load fisheriris;
t = treefit(meas,species);
treedisp(t,'names',{'SL' 'SW' 'PL' 'PW'});
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treeprune` | `treetest`

treefit

Fit tree

Note: `treefit` will be removed in a future release. Use `fitctree` or `fitrtree` instead.

Syntax

```
t = treefit(X,y)
t = treefit(X,y,param1,val1,param2,val2,...)
```

Description

`t = treefit(X,y)` creates a decision tree `t` for predicting response `y` as a function of predictors `X`. `X` is an `n`-by-`m` matrix of predictor values. `y` is either a vector of `n` response values (for regression), or a character array or cell array of strings containing `n` class names (for classification). Either way, `t` is a binary tree where each non-terminal node is split based on the values of a column of `X`.

`t = treefit(X,y,param1,val1,param2,val2,...)` specifies optional parameter name-value pairs. Valid parameter strings are:

The following table lists parameters available for all trees.

Parameter	Value
`'catidx'`	Vector of indices of the columns of `X`. `treefit` treats these columns as unordered categorical values.
`'method'`	Either `'classification'` (default if `y` is text) or `'regression'` (default if `y` is numeric).
`'splitmin'`	A number `n` such that impure nodes must have `n` or more observations to be split (default 10).

Parameter	Value
`'prune'`	`'on'` (default) to compute the full tree and a sequence of pruned subtrees, or `'off'` for the full tree without pruning.

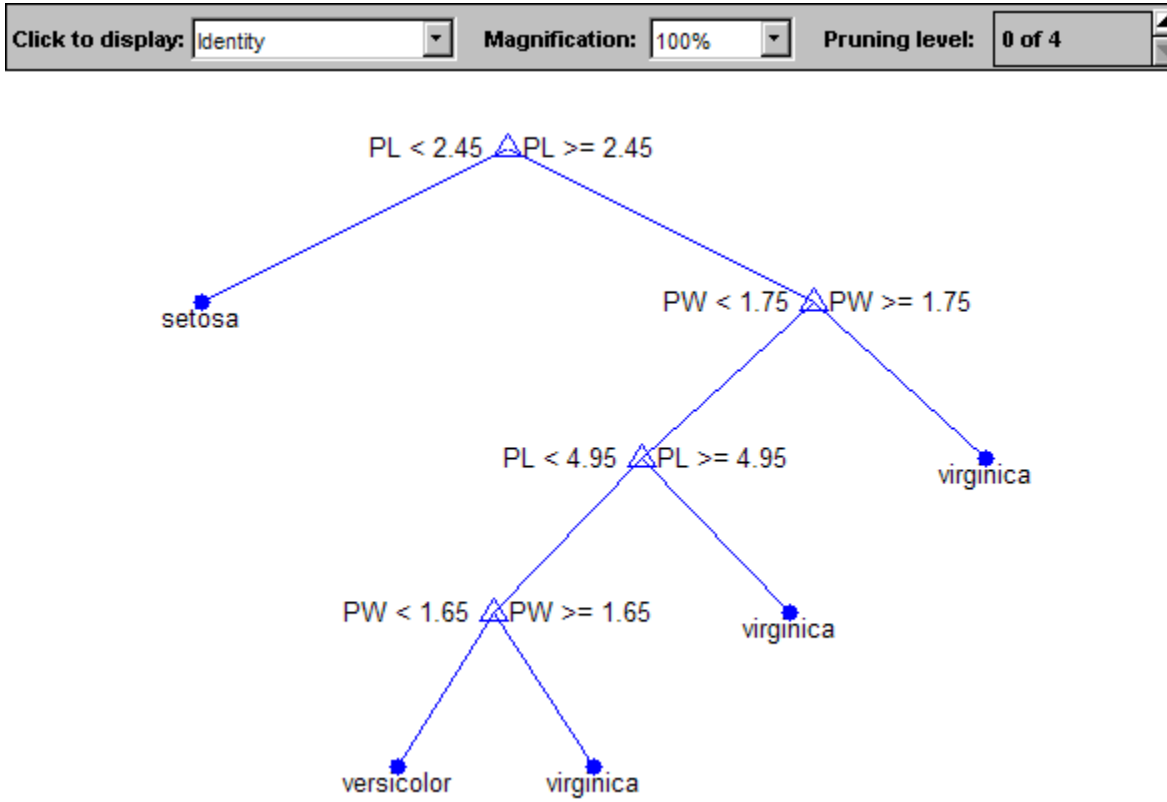
The following table lists parameters available for classification trees only.

Parameter	Value
`'cost'`	`p`-by-`p` matrix `C`, where `p` is the number of distinct response values or class names in the input `y`. `C(i,j)` is the cost of classifying a point into class `j` if its true class is `i`. (The default has `C(i,j)=1` if `i~=j`, and `C(i,j)=0` if `i=j`.) `C` can also be a structure `S` with two fields: `S.group` containing the group names, and `S.cost` containing a matrix of cost values.
`'splitcriterion'`	Criterion for choosing a split: either `'gdi'` (default) for Gini's diversity index, `'twoing'` for the twoing rule, or `'deviance'` for maximum deviance reduction.
`'priorprob'`	Prior probabilities for each class, specified as a vector (one value for each distinct group name) or as a structure `S` with two fields: `S.group` containing the group names, and `S.prob` containing a vector of corresponding probabilities.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;
t = treefit(meas,species);
treedisp(t,'names',{'SL' 'SW' 'PL' 'PW'});
```



More About

- "Grouping Variables" on page 2-52

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treedisp` | `treetest`

treeprune

Prune tree

Compatibility

`treeprune` will be removed in a future release. Use `fitctree` or `fitrtree` to grow a tree. Then use `prune` (`ClassificationTree`) or `prune` (`RegressionTree`) instead of `treeprune`.

Syntax

```
t2 = treeprune(t1,'level',level)
t2 = treeprune(t1,'nodes',nodes)
t2 = treeprune(t1)
```

Description

`t2 = treeprune(t1,'level',level)` takes a decision tree `t1` as created by the `treefit` function, and a pruning level, and returns the decision tree `t2` pruned to that level. Setting `level` to `0` means no pruning. Trees are pruned based on an optimal pruning scheme that first prunes branches giving less improvement in error cost.

`t2 = treeprune(t1,'nodes',nodes)` prunes the nodes listed in the `nodes` vector from the tree. Any `t1` branch nodes listed in `nodes` become leaf nodes in `t2`, unless their parent nodes are also pruned. The `treedisp` function can display the node numbers for any node you select.

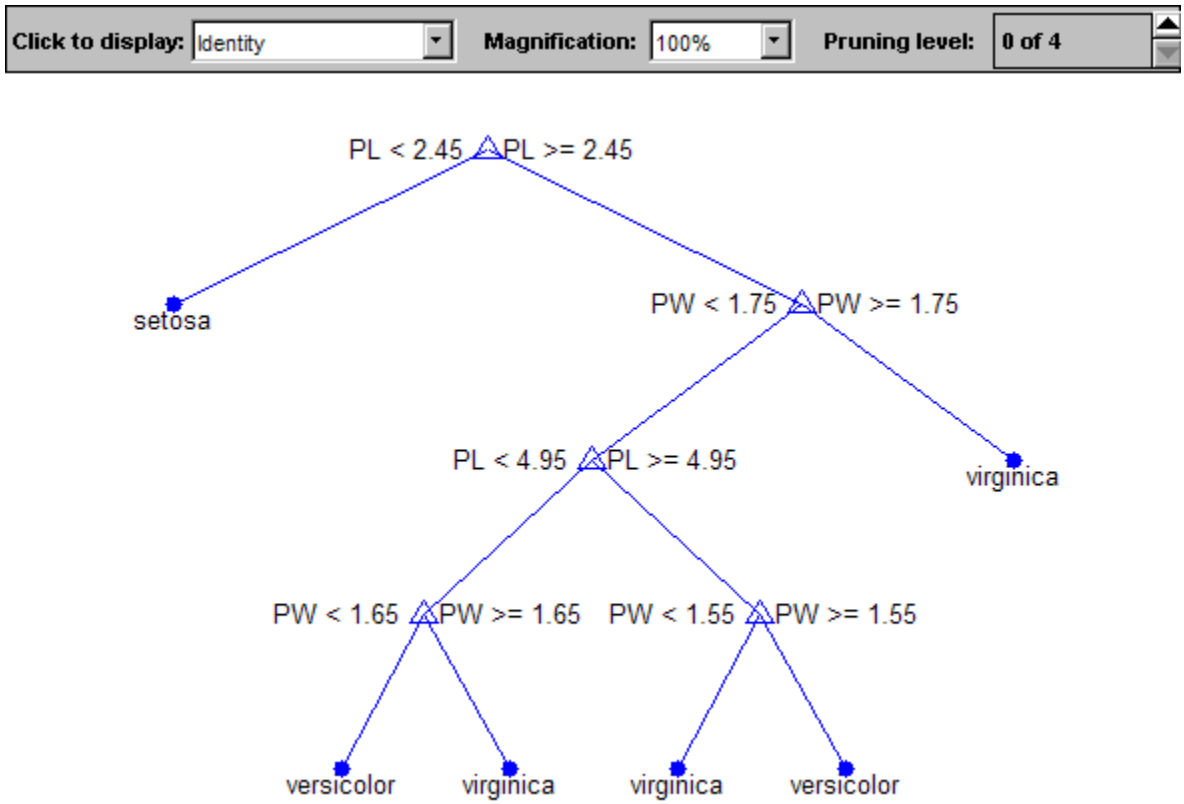
`t2 = treeprune(t1)` returns the decision tree `t2` that is the same as `t1`, but with the optimal pruning information added. This is useful only if you created `t1` by pruning another tree, or by using the `treefit` function with pruning set `'off'`. If you plan to prune a tree multiple times, it is more efficient to create the optimal pruning sequence first.

Pruning is the process of reducing a tree by turning some branch nodes into leaf nodes, and removing the leaf nodes under the original branch.

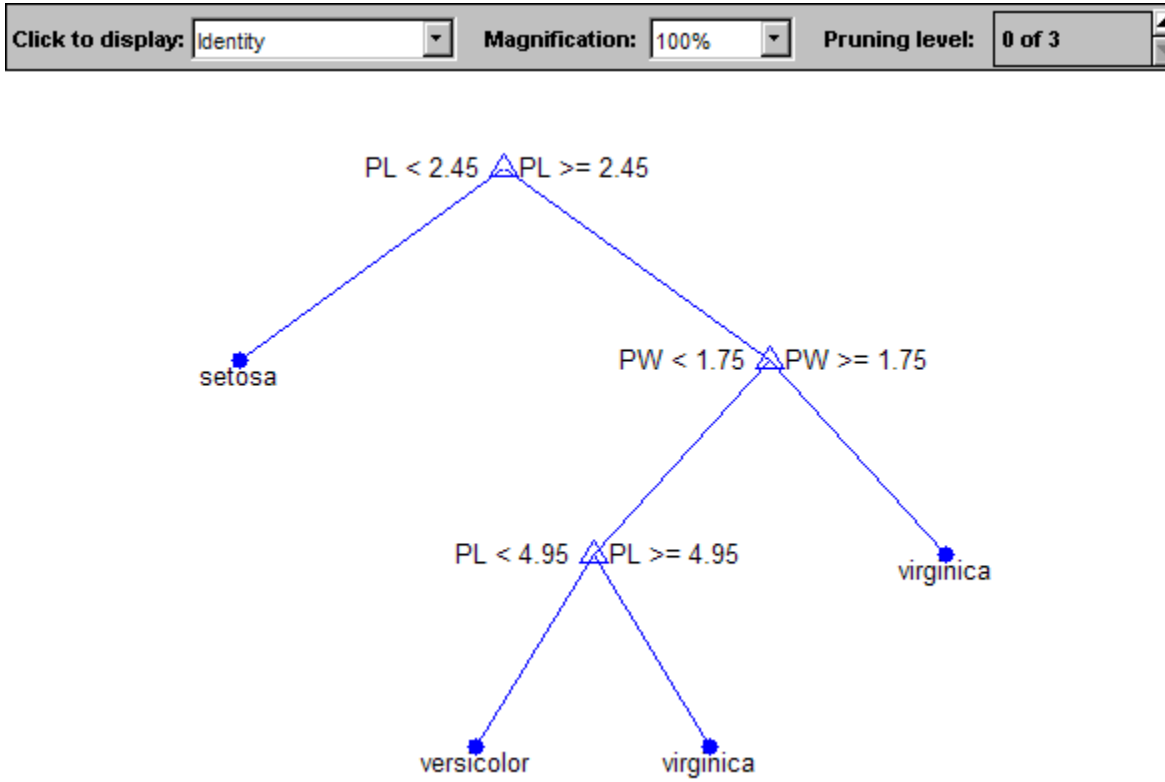
Examples

Display the full tree for Fisher's iris data, as well as the next largest tree from the optimal pruning sequence:

```
load fisheriris;
t1 = treefit(meas,species,'splitmin',5);
treedisp(t1,'names',{'SL' 'SW' 'PL' 'PW'});
```




```
t2 = treeprune(t1,'level',1);
treedisp(t2,'names',{'SL' 'SW' 'PL' 'PW'});
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treetest` | `treedisp`

Trees property

Class: TreeBagger

Decision trees in ensemble

Description

The `Trees` property is a cell array of size `NTrees`-by-1 containing the trees in the ensemble.

See Also

`NTrees`

treetest

Error rate

Syntax

```
cost = treetest(t,'resubstitution')
cost = treetest(t,'test',X,y)
cost = treetest(t,'crossvalidate',X,y)
[cost,secost,ntnodes,bestlevel] = treetest(...)
[...] = treetest(...,param1,val1,param2,val2,...)
```

Compatibility

`treetest` will be removed in a future release. Use `fitctree` or `fitrtree` to grow a tree. Then use `resubLoss` (`ClassificationTree`) or `resubLoss` (`RegressionTree`) instead of `treetest(T,'resubstitution')`. Use `loss` (`ClassificationTree`) or `loss` (`RegressionTree`) instead of `treetest(T,'test',X,Y)`. Use `cvLoss` (`ClassificationTree`) or `cvLoss` (`RegressionTree`) instead of `treetest(T,'crossvalidate',X,Y)`.

Description

`cost = treetest(t,'resubstitution')` computes the cost of the tree `t` using a resubstitution method. `t` is a decision tree as created by the `treefit` function. The cost of the tree is the sum over all terminal nodes of the estimated probability of that node times the node's cost. If `t` is a classification tree, the cost of a node is the sum of the misclassification costs of the observations in that node. If `t` is a regression tree, the cost of a node is the average squared error over the observations in that node. `cost` is a vector of cost values for each subtree in the optimal pruning sequence for `t`. The resubstitution cost is based on the same sample that was used to create the original tree, so it underestimates the likely cost of applying the tree to new data.

`cost = treetest(t,'test',X,y)` uses the predictor matrix `X` and response `y` as a test sample, applies the decision tree `t` to that sample, and returns a vector `cost` of cost

values computed for the test sample. `X` and `y` should not be the same as the learning sample, which is the sample that was used to fit the tree `t`.

`cost = treetest(t,'crossvalidate',X,y)` uses 10-fold cross-validation to compute the cost vector. `X` and `y` should be the learning sample, which is the sample that was used to fit the tree `t`. The function partitions the sample into 10 subsamples, chosen randomly but with roughly equal size. For classification trees, the subsamples also have roughly the same class proportions. For each subsample, `treetest` fits a tree to the remaining data and uses it to predict the subsample. It pools the information from all subsamples to compute the cost for the whole sample.

`[cost,secost,ntnodes,bestlevel] = treetest(...)` also returns the vector `secost` containing the standard error of each `cost` value, the vector `ntnodes` containing number of terminal nodes for each subtree, and the scalar `bestlevel` containing the estimated best level of pruning. `bestlevel = 0` means no pruning, i.e., the full unpruned tree. The best level is the one that produces the smallest tree that is within one standard error of the minimum-cost subtree.

`[...] = treetest(...,param1,val1,param2,val2,...)` specifies optional parameter name-value pairs chosen from the following table.

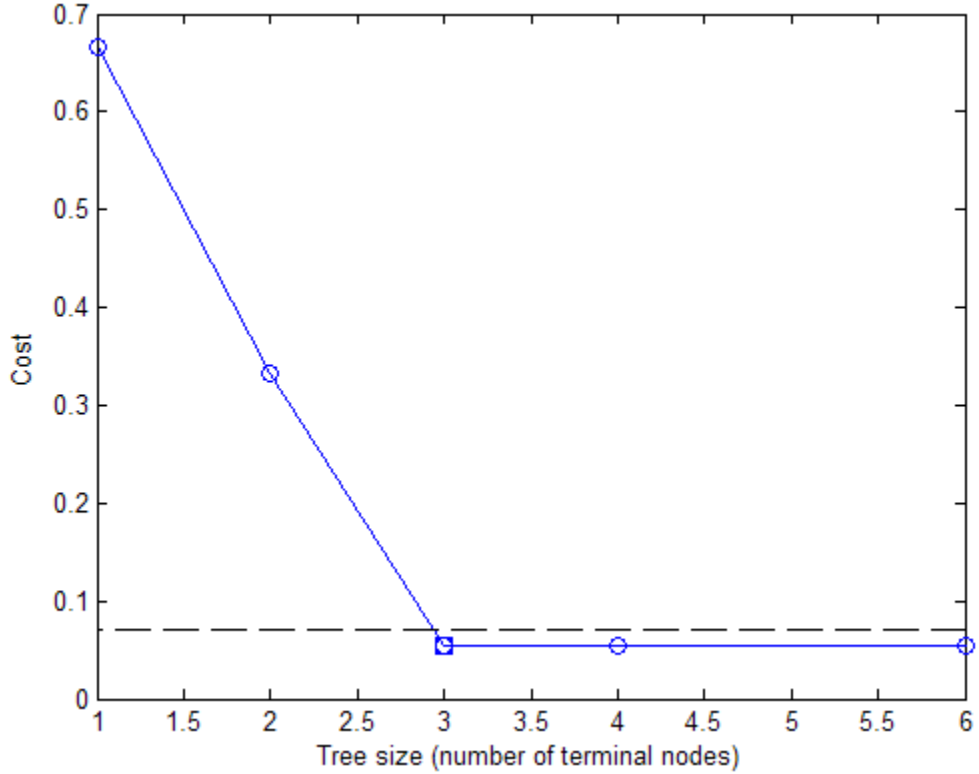
Parameter	Value
`'nsamples'`	The number of cross-validations samples (default is 10).
`'treesize'`	Either `'se'` (default) to choose the smallest tree whose cost is within one standard error of the minimum cost, or `'min'` to choose the minimal cost tree.

Examples

Find the best tree for Fisher's iris data using cross-validation. The solid line shows the estimated cost for each tree size, the dashed line marks one standard error above the minimum, and the square marks the smallest tree under the dashed line.

```
% Start with a large tree.
load fisheriris;
t = treefit(meas,species','splitmin',5);

% Find the minimum-cost tree.
[c,s,n,best] = treetest(t,'cross',meas,species);
```

```
tmin = treeprune(t,'level',best);

% Plot smallest tree within 1 std of minimum cost tree.
[mincost,minloc] = min(c);
plot(n,c,'b-o',...
     n(best+1),c(best+1),'bs',...
     n,(mincost+s(minloc))*ones(size(n)),'k--');
xlabel('Tree size (number of terminal nodes)')
ylabel('Cost')
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treedisp`

treeval

Predicted responses

Compatibility

`treeval` will be removed in a future release. Use `fitctree` or `fitrtree` to grow a tree. Then use `predict` (`ClassificationTree`) or `predict` (`RegressionTree`) instead of `treeval`.

Syntax

```
yfit = treeval(t,X)
yfit = treeval(t,X,subtrees)
[yfit,node] = treeval(...)
[yfit,node,cname] = treeval(...)
```

Description

`yfit = treeval(t,X)` takes a classification or regression tree `t` as produced by the `treefit` function and a matrix `X` of predictor values, and produces a vector `yfit` of predicted response values. For a regression tree, `yfit(i)` is the fitted response value for a point having the predictor values `X(i,:)`. For a classification tree, `yfit(i)` is the class number into which the tree would assign the point with data `X(i,:)`. To convert the number into a class name, use the third output argument, `cname` (described below).

`yfit = treeval(t,X,subtrees)` takes an additional vector `subtrees` of pruning levels, with `0` representing the full, unpruned tree. `T` must include a pruning sequence as created by the `treefit` or `prunetree` function. If `subtree` has k elements and `X` has n rows, the output `yfit` is an n-by-k matrix, with the `j`th column containing the fitted values produced by the `subtrees(j)` subtree. `subtrees` must be sorted in ascending order.

`[yfit,node] = treeval(...)` also returns an array `node` of the same size as `yfit` containing the node number assigned to each row of `X`. The `treedisp` function can display the node numbers for any node you select.

`[yfit,node,cname] = treeval(...)` is valid only for classification trees. It returns a cell array `cname` containing the predicted class names.

Examples

Find the predicted classifications for Fisher's iris data:

```
load fisheriris;
t = treefit(meas,species);  % Create decision tree
sfit = treeval(t,meas);     % Find assigned class numbers
sfit = t.classname(sfit);   % Get class names
mean(strcmp(sfit,species))  % Proportion in correct class
ans =
   0.9800
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`treefit` | `treeprune` | `treetest`

prob.TriangularDistribution class

Package: prob
Superclasses: prob.ParametricTruncatableDistribution

Triangular probability distribution object

Description

`prob.TriangularDistribution` is an object consisting of parameters and a model description for a triangular probability distribution. Create a probability distribution object with specified parameters using `makedist`.

Construction

`pd = makedist('Triangular')` creates a triangular probability distribution object using the default parameter values.

`pd = makedist('Triangular','a',a,'b',b,'c',c)` creates a triangular distribution object using the specified parameter values.

Input Arguments

a — Lower limit

`0` (default) | scalar value

Lower limit for the triangular distribution, specified as a scalar value.

Data Types: `single` | `double`

b — Peak location

`0.5` (default) | scalar value

Peak location for the triangular distribution, specified as a scalar value greater than or equal to a.

Data Types: `single` | `double`

c — Upper limit

1 (default) | scalar value

Upper limit for the triangular distribution, specified as a scalar value greater than or equal to b.

Data Types: `single` | `double`

Properties

a — Lower limit

scalar value

Lower limit for the triangular distribution, stored as a scalar value.

Data Types: `single` | `double`

b — Peak location

scalar value

Location of the peak for the triangular distribution, stored as a scalar value greater than or equal to a.

Data Types: `single` | `double`

c — Upper limit

scalar value

Upper limit for the triangular distribution, stored as a scalar value greater than or equal to b.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`IsTruncated` — Logical flag for truncated distribution

0 | 1

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Triangular Distribution

The triangular distribution is frequently used in simulations when limited sample data is available. The lower and upper limits represent the smallest and largest values, and the location of the peak represents an estimate of the mode.

The triangular distribution uses the following parameters.

Parameter	Description	Support
a	Lower limit	$a \le b$
b	Peak location	$a \le b \le c$
c	Upper limit	$c \ge b$

The probability density function (pdf) is

$$f(x \mid a,b,c) = \begin{cases} \dfrac{2(x-a)}{(c-a)(b-a)} & ; \quad a \le x \le b \\ \dfrac{2(c-x)}{(c-a)(c-b)} & ; \quad b < x \le c \\ 0 & ; \quad x < a \,,\, x > c \end{cases} .$$

and

$$f(x \mid a,b,c) = \frac{2(c-x)}{(c-a)(c-b)} \quad ; \quad b < x \le c \,.$$

The value of the pdf is 0 when $x < a$ or $x > c$.

Examples

Create a Triangular Distribution Object Using Default Parameters

Create a triangular distribution object using the default parameter values.

```
pd = makedist('Triangular')

pd =

  TriangularDistribution

A = 0, B = 0.5, C = 1
```

Create a Triangular Distribution Object Using Specified Parameters

Create a triangular distribution object by specifying parameter values.

```
pd = makedist('Triangular', 'a',-2,'b',1,'c',5)

pd =

  TriangularDistribution

A = -2, B = 1, C = 5
```

Compute the mean of the distribution.

```
m = mean(pd)

m =

    1.3333
```

See Also

`makedist`

More About

- Class Attributes
- Property Attributes

trimmean

Mean excluding outliers

Syntax

```
m = trimmean(X,percent)
trimmean(X,percent,dim)
m = trimmean(X,percent,flag)
m = trimmean(x,percent,flag,dim)
```

Description

`m = trimmean(X,percent)` calculates the trimmed mean of the values in `X`. For a vector input, `m` is the mean of `X`, excluding the highest and lowest `k` data values, where `k=n*(percent/100)/2` and where `n` is the number of values in `X`. For a matrix input, `m` is a row vector containing the trimmed mean of each column of `X`. For `n`-D arrays, `trimmean` operates along the first non-singleton dimension. `percent` is a scalar between 0 and 100.

`trimmean(X,percent,dim)` takes the trimmed mean along dimension `dim` of `X`.

`m = trimmean(X,percent,flag)` controls how to trim when `k` is not an integer. `flag` can be chosen from the following:

`'round'`	Round `k` to the nearest integer (round to a smaller integer if `k` is a half integer). This is the default.
`'floor'`	Round `k` down to the next smaller integer.
`'weight'`	If `k=i+f` where `i` is the integer part and `f` is the fraction, compute a weighted mean with weight `(1-f)` for the `(i+1)th` and `(n-i)th` values, and full weight for the values between them.

`m = trimmean(x,percent,flag,dim)` takes the trimmed mean along dimension `dim` of `x`.

Examples

Efficiency of the Trimmed Mean

Generate a 100-by-100 matrix of random numbers from the standard normal distribution. This represents 100 samples, each containing 100 data points.

```
rng default;  % For reproducibility
x = normrnd(0,1,100,100);
```

Compute the sample mean and the 10% trimmed mean for each column of the data matrix.

```
m = mean(x);
trim = trimmean(x,10);
```

Compute the efficiency of the 10% trimmed mean relative to the sample mean for the data.

```
sm = std(m);
strim = std(trim);
efficiency = (sm/strim).^2
```

```
efficiency =

    0.9663
```

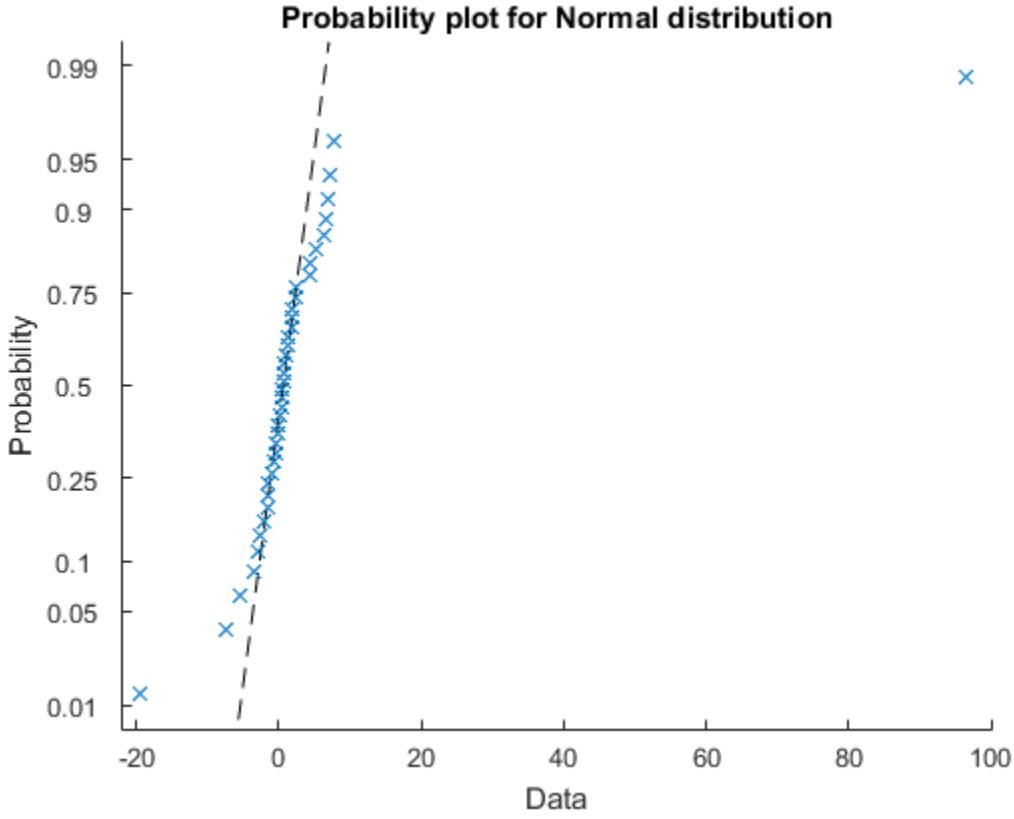
Trimmed Mean for Distributions with Outliers

Generate random data from the *t* location-scale distribution, which tends to have outliers.

```
rng default;  % For reproducibility
x = trnd(1,40,1);
```

Visualize the distribution using a normal probability plot.

```
probplot(x)
```



Although the distribution is symmetric around zero, there are several outliers which will affect the mean. The trimmed mean is closer to zero, which is more representative of the data.

```
mean = mean(x)
tmean = trimmean(x,25)
```

```
mean =

    2.7991


tmean =
```

```
    0.8797
```

More About

Tips

The trimmed mean is a robust estimate of the location of a sample. If there are outliers in the data, the trimmed mean is a more representative estimate of the center of the body of the data than the mean. However, if the data is all from the same probability distribution, then the trimmed mean is less efficient than the sample mean as an estimator of the location of the data.

See Also

`mean` | `median` | `geomean` | `harmmean`

trnd

Student's *t* random numbers

Syntax

```
r = trnd(nu)
r = trnd(nu,m,n,...)
r = trnd(nu,[m,n,...])
```

Description

`r = trnd(nu)` generates random numbers from Student's *t* distribution with `nu` degrees of freedom. `nu` can be a vector, a matrix, or a multidimensional array. The size of `r` is equal to the size of `nu`.

`r = trnd(nu,m,n,...)` or `r = trnd(nu,[m,n,...])` generates an `m`-by-`n`-by-... array. The `nu` parameter can be a scalar or an array of the same size as `r`.

Examples

Generate Student's *t* Distribution Random Numbers

```
r1 = trnd(ones(1,6))
```

```
r1 =

    0.2108    7.8450  -11.0511    0.4134    4.3293   -0.8323
```

```
r2 = trnd(1:6,[1 6])
```

```
r2 =

    8.9290   -0.1908    0.3496   -0.7658    1.3234   -1.2808
```

```
r3 = trnd(3,2,6)

r3 =

    1.3157    0.7010    0.1591   -1.3840    4.1354    0.2442
    0.9789   -2.4700   -1.8884   -0.0116   -0.9496   -0.2340
```

More About

- "Student's t Distribution" on page B-146

See Also

`tpdf` | `tcdf` | `tinv` | `tstat` | `random`

prob.TruncatableDistribution class

Package: prob

Truncatable probability distribution object

Description

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object

See Also

`dfittool` | `fitdist` | `makedist`

More About

- Class Attributes
- Property Attributes

truncate

Truncate probability distribution object

Syntax

```
t = truncate(pd,lower,upper)
```

Description

`t = truncate(pd,lower,upper)` returns a probability distribution t, which is the probability distribution pd truncated to the specified interval with lower limit, lower, and upper limit, upper.

Examples

Truncate a Probability Distribution

Create a standard normal probability distribution object.

```
pd = makedist('Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Truncate the distribution to have a lower limit of -2 and an upper limit of 2.

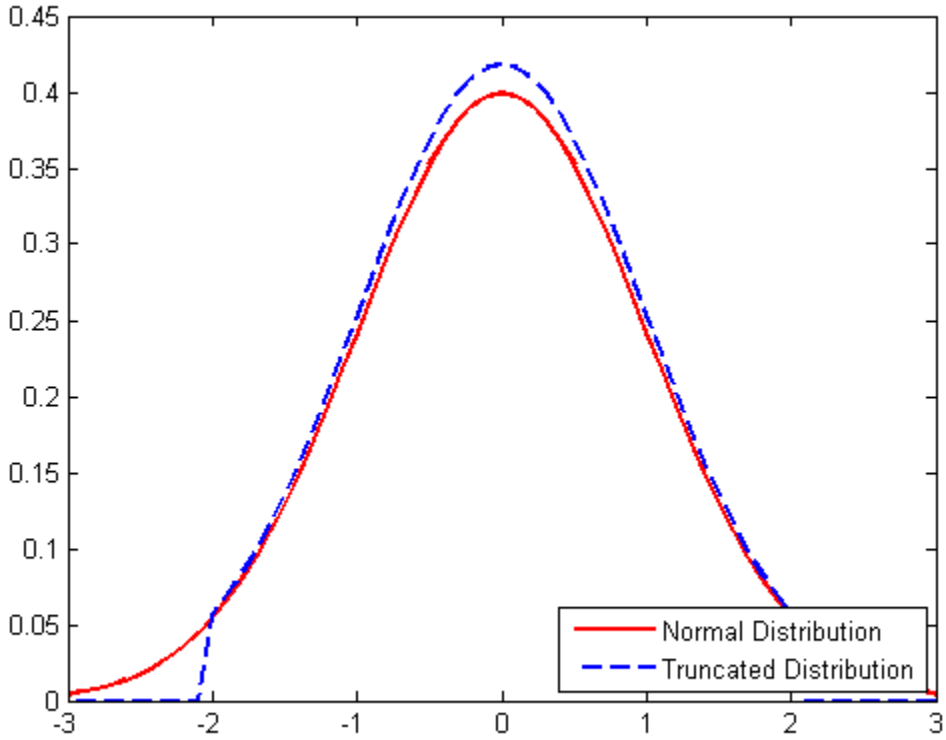
```
t = truncate(pd,-2,2)
```

```
t =

  NormalDistribution

  Normal distribution
       mu = 0
```

```
    sigma = 1
  Truncated to the interval [-2, 2]
```

Plot the pdf of the original and truncated distributions for a visual comparison.

```
x = -3:.1:3;
figure;
plot(x,pdf(pd,x),'Color','red','LineWidth',2)
hold on;
plot(x,pdf(t,x),'Color','blue','LineWidth',2)
hold off;
```



Generate Random Numbers from a Truncated Distribution

Create a standard normal probability distribution object.

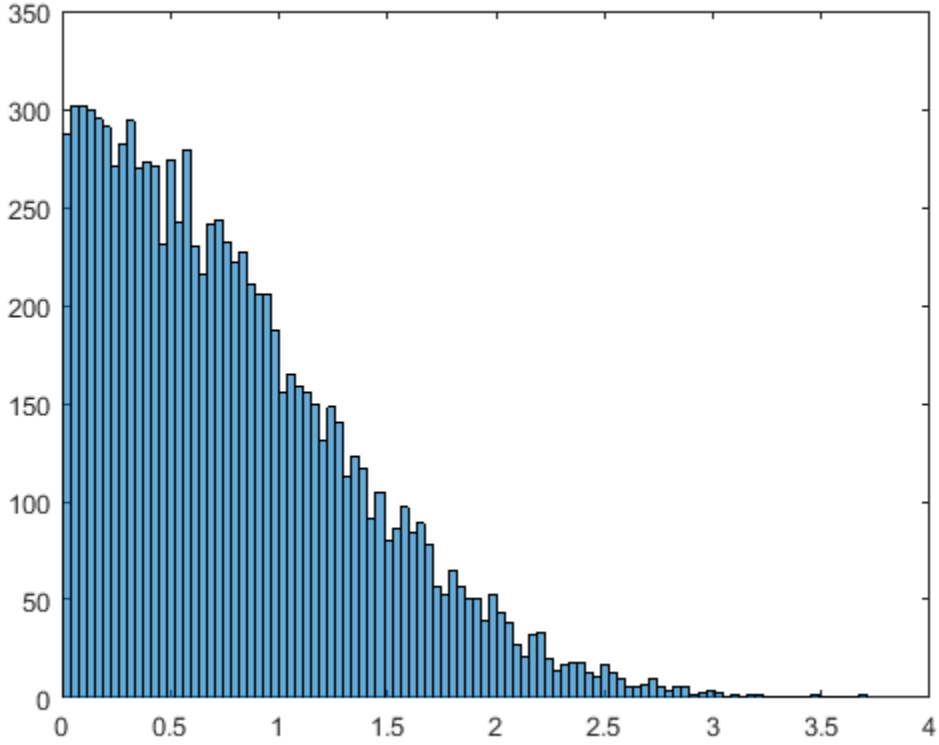
```
pd = makedist('Normal')

pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Truncate the distribution by restricting it to positive values. Set the lower limit to 0 and the upper limit to infinity.

```
t = truncate(pd,0,inf)

t =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
  Truncated to the interval [0, Inf]
```

Generate random numbers from the truncated distribution and visualize with a histogram.

```
r = random(t,10000,1);
histogram(r,100)
```



Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

`lower` — Lower truncation limit

scalar value

Lower truncation limit, specified as a scalar value.

Data Types: `single` | `double`

`upper` — Upper truncation limit

scalar value

Upper truncation limit, specified as a scalar value.

Data Types: `single` | `double`

Output Arguments

`t` — Truncated distribution

probability distribution object

Truncated distribution, returned as a probability distribution object. The pdf of t is 0 outside the truncation interval. Inside the truncation interval, the pdf of t is equal to the pdf of pd, but divided by the probability assigned to that interval by pd.

See Also

`dfittool` | `fitdist` | `makedist`

truncate

Class: prob.TruncatableDistribution
Package: prob

Truncate probability distribution object

Syntax

```
t = truncate(pd,lower,upper)
```

Description

`t = truncate(pd,lower,upper)` returns a probability distribution t, which is the probability distribution pd truncated to the specified interval with lower limit, lower, and upper limit, upper.

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, for fittable distributions, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

`lower` — Lower truncation limit

scalar value

Lower truncation limit, specified as a scalar value.

Data Types: `single` | `double`

`upper` — Upper truncation limit

scalar value

Upper truncation limit, specified as a scalar value.

Data Types: `single` | `double`

Output Arguments

`t` — Truncated distribution

probability distribution object

Truncated distribution, returned as a probability distribution object. The pdf of t is 0 outside the truncation interval. Inside the truncation interval, the pdf of t is equal to the pdf of pd, but divided by the probability assigned to that interval by pd.

Examples

Truncate a Probability Distribution

Create a standard normal probability distribution object.

```
pd = makedist('Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Truncate the distribution to have a lower limit of -2 and an upper limit of 2.

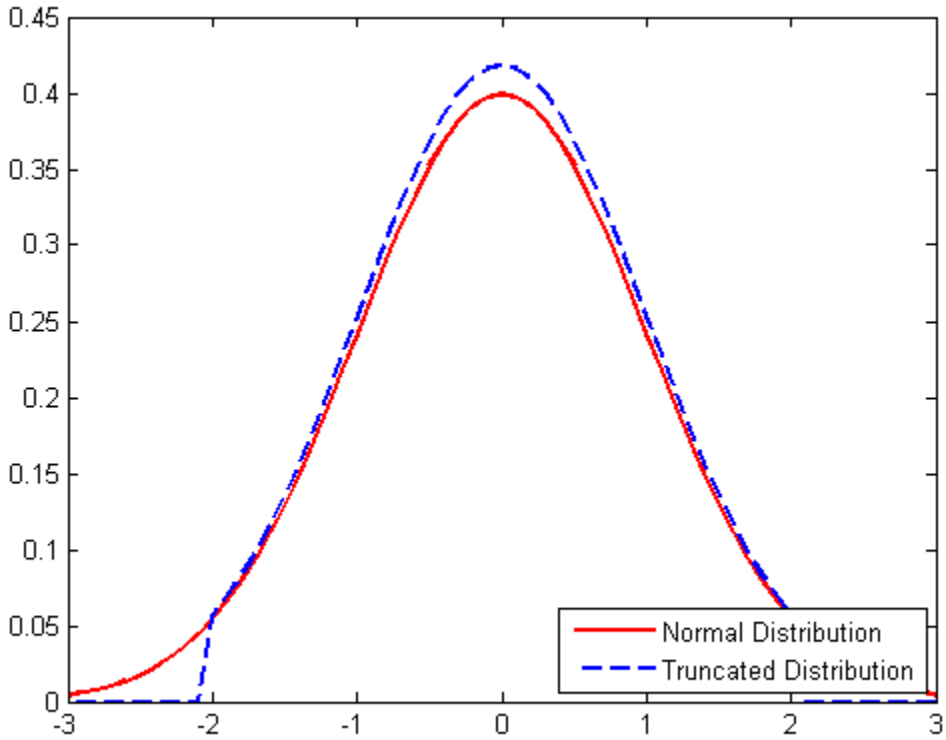
```
t = truncate(pd,-2,2)
```

```
t =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

```
  Truncated to the interval [-2, 2]
```

Plot the pdf of the original and truncated distributions for a visual comparison.

```
x = -3:.1:3;
figure;
plot(x,pdf(pd,x),'Color','red','LineWidth',2)
hold on;
plot(x,pdf(t,x),'Color','blue','LineWidth',2)
hold off;
```



Generate Random Numbers from a Truncated Distribution

Create a standard normal probability distribution object.

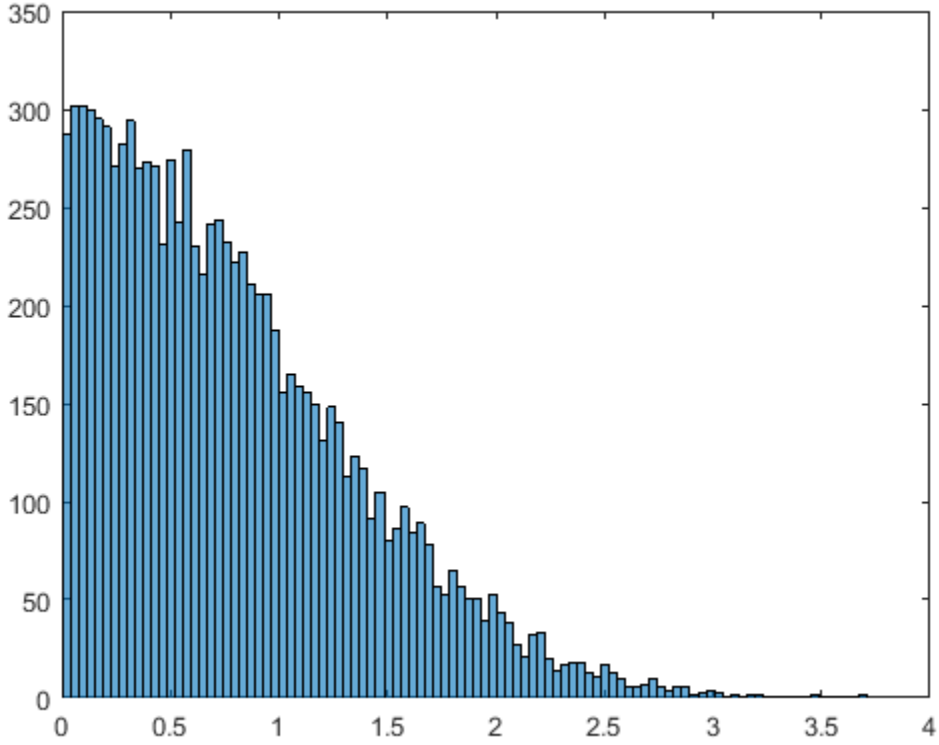
```
pd = makedist('Normal')

pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Truncate the distribution by restricting it to positive values. Set the lower limit to 0 and the upper limit to infinity.

```
t = truncate(pd,0,inf)

t =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
  Truncated to the interval [0, Inf]
```

Generate random numbers from the truncated distribution and visualize with a histogram.

```
rng default  % For reproducibility
r = random(t,10000,1);
histogram(r,100)
```



See Also

`dfittool` | `fitdist` | `makedist`

More About

- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

tstat

Student's t mean and variance

Syntax

```
[m,v] = tstat(nu)
```

Description

`[m,v] = tstat(nu)` returns the mean of and variance for Student's t distribution using the degrees of freedom in `nu`. `nu` can a vectors, matrix, or multidimensional array. The returned values for `m` and `v` are the same size as `nu`.

Examples

Compute Student's *t* Mean and Variance

Compute the mean and variance for Student's t distributions with degrees of freedom *nu* equal to 1 through 30.

```
nu = reshape(1:30,6,5);
[m,v] = tstat(nu)
```

```
m =

   NaN     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0


v =

       NaN    1.4000    1.1818    1.1176    1.0870
```

```
   NaN    1.3333    1.1667    1.1111    1.0833
3.0000    1.2857    1.1538    1.1053    1.0800
2.0000    1.2500    1.1429    1.1000    1.0769
1.6667    1.2222    1.1333    1.0952    1.0741
1.5000    1.2000    1.1250    1.0909    1.0714
```

Note that the variance does not exist for one and two degrees of freedom.

More About

Student's *t* Mean and Variance

The mean of the Student's t distribution is

$$\text{mean} = 0$$

for degrees of freedom ν greater than 1. If ν equals 1, then the mean is undefined.

The variance of the Student's t distribution is

$$\text{var} = \frac{\nu}{\nu - 2}$$

for degrees of freedom ν greater than 2. If ν is less than or equal to 2, then the variance is undefined.

- "Student's t Distribution" on page B-146

See Also

`tpdf` | `tcdf` | `tinv` | `trnd`

ttest

One-sample and paired-sample *t*-test

Syntax

```
h = ttest(x)

h = ttest(x,y)
h = ttest(x,y,Name,Value)

h = ttest(x,m)
h = ttest(x,m,Name,Value)

[h,p] = ttest(___)
[h,p,ci,stats] = ttest(___)
```

Description

`h = ttest(x)` returns a test decision for the null hypothesis that the data in x comes from a normal distribution with mean equal to zero and unknown variance, using the one-sample *t*-test. The alternative hypothesis is that the population distribution does not have a mean equal to zero. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = ttest(x,y)` returns a test decision for the null hypothesis that the data in `x – y` comes from a normal distribution with mean equal to zero and unknown variance, using the paired-sample *t*-test.

`h = ttest(x,y,Name,Value)` returns a test decision for the paired-sample *t*-test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level or conduct a one-sided test.

`h = ttest(x,m)` returns a test decision for the null hypothesis that the data in x comes from a normal distribution with mean m and unknown variance. The alternative hypothesis is that the mean is not m.

`h = ttest(x,m,Name,Value)` returns a test decision for the one-sample *t*-test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level or conduct a one-sided test.

`[h,p] = ttest( ___ )` also returns the *p*-value, p, of the test, using any of the input arguments from the previous syntax groups.

`[h,p,ci,stats] = ttest( ___ )` also returns the confidence interval ci for the mean of `x`, or of `x − y` for the paired *t*-test, and the structure stats containing information about the test statistic.

Examples

Test for a Mean Equal to Zero

Load the sample data. Create a vector containing the third column of the stock returns data.

```
load stockreturns;
x = stocks(:,3);
```

Test the null hypothesis that the sample data comes from a population with mean equal to zero.

```
[h,p,ci,stats] = ttest(x)
```

```
h =
     1

p =

    0.0106

ci =
   -0.7357
   -0.0997

stats =
    tstat: -2.6065
       df: 99
       sd: 1.6027
```

The returned value `h = 1` indicates that `ttest` rejects the null hypothesis at the 5% significance level.

Test Hypothesis at a Different Significance Level

Load the sample data. Create a vector containing the third column of the stock returns data.

```
load stockreturns;
x = stocks(:,3);
```

Test the null hypothesis that the sample data are from a population with mean equal to zero at the 1% significance level.

```
h = ttest(x,0,'Alpha',0.01)
```

```
h =
     0
```

The returned value `h = 0` indicates that `ttest` does not reject the null hypothesis at the 1% significance level.

Paired-Sample *t*-Test

Load the sample data. Create vectors containing the first and second columns of the data matrix to represent students' grades on two exams.

```
load examgrades;
x = grades(:,1);
y = grades(:,2);
```

Test the null hypothesis that the pairwise difference between data vectors `x` and `y` has a mean equal to zero.

```
[h,p] = ttest(x,y)
```

```
h =
     0

p =
    0.9805
```

The returned value of `h = 0` indicates that `ttest` does not reject the null hypothesis at the default 5% significance level.

Paired-Sample *t*-Test at a Different Significance Level

Load the sample data. Create vectors containing the first and second columns of the data matrix to represent students' grades on two exams.

```
load examgrades;
x = grades(:,1);
y = grades(:,2);
```

Test the null hypothesis that the pairwise difference between data vectors `x` and `y` has a mean equal to zero at the 1% significance level.

```
[h,p] = ttest(x,y,'Alpha',0.01)
```

```
h =
     0

p =
    0.9805
```

The returned value of `h = 0` indicates that `ttest` does not reject the null hypothesis at the 1% significance level.

Test for a Hypothesized Mean

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that sample data comes from a distribution with mean `m = 75`.

```
h = ttest(x,75)
```

```
h =
     0
```

The returned value of `h = 0` indicates that `ttest` does not reject the null hypothesis at the 5% significance level.

One-Sided Hypothesis Test

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that the data comes from a population with mean equal to 65, against the alternative that the mean is greater than 65.

```
h = ttest(x,65,'Tail','right')
```

```
h =
     1
```

The returned value of `h = 1` indicates that `ttest` rejects the null hypothesis at the 5% significance level, in favor of the alternate hypothesis that the data comes from a population with a mean greater than 65.

Input Arguments

x — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array. `ttest` performs a separate *t*-test along each column and returns a vector of results. If y sample data is specified, x and y must be the same size.

Data Types: `single` | `double`

y — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array. If y sample data is specified, x and y must be the same size.

Data Types: `single` | `double`

`m` — Hypothesized population mean

0 (default) | scalar value

Hypothesized population mean, specified as a scalar value.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Alpha',0.01` conducts a right-tailed hypothesis test at the 1% significance level.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Dim'` — Dimension

first nonsingleton dimension (default) | positive integer value

Dimension of the input matrix along which to test the means, specified as the comma-separated pair consisting of `'Dim'` and a positive integer value. For example, specifying `'Dim',1` tests the column means, while `'Dim',2` tests the row means.

Example: `'Dim',2`

Data Types: `single` | `double`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the population mean is not `m`.
`'right'`	Test the alternative hypothesis that the population mean is greater than `m`.
`'left'`	Test the alternative hypothesis that the population mean is less than `m`.

Example: `'Tail','right'`

Output Arguments

h — Hypothesis test result

`1 | 0`

Hypothesis test result, returned as a logical value.

- If h = `1`, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = `0`, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

ci — Confidence interval

vector

Confidence interval for the true population mean, returned as a two-element vector containing the lower and upper boundaries of the 100 × (1 – Alpha)% confidence interval.

stats — Test statistics

structure

Test statistics, returned as a structure containing the following:

- `tstat` — Value of the test statistic.
- `df` — Degrees of freedom of the test.

- `sd` — Estimated population standard deviation. For a paired *t*-test, this is the standard deviation of `x - y`.

More About

One-Sample t-Test

The one-sample *t*-test is a parametric test of the location parameter when the population standard deviation is unknown.

The test statistic is

$$t = \frac{\bar{x} - \mu}{s / \sqrt{n}},$$

where $\bar{x}$ is the sample mean, μ is the hypothesized population mean, s is the sample standard deviation, and n is the sample size. Under the null hypothesis, the test statistic has Student's t distribution with $n - 1$ degrees of freedom.

Multidimensional Array

A multidimensional array has more than two dimensions. For example, if `x` is a 1-by-3-by-4 array, then `x` is a three-dimensional array.

First Nonsingleton Dimension

The first nonsingleton dimension is the first dimension of an array whose size is not equal to 1. For example, if `x` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `x`.

See Also

`ttest2` | `ztest`

ttest2

Two-sample *t*-test

Syntax

```
h = ttest2(x,y)
h = ttest2(x,y,Name,Value)
[h,p] = ttest2(___)
[h,p,ci,stats] = ttest2(___)
```

Description

`h = ttest2(x,y)` returns a test decision for the null hypothesis that the data in vectors x and y comes from independent random samples from normal distributions with equal means and equal but unknown variances, using the two-sample *t*-test. The alternative hypothesis is that the data in x and y comes from populations with unequal means. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = ttest2(x,y,Name,Value)` returns a test decision for the two-sample *t*-test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level or conduct the test without assuming equal variances.

`[h,p] = ttest2(___)` also returns the *p*-value, p, of the test, using any of the input arguments in the previous syntaxes.

`[h,p,ci,stats] = ttest2(___)` also returns the confidence interval on the difference of the population means, ci, and the structure stats containing information about the test statistic.

Examples

Test for Equal Means

Load the data set. Create vectors containing the first and second columns of the data matrix to represent students' grades on two exams.

```
load examgrades;
x = grades(:,1);
y = grades(:,2);
```

Test the null hypothesis that the two data samples are from populations with equal means.

```
[h,p,ci,stats] = ttest2(x,y)
```

```
h =
     0

p =
    0.9867

ci =
   -1.9438
    1.9771

stats =
    tstat: 0.0167
       df: 238
       sd: 7.7084
```

The returned value of `h = 0` indicates that `ttest2` does not reject the null hypothesis at the default 5% significance level.

Test for Equal Means Without Assuming Equal Variances

Load the data set. Create vectors containing the first and second columns of the data matrix to represent students' grades on two exams.

```
load examgrades;
x = grades(:,1);
y = grades(:,2);
```

Test the null hypothesis that the two data vectors are from populations with equal means, without assuming that the populations also have equal variances.

```
[h,p] = ttest2(x,y,'Vartype','unequal')
```

```
h =
     0

p =
```

```
    0.9867
```

The returned value of `h = 0` indicates that `ttest2` does not reject the null hypothesis at the default 5% significance level even if equal variances are not assumed.

Input Arguments

x — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array. `ttest2` treats `NaN` values as missing data and ignores them.

- If x and y are specified as vectors, they do not need to be the same length.
- If x and y are specified as matrices, they must have the same number of columns. `ttest2` performs a separate *t*-test along each column and returns a vector of results.
- If x and y are specified as multidimensional arrays, they must have the same size along all but the first nonsingleton dimension.

Data Types: `single` | `double`

y — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array. `ttest2` treats `NaN` values as missing data and ignores them.

- If x and y are specified as vectors, they do not need to be the same length.
- If x and y are specified as matrices, they must have the same number of columns. `ttest2` performs a separate *t*-test along each column and returns a vector of results.
- If x and y are specified as multidimensional arrays, they must have the same size along all but the first nonsingleton dimension. `ttest2` works along the first nonsingleton dimension.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Alpha',0.01,'Vartype','unequal'` specifies a right-tailed test at the 1% significance level, and does not assume that `x` and `y` have equal population variances.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Dim'` — Dimension

first nonsingleton dimension (default) | positive integer value

Dimension of the input matrix along which to test the means, specified as the comma-separated pair consisting of `'Dim'` and a positive integer value. For example, specifying `'Dim',1` tests the column means, while `'Dim',2` tests the row means.

Example: `'Dim',2`

Data Types: `single` | `double`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the population means are not equal.
`'right'`	Test the alternative hypothesis that the population mean of x is greater than the population mean of y.
`'left'`	Test the alternative hypothesis that the population mean of x is less than the population mean of y.

Example: `'Tail','right'`

'Vartype' — Variance type

'equal' (default) | 'unequal'

Variance type, specified as the comma-separated pair consisting of 'Vartype' and one of the following.

'equal'	Conduct test using the assumption that x and y are from normal distributions with unknown but equal variances.
'unequal'	Conduct test using the assumption that x and y are from normal distributions with unknown and unequal variances. This is called the Behrens-Fisher problem. ttest2 uses Satterthwaite's approximation for the effective degrees of freedom.

Vartype must be a single string, even when x is a matrix or a multidimensional array.

Example: 'Vartype','unequal'

Output Arguments

h — Hypothesis test result

1 | 0

Hypothesis test result, returned as a logical value.

- If h = 1, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = 0, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

ci — Confidence interval

vector

Confidence interval for the difference in population means of x and y, returned as a two-element vector containing the lower and upper boundaries of the 100 × (1 – Alpha)% confidence interval.

`stats` — Test statistics

structure

Test statistics for the two-sample *t*-test, returned as a structure containing the following:

- `tstat` — Value of the test statistic.
- `df` — Degrees of freedom of the test.
- `sd` — Pooled estimate of the population standard deviation (for the equal variance case) or a vector containing the unpooled estimates of the population standard deviations (for the unequal variance case).

More About

Two-Sample *t*-test

The two-sample *t*-test is a parametric test that compares the location parameter of two independent data samples.

The test statistic is

$$t = \frac{\bar{x} - \bar{y}}{\sqrt{\frac{s_x^2}{n} + \frac{s_y^2}{m}}},$$

where $\bar{x}$ and $\bar{y}$ are the sample means, s_x and s_y are the sample standard deviations, and n and m are the sample sizes.

In the case where it is assumed that the two data samples are from populations with equal variances, the test statistic under the null hypothesis has Student's t distribution with $n + m - 2$ degrees of freedom, and the sample standard deviations are replaced by the pooled standard deviation

$$s = \sqrt{\frac{(n-1)s_x^2 + (m-1)s_y^2}{n+m-2}}.$$

In the case where it is not assumed that the two data samples are from populations with equal variances, the test statistic under the null hypothesis has an approximate Student's t distribution with a number of degrees of freedom given by Satterthwaite's approximation. This test is sometimes called Welch's t-test.

Multidimensional Array

A multidimensional array has more than two dimensions. For example, if `x` is a 1-by-3-by-4 array, then `x` is a three-dimensional array.

First Nonsingleton Dimension

The first nonsingleton dimension is the first dimension of an array whose size is not equal to 1. For example, if `x` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `x`.

See Also

`ttest` | `ztest`

type

Class: classregtree

Tree type

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
ttype = type(t)
```

Description

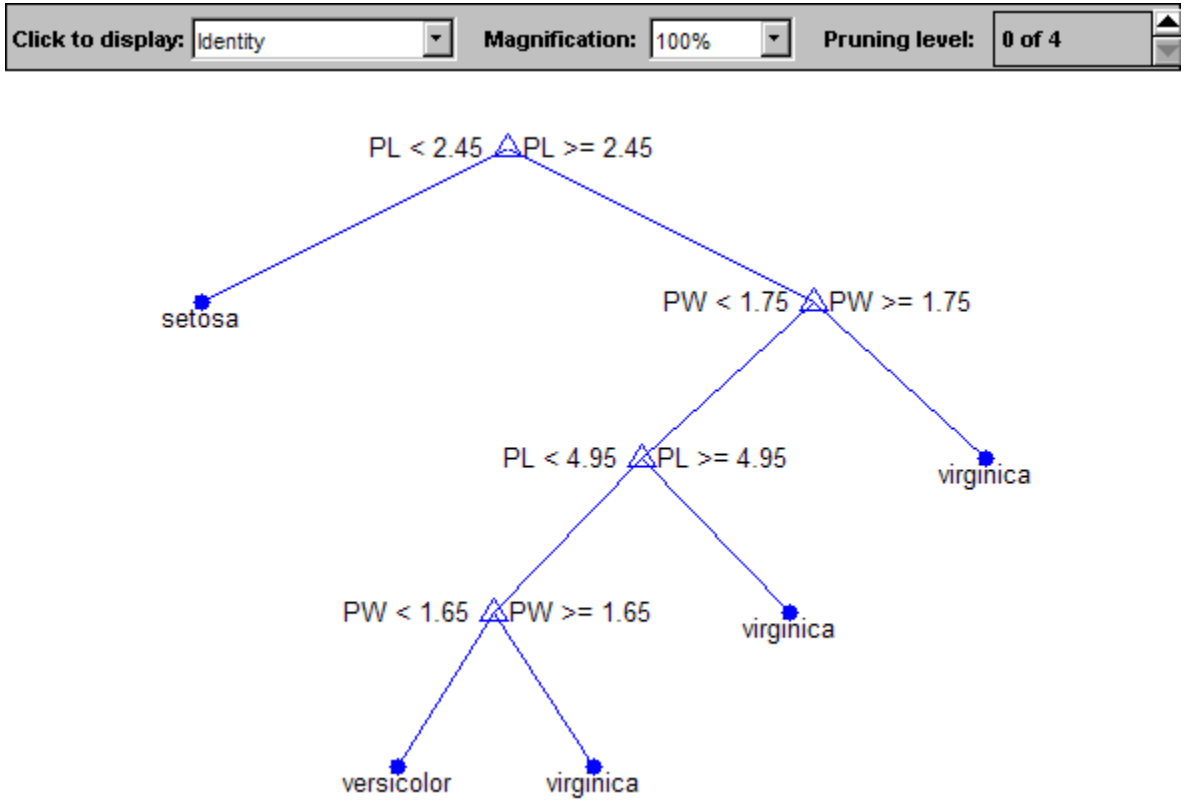
`ttype = type(t)` returns the type of the tree `t`. `ttype` is `'regression'` for regression trees and `'classification'` for classification trees.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
```

```
9  class = virginica

view(t)
```




```
ttype = type(t)
ttype =
classification
```

References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree`

Type property

Class: cvpartition

Type of partition

Description

The type of validation partition. It is `'kfold'`, `'holdout'`, `'leaveout'`, or `'resubstitution'`.

See Also

`trainsize`

Type property

Class: qrandset

Name of sequence on which point set `P` is based

Description

`P.Type` returns a string that contains the name of the sequence on which the point set `P` is based, for example `'Sobol'`. You cannot change the `Type` property for a point set.

Using BetaDistribution Objects

Beta probability distribution object

A `BetaDistribution` object consist of parameters, a model description, and sample data for a beta probability distribution.

The beta distribution describes a family of curves that are unique in that they are nonzero only on the interval (0,1). A more general version of the distribution assigns parameters to the endpoints of the interval.

The beta distribution uses the following parameters.

Parameter	Description	Support
a	First shape parameter	$a > 0$
b	Second shape parameter	$b > 0$

Examples

Create a Beta Distribution Object Using Default Parameters

Create a beta distribution object using the default parameter values.

```
pd = makedist('Beta')
```

```
pd =

  BetaDistribution

  Beta distribution
    a = 1
    b = 1
```

Create a Beta Distribution Object Using Specified Parameters

Create a beta distribution object by specifying the parameter values.

```
pd = makedist('Beta','a',2,'b',4)
```

```
pd =
```

```
  BetaDistribution

  Beta distribution
    a = 2
    b = 4
```

Compute the mean of the distribution.

```
m = mean(pd)

m =

    0.3333
```

Properties

a — First shape parameter
positive scalar value

First shape parameter of the beta distribution, stored as a positive scalar value.

Data Types: `single | double`

b — Second shape parameter
positive scalar value

Second shape parameter of the beta distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single` | `double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `BetaDistribution` probability distribution object.

- Create a `BetaDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Beta')` creates a `BetaDistribution` object using the default parameter values for the first shape parameter (`a = 1`) and the second shape parameter (`b = 1`).

  `pd = makedist('Beta','a',a,'b',b)` creates a `BetaDistribution` object using the parameter values specified for `a` and `b`.

  For additional syntax options, see `makedist`.
- Fit a `BetaDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Beta')` creates a `BetaDistribution` object by fitting a beta distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `BetaDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Beta Distribution"

Using BinomialDistribution Objects

Binomial probability distribution object

A `BinomialDistribution` object consists of parameters, a model description, and sample data for a binomial probability distribution

The binomial distribution models the total number of successes in repeated trials from an infinite population under the following conditions:

- Only two outcomes are possible for each of n trials.
- The probability of success for each trial is constant.
- All trials are independent of each other.

The binomial distribution uses the following parameters.

Parameter	Description	Support
`N`	Number of trials	positive integer
`p`	Probability of success	$0 \le p \le 1$

Examples

Create a Binomial Distribution Object Using Default Parameters

Create a binomial distribution object using the default parameter values.

```
pd = makedist('Binomial')
```

```
pd =

  BinomialDistribution

  Binomial distribution
    N =   1
    p = 0.5
```

Create a Binomial Distribution Object Using Specified Parameters

Create a binomial distribution object by specifying the parameter values.

```
pd = makedist('Binomial','N',30,'p',0.25)
```

```
pd =

  BinomialDistribution

  Binomial distribution
    N =   30
    p = 0.25
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    7.5000
```

Properties

`N` — Number of trials

positive integer value

Number of trials for the binomial distribution, stored as a positive integer value.

Data Types: `single` | `double`

`p` — Probability of success

positive scalar value in the range `[0,1]`

Probability of success of any individual trial for the binomial distribution, stored as a positive scalar value in the range `[0,1]`.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `fiqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `BinomialDistribution` probability distribution object.

- Create a `BinomialDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Binomial')` creates a `BinomialDistribution` object using the default parameter values for the number of trials (`N = 1`) and the probability of success (`p = 0.5`).

  `pd = makedist('Binomial','N',N,'p',p)` creates a `BinomialDistribution` object using the parameter values specified for `N` and `p`.

  For additional syntax options, see `makedist`.

- Fit a `BinomialDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Binomial')` creates a `BinomialDistribution` object by fitting a binomial distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit a `BinomialDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Binomial Distribution"
- "Bernoulli Distribution"

Using BirnbaumSaundersDistribution Objects

Birnbaum-Saunders probability distribution object

A `BirnbaumSaundersDistribution` object consists of parameters, a model description, and sample data for a Birnbaum-Saunders probability distribution.

The Birnbaum-Saunders distribution was originally proposed as a lifetime model for materials subject to cyclic patterns of stress and strain, where the ultimate failure of the material comes from the growth of a prominent flaw. In materials science, Miner's Rule suggests that the damage occurring after n cycles, at a stress level with an expected lifetime of N cycles, is proportional to n / N. Whenever Miner's Rule applies, the Birnbaum-Saunders model is a reasonable choice for a lifetime distribution model.

The Birnbaum-Saunders distribution uses the following parameters.

Parameter	Description	Support
`beta`	scale parameter	$\beta > 0$
`gamma`	shape parameter	$\gamma > 0$

Examples

Create a Birnbaum-Saunders Distribution Object Using Default Parameters

Create a Birnbaum-Saunders distribution object using the default parameter values.

```
pd = makedist('BirnbaumSaunders')
```

```
pd =

  BirnbaumSaundersDistribution

  Birnbaum-Saunders distribution
     beta = 1
    gamma = 1
```

Create a Birnbaum-Saunders Distribution Object Using Specified Parameter Values

Create a Birnbaum-Saunders distribution object by specifying the parameter values.

```
pd = makedist('BirnbaumSaunders','beta',2,'gamma',5)
```

```
pd =

  BirnbaumSaundersDistribution

  Birnbaum-Saunders distribution
     beta = 2
    gamma = 5
```

Compute the mean of the distribution.

```
m = mean(pd)

m =

    27
```

Properties

`beta` — Scale parameter

positive scalar value

Scale parameter of the Birnbaum-Saunders distribution, stored as a positive scalar value.

Data Types: `single | double`

`gamma` — Shape parameter

positive scalar value

Shape parameter of the Birnbaum-Saunders distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncatevar`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `BirnbaumSaundersDistribution` probability distribution object.

- Create a `BirnbaumSaundersDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('BirnbaumSaunders')` creates a `BirnbaumSaundersDistribution` object using the default parameter values for the scale parameter (`beta = 1`) and the shape parameter (`gamma = 1`).

  `pd = makedist('BirnbaumSaunders','beta',beta,'gamma',gamma)` creates a `BirnbaumSaundersDistribution` object using the parameter values specified for `beta` and `gamma`.

  For additional syntax options, see `makedist`.

- Fit a `BirnbaumSaundersDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'BirnbaumSaunders')` creates a `BirnbaumSaundersDistribution` object by fitting a Birnbaum-Saunders distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit a `BirnbaumSaundersDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Birnbaum-Saunders Distribution"

Using BurrDistribution Objects

Burr probability distribution object

A `BurrDistribution` object consists of parameters, a model description, and sample data for a Burr probability distribution.

The Burr distribution is a three-parameter family of distributions on the positive real line. It can fit a wide range of empirical data, and is used in various fields such as finance, hydrology, and reliability to model a variety of data types.

The Burr distribution uses the following parameters.

Parameter	Description	Support
`alpha`	Scale parameter	$\alpha > 0$
`c`	First shape parameter	$c > 0$
`k`	Second shape parameter	$k > 0$

Examples

Create a Burr Distribution Object Using Default Parameters

Create a Burr distribution object using the default parameter values.

```
pd = makedist('Burr')
```

```
pd =

  BurrDistribution

  Burr distribution
    alpha = 1
        c = 1
        k = 1
```

Create a Burr Distribution Object Using Specified Parameters

Create a Burr distribution object by specifying parameter values.

```
pd = makedist('Burr','alpha',1,'c',2,'k',5)

pd =

  BurrDistribution

  Burr distribution
    alpha = 1
        c = 2
        k = 5
```

Compute the mean of the distribution.

```
m = mean(pd)

m =

    0.4295
```

Properties

`alpha` — Scale parameter
positive scalar value

Scale parameter of the Burr distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`c` — First shape parameter
positive scalar value

First shape parameter of the Burr distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`k` — Second shape parameter
positive scalar value

Second shape parameter of the Burr distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated

by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single` | `double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single` | `double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `BurrDistribution` probability distribution object.

- Create a `BurrDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Burr')` creates a `BurrDistribution` object using the default parameter values for the scale parameter (`alpha = 1`), the first shape parameter (`c = 1`), and the second shape parameter (`k = 1`).

  `pd = makedist('Burr','alpha',alpha,'c',c,'k',k)` creates a `BurrDistribution` object using the parameter values specified for `alpha`, `c`, and `k`.

  For additional syntax options, see `makedist`.
- Fit a `BurrDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Burr')` creates a `BurrDistribution` object by fitting a Burr distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `BurrDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Burr Type XII Distribution"

Using ExponentialDistribution Objects

Exponential probability distribution object

An `ExponentialDistribution` object consists of parameters, a model description, and sample data for an exponential probability distribution.

The exponential distribution is used to model events that occur randomly over time, and its main application area is studies of lifetimes. It is a special case of the gamma distribution with the shape parameter $a = 1$.

The exponential distribution uses the following parameters.

Parameter	Description	Support
`mu`	Mean	$\mu > 0$

Examples

Create an Exponential Distribution Object Using Default Parameters

Create an exponential distribution object using the default parameter values.

```
pd = makedist('Exponential')
```

```
pd =

  ExponentialDistribution

  Exponential distribution
    mu = 1
```

Create an Exponential Distribution Object Using Specified Parameters

Create an exponential distribution object by specifying the parameter values.

```
pd = makedist('Exponential','mu',2)
```

```
pd =
```

```
  ExponentialDistribution

  Exponential distribution
    mu = 2
```

Compute the variance of the distribution.

```
v = var(pd)
```

```
v =

     4
```

Properties

`mu` — Mean

positive scalar value

Mean of the exponential distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create an `ExponentialDistribution` probability distribution object.

- Create an `ExponentialDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Exponential')` creates a `ExponentialDistribution` object using the default parameter value for the mean (`mu = 1`).

  `pd = makedist('Exponential','mu',mu)` creates an `ExponentialDistribution` object using the parameter value specified for `mu`.

For additional syntax options, see `makedist`.

- Fit an `ExponentialDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Exponential')` creates an `ExponentialDistribution` object by fitting an exponential distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit an `ExponentialDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Exponential Distribution"

Using ExtremeValueDistribution Objects

Extreme value probability distribution object

An `ExtremeValueDistribution` object consists of parameters, a model description, and sample data for an extreme value probability distribution.

The extreme value distribution is appropriate for modeling the smallest value from a distribution whose tails decay exponentially fast, for example, the normal distribution. It can also model the largest value from a distribution, such as the normal or exponential distributions, by using the negative of the original values.

The extreme value distribution uses the following parameters.

Parameter	Description	Support
`mu`	Location parameter	$-\infty < \mu < \infty$
`sigma`	Scale parameter	$\sigma \geq 0$

Examples

Create an Extreme Value Distribution Object Using Default Parameters

Create an extreme value distribution object using the default parameter values.

```
pd = makedist('ExtremeValue')
```

```
pd =

  ExtremeValueDistribution

  Extreme Value distribution
       mu = 0
    sigma = 1
```

Create an Extreme Value Distribution Object Using Specified Parameters

Create an extreme value distribution object by specifying the parameter values.

```
pd = makedist('ExtremeValue', 'mu',-1,'sigma',2)
```

```
pd =

  ExtremeValueDistribution

  Extreme Value distribution
       mu = -1
    sigma =  2
```

Compute the standard deviation for the distribution.

```
s = std(pd)
```

```
s =

    2.5651
```

Properties

`mu` — Location parameter

scalar value

Location parameter of the extreme value distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

nonnegative scalar value

Scale parameter of the extreme value distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create an `ExtremeValueDistribution` probability distribution object.

- Create an `ExtremeValueDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('ExtremeValue')` creates an `ExtremeValueDistribution` object using the default parameter values for the location parameter (`mu = 0`) and the scale parameter (`sigma = 1`).

  `pd = makedist('ExtremeValue','mu',mu,'sigma',sigma)` creates an `ExtremeValueDistribution` object using the parameter values specified for `mu` and `sigma`.

  For additional syntax options, see `makedist`.
- Fit an `ExtremeValueDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'ExtremeValue')` creates an `ExtremeValueDistribution` object by fitting an extreme value distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `ExtremeValueDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Extreme Value Distribution"

Using GammaDistribution Objects

Gamma probability distribution object

A `GammaDistribution` object consists of parameters, a model description, and sample data for a gamma probability distribution.

The gamma distribution is a two-parameter family of distributions used to model sums of exponentially distributed random variables. The chi-square and the exponential distributions, which are special cases of the gamma distribution, are one-parameter distributions that fix one of the two gamma parameters.

The gamma distribution uses the following parameters.

Parameter	Description	Support
a	Shape parameter	$a > 0$
b	Scale parameter	$b \geq 0$

Examples

Create a Gamma Distribution Object Using Default Parameters

Create a gamma distribution object using the default parameter values.

```
pd = makedist('Gamma')
```

```
pd =

  GammaDistribution

  Gamma distribution
    a = 1
    b = 1
```

Create a Gamma Distribution Object Using Specified Parameters

Create a gamma distribution object by specifying the parameter values.

```
pd = makedist('Gamma', 'a',2,'b',4)
```

```
pd =

  GammaDistribution

  Gamma distribution
    a = 2
    b = 4
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

     8
```

Properties

a — Shape parameter
positive scalar value

Shape parameter for the gamma distribution, stored as a positive scalar value.

Data Types: `single | double`

b — Scale parameter
nonnegative scalar value

Scale parameter for the gamma distribution, stored as a nonnegative scalar value.

Data Types: `single | double`

DistributionName — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

InputData — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single` | `double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `GammaDistribution` probability distribution object.

- Create a `GammaDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Gamma')` creates a `GammaDistribution` object using the default parameter values for the shape parameter (`a = 1`) and the scale parameter (`b = 1`).

  `pd = makedist('Gamma','a',a,'b',b)` creates a `GammaDistribution` object using the parameter values specified for `a` and `b`.

  For additional syntax options, see `makedist`.

- Fit a `GammaDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Gamma')` creates a `GammaDistribution` object by fitting a gamma distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit a `GammaDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Gamma Distribution"

Using GeneralizedExtremeValueDistribution Objects

Generalized extreme value probability distribution object

A `GeneralizedExtremeValueDistribution` object consists of parameters, a model description, and sample data for a generalized extreme value probability distribution.

The generalized extreme value distribution is often used to model the smallest or largest value among a large set of independent, identically distributed random values representing measurements or observations. It combines three simpler distributions into a single form, allowing a continuous range of possible shapes that include all three of the simpler distributions.

The three distribution types correspond to the limiting distribution of block maxima from different classes of underlying distributions:

- Type 1 — Distributions whose tails decrease exponentially, such as the normal distribution
- Type 2 — Distributions whose tails decrease as a polynomial, such as Student's t distribution
- Type 3 — Distributions whose tails are finite, such as the beta distribution

The generalized extreme value distribution uses the following parameters.

Parameter	Description	Support
`k`	Shape parameter	$-\infty \le k \le \infty$
`sigma`	Scale parameter	$\sigma \ge 0$
`mu`	Location parameter	$-\infty \le \mu \le \infty$

Examples

Create a Generalized Extreme Value Distribution Object Using Default Parameters

Create a generalized extreme value distribution object using the default parameter values.

```
pd = makedist('GeneralizedExtremeValue')

pd =

  GeneralizedExtremeValueDistribution

  Generalized Extreme Value distribution
        k = 0
    sigma = 1
       mu = 0
```

Create a Generalized Extreme Value Distribution Object Using Specified Parameters

Create a generalized extreme value distribution object by specifying values for the parameters.

```
pd = makedist('GeneralizedExtremeValue','k',0,'sigma',2,'mu',1)

pd =

  GeneralizedExtremeValueDistribution

  Generalized Extreme Value distribution
        k = 0
    sigma = 2
       mu = 1
```

Compute the mean of the distribution.

```
m = mean(pd)

m =

    2.1544
```

Properties

k — Shape parameter

scalar value

Shape parameter of the generalized extreme value distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

nonnegative scalar value

Scale parameter of the generalized extreme value distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`mu` — Location parameter

scalar value

Location parameter of the generalized extreme value distribution, stored as a scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `GeneralizedExtremeValueDistribution` probability distribution object.

- Create a `GeneralizedExtremeValueDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('GeneralizedExtremeValue')` creates a `GeneralizedExtremeValueDistribution` object using the default parameter values for the shape parameter (`k = 0`) , the scale parameter (`sigma = 1`), and the location parameter (`mu = 0`).

  `pd = makedist('GeneralizedExtremeValue','k',k,'sigma',sigma,'mu', mu)` creates a `GeneralizedExtremeValueDistribution` object using the parameter values specified for `k`, `sigma`, and `mu`.

  For additional syntax options, see `makedist`.
- Fit a `GeneralizedExtremeValueDistribution` object to data using `fitdist`.

`pd = fitdist(x,'GeneralizedExtremeValue')` creates a `GeneralizedExtremeValueDistribution` object by fitting a generalized extreme value distribution to the data contained in the column vector, `x`.

For additional syntax options, see `fitdist`.

- Interactively fit a `GeneralizedExtremeValueDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Generalized Extreme Value Distribution"

Using GeneralizedParetoDistribution Objects

Generalized Pareto probability distribution object

A `GeneralizedParetoDistribution` object consists of parameters, a model description, and sample data for a generalized Pareto probability distribution.

The generalized Pareto distribution is used to model the tails of another distribution. It allows a continuous range of possible shapes that include both the exponential and Pareto distributions as special cases. It has three basic forms, each corresponding to a limiting distribution of exceedence data from a different class of underlying distributions.

- Distributions whose tails decrease exponentially, such as the normal, lead to a generalized Pareto shape parameter of zero.
- Distributions whose tails decrease polynomially, such as the Student's *t*, lead to a positive shape parameter.
- Distributions whose tails are finite, such as the beta, lead to a negative shape parameter.

The generalized Pareto distribution uses the following parameters.

Parameter	Description	Support
`k`	Shape parameter	$-\infty < k < \infty$
`sigma`	Scale parameter	$\sigma \geq 0$
`theta`	Location parameter	$-\infty < \theta < \infty$

Examples

Create a Generalized Pareto Distribution Object Using Default Parameters

Create a generalized Pareto distribution object using the default parameter values.

```
pd = makedist('GeneralizedPareto')
```

```
pd =

  GeneralizedParetoDistribution
```

```
  Generalized Pareto distribution
        k = 1
    sigma = 1
    theta = 1
```

Create a Generalized Pareto Distribution Object Using Specified Parameters

Create a generalized Pareto distribution object by specifying parameter values.

```
pd = makedist('GeneralizedPareto','k',0,'sigma',2,'theta',1)
```

```
pd =

  GeneralizedParetoDistribution

  Generalized Pareto distribution
        k = 0
    sigma = 2
    theta = 1
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    2.1544
```

Properties

k — Shape parameter

scalar value

Shape parameter for the generalized Pareto distribution, stored as a scalar value.

Data Types: `single` | `double`

sigma — Scale parameter

nonnegative scalar value

Scale parameter for the generalized Pareto distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`theta` — Location parameter

scalar value

Location parameter for the generalized Pareto distribution, stored as a scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `GeneralizedParetoDistribution` probability distribution object.

- Create a `GeneralizedParetoDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('GeneralizedPareto')` creates a `GeneralizedParetoDistribution` object using the default parameter values for the shape parameter (`k = 1`), the scale parameter (`sigma = 1`), and the location parameter (`theta = 1`).

  `pd = makedist('GeneralizedPareto','k',k,'sigma',sigma,'theta', theta)` creates a `GeneralizedParetoDistribution` object using the parameter values specified for `k`, `sigma`, and `theta`.

  For additional syntax options, see `makedist`.
- Fit a `GeneralizedParetoDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'GeneralizedPareto')` creates a `GeneralizedParetoDistribution` object by fitting a generalized Pareto distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `GeneralizedParetoDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Generalized Pareto Distribution"

Using InverseGaussianDistribution Objects

Inverse Gaussian probability distribution object

An `InverseGaussianDistribution` object consists of parameters, a model description, and sample data for an inverse Gaussian probability distribution.

Also known as the Wald distribution, the inverse Gaussian is used to model nonnegative positively skewed data. Inverse Gaussian distributions have many similarities to standard Gaussian (normal) distributions, which lead to applications in inferential statistics.

The inverse Gaussian distribution uses the following parameters.

Parameter	Description	Support
`mu`	Scale parameter	$\mu > 0$
`lambda`	Shape parameter	$\lambda > 0$

Examples

Create an Inverse Gaussian Distribution Object Using Default Parameters

Create an inverse Gaussian distribution object using the default parameter values.

```
pd = makedist('InverseGaussian')
```

```
pd =

  InverseGaussianDistribution

  Inverse Gaussian distribution
        mu = 1
    lambda = 1
```

Create an Inverse Gaussian Distribution Object Using Specified Parameters

Create an inverse Gaussian distribution object by specifying parameter values.

```
pd = makedist('InverseGaussian','mu',2,'lambda',4)
```

```
pd =

  InverseGaussianDistribution

  Inverse Gaussian distribution
        mu = 2
    lambda = 4
```

Compute the standard deviation of the distribution.

```
s = std(pd)
```

```
s =

    1.4142
```

Properties

`mu` — Scale parameter
positive scalar value

Scale parameter for the inverse Gaussian distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`lambda` — Shape parameter
positive scalar value

Shape parameter for the inverse Gaussian distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create an `InverseGaussianDistribution` probability distribution object.

- Create an `InverseGaussianDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('InverseGaussian')` creates an `InverseGaussianDistribution` object using the default parameter values for the scale parameter (`mu = 1`) and the shape parameter (`lambda = 1`).

  `pd = makedist('InverseGaussian','mu',mu,'lambda',lambda)` creates an `InverseGaussianDistribution` object using the parameter values specified for `mu` and `lambda`.

  For additional syntax options, see `makedist`.

- Fit an `InverseGaussianDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'InverseGaussian')` creates an `InverseGaussianDistribution` object by fitting an inverse Gaussian distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit an `InverseGaussianDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Inverse Gaussian Distribution"

Using KernelDistribution Objects

Kernel probability distribution object

A `KernelDistribution` object consists of parameters, a model description, and sample data for a nonparametric kernel-smoothing distribution.

The kernel distribution is a nonparametric estimation of the probability density function (pdf) of a random variable.

The kernel distribution uses the following options.

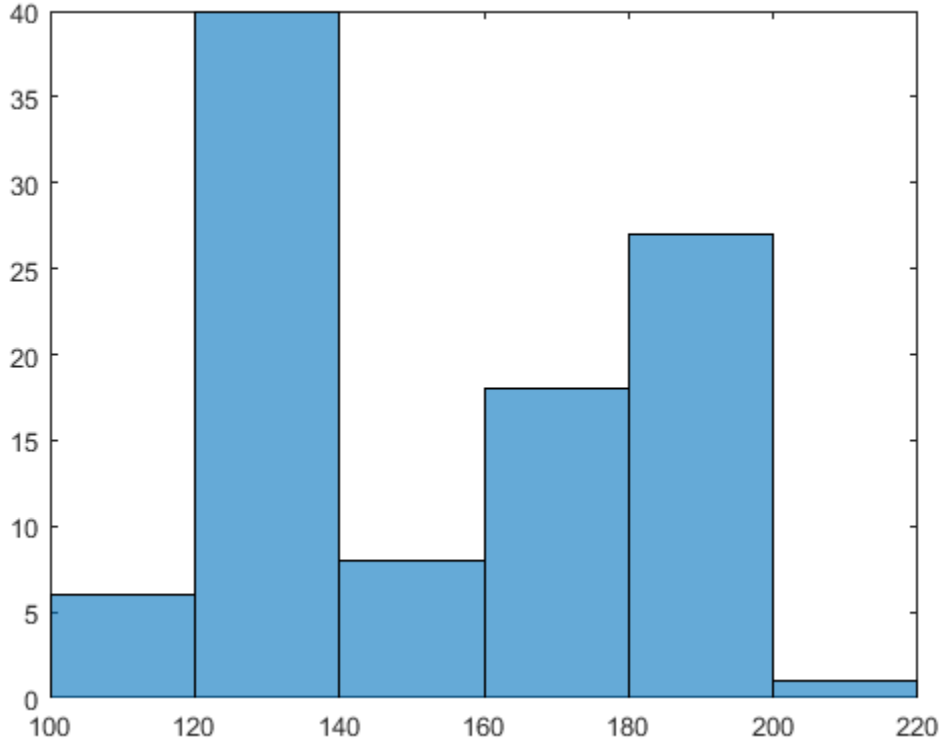
Option	Description	Possible Values
`Kernel`	Kernel function type	`normal`, `box`, `triangle`, `epanechnikov`
`BandWidth`	Kernel smoothing parameter	`BandWidth > 0`

Examples

Fit a Kernel Distribution Object to Data

Load the sample data. Visualize the patient weight data using a histogram.

```
load hospital;
histogram(hospital.Weight)
```



The histogram shows that the data has two modes, one for female patients and one for male patients.

Create a probability distribution object by fitting a kernel distribution to the patient weight data.

```
pd_kernel = fitdist(hospital.Weight,'Kernel')
```

```
pd_kernel =

  KernelDistribution

    Kernel = normal
    Bandwidth = 14.3792
```

```
    Support = unbounded
```

For comparison, create another probability distribution object by fitting a normal distribution to the patient weight data.

```
pd_normal = fitdist(hospital.Weight,'Normal')
```

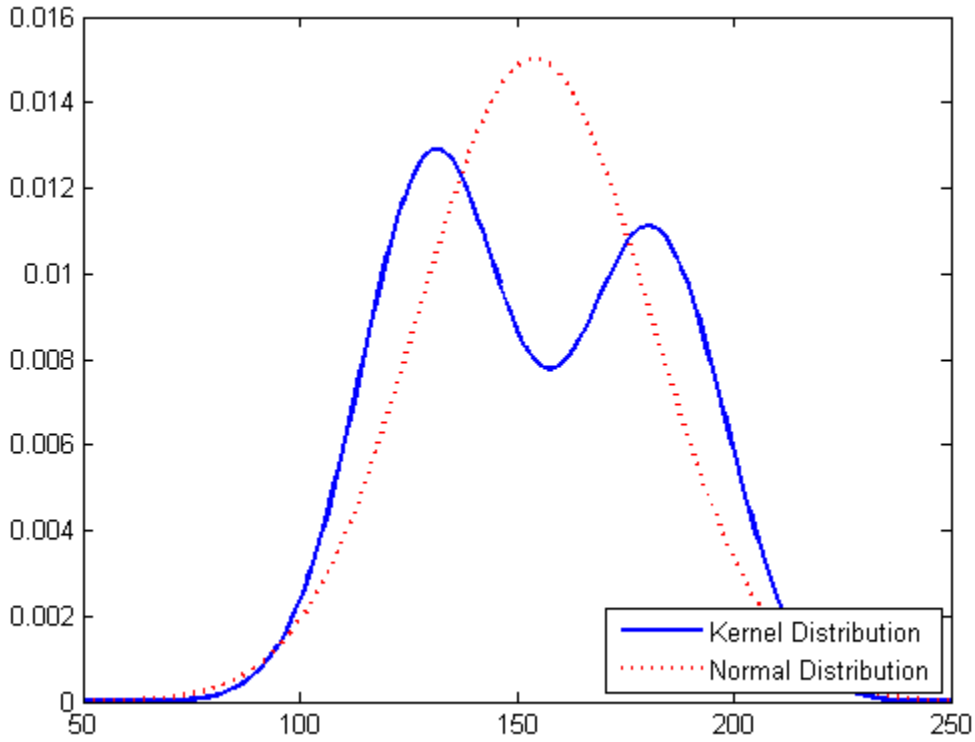
```
pd_normal =

  NormalDistribution

  Normal distribution
       mu =     154   [148.728, 159.272]
    sigma = 26.5714   [23.3299, 30.8674]
```

Define the x values and compute the pdf of each distribution.

```
x = 50:1:250;
pdf_kernel = pdf(pd_kernel,x);
pdf_normal = pdf(pd_normal,x);
```

Plot the pdf of each distribution.

```
plot(x,pdf_kernel,'Color','b','LineWidth',2);
hold on;
plot(x,pdf_normal,'Color','r','LineStyle',':','LineWidth',2);
legend('Kernel Distribution','Normal Distribution','Location','SouthEast');
hold off;
```



Fitting a kernel distribution instead of a unimodal distribution such as the normal reveals the separate modes for the female and male patients.

- “Fit Kernel Distribution Object to Data” on page 5-49
- “Fit Probability Distribution Objects to Grouped Data” on page 5-124
- “Compare Multiple Distribution Fits” on page 5-117

Properties

`Kernel` — Kernel smoother type

`'normal' | 'box' | 'triangle' | 'epanechnikov'`

Kernel function type, stored as a valid kernel function type name.

`BandWidth` — Bandwidth of kernel smoothing window

positive scalar value

Bandwidth of the kernel smoothing window, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `pdf` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `KernelDistribution` probability distribution object.

- Fit a `KernelDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Kernel')` creates a `KernelDistribution` object by fitting a kernel distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `KernelDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist`

More About

- “Working with Probability Distributions” on page 5-3
- “Nonparametric and Empirical Probability Distributions” on page 5-40
- “Kernel Distribution”

Using LogisticDistribution Objects

Logistic probability distribution object

A `LogisticDistribution` object consists of parameters, a model description, and sample data for a logistic probability distribution.

The logistic distribution is used for growth models and in logistic regression. It has longer tails and a higher kurtosis than the normal distribution.

The logistic distribution uses the following parameters.

Parameter	Description	Support
`mu`	Mean	$-\infty < \mu < \infty$
`sigma`	Scale parameter	$\sigma \geq 0$

Examples

Create a Logistic Distribution Object Using Default Parameters

Create a logistic distribution object using the default parameter values.

```
pd = makedist('Logistic')
```

```
pd =

  LogisticDistribution

  Logistic distribution
       mu = 0
    sigma = 1
```

Create a Logistic Distribution Object Using Specified Parameters

Create a logistic distribution object by specifying parameter values.

```
pd = makedist('Logistic', 'mu',2,'sigma',4)
```

```
pd =
```

```
  LogisticDistribution

  Logistic distribution
       mu = 2
    sigma = 4
```

Compute the standard deviation of the distribution.

```
s = std(pd)
```

```
s =

    7.2552
```

- "Compare Multiple Distribution Fits" on page 5-117

Properties

`mu` — Mean

scalar value

Mean of the logistic distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter

nonnegative scalar value

Scale parameter of the logistic distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `LogisticDistribution` probability distribution object.

- Create a `LogisticDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Logistic')` creates a `LogisticDistribution` object using the default parameter values for the mean (`mu = 0`) and the scale parameter (`sigma = 1`).

  `pd = makedist('Logistic','mu',mu,'sigma',sigma)` creates a `LogisticDistribution` object using the parameter values specified for `mu` and `sigma`.

  For additional syntax options, see `makedist`.
- Fit a `LogisticDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Logistic')` creates a `LogisticDistribution` object by fitting a logistic distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `LogisticDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Logistic Distribution"

Using LoglogisticDistribution Objects

Loglogistic probability distribution object

A `LoglogisticDistribution` object consists of parameters, a model description, and sample data for a loglogistic probability distribution.

The loglogistic distribution is closely related to the logistic distribution. If x is distributed loglogistically with parameters μ and σ, then $\log(x)$ is distributed logistically with mean and standard deviation. This distribution is often used in survival analysis to model events that experience an initial rate increase, followed by a rate decrease.

The loglogistic distribution uses the following parameters.

Parameter	Description	Support
`mu`	Log mean	$\mu > 0$
`sigma`	Log scale parameter	$\sigma > 0$

Examples

Create a Loglogistic Distribution Object Using Default Parameters

Create a loglogistic distribution object using the default parameter values.

```
pd = makedist('Loglogistic')
```

```
pd =

  LoglogisticDistribution

  Log-Logistic distribution
       mu = 0
    sigma = 1
```

Create a Loglogistic Distribution Object Using Specified Parameters

Create a loglogistic distribution object by specifying the parameter values.

```
pd = makedist('Loglogistic','mu',5,'sigma',2)

pd =

  LoglogisticDistribution

  Log-Logistic distribution
       mu = 5
    sigma = 2
```

Generate random numbers from the loglogistic distribution and compute their log values.

```
rng(19) % for reproducibility
x = random(pd,10000,1);
logx = log(x);
```

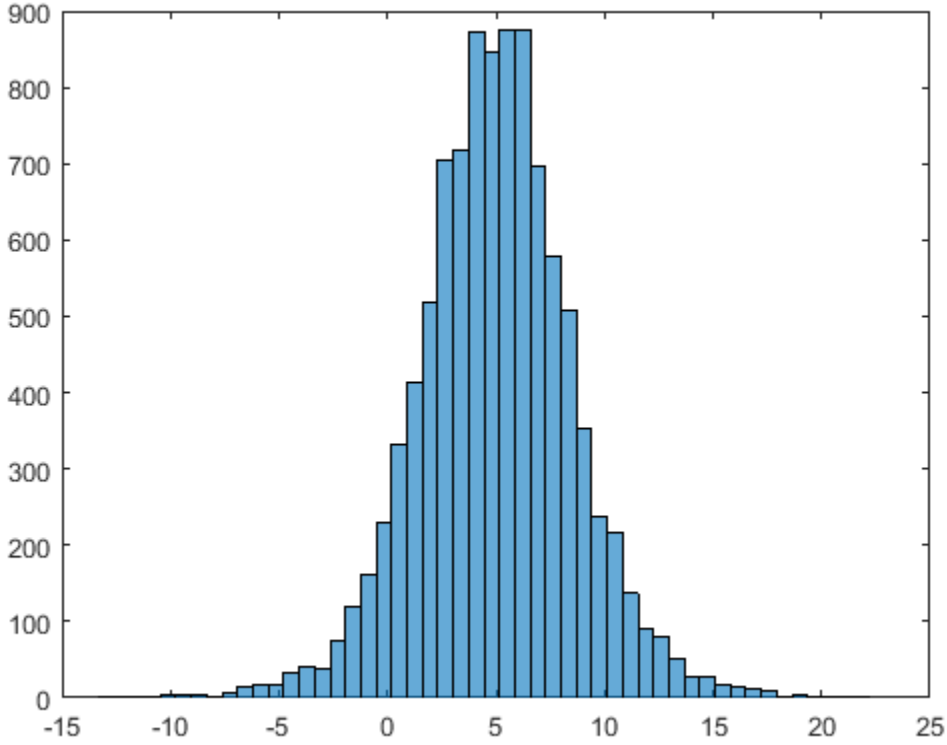
Compute the mean of the log values.

```
m = mean(logx)

m =

    4.9828
```

The mean of the log of `x` is equal to the `mu` parameter of `x`, since `x` has a loglogistic distribution.

Plot `logx`.

```
histogram(logx,50)
```



The plot shows that the log values of `x` have a logistic distribution.

Properties

`mu` — Log mean
positive scalar value

Log mean for the loglogistic distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`sigma` — Log scale parameter
positive scalar value

Log scale parameter for the loglogistic distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions
cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `LoglogisticDistribution` probability distribution object.

- Create a `LoglogisticDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Loglogistic')` creates a `LoglogisticDistribution` object using the default parameter values for the log mean (`mu = 0`) and the log scale parameter (`sigma = 1`).

  `pd = makedist('Loglogistic','mu',mu,'sigma',sigma)` creates a `LoglogisticDistribution` object using the parameter values specified for `mu` and `sigma`.

  For additional syntax options, see `makedist`.

- Fit a `LoglogisticDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Loglogistic')` creates a `LoglogisticDistribution` object by fitting a loglogistic distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit a `LoglogisticDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Working with Probability Distributions" on page 5-3
- "Loglogistic Distribution"

Using LognormalDistribution Objects

Lognormal probability distribution object

A `LognormalDistribution` object consists of parameters, a model description, and sample data for a lognormal probability distribution.

The lognormal distribution is a probability distribution whose logarithm has a normal distribution. It is sometimes called the Galton distribution. The lognormal distribution is applicable when the quantity of interest must be positive, since log(x) exists only when x is positive.

The lognormal distribution uses the following parameters.

Parameter	Description	Support
`mu`	Log mean	$-\infty < \mu < \infty$
`sigma`	Log standard deviation	$\sigma \geq 0$

Examples

Create a Lognormal Distribution Object Using Default Parameters

Create a lognormal distribution object using the default parameter values.

```
pd = makedist('Lognormal')
```

```
pd =

  LognormalDistribution

  Lognormal distribution
       mu = 0
    sigma = 1
```

Create a Lognormal Distribution Object Using Specified Parameters

Create a lognormal distribution object by specifying the parameter values.

```
pd = makedist('Lognormal','mu',5,'sigma',2)

pd =

  LognormalDistribution

  Lognormal distribution
       mu = 5
    sigma = 2
```

Compute the mean of the lognormal distribution.

```
mean(pd)

ans =

   1.0966e+03
```

The mean of the lognormal distribution is not equal to the `mu` parameter.

Generate random numbers from the lognormal distribution and compute their log values.

```
rng(47);  % for reproducibility
x = random(pd,10000,1);
logx = log(x);
```

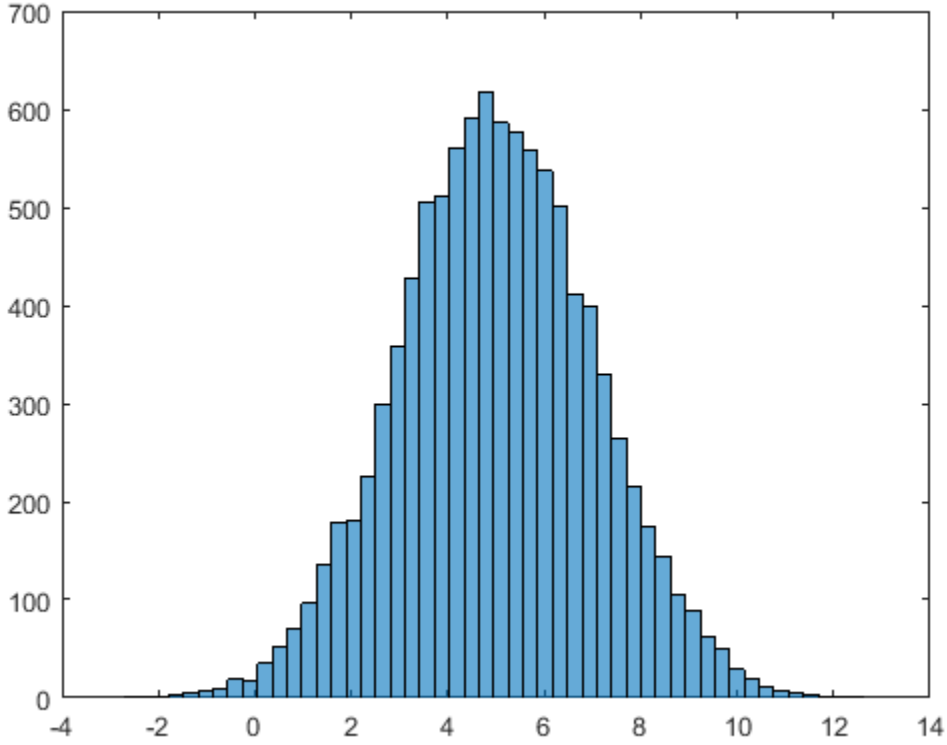
Compute the mean of the log values.

```
m = mean(logx)

m =

    4.9999
```

The mean of the log of `x` is equal to the `mu` parameter of `x`, since `x` has a lognormal distribution.

Plot `logx`.

```
histogram(logx,50)
```



The plot shows that the log values of `x` are normally distributed with a mean equal to 5 and a standard deviation equal to 2.

Properties

`mu` — Log mean
scalar value

Log mean for the lognormal distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Log standard deviation

nonnegative scalar value

Log standard deviation for the lognormal distribution, stored as a nonnegative scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates
matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions
cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single` | `double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `LognormalDistribution` probability distribution object.

- Create a `LognormalDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Lognormal')` creates a `LognormalDistribution` object using the default parameter values for the log mean (`mu = 0`) and the log standard deviation (`sigma = 1`).

  `pd = makedist('Lognormal','mu',mu,'sigma',sigma)` creates a `LognormalDistribution` object using the parameter values specified for `mu` and `sigma`.

  For additional syntax options, see `makedist`.
- Fit a `LognormalDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Lognormal')` creates a `LognormalDistribution` object by fitting a lognormal distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `LognormalDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Working with Probability Distributions" on page 5-3
- "Lognormal Distribution"
- "Supported Distributions" on page 5-17

Using MultinomialDistribution Objects

Multinomial probability distribution object

A `MultinomialDistribution` object consists of parameters and a model description for a multinomial probability distribution.

The multinomial distribution is a generalization of the binomial distribution. While the binomial distribution gives the probability of the number of "successes" in n independent trials of a two-outcome process, the multinomial distribution gives the probability of each combination of outcomes in n independent trials of a k-outcome process. The probability of each outcome in any one trial is given by the fixed probabilities p_1, ..., p_k.

The multinomial distribution uses the following parameters.

Parameter	Description	Support
`probabilities`	Outcome probabilities	$0 \le probabilities(i) \le 1$; $\sum_{all(i)} probabilities(i) = 1$

Examples

Create a Multinomial Distribution Object Using Default Parameters

Create a multinomial distribution object using the default parameter values.

```
pd = makedist('Multinomial')
```

```
pd =

  MultinomialDistribution

  Probabilities:
    0.5000    0.5000
```

Create a Multinomial Distribution Object Using Specified Parameters

Create a multinomial distribution object for a distribution with three possible outcomes. Outcome 1 has a probability of 1/2, outcome 2 has a probability of 1/3, and outcome 3 has a probability of 1/6.

```
pd = makedist('Multinomial','probabilities',[1/2 1/3 1/6])
```

```
pd =

  MultinomialDistribution

  Probabilities:
    0.5000    0.3333    0.1667
```

Generate a random outcome from the distribution.

```
rng('default');  % for reproducibility
r = random(pd)

r =

     2
```

The result of this trial is outcome 2. By default, the number of trials in each experiment, n, equals 1.

Generate random outcomes from the distribution when the number of trials in each experiment, n, equals 1, and the experiment is repeated ten times.

```
rng('default');  % for reproducibility
r = random(pd,10,1)

r =

     2
     3
     1
     3
     2
     1
     1
     2
     3
     3
```

Each element in the array is the outcome of an individual experiment that contains one trial.

Generate random outcomes from the distribution when the number of trials in each experiment, n, equals 5, and the experiment is repeated ten times.

```
rng('default');  % for reproducibility
```

```
r = random(pd,10,5)

r =

     2     1     2     2     1
     3     3     1     1     1
     1     3     3     1     2
     3     1     3     1     2
     2     2     2     1     1
     1     1     2     2     1
     1     1     2     2     1
     2     3     1     1     2
     3     2     2     3     2
     3     3     1     1     2
```

Each element in the resulting matrix is the outcome of one trial. The columns correspond to the five trials in each experiment, and the rows correspond to the ten experiments. For example, in the first experiment (corresponding to the first row), 2 of the 5 trials resulted in outcome 1, and 3 of the 5 trials resulted in outcome 2.

- "Multinomial Probability Distribution Objects" on page 5-128
- "Multinomial Probability Distribution Functions" on page 5-132

Properties

`probabilities` — outcome probabilities

vector of scalar values in the range `[0,1]`

Outcome probabilities for the multinomial distribution, stored as a vector of scalar values in the range `[0,1]`. The values in `probabilities` must sum to 1.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `pdf` `random` `std` `truncate` `var`

Create Object

Create a `MultinomialDistribution` object with specified parameter values using `makedist`.

`pd = makedist('Multinomial')` creates a `MultinomialDistribution` object using the default parameter values for the probabilities (`probabilities = [0.500,0.500]`).

`pd = makedist('Multinomial','Probabilities',probabilities)` creates a `MultinomialDistribution` object using the parameter values specified for `probabilities`.

For additional syntax options, see `makedist`.

See Also

`makedist`

More About

- "Multinomial Distribution"

Using NakagamiDistribution Objects

Nakagami probability distribution object

A `NakagamiDistribution` object consists of parameters, a model description, and sample data for a Nakagami probability distribution.

The Nakagami distribution is commonly used in communication theory to model scattered signals that reach a receiver using multiple paths.

The Nakagami distribution uses the following parameters.

Parameter	Description	Support
`mu`	Shape parameter	$\mu > 0$
`omega`	Scale parameter	$\omega > 0$

Examples

Create a Nakagami Distribution Object Using Default Parameters

Create a Nakagami distribution object using the default parameter values.

```
pd = makedist('Nakagami')
```

```
pd =

  NakagamiDistribution

  Nakagami distribution
       mu = 1
    omega = 1
```

Create a Nakagami Distribution Object Using Specified Parameters

Create a Nakagami distribution object by specifying parameter values.

```
pd = makedist('Nakagami','mu',5,'omega',2)
```

```
pd =
```

```
  NakagamiDistribution

  Nakagami distribution
       mu = 5
    omega = 2
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    1.3794
```

Properties

`mu` — Shape parameter
positive scalar value

Shape parameter for the Nakagami distribution, stored as a positive scalar value.

Data Types: `single | double`

`omega` — Scale parameter
positive scalar value

Scale parameter for the Nakagami distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single` | `double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `NakagamiDistribution` probability distribution object.

- Create a `NakagamiDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Nakagami')` creates a `NakagamiDistribution` object using the default parameter values for the shape parameter (`mu = 1`) and the scale parameter (`omega = 1`).

  `pd = makedist('Nakagami','mu',mu,'omega',omega)` creates a `NakagamiDistribution` object using the parameter values specified for `mu` and `omega`.

  For additional syntax options, see `makedist`.
- Fit a `NakagamiDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Nakagami')` creates a `NakagamiDistribution` object by fitting a Nakagami distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `NakagamiDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Nakagami Distribution"

Using NegativeBinomialDistribution Objects

Negative binomial distribution object

A `NegativeBinomialDistribution` object consists of parameters, a model description, and sample data for a negative binomial probability distribution.

The negative binomial distribution models the number of failures x before a specified number of successes, R, is reached in a series of independent, identical trials. This distribution can also model count data, in which case R does not need to be an integer value.

The negative binomial distribution uses the following parameters.

Parameter	Description	Support
R	Number of successes	$r > 0$
p	Probability of success	$0 < p \le 1$

Examples

Create a Negative Binomial Distribution Object Using Default Parameters

Create a negative binomial distribution object using the default parameter values.

```
pd = makedist('NegativeBinomial')
```

```
pd =

  NegativeBinomialDistribution

  Negative Binomial distribution
    R =   1
    P = 0.5
```

Create a Negative Binomial Distribution Object Using Specified Parameters

Create a negative binomial distribution object by specifying the parameter values.

```
pd = makedist('NegativeBinomial','R',5,'p',.1)
```

```
pd =

  NegativeBinomialDistribution

  Negative Binomial distribution
    R =   5
    P = 0.1
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    45
```

Properties

`R` — Number of successes

positive scalar value

Number of successes for the negative binomial distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`p` — Probability of success

positive scalar value in the range (0,1]

Probability of success of any individual trial for the negative binomial distribution, specified as a positive scalar value in the range (0,1].

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `NegativeBinomialDistribution` probability distribution object.

- Create a `NegativeBinomialDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('NegativeBinomial')` creates a `NegativeBinomialDistribution` object using the default parameter values for the number of successes (`R = 1`) and the probability of success (`p = 0.5`).

  `pd = makedist('NegativeBinomial','R',R,'p',p)` creates a `NegativeBinomialDistribution` object using the parameter values specified for `R` and `p`.

  For additional syntax options, see `makedist`.

- Fit a `NegativeBinomialDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'NegativeBinomial')` creates a `NegativeBinomialDistribution` object by fitting a negative binomial distribution to the data contained in the column vector, `x`.

- Interactively fit a `NegativeBinomialDistribution` object to data using the Distribution Fitting app, `dfittool`.

  For additional syntax options, see `fitdist`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Negative Binomial Distribution"

Using NormalDistribution Objects

Normal probability distribution object

A `NormalDistribution` object consists of parameters, a model description, and sample data for a normal probability distribution.

The normal distribution, sometimes called the Gaussian distribution, is a two-parameter family of curves. The usual justification for using the normal distribution for modeling is the Central Limit theorem, which states (roughly) that the sum of independent samples from any distribution with finite mean and variance converges to the normal distribution as the sample size goes to infinity.

The normal distribution uses the following parameters.

Parameter	Description	Support
`mu`	Mean	$-\infty < \mu < \infty$
`sigma`	Standard deviation	$\sigma \geq 0$

Examples

Create a Normal Distribution Object Using Default Parameters

Create a normal distribution object using the default parameter values.

```
pd = makedist('Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 0
    sigma = 1
```

Create a Normal Distribution Object Using Specified Parameters

Create a normal distribution object by specifying the parameter values.

```
pd = makedist('Normal','mu',75,'sigma',10)

pd =

  NormalDistribution

  Normal distribution
       mu = 75
    sigma = 10
```

Compute the interquartile range of the distribution.

```
r = iqr(pd)

r =

   13.4898
```

Fit a Normal Distribution Object

Load the sample data. Create a vector containing the first column of students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Create a normal distribution object by fitting it to the data.

```
pd = fitdist(x,'Normal')

pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

- "Compare Multiple Distribution Fits" on page 5-117

Properties

`mu` — Mean

scalar value

Mean of the normal distribution, stored as a scalar value.

Data Types: `single | double`

`sigma` — Standard deviation

nonnegative scalar value

Standard deviation of the normal distribution, stored as a nonnegative scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates
matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions
cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `NormalDistribution` probability distribution object.

- Create a `NormalDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Normal')` creates a `NormalDistribution` object using the default parameter values for the mean (`mu = 0`) and the standard deviation (`sigma = 1`).

  `pd = makedist('Normal','mu',mu,'sigma',sigma)` creates a `NormalDistribution` object using the parameter values specified for `mu` and `sigma`.

  For additional syntax options, see `makedist`.
- Fit a `NormalDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Normal')` creates a `NormalDistribution` object by fitting a normal distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `NormalDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Normal Distribution"

Using PiecewiseLinearDistribution Objects

Piecewise linear probability distribution object

A `PiecewiseLinearDistribution` object consists of a model description for a piecewise linear probability distribution.

The piecewise linear distribution is a nonparametric probability distribution created using a piecewise linear representation of the cumulative distribution function (cdf). The options specified for the piecewise linear distribution specify the form of the cdf. The probability density function (pdf) is a step function.

The piecewise linear distribution uses the following parameters.

Parameter	Description
`x`	Vector of x values at which the cdf changes slope
`Fx`	Vector of cdf values that correspond to each value in `x`

Examples

Create a Piecewise Linear Distribution Object Using Default Parameters

Create a piecewise linear distribution object using the default parameter values.

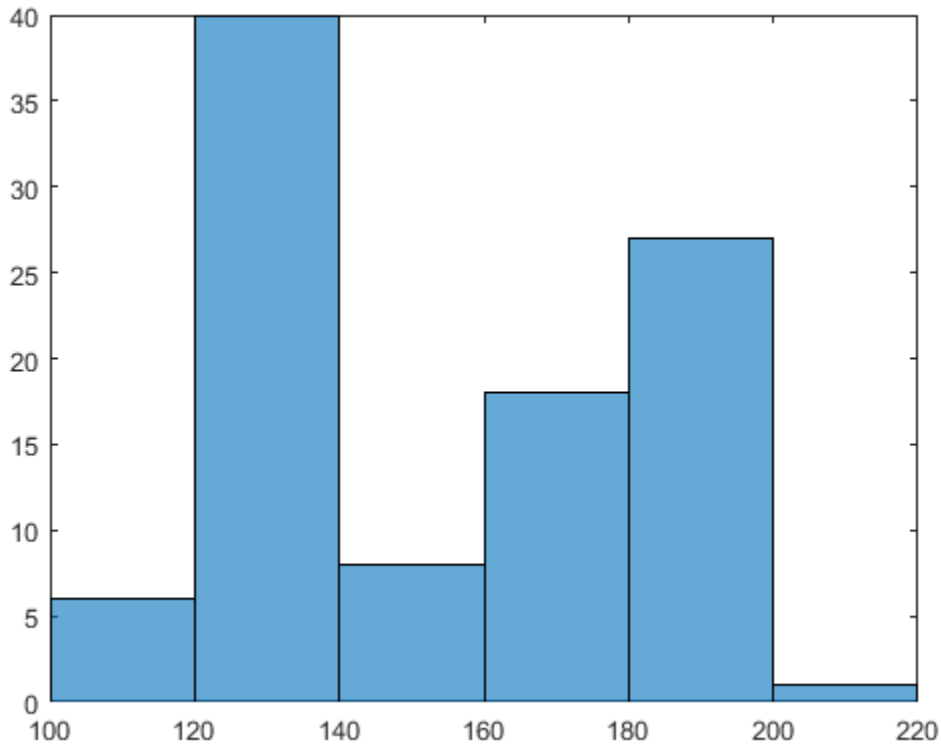
```
pd = makedist('PiecewiseLinear')
```

```
pd =

  PiecewiseLinearDistribution

F(0) = 0
F(1) = 1
```

Create a Piecewise Linear Distribution Object Using Specified Parameters

Load the sample data. Visualize the patient weight data using a histogram.

```
load hospital
histogram(hospital.Weight)
```



The histogram shows that the data has two modes, one for female patients and one for male patients.

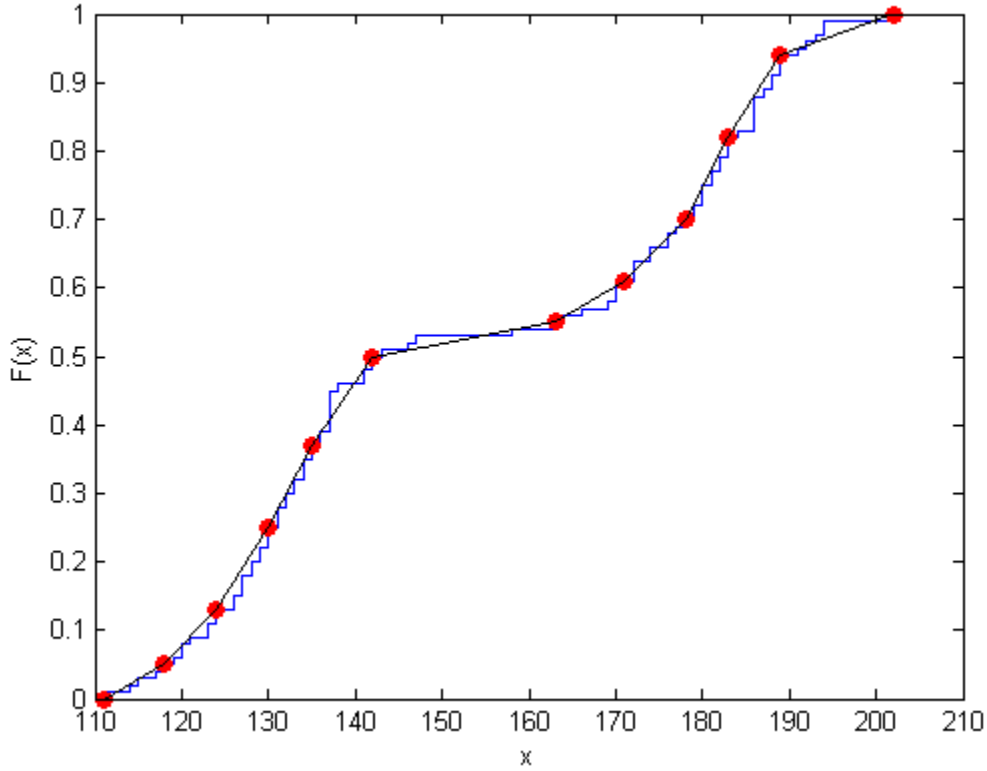
Compute the empirical cumulative distribution function (ecdf) for the data.

```
[f,x] = ecdf(hospital.Weight);
```

Construct a piecewise linear approximation to the ecdf and plot both functions.

```
f = f(1:5:end); % keep a less dense grid of points
```

```
x = x(1:5:end);

figure;
ecdf(hospital.Weight)
hold on
plot(x,f,'ro','MarkerFace','r') % overlay grid
plot(x,f,'k') % show interpolation
```



Create a piecewise linear probability distribution object using the piecewise approximation of the ecdf.

```
pd = makedist('PiecewiseLinear','x',x,'Fx',f)
```

```
pd =
```

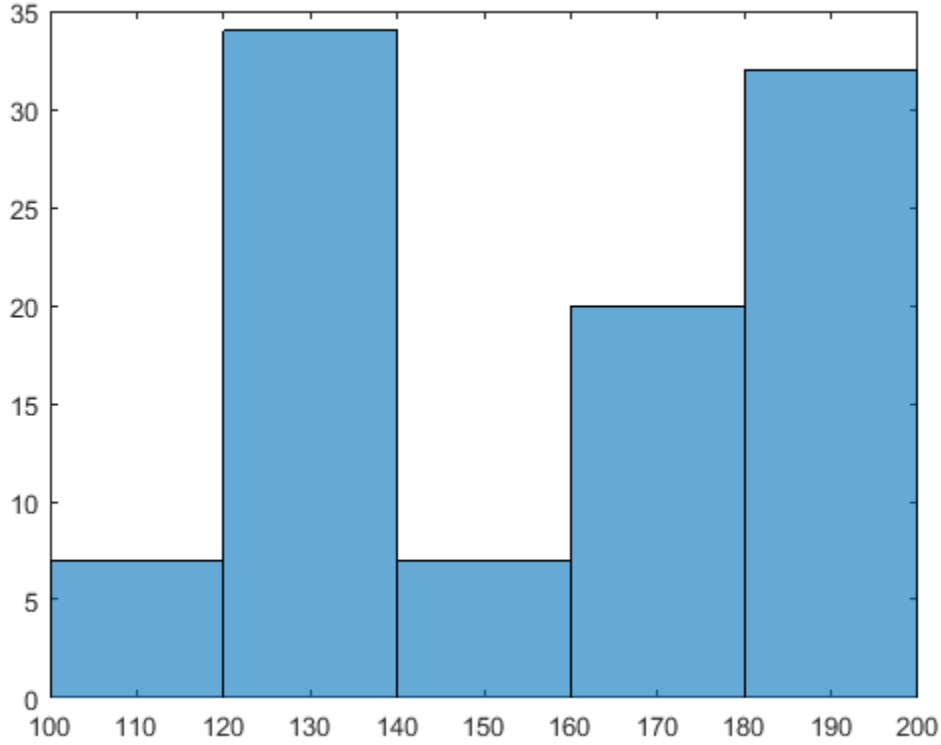
```
  PiecewiseLinearDistribution

F(111) = 0
F(118) = 0.05
F(124) = 0.13
F(130) = 0.25
F(135) = 0.37
F(142) = 0.5
F(163) = 0.55
F(171) = 0.61
F(178) = 0.7
F(183) = 0.82
F(189) = 0.94
F(202) = 1
```

Generate 100 random numbers from the distribution.

```
rw = random(pd,100,1);
```

Plot the random numbers to visually compare their distribution to the original data.

```
figure;
histogram(rw)
```



The random numbers generated from the piecewise linear distribution have the same bimodal distribution as the original data.

- "Fit a Nonparametric Distribution with Pareto Tails" on page 5-61

Properties

x — Data values

vector of scalar values

Data values at which the cumulative distribution function (cdf) changes slope, stored as a vector of scalar values.

Data Types: `single | double`

`Fx` — cdf value

vector of scalar values

cdf value at each value in `x`, stored as a vector of scalar values.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `pdf` `random` `std` `truncate` `var`

Create Object

Create a `PiecewiseLinearDistribution` object with specified parameter values using `makedist`.

`pd = makedist('PiecewiseLinear')` creates a `PiecewiseLinearDistribution` object using the default parameter values for the data values (`x = 1`) and the cdf values (`Fx = 1`).

`pd = makedist('PiecewiseLinear','x',x,'Fx',Fx)` creates a `PiecewiseLinearDistribution` object using the parameter values specified for `x` and `Fx`.

For additional syntax options, see `makedist`.

See Also

`makedist`

More About

- "Working with Probability Distributions" on page 5-3
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Piecewise Linear Distribution"

Using PoissonDistribution Objects

Poisson probability distribution object

A `PoissonDistribution` object consists of parameters, a model description, and sample data for a Poisson probability distribution.

The Poisson distribution is appropriate for applications that involve counting the number of times a random event occurs in a given amount of time, distance, area, etc. If the number of counts follows the Poisson distribution, then the interval between individual counts follows the exponential distribution.

The Poisson distribution uses the following parameters.

Parameter	Description	Support
`lambda`	Mean	$\lambda \geq 0$

Examples

Create a Poisson Distribution Object Using Default Parameters

Create a Poisson distribution object using the default parameter values.

```
pd = makedist('Poisson')
```

```
pd =

  PoissonDistribution

  Poisson distribution
    lambda = 1
```

Create a Poisson Distribution Object Using Specified Parameters

Create a Poisson distribution object by specifying the parameter values.

```
pd = makedist('Poisson','lambda',5)
```

```
pd =

  PoissonDistribution
```

```
  Poisson distribution
    lambda = 5
```

Compute the variance of the distribution.

```
v = var(pd)
```

```
v =

     5
```

For the Poisson distribution, both the mean and variance are equal to the parameter lambda.

Properties

`lambda` — Mean

nonnegative scalar value

Mean of the Poisson distribution, stored as a nonnegative scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the

corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `PoissonDistribution` probability distribution object.

- Create a `PoissonDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Poisson')` creates a `PoissonDistribution` object using the default parameter value for the mean (`lambda = 1`).

`pd = makedist('Poisson','lambda',lambda)` creates a `PoissonDistribution` object using the parameter value specified for `lambda`.

For additional syntax options, see `makedist`.

- Fit a `PoissonDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Poisson')` creates a `PoissonDistribution` object by fitting a Poisson distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit a `PoissonDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Poisson Distribution"

Using RayleighDistribution Objects

Rayleigh probability distribution object

A `RayleighDistribution` object consists of parameters, a model description, and sample data for a normal probability distribution.

The Rayleigh distribution is a special case of the Weibull distribution. It is often used in communication theory to model scattered signals that reach a receiver by multiple paths.

The Rayleigh distribution uses the following parameter.

Parameter	Description	Support
b	Defining parameter	$b > 0$

Examples

Create a Rayleigh Distribution Object Using Default Parameters

Create a Rayleigh distribution object using the default parameter values.

```
pd = makedist('Rayleigh')
```

```
pd =

  RayleighDistribution

  Rayleigh distribution
    B = 1
```

Create a Rayleigh Distribution Object Using Specified Parameters

Create a Rayleigh distribution object by specifying the parameter values.

```
pd = makedist('Rayleigh','b',3)
```

```
pd =

  RayleighDistribution
```

```
  Rayleigh distribution
    B = 3
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    3.7599
```

Properties

b — Defining parameter

positive scalar value

Defining parameter for the Rayleigh distribution, stored as a positive scalar value.

Data Types: `single | double`

DistributionName — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

InputData — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `RayleighDistribution` probability distribution object.

- Create a `RayleighDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Rayleigh')` creates a `RayleighDistribution` object using the default parameter value for defining parameter (`b = 1`).

  `pd = makedist('Rayleigh','b',b)` creates a `RayleighDistribution` object using the parameter value specified for `b`.

For additional syntax options, see `makedist`.

- Fit a `RayleighDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Rayleigh')` creates a `RayleighDistribution` object by fitting a Rayleigh distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit a `RayleighDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Rayleigh Distribution"

Using RicianDistribution Objects

Rician probability distribution object

A `RicianDistribution` object consists of parameters, a model description, and sample data for a Rician probability distribution.

The Rician distribution is used in communications theory to model scattered signals that reach a receiver using multiple paths.

The Rician distribution uses the following parameters.

Name	Description	Support
`s`	Noncentrality parameter	$s \geq 0$
`sigma`	Scale parameter	$\sigma > 0$

Examples

Create a Rician Distribution Object Using Default Parameters

Create a Rician distribution object using the default parameter values.

```
pd = makedist('Rician')
```

```
pd =

  RicianDistribution

  Rician distribution
        s = 1
    sigma = 1
```

Create a Rician Distribution Object Using Specified Parameters

Create a Rician distribution object by specifying the parameter values.

```
pd = makedist('Rician','s',0,'sigma',2)
```

```
pd =
```

```
  RicianDistribution

  Rician distribution
        s = 0
    sigma = 2
```

Compute the mean of the distribution.

```
m = mean(pd)

m =

    2.5066
```

Properties

s — Noncentrality parameter
nonnegative scalar value

Noncentrality parameter of the Rician distribution, stored as a nonnegative scalar value.

Data Types: `single | double`

sigma — scale parameter
positive scalar value

Scale parameter for the Rician distribution, stored as a positive scalar value.

Data Types: `single | double`

DistributionName — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

InputData — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single` | `double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `RicianDistribution` probability distribution object.

- Create a `RicianDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Rician')` creates a `RicianDistribution` object using the default parameter values for the noncentrality parameter (`s = 1`) and the scale parameter (`sigma = 1`).

  `pd = makedist('Binomial','s',s,'sigma',sigma)` creates a `RicianDistribution` object using the parameter values specified for `s` and `sigma`.

  For additional syntax options, see `makedist`.
- Fit a `RicianDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Rician')` creates a `RicianDistribution` object by fitting a Rician distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `RicianDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Rician Distribution"

Using tLocationScaleDistribution Objects

t Location-Scale probability distribution object

A `tLocationScaleDistribution` object consists of parameters, a model description, and sample data for a *t* location-scale probability distribution.

The *t* location-scale distribution is useful for modeling data distributions with heavier tails (more prone to outliers) than the normal distribution. It approaches the normal distribution as ν approaches infinity, and smaller values of ν yield heavier tails.

The *t* location-scale distribution uses the following parameters.

Parameter	Description	Support
`mu`	Location parameter	$-\infty < \mu < \infty$
`sigma`	Scale parameter	$\sigma > 0$
`nu`	Shape parameter	$\nu > 0$

Examples

Create a *t* Location-Scale Distribution Object Using Default Parameters

Create a *t* location scale distribution object using the default parameter values.

```
pd = makedist('tLocationScale')
```

```
pd =

  tLocationScaleDistribution

  t Location-Scale distribution
       mu = 0
    sigma = 1
       nu = 5
```

Create a *t* Location-Scale Distribution Object Using Specified Parameters

Create a *t* location-scale distribution object by specifying the parameter values.

```
pd = makedist('tLocationScale','mu',-2,'sigma',1,'nu',20)

pd =

  tLocationScaleDistribution

  t Location-Scale distribution
       mu = -2
    sigma =  1
       nu = 20
```

Compute the interquartile range of the distribution.

```
r = iqr(pd)

r =

    1.3739
```

- “Represent Cauchy Distribution Using *t* Location-Scale” on page 5-138

Properties

`mu` — Location parameter
scalar value

Location parameter of the *t* location-scale distribution, stored as a scalar value.

Data Types: `single` | `double`

`sigma` — Scale parameter
positive scalar value

Scale parameter of the *t* location-scale distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`nu` — Degrees of freedom
positive scalar value

Degrees of freedom of the *t* location-scale distribution, stored as a positive scalar value.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the

estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Object Functions

`cdf` `icdf` `fiqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `tLocationScaleDistribution` probability distribution object.

- Create a `tLocationScaleDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('tLocationScale')` creates a `tLocationScaleDistribution` object using the default parameter values for the location parameter (`mu = 0`), the scale parameter (`sigma = 1`), and the degrees of freedom (`nu = 5`).

  `pd = makedist('tLocationScale','mu',mu,'sigma',sigma,'nu',nu)` creates a `tLocationScaleDistribution` object using the parameter values specified for `mu`, `sigma`, and `nu`.

  For additional syntax options, see `makedist`.
- Fit a `tLocationScaleDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'tLocationScale')` creates a `tLocationScaleDistribution` object by fitting a *t* location-scale distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.
- Interactively fit a `tLocationScaleDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "t Location-Scale Distribution"

Using TriangularDistribution Objects

Triangular probability distribution object

A `TriangularDistribution` object consists of parameters and a model description for a triangular probability distribution.

The triangular distribution is frequently used in simulations when limited sample data is available. The lower and upper limits represent the smallest and largest values, and the location of the peak represents an estimate of the mode.

The triangular distribution uses the following parameters.

Parameter	Description	Support
a	Lower limit	$a \le b$
b	Peak location	$a \le b \le c$
c	Upper limit	$c \ge b$

Examples

Create a Triangular Distribution Object Using Default Parameters

Create a triangular distribution object using the default parameter values.

```
pd = makedist('Triangular')
```

```
pd =

  TriangularDistribution

A = 0, B = 0.5, C = 1
```

Create a Triangular Distribution Object Using Specified Parameters

Create a triangular distribution object by specifying parameter values.

```
pd = makedist('Triangular', 'a',-2,'b',1,'c',5)
```

```
pd =
```

```
  TriangularDistribution

A = -2, B = 1, C = 5
```

Compute the mean of the distribution.

```
m = mean(pd)

m =

    1.3333
```

- "Generate Random Numbers Using the Triangular Distribution" on page 5-66

Properties

a — Lower limit

scalar value

Lower limit for the triangular distribution, stored as a scalar value.

Data Types: `single` | `double`

b — Peak location

scalar value

Location of the peak for the triangular distribution, stored as a scalar value greater than or equal to `a`.

Data Types: `single` | `double`

c — Upper limit

scalar value

Upper limit for the triangular distribution, stored as a scalar value greater than or equal to `b`.

Data Types: `single` | `double`

DistributionName — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `pdf` `random` `std` `truncate` `var`

Create Object

Create a `TriangularDistribution` object with specified parameter values using `makedist`.

`pd = makedist('Triangular')` creates a `TriangularDistribution` object using the default parameter values for the lower limit (`a = 0`), the peak location (`b = 0.5`), and the upper limit (`c = 1`).

`pd = makedist('Triangular','a',a,'b',b,'c',c)` creates a `TriangularDistribution` object using the parameter values specified for `a`, `b`, and `c`.

For additional syntax options, see `makedist`.

See Also

`makedist`

More About

- “Triangular Distribution” on page B-157

Using UniformDistribution Objects

Uniform probability distribution object

A `UniformDistribution` object consists of parameters and a model description for a uniform probability distribution.

The uniform distribution has a constant probability density function between its two parameters, lower (the minimum) and upper (the maximum). This distribution is appropriate for representing round-off errors in values tabulated to a particular number of decimal places.

The uniform distribution uses the following parameters.

Parameter	Description	Support
`lower`	Lower parameter	$-\infty < lower < upper$
`upper`	Upper parameter	$lower < upper < \infty$

Examples

Create a Uniform Distribution Object Using Default Parameters

Create a uniform distribution object using the default parameter values.

```
pd = makedist('Uniform')
```

```
pd =

  UniformDistribution

  Uniform distribution
    Lower = 0
    Upper = 1
```

Create a Uniform Distribution Object Using Specified Parameters

Create a uniform distribution object by specifying parameter values.

```
pd = makedist('Uniform','Lower',-4,'Upper',2)

pd =

  UniformDistribution

  Uniform distribution
    Lower = -4
    Upper =  2
```

Compute the interquartile range of the distribution

```
r = iqr(pd)

r =

     3
```

- "Generate Random Numbers Using Uniform Distribution Inversion" on page 5-135

Properties

`lower` — Lower parameter

scalar value

Lower parameter for the uniform distribution, stored as a scalar value.

Data Types: `single` | `double`

`upper` — Upper parameter

scalar value

Upper parameter for the uniform distribution, stored as a scalar value greater than `lower`.

Data Types: `single` | `double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`IsTruncated` — Logical flag for truncated distribution

`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `pdf` `random` `std` `truncate` `var`

Create Object

Create a `UniformDistribution` object with specified parameter values using `makedist`.

`pd = makedist('Uniform')` creates a `UniformDistribution` object using the default parameter values for the lower parameter (`lower = 0`) and the upper parameter (`upper = 1`).

`pd = makedist('Uniform','lower',lower,'upper',upper)` creates a `UniformDistribution` object using the parameter values specified for `lower` and `upper`.

For additional syntax options, see `makedist`.

See Also

`makedist`

More About

- "Uniform Distribution (Continuous)"

Using WeibullDistribution Objects

Weibull probability distribution object

A `WeibullDistribution` object consists of parameters, a model description, and sample data for a Weibull probability distribution.

The Weibull distribution is used in reliability and lifetime modeling, and to model the breaking strength of materials.

The Weibull distribution uses the following parameters.

Parameter	Description	Support
a	Scale parameter	$a > 0$
b	Shape parameter	$b > 0$

Examples

Create a Weibull Distribution Object Using Default Parameters

Create a Weibull distribution object using the default parameter values.

```
pd = makedist('Weibull')
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 1
    B = 1
```

Create a Weibull Distribution Object Using Specified Parameter Values

Create a Weibull distribution object by specifying the parameter values.

```
pd = makedist('Weibull','a',2,'b',5)
```

```
pd =

  WeibullDistribution
```

```
  Weibull distribution
    A = 2
    B = 5
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    1.8363
```

- "Fit Probability Distribution Objects to Grouped Data" on page 5-124
- "Compare Multiple Distribution Fits" on page 5-117

Properties

a — Scale parameter

positive scalar value

Scale parameter of the Weibull distribution, stored as a positive scalar value.

Data Types: `single | double`

b — Shape parameter

positive scalar value

Shape parameter of the Weibull distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name

probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting

structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution

`0` | `1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single` | `double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single` | `double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters
array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Object Functions

`cdf` `icdf` `iqr` `mean` `median` `negloglik` `paramci` `pdf` `proflik` `random` `std` `truncate` `var`

Create Object

Statistics and Machine Learning Toolbox provides several ways to create a `WeibullDistribution` probability distribution object.

- Create a `WeibulllDistribution` object with specified parameter values using `makedist`.

  `pd = makedist('Weibull')` creates a `WeibullDistribution` object using the default parameter values for the scale parameter (`a = 1`) and the shape parameter (`b = 1`).

  `pd = makedist('Weibull','a',a,'b',b)` creates a `WeibullDistribution` object using the parameter values specified for `a` and `b`.

  For additional syntax options, see `makedist`.

- Fit a `WeibullDistribution` object to data using `fitdist`.

  `pd = fitdist(x,'Weibull')` creates a `WeibullDistribution` object by fitting a Weibull distribution to the data contained in the column vector, `x`.

  For additional syntax options, see `fitdist`.

- Interactively fit a `WeibullDistribution` object to data using the Distribution Fitting app, `dfittool`.

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Weibull Distribution"

prob.UniformDistribution class

Package: prob
Superclasses: prob.ParametricTruncatableDistribution

Uniform probability distribution object

Description

`prob.UniformDistribution` is an object consisting of parameters and a model description for a uniform probability distribution. Create a probability distribution object with specified parameters using `makedist`.

Construction

`pd = makedist('Uniform')` creates a uniform probability distribution object using the default parameter values.

`pd = makedist('Uniform','Lower',lower,'Upper',upper)` creates a uniform distribution object using the specified parameter values.

Input Arguments

`lower` — Lower parameter
0 (default) | scalar value

Lower limit for the uniform distribution, specified as a scalar value.

Data Types: `single` | `double`

`upper` — Upper parameter
1 (default) | scalar value

Upper parameter for the uniform distribution, specified as a scalar value greater than `lower`.

Data Types: `single` | `double`

Properties

`lower` — Lower parameter
scalar value

Lower parameter for the uniform distribution, stored as a scalar value.

Data Types: `single | double`

`upper` — Upper parameter
scalar value

Upper parameter for the uniform distribution, stored as a scalar value greater than `lower`.

Data Types: `single | double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`IsTruncated` — Logical flag for truncated distribution
`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters
positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions
cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterNames` — Distribution parameter names
cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values
vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single | double`

`Truncation` — Truncation interval
vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single | double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object

median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object
mean	Mean of probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Uniform Distribution

The uniform distribution has a constant probability density function between its two parameters, lower (the minimum) and upper (the maximum). This distribution is appropriate for representing round-off errors in values tabulated to a particular number of decimal places.

The uniform distribution uses the following parameters.

Parameter	Description	Support
`lower`	Lower parameter	$-\infty < lower < upper$
`upper`	Upper parameter	$lower < upper < \infty$

The probability density function (pdf) is

$$f(x \mid lower, upper) = \begin{cases} \left(\frac{1}{upper - lower}\right) & ; \quad lower \le x \le upper \\ 0 & ; \quad otherwise \end{cases}.$$

and 0 otherwise.

Examples

Create a Uniform Distribution Object Using Default Parameters

Create a uniform distribution object using the default parameter values.

```
pd = makedist('Uniform')
```

```
pd =

  UniformDistribution

  Uniform distribution
    Lower = 0
    Upper = 1
```

Create a Uniform Distribution Object Using Specified Parameters

Create a uniform distribution object by specifying parameter values.

```
pd = makedist('Uniform','Lower',-4,'Upper',2)
```

```
pd =

  UniformDistribution

  Uniform distribution
    Lower = -4
    Upper =  2
```

Compute the interquartile range of the distribution

```
r = iqr(pd)
```

```
r =
```

```
3
```

See Also

`makedist`

More About

- "Uniform Distribution (Continuous)"
- Class Attributes
- Property Attributes

union

Class: dataset

Set union for dataset array observations

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
C = union(A,B)
C = union(A,B,vars)
C = union(A,B,vars,setOrder)
[C,iA,iB] = union( ___ )
```

Description

`C = union(A,B)` for `dataset` arrays `A` and `B` returns the combined set of observations from the two arrays, with repetitions removed. The observations in the dataset array C are sorted.

`C = union(A,B,vars)` returns the combined set of observations from the two arrays, with repetitions of unique combinations of the variables specified in vars removed. The observations in the dataset array C are sorted by those variables.

The values for variables not specified in vars for each observation in C are taken from the corresponding observation in `A` or `B`, or from A if there are common observations in both `A` and `B`. If there are multiple observations in `A` or `B` that correspond to an observation in C, those values are taken from the first occurrence.

`C = union(A,B,vars,setOrder)` returns the observations in C in the order specified by setOrder.

`[C,iA,iB] = union( ___ )` also returns index vectors iA and iB such that C is a sorted combination of the values `A(iA,:)` and `B(iB,:)`. If there are common observations in `A` and `B`, then `union` returns only the index from `A`, in iA. If there are repeated observations in `A` or `B`, then the index of the first occurrence is returned. You can use any of the previous input arguments.

Input Arguments

`A,B`

Input dataset arrays.

`vars`

Cell array of strings containing variable names or a vector of integers containing variable column numbers, indicating the variables for which `union` removes repetitions of unique combinations of the variables.

Specify `vars` as `[]` to use its default value of all variables.

`setOrder`

Flag indicating the sorting order for the observations in C. The possible values of `setOrder` are:

`'sorted'`	Observations in C are in sorted order (default).
`'stable'`	Observations in C are in the same order that they appear in `A`, then `B`.

Output Arguments

`C`

Dataset array with the combined observations of `A` and `B`, with repetitions removed. C is in sorted order (by default), or the order specified by setOrder.

`iA`

Index vector, indicating the observations in `A` that contribute to the union. `iA` contains the index to the first occurrence of any repeated observations in `A`.

iB

Index vector, indicating the observations in B that contribute to the union. If there are common observations in A and B, then union returns only the index from A, in iA. iB contains the index to the first occurrence of any repeated observations in B.

Examples

Union of Two Dataset Arrays

Navigate to the folder containing sample data, and load sample data.

```
cd(matlabroot)
cd('help/toolbox/stats/examples')

A = dataset('XLSFile','hospitalSmall.xlsx');
B = dataset('XLSFile','hospitalSmall.xlsx','Sheet',2);
[length(A) length(B)]
```

```
ans =

    14     8
```

The first dataset array, A, has 14 observations. The second dataset array, B, has 8 observations.

Return the union.

```
C = union(A,B);
length(C)
```

```
ans =

    21
```

The union of the two dataset arrays has 21 observations, indicating that there was one observation replicated in A and B.

- “Create a Dataset Array from a File” on page 2-69
- “Merge Dataset Arrays” on page 2-99

See Also

dataset | intersect | ismember | setdiff | setxor | sortrows | unique

More About

- “Dataset Arrays” on page 2-132

unique

Class: dataset

Unique observations in dataset array

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
C = unique(A)
[C,ia,ic] = unique(A)
C = unique(A,vars)
[C,ia,ic] = unique(A,vars)
[...] = unique(A,vars,occurrence)
[...] = unique(...,'R2012a')
[...] = unique(...,'legacy')
[...] = unique(A,vars,setOrder)
```

Description

Note: The behavior of `dataset.unique` is consistent with the MATLAB function `unique`. For a demonstration of using the `'legacy'` flag to preserve the behavior from R2012b and prior in your existing code, see the documentation for `unique`.

`C = unique(A)` returns a copy of the dataset A that contains only the sorted unique observations. `A` must contain only variables whose class has a `unique` method, including:

- numeric
- character

- logical
- categorical
- cell arrays of strings

For a variable with multiple columns, its class's `unique` method must support the `'rows'` flag.

`[C,ia,ic] = unique(A)` also returns index vectors `ia` and `ic` such that `C = A(ia,:)` and `A = C(ic,:)`.

`C = unique(A,vars)` returns a dataset that contains only one observation for each unique combination of values for the variables in `A` specified in `vars`. `vars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. `C` includes all variables from `A`. The values in `C` for the variables not specified in `vars` are taken from the last occurrence among observations in `A` with each unique combination of values for the variables specified in `vars`.

`[C,ia,ic] = unique(A,vars)` also returns index vectors `ia` and `ic` such that `C = A(ia,:)` and `A(:,vars) = C(ic,vars)`.

`[...] = unique(A,vars,occurrence)` specifies which index is returned in `ia` in the case of repeated observations in `A`. The default value is `occurrence='last'`, which returns the index of the last occurrence of each repeated observation in `A`. `occurrence='first'` returns the index of the first occurrence of each repeated observation in `A`. The values in `C` for variables not specified in `vars` are taken from the observations `A(ia,:)`. Specify `vars` as `[]` to use the default value of all variables.

`[...] = unique(...,'R2012a')` adopts the future behavior of `unique`. You can specify the flag as the final argument with any previous syntax that accepts `A`, `vars`, or `occurrence`.

`[...] = unique(...,'legacy')` preserves the current behavior of `unique`. You can specify the flag as the final argument with any previous syntax that accepts `A`, `vars`, or `occurrence`.

`[...] = unique(A,vars,setOrder)` returns the observations of `C` in a specific order. `setOrder='sorted'` returns the values of `C` in sorted order. `setOrder='stable'` returns the values of `C` in the same order as `A`. If there are repeated observations in `A`, then `ia` returns the index of the first occurrence of each repeated observation. Specify `vars` as `[]` to use the default value of all variables.

See Also

`dataset` | `set` | `subsasgn`

Units property

Class: dataset

Units of variables in data set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

A cell array of strings giving the units of the variables in the data set. This property may be empty, but if not empty, the number of strings must equal the number of variables. Any individual string may be empty for a variable that does not have units defined. The default is an empty cell array.

unidcdf

Discrete uniform cumulative distribution function

Syntax

```
p = unidcdf(x,N)
p = unidcdf(x,N,'upper')
```

Description

`p = unidcdf(x,N)` returns the discrete uniform cdf at each value in `x` using the corresponding maximum observable value in `N`. `x` and `N` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The maximum observable values in `N` must be positive integers.

`p = unidcdf(x,N,'upper')` returns the complement of the discrete uniform cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The discrete uniform cdf is

$$p = F(x \mid N) = \frac{floor(x)}{N} I_{(1,\ldots,N)}(x)$$

The result, p, is the probability that a single observation from the discrete uniform distribution with maximum N will be a positive integer less than or equal to x. The values x do not need to be integers.

Examples

Compute Discrete Uniform Distribution cdf

What is the probability of drawing a number 20 or less from a hat with the numbers from 1 to 50 inside?

```
probability = unidcdf(20,50)

probability =
  0.4000
```

More About

- "Uniform Distribution (Discrete)" on page B-169

See Also

cdf | unidpdf | unidinv | unidstat | unidrnd | mle

unidinv

Discrete uniform inverse cumulative distribution function

Syntax

```
X = unidinv(P,N)
```

Description

`X = unidinv(P,N)` returns the smallest positive integer `X` such that the discrete uniform cdf evaluated at `X` is equal to or exceeds `P`. You can think of `P` as the probability of drawing a number as large as `X` out of a hat with the numbers `1` through `N` inside.

`P` and `N` can be vectors, matrices, or multidimensional arrays that have the same size, which is also the size of `X`. A scalar input for `N` or `P` is expanded to a constant array with the same dimensions as the other input. The values in `P` must lie on the interval [0 1] and the values in `N` must be positive integers.

Examples

```
x = unidinv(0.7,20)
x =
    14

y = unidinv(0.7 + eps,20)
y =
    15
```

A small change in the first parameter produces a large jump in output. The cdf and its inverse are both step functions. The example shows what happens at a step.

More About

- “Uniform Distribution (Discrete)” on page B-169

See Also

icdf | unidcdf | unidpdf | unidstat | unidrnd

unidpdf

Discrete uniform probability density function

Syntax

```
Y = unidpdf(X,N)
```

Description

`Y = unidpdf(X,N)` computes the discrete uniform pdf at each of the values in `X` using the corresponding maximum observable value in `N`. `X` and `N` can be vectors, matrices, or multidimensional arrays that have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `N` must be positive integers.

The discrete uniform pdf is

$$y = f(x \mid N) = \frac{1}{N} I_{(1,\ldots,N)}(x)$$

You can think of y as the probability of observing any one number between 1 and n.

Examples

For fixed `n`, the uniform discrete pdf is a constant.

```
y = unidpdf(1:6,10)
y =
  0.1000  0.1000  0.1000  0.1000  0.1000  0.1000
```

Now fix `x`, and vary `n`.

```
likelihood = unidpdf(5,4:9)
likelihood =
  0  0.2000  0.1667  0.1429  0.1250  0.1111
```

More About

- "Uniform Distribution (Discrete)" on page B-169

See Also

`pdf` | `unidcdf` | `unidinv` | `unidstat` | `unidrnd`

unidrnd

Discrete uniform random numbers

Syntax

```
R = unidrnd(N)
R = unidrnd(N,m,n,...)
R = unidrnd(N,[m,n,...])
```

Description

`R = unidrnd(N)` generates random numbers for the discrete uniform distribution with maximum `N`. The parameters in `N` must be positive integers. `N` can be a vector, a matrix, or a multidimensional array. The size of `R` is the size of `N`. The discrete uniform distribution arises from experiments equivalent to drawing a number from one to `N` out of a hat.

`R = unidrnd(N,m,n,...)` or `R = unidrnd(N,[m,n,...])` generates an `m`-by-`n`-by-... array. The `N` parameter can be a scalar or an array of the same size as `R`.

Examples

In the Massachusetts lottery, a player chooses a four-digit number. Generate random numbers for Monday through Saturday.

```
numbers = unidrnd(10000,1,6)-1
numbers =
    4564   185  8214  4447  6154  7919
```

More About

- “Uniform Distribution (Discrete)” on page B-169

See Also

`random` | `unidpdf` | `unidcdf` | `unidinv` | `unidstat`

unidstat

Discrete uniform mean and variance

Syntax

```
[M,V] = unidstat(N)
```

Description

`[M,V] = unidstat(N)` returns the mean and variance of the discrete uniform distribution with minimum value `1` and maximum value `N`.

The mean of the discrete uniform distribution with parameter N is $(N + 1)/2$. The variance is $(N^2 - 1)/12$.

Examples

```
[m,v] = unidstat(1:6)
m =
  1.0000   1.5000   2.0000   2.5000   3.0000   3.5000
v =
  0   0.2500   0.6667   1.2500   2.0000   2.9167
```

More About

- "Uniform Distribution (Discrete)" on page B-169

See Also

`unidpdf` | `unidcdf` | `unidinv` | `unidrnd`

unifcdf

Continuous uniform cumulative distribution function

Syntax

```
p = unifcdf(x,a,b)
p = unifcdf(x,a,b,'upper')
```

Description

`p = unifcdf(x,a,b)` returns the uniform cdf at each value in `x` using the corresponding lower endpoint (minimum), `a` and upper endpoint (maximum), `b`. `x`, `a`, and `b` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant matrix with the same dimensions as the other inputs.

`p = unifcdf(x,a,b,'upper')` returns the complement of the uniform cdf at each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities.

The uniform cdf is

$$p = F(x \mid a,b) = \frac{x-a}{b-a} I_{[a,b]}(x)$$

The standard uniform distribution has a = 0 and b = 1.

Examples

Compute Uniform Distribution cdf

What is the probability that an observation from a standard uniform distribution will be less than 0.75?

```
probability = unifcdf(0.75)
```

```
probability =
  0.7500
```

What is the probability that an observation from a uniform distribution with `a = -1` and `b = 1` will be less than 0.75?

```
probability = unifcdf(0.75,-1,1)
```

```
probability =
  0.8750
```

More About

- "Uniform Distribution (Continuous)" on page B-163

See Also

`cdf` | `unifpdf` | `unifinv` | `unifstat` | `unifit` | `unifrnd`

unifinv

Continuous uniform inverse cumulative distribution function

Syntax

```
X = unifinv(P,A,B)
```

Description

`X = unifinv(P,A,B)` computes the inverse of the uniform cdf with parameters `A` and `B` (the minimum and maximum values, respectively) at the corresponding probabilities in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs.

The inverse of the uniform cdf is

$$x = F^{-1}(p \mid a,b) = a + p(a-b)I_{[0,1]}(p)$$

The standard uniform distribution has A = `0` and B = `1`.

Examples

What is the median of the standard uniform distribution?

```
median_value = unifinv(0.5)
median_value =
  0.5000
```

What is the 99th percentile of the uniform distribution between -1 and 1?

```
percentile = unifinv(0.99,-1,1)
percentile =
  0.9800
```

More About

- "Uniform Distribution (Continuous)" on page B-163

See Also

`icdf` | `unifcdf` | `unifpdf` | `unifstat` | `unifit` | `unifrnd`

unifit

Continuous uniform parameter estimates

Syntax

```
[ahat,bhat] = unifit(data)
[ahat,bhat,ACI,BCI] = unifit(data)
[ahat,bhat,ACI,BCI] = unifit(data,alpha)
```

Description

`[ahat,bhat] = unifit(data)` returns the maximum likelihood estimates (MLEs) of the parameters of the uniform distribution given the data in `data`.

`[ahat,bhat,ACI,BCI] = unifit(data)` also returns 95% confidence intervals, `ACI` and `BCI`, which are matrices with two rows. The first row contains the lower bound of the interval for each column of the matrix `data`. The second row contains the upper bound of the interval.

`[ahat,bhat,ACI,BCI] = unifit(data,alpha)` enables you to control of the confidence level `alpha`. For example, if `alpha = 0.01` then `ACI` and `BCI` are 99% confidence intervals.

Examples

```
r = unifrnd(10,12,100,2);
[ahat,bhat,aci,bci] = unifit(r)
ahat =
  10.0154  10.0060
bhat =
  11.9989  11.9743
aci =
  9.9551  9.9461
  10.0154  10.0060
bci =
  11.9989  11.9743
```

```
  12.0592   12.0341
```

More About

- "Uniform Distribution (Continuous)" on page B-163

See Also

`mle` | `unifpdf` | `unifcdf` | `unifinv` | `unifstat` | `unifrnd`

unifpdf

Continuous uniform probability density function

Syntax

```
Y = unifpdf(X,A,B)
```

Description

`Y = unifpdf(X,A,B)` computes the continuous uniform pdf at each of the values in `X` using the corresponding lower endpoint (minimum), `A` and upper endpoint (maximum), `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array with the same dimensions as the other inputs. The parameters in `B` must be greater than those in `A`.

The continuous uniform distribution pdf is

$$y = f(x \mid a,b) = \frac{1}{b-a} I_{[a,b]}(x)$$

The standard uniform distribution has A = `0` and B = `1`.

Examples

For fixed `a` and `b`, the uniform pdf is constant.

```
x = 0.1:0.1:0.6;
y = unifpdf(x)
y =
   1   1   1   1   1   1
```

What if `x` is not between `a` and `b`?

```
y = unifpdf(-1,0,1)
y =
   0
```

More About

- "Uniform Distribution (Continuous)" on page B-163

See Also

`pdf` | `unifcdf` | `unifinv` | `unifstat` | `unifit` | `unifrnd`

unifrnd

Continuous uniform random numbers

Syntax

```
R = unifrnd(A,B)
R = unifrnd(A,B,m,n,...)
R = unifrnd(A,B,[m,n,...])
```

Description

`R = unifrnd(A,B)` returns an array `R` of random numbers generated from the continuous uniform distributions with lower and upper endpoints specified by `A` and `B`, respectively. If `A` and `B` are arrays, `R(i,j)` is generated from the distribution specified by the corresponding elements of `A` and `B`. If either `A` or `B` is a scalar, it is expanded to the size of the other input.

`R = unifrnd(A,B,m,n,...)` or `R = unifrnd(A,B,[m,n,...])` returns an `m`-by-`n`-by-... array. If `A` and `B` are scalars, all elements of `R` are generated from the same distribution. If either `A` or `B` is an array, they must be `m`-by-`n`-by-... .

Examples

Generate one random number each from the continuous uniform distributions on the intervals (0,1), (0,2), ..., (0,5):

```
a = 0; b = 1:5;
r1 = unifrnd(a,b)
r1 =
    0.8147    1.8116    0.3810    3.6535    3.1618
```

Generate five random numbers each from the same distributions:

```
B = repmat(b,5,1);
R = unifrnd(a,B)
R =
```

```
    0.0975    0.3152    0.4257    2.6230    3.7887
    0.2785    1.9412    1.2653    0.1428    3.7157
    0.5469    1.9143    2.7472    3.3965    1.9611
    0.9575    0.9708    2.3766    3.7360    3.2774
    0.9649    1.6006    2.8785    2.7149    0.8559
```

Generate five random numbers from the continuous uniform distribution on (0,2):

```
r2 = unifrnd(a,b(2),1,5)
r2 =
    1.4121    0.0637    0.5538    0.0923    0.1943
```

More About

- "Uniform Distribution (Continuous)" on page B-163

See Also

`rand` | `random` | `unifpdf` | `unifcdf` | `unifinv` | `unifstat` | `unifit`

unifstat

Continuous uniform mean and variance

Syntax

```
[M,V] = unifstat(A,B)
```

Description

`[M,V] = unifstat(A,B)` returns the mean of and variance for the continuous uniform distribution using the corresponding lower endpoint (minimum), `A` and upper endpoint (maximum), `B`. Vector or matrix inputs for `A` and `B` must have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant matrix with the same dimensions as the other input.

The mean of the continuous uniform distribution with parameters a and b is $(a + b)/2$, and the variance is $(a - b)^2/12$.

Examples

```
a = 1:6;
b = 2.*a;
[m,v] = unifstat(a,b)
m =
  1.5000  3.0000  4.5000  6.0000  7.5000  9.0000
v =
  0.0833  0.3333  0.7500  1.3333  2.0833  3.0000
```

More About

- “Uniform Distribution (Continuous)” on page B-163

See Also

`unifpdf` | `unifcdf` | `unifinv` | `unifit` | `unifrnd`

unstack

Class: dataset

Unstack data from single variable into multiple variables

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
wide = unstack(tall,datavar,indvar)
[wide,itall] = unstack(tall,datavar,indvar)
wide = unstack(tall,datavar,indvar,'Parameter',value)
```

Description

`wide = unstack(tall,datavar,indvar)` converts a dataset array `tall` to an equivalent dataset array `wide` that is in wide format, by unstacking a single variable in `tall` into multiple variables in `wide`. In general `wide` contains more variables, but fewer observations, than `tall`.

`datavar` specifies the data variable in `tall` to unstack. `indvar` specifies an indicator variable in `tall` that determines which variable in `wide` each value in `datavar` is unstacked into. `unstack` treats the remaining variables in `tall` as grouping variables. Each unique combination of their values defines a group of observations in `tall` that will be unstacked into a single observation in `wide`.

`unstack` creates `m` data variables in `wide`, where `m` is the number of group levels in `indvar`. The values in `indvar` indicate which of those `m` variables receive which values from `datavar`. The `j`-th data variable in `wide` contains the values from `datavar` that correspond to observations whose `indvar` value was the `j`-th of the `m` possible levels.

Elements of those `m` variables for which no corresponding data value in `tall` exists contain a default value.

`datavar` is a positive integer, a variable name, or a logical vector containing a single true value. `indvar` is a positive integer, a variable name, or a logical vector containing a single true value.

`[wide,itall] = unstack(tall,datavar,indvar)` returns an index vector `itall` indicating the correspondence between observations in `wide` and those in `tall`. For each observation in `wide`, `itall` contains the index of the first in the corresponding group of observations in `tall`.

For more information on grouping variables, see “Grouping Variables” on page 2-52.

Input Arguments

`wide = unstack(tall,datavar,indvar,'Parameter',value)` uses the following parameter name/value pairs to control how `unstack` converts variables in `tall` to variables in `wide`:

`'GroupVars'`	Grouping variables in `tall` that define groups of observations. `groupvars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. The default is all variables in `tall` not listed in `datavar` or `indvar`.
`'NewDataVarNames'`	A cell array of strings containing names for the data variables `unstack` should create in `wide`. Default is the group names of the grouping variable specified in `indvar`.
`'AggregationFun'`	A function handle that accepts a subset of values from `datavar` and returns a single value. `stack` applies this function to observations from the same group that have the same value of `indvar`. The function must aggregate the data values into a single value, and in such cases it is not possible to recover `tall` from `wide` using `stack`. The default is `@sum` for numeric data variables. For non-numeric variables, there is no default, and you must specify `'AggregationFun'` if multiple observations in the same group have the same values of `indvar`.

`'ConstVars'`	Variables in `tall` to copy to `wide` without unstacking. The values for these variables in `wide` are taken from the first observation in each group in `tall`, so these variables should typically be constant within each group. `ConstVars` is a positive integer, a vector of positive integers, a variable name, a cell array containing one or more variable names, or a logical vector. The default is no variables.

You can also specify more than one data variable in `tall`, each of which becomes a set of `m` variables in `wide`. In this case, specify `datavar` as a vector of positive integers, a cell array containing variable names, or a logical vector. You may specify only one variable with `indvar`. The names of each set of data variables in `wide` are the name of the corresponding data variable in `tall` concatenated with the names specified in `'NewDataVarNames'`. The function specified in `'AggregationFun'` must return a value with a single row.

Examples

Convert a "wide format" data set to "tall format", and then back to a different "wide format":

```
load flu

% FLU has a 'Date' variable, and 10 variables for estimated
% influenza rates (in 9 different regions, estimated from
% Google searches, plus a nationwide extimate from the
% CDC). Combine those 10 variables into a "tall" array that
% has a single data variable, 'FluRate', and an indicator
% variable, 'Region', that says which region each estimate
% is from.
[flu2,iflu] = stack(flu, 2:11, 'NewDataVarName','FluRate', ...
    'IndVarName','Region')

% The second observation in FLU is for 10/16/2005.  Find the
% observations in FLU2 that correspond to that date.
flu(2,:)
flu2(iflu==2,:)

% Use the 'Date' variable from that tall array to split
% 'FluRate' into 52 separate variables, each containing the
% estimated influenza rates for each unique date.  The new
```

```
% "wide" array has one observation for each region.  In
% effect, this is the original array FLU "on its side".
dateNames = cellstr(datestr(flu.Date,'mmm_DD_YYYY'));
[flu3,iflu2] = unstack(flu2, 'FluRate', 'Date', ...
    'NewDataVarNames',dateNames)

% Since observations in FLU3 represent regions, IFLU2
% indicates the first occurrence in FLU2 of each region.
flu2(iflu2,:)
```

See Also

`dataset.stack` | `dataset.join`

How To

- “Grouping Variables” on page 2-52

upperparams

Class: paretotails

Upper Pareto tails parameters

Syntax

```
params = upperparams(obj)
```

Description

`params = upperparams(obj)` returns the 2-element vector `params` of shape and scale parameters, respectively, of the upper tail of the Pareto tails object `obj`. `upperparams` does not return a location parameter.

Examples

Fit Pareto tails to a t distribution at cumulative probabilities 0.1 and 0.9:

```
t = trnd(3,100,1);
obj = paretotails(t,0.1,0.9);

lowerparams(obj)
ans =
   -0.1901    1.1898
upperparams(obj)
ans =
    0.3646    0.5103
```

See Also

`paretotails` | `lowerparams`

UserData property

Class: dataset

Variable containing additional information associated with data set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

Any variable containing additional information to be associated with the data set. The default is an empty array.

var

Variance of probability distribution

Syntax

```
v = var(pd)
```

Description

`v = var(pd)` returns the variance v of the probability distribution pd.

Examples

Variance of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the variance of the fitted distribution.

```
v = var(pd)
```

```
v =
```

```
   76.0419
```

For a normal distribution, the variance is equal to the square of the parameter `sigma`.

Variance of a Skewed Distribution

Create a Weibull probability distribution object.

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Compute the variance of the distribution.

```
v = var(pd)
```

```
v =
    5.3650
```

Input Arguments

`pd` — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

`v` — Variance

nonnegative scalar value

Variance of the probability distribution, returned as a nonnegative scalar value.

See Also

`dfittool` | `fitdist` | `makedist`

var

Class: prob.KernelDistribution
Package: prob

Variance of probability distribution object

Syntax

```
v = var(pd)
```

Description

`v = var(pd)` returns the variance v of the probability distribution pd.

Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Fit a probability distribution object to data using `fitdist` or the Distribution Fitting app.

Output Arguments

v — Variance

nonnegative scalar value

Variance of the probability distribution, returned as a nonnegative scalar value.

Examples

Variance of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a kernel distribution object to the data.

```
pd = fitdist(x,'Kernel')
```

```
pd =

  KernelDistribution

    Kernel = normal
    Bandwidth = 3.61677
    Support = unbounded
```

Compute the variance of the fitted distribution.

```
v = var(pd)
```

```
v =

   88.4893
```

See Also

`dfittool` | `fitdist`

var

Class: ProbDistUnivParam

Return variance of ProbDistUnivParam object

Syntax

```
V = var(PD)
```

Description

`V = var(PD)` returns *V*, the variance of the ProbDistUnivParam object *PD*.

Input Arguments

PD	An object of the class `ProbDistUnivParam`.

Output Arguments

V	The variance of the ProbDistUnivParam object *PD*.

See Also

`var`

var

Class: prob.ParametricTruncatableDistribution
Package: prob

Variance of probability distribution object

Syntax

```
v = var(pd)
```

Description

`v = var(pd)` returns the variance v of the probability distribution pd.

Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`.

Output Arguments

v — Variance

nonnegative scalar value

Variance of the probability distribution, returned as a nonnegative scalar value.

Examples

Variance of a Triangular Distribution

Create a triangular distribution object.

```
pd = makedist('Triangular','a',-3,'b',1,'c',3)
```

```
pd =

  TriangularDistribution

A = -3, B = 1, C = 3
```

Compute the variance of the distribution.

```
v = var(pd)
```

```
v =

    1.5556
```

See Also

`makedist`

var

Class: prob.ToolboxFittableParametricDistribution
Package: prob

Variance of probability distribution object

Syntax

```
v = var(pd)
```

Description

`v = var(pd)` returns the variance v of the probability distribution pd.

Input Arguments

pd — Probability distribution

probability distribution object

Probability distribution, specified as a probability distribution object. Create a probability distribution object with specified parameter values using `makedist`. Alternatively, create a probability distribution object by fitting it to data using `fitdist` or the Distribution Fitting app.

Output Arguments

v — Variance

nonnegative scalar value

Variance of the probability distribution, returned as a nonnegative scalar value.

Examples

Variance of a Fitted Distribution

Load the sample data. Create a vector containing the first column of students' exam grade data.

```
load examgrades;
x = grades(:,1);
```

Fit a normal distribution object to the data.

```
pd = fitdist(x,'Normal')
```

```
pd =

  NormalDistribution

  Normal distribution
       mu = 75.0083   [73.4321, 76.5846]
    sigma =  8.7202   [7.7391, 9.98843]
```

Compute the variance of the fitted distribution.

```
v = var(pd)
```

```
v =

   76.0419
```

For a normal distribution, the variance is equal to the square of the parameter `sigma`.

Variance of a Skewed Distribution

Create a Weibull probability distribution object.

```
pd = makedist('Weibull','a',5,'b',2)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 5
    B = 2
```

Compute the variance of the distribution.

```
v = var(pd)
```

```
v =
    5.3650
```

See Also

`dfittool` | `fitdist` | `makedist`

VarDescription property

Class: dataset

Cell array of strings giving descriptions of variables in data set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

A cell array of strings giving the descriptions of the variables in the data set. This property may be empty, but if not empty, the number of strings must equal the number of variables. Any individual string may be empty for a variable that does not have a description defined. The default is an empty cell array.

varimportance

Class: classregtree

Compute embedded estimates of input feature importance

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
imp = varimportance(t)
```

Description

`imp = varimportance(t)` computes estimates of input feature importance for tree `t` by summing changes in the risk due to splits on every feature. The returned vector `imp` has one element for each input variable in the data used to train this tree. At each node, the risk is estimated as node impurity if impurity was used to split nodes and node error otherwise. This risk is weighted by the node probability. Variable importance associated with this split is computed as the difference between the risk for the parent node and the total risk for the two children.

See Also

`risk`

VarNames property

Class: dataset

Cell array giving names of variables in data set

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Description

A cell array of nonempty, distinct strings giving the names of the variables in the data set. The number of strings must equal the number of variables. The default is the cell array of string names for the variables used to create the data set.

VarNames property

Class: TreeBagger

Variable names

Description

The `VarNames` property is a cell array containing the names of the predictor variables (features). `TreeBagger` takes these names from the optional `'names'` parameter. The default names are `'x1'`, `'x2'`, etc.

vartest

Chi-square variance test

Syntax

```
h = vartest(x,v)
h = vartest(x,v,Name,Value)
[h,p] = vartest( ___ )
[h,p,ci,stats] = vartest( ___ )
```

Description

`h = vartest(x,v)` returns a test decision for the null hypothesis that the data in vector x comes from a normal distribution with variance v, using the chi-square variance test. The alternative hypothesis is that x comes from a normal distribution with a different variance. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = vartest(x,v,Name,Value)` performs the chi-square variance test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level or conduct a one-sided test.

`[h,p] = vartest( ___ )` also returns the *p*-value of the test, p, using any of the input arguments in the previous syntaxes.

`[h,p,ci,stats] = vartest( ___ )` also returns the confidence interval for the true variance, ci, and the structure stats containing information about the test statistic.

Examples

Test for a Specified Variance

Load the sample data. Create a vector containing the first column of the students' exam grades matrix.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that the data comes from a distribution with a variance of 25.

```
[h,p,ci,stats] = vartest(x,25)
```

```
h =
     1

p =
     0

ci =
   59.8936
   99.7688

stats =
    chisqstat: 361.9597
           df: 119
```

The returned value `h = 1` indicates that `vartest` rejects the null hypothesis at the default 5% significance level. `ci` shows the lower and upper boundaries of the 95% confidence interval for the true variance, and suggests that the true variance is greater than 25.

One-Sided Hypothesis Test

Load the sample data. Create a vector containing the first column of the students' exam grades matrix.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that the data comes from a distribution with a variance of 25, against the alternative hypothesis that the variance is greater than 25.

```
[h,p] = vartest(x,25,'Tail','right')
```

```
h =
     1

p =
   2.4269e-26
```

The returned value of `h = 1` indicates that `vartest` rejects the null hypothesis at the default 5% significance level, in favor of the alternative hypothesis that the variance is greater than 25.

Input Arguments

x — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array. For matrices, `vartest` performs separate tests along each column of x, and returns a row vector of results. For multidimensional arrays, `vartest` works along the first nonsingleton dimension of x.

Data Types: `single` | `double`

v — Hypothesized variance

nonnegative scalar value

Hypothesized variance, specified as a nonnegative scalar value.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Alpha',0.01` specifies a right-tailed hypothesis test at the 1% significance level.

'Alpha' — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Dim'` — Dimension

first nonsingleton dimension (default) | positive integer value

Dimension of the input matrix to test along, specified as the comma-separated pair consisting of `'Dim'` and a positive integer value. For example, specifying `'Dim',1` tests the data in each column for equality to the hypothesized variance, while `'Dim',2` tests the data in each row.

Example: `'Dim',2`

Data Types: `single` | `double`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the population variance is not `v`.
`'right'`	Test the alternative hypothesis that the population variance is greater than `v`.
`'left'`	Test the alternative hypothesis that the population variance is less than `v`.

Example: `'Tail','right'`

Output Arguments

`h` — Hypothesis test result

`1` | `0`

Hypothesis test result, returned as a logical value.

- If `h = 1`, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If `h = 0`, this indicates a failure to reject the null hypothesis at the Alpha significance level.

`p` — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

`ci` — Confidence interval

vector

Confidence interval for the true variance, returned as a two-element vector containing the lower and upper boundaries of the 100 × (1 – Alpha)% confidence interval.

`stats` — Test statistics

structure

Test statistics for the chi-square variance test, returned as a structure containing:

- `chisqstat` — Value of the test statistic.
- `df` — Degrees of freedom of the test.

More About

Chi-Square Variance Test

The chi-square variance test is used to test if the variance of a population is equal to a hypothesized value.

The test statistic is

$$T = (n-1)\left(\frac{s}{\sigma_0}\right)^2,$$

where n is the sample size, s is the sample standard deviation, and σ_0 is the hypothesized standard deviation. The denominator is the ratio of the sample standard deviation to the hypothesized standard deviation. The further this ratio deviates from 1, the more likely you are to reject the null hypothesis. The test statistic T has a chi-square distribution with $n - 1$ degrees of freedom under the null hypothesis.

Multidimensional Array

A multidimensional array has more than two dimensions. For example, if `x` is a 1-by-3-by-4 array, then `x` is a three-dimensional array.

First Nonsingleton Dimension

The first nonsingleton dimension is the first dimension of an array whose size is not equal to 1. For example, if `x` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `x`.

See Also

`vartest2` | `vartestn`

vartest2

Two-sample *F*-test for equal variances

Syntax

```
h = vartest2(x,y)
h = vartest2(x,y,Name,Value)
[h,p] = vartest2(___)
[h,p,ci,stats] = vartest2(___)
```

Description

`h = vartest2(x,y)` returns a test decision for the null hypothesis that the data in vectors x and y comes from normal distributions with the same variance, using the two-sample *F*-test. The alternative hypothesis is that they come from normal distributions with different variances. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h = vartest2(x,y,Name,Value)` returns a test decision for the two-sample *F*-test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level or conduct a one-sided test.

`[h,p] = vartest2(___)` also returns the *p*-value of the test, p, using any of the input arguments in the previous syntaxes.

`[h,p,ci,stats] = vartest2(___)` also returns the confidence interval for the true variance ratio, ci, and the structure stats containing information about the test statistic.

Examples

Test for Equal Variances

Load the sample data. Create vectors containing the first and second columns of the data matrix to represent students' grades on two exams.

```
load examgrades;
x = grades(:,1);
```

```
y = grades(:,2);
```

Test the null hypothesis that the data in `x` and `y` comes from distributions with the same variance.

```
[h,p,ci,stats] = vartest2(x,y)
```

```
h =
     1

p =
    0.0019

ci =
    1.2383
    2.5494

stats =
    fstat: 1.7768
      df1: 119
      df2: 119
```

The returned result `h = 1` indicates that `vartest2` rejects the null hypothesis at the default 5% significance level. `ci` contains the lower and upper boundaries of the 95% confidence interval for the true variance ratio. `stats` contains the value of the test statistic for the *F*-test and the numerator and denominator degrees of freedom.

One-Sided Hypothesis Test

Load the sample data. Create vectors containing the first and second columns of the data matrix to represent students' grades on two exams.

```
load examgrades;
x = grades(:,1);
y = grades(:,2);
```

Test the null hypothesis that the data in `x` and `y` comes from distributions with the same variance, against the alternative that the population variance of `x` is greater than that of `y`.

```
vartest2(x,y,'Tail','right')
```

```
h =
     1

p =
```

```
    9.4364e-04
```

The returned result `h = 1` indicates that `vartest2` rejects the null hypothesis at the default 5% significance level, in favor of the alternative hypothesis that the population variance of `x` is greater than that of `y`.

Input Arguments

x — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array.

- If `x` and `y` are vectors, they do not need to be the same length.
- If `x` and `y` are matrices, they must have the same number of columns, but do not need to have the same number of rows. `vartest2` performs separate tests along each column and returns a vector of the results.
- If x and y are multidimensional arrays, they must have the same number of dimensions, and the same size along all but the first nonsingleton dimension.

Data Types: `single` | `double`

y — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array.

- If `x` and `y` are vectors, they do not need to be the same length.
- If `x` and `y` are matrices, they must have the same number of columns, but do not need to have the same number of rows. `vartest2` performs separate tests along each column and returns a vector of the results.
- If x and y are multidimensional arrays, they must have the same number of dimensions, and the same size along all but the first nonsingleton dimension.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Alpha',0.01` specifies a right-tailed hypothesis test at the 1% significance level.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Dim'` — Dimension

first nonsingleton dimension (default) | positive integer value

Dimension of the input matrix to test along, specified as the comma-separated pair consisting of `'Dim'` and a positive integer value. For example, specifying `'Dim',1` tests the data in each column for variance equality, while `'Dim',2` tests the data in each row.

Example: `'Dim',2`

Data Types: `single` | `double`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis to evaluate using the *F*-test, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the population variances are not equal.
`'right'`	Test the alternative hypothesis that the population variance of x is greater than that of y.
`'left'`	Test the alternative hypothesis that the population variance of x is less than that of y.

Example: `'Tail','right'`

Output Arguments

h — Hypothesis test result

1 | 0

Hypothesis test result, returned as a logical value.

- If h = 1, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = 0, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

ci — Confidence interval

vector

Confidence interval for the true ratio of the population variances, returned as a two-element vector containing the lower and upper boundaries of the 100 × (1 – Alpha)% confidence interval.

stats — Test statistics

structure

Test statistics for the hypothesis test, returned as a structure containing:

- fstat — Value of the test statistic.
- df1 — Numerator degrees of freedom of the test.
- df2 — Denominator degrees of freedom of the test.

More About

Two-Sample *F*-Test

The two-sample *F*-test is used to test if the variances of two populations are equal.

The test statistic is

$$F = \frac{{s_1}^2}{{s_2}^2},$$

where s_1 and s_2 are the sample standard deviations. The test statistic is a ratio of the two sample variances. The further this ratio deviates from 1, the more likely you are to reject the null hypothesis. Under the null hypothesis, the test statistic F has a F-distribution with numerator degrees of freedom equal to $N_1 - 1$ and denominator degrees of freedom equal to $N_2 - 1$, where N_1 and N_2 are the sample sizes of the two data sets.

Multidimensional Array

A multidimensional array has more than two dimensions. For example, if `x` is a 1-by-3-by-4 array, then `x` is a three-dimensional array.

First Nonsingleton Dimension

The first nonsingleton dimension is the first dimension of an array whose size is not equal to 1. For example, if `x` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `x`.

See Also

`vartest` | `vartestn`

vartestn

Multiple-sample tests for equal variances

Syntax

```
vartestn(x)
vartestn(x,Name,Value)

vartestn(x,group)
vartestn(x,group,Name,Value)

p = vartestn(___)
[p,stats] = vartestn(___)
```

Description

`vartestn(x)` returns a summary table of statistics and a box plot for a Bartlett test of the null hypothesis that the columns of data vector x come from normal distributions with the same variance. The alternative hypothesis is that not all columns of data have the same variance.

`vartestn(x,Name,Value)` returns a summary table of statistics and a box plot for a test of unequal variances with additional options specified by one or more name-value pair arguments. For example, you can specify a different type of hypothesis test or change the display settings for the test results.

`vartestn(x,group)` returns a summary table of statistics and a box plot for a Bartlett test of the null hypothesis that the data in each categorical group comes from normal distributions with the same variance. The alternative hypothesis is that not all groups have the same variance.

`vartestn(x,group,Name,Value)` returns a summary table of statistics and a box plot for a test of unequal variances with additional options specified by one or more name-value pair arguments. For example, you can specify a different type of hypothesis test or change the display settings for the test results.

`p = vartestn( ___ )` also returns the *p*-value of the test, p, using any of the input arguments in the previous syntaxes.

`[p,stats] = vartestn( ___ )` also returns the structure stats containing information about the test statistic.

Examples

Test Data for Equal Variances

Load the sample data.

```
load examgrades;
```

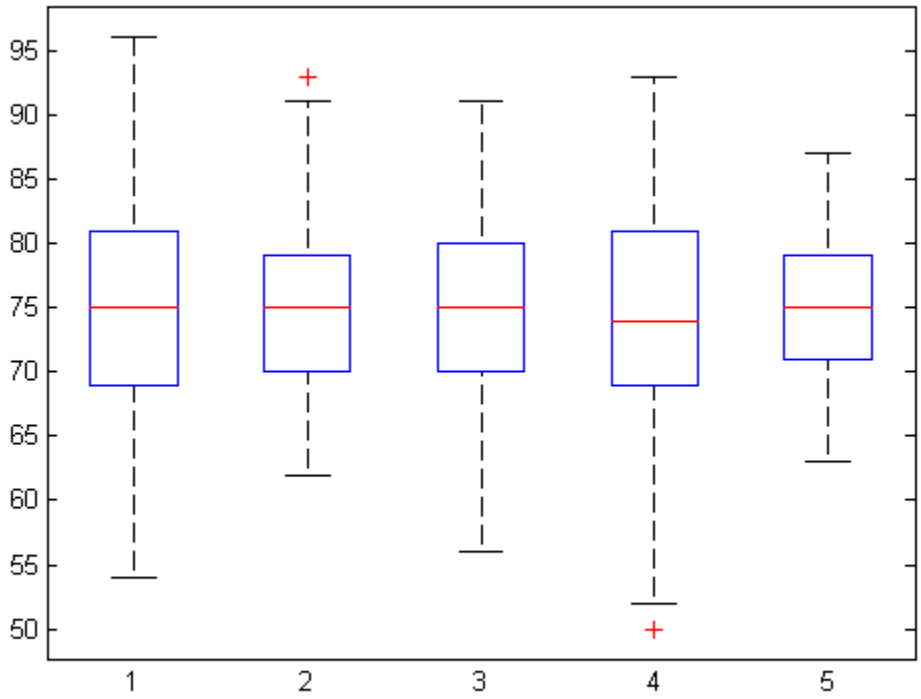
Test the null hypothesis that the variances are equal across the five columns of data in the students' exam grades matrix, `grades`.

```
vartestn(grades)
```

Group Summary Table

Group	Count	Mean	Std Dev
1	120	75.0083	8.7202
2	120	74.9917	6.54204
3	120	74.9917	7.43091
4	120	75.0333	8.60128
5	120	74.9917	5.25884
Pooled	600	75.0033	7.42558

Bartlett's statistic	38.7332
Degrees of freedom	4
p-value	0



The low *p*-value, `p = 0`, indicates that `vartestn` rejects the null hypothesis that the variances are equal across all five columns, in favor of the alternative hypothesis that at least one column has a different variance.

Test Grouped Data for Equal Variances

Load the sample data.

```
load carsmall;
```

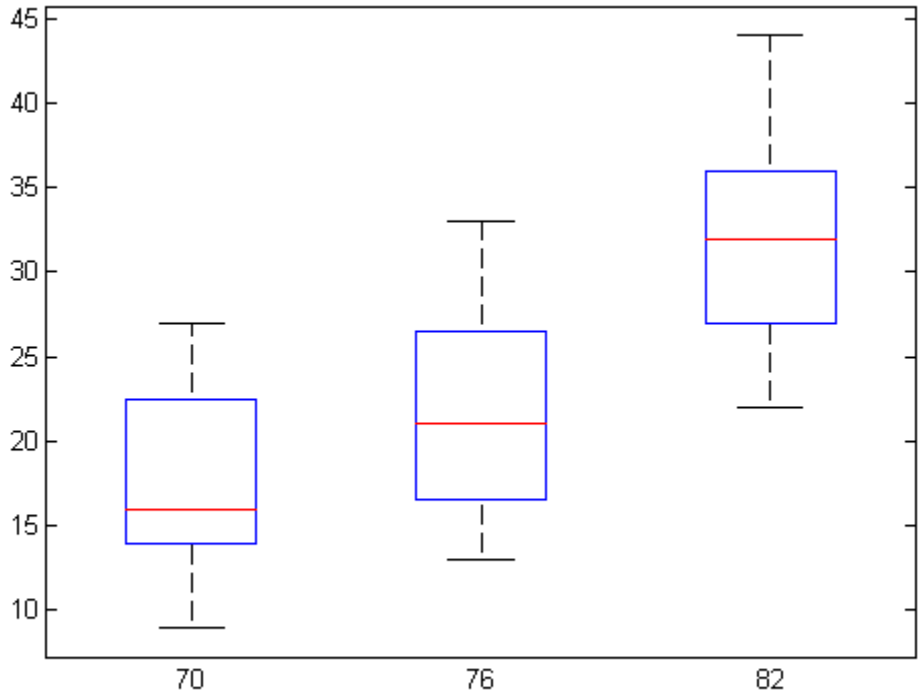
Test the null hypothesis that the variances in miles per gallon (`MPG`) are equal across different model years.

```
vartestn(MPG,Model_Year)
```

Group Summary Table

Group	Count	Mean	Std Dev
70	29	17.6897	5.33923
76	34	21.5735	5.8893
82	31	31.7097	5.39255
Pooled	94	23.7181	5.562

Bartlett's statistic	0.36619
Degrees of freedom	2
p-value	0.83269



The high *p*-value, `p = 0.83269`, indicates that `vartestn` does not reject the null hypothesis that the variances in miles per gallon (`MPG`) are equal across different model years.

Test for Equal Variances Using Levene's Test

Load the sample data.

```
load carsmall;
```

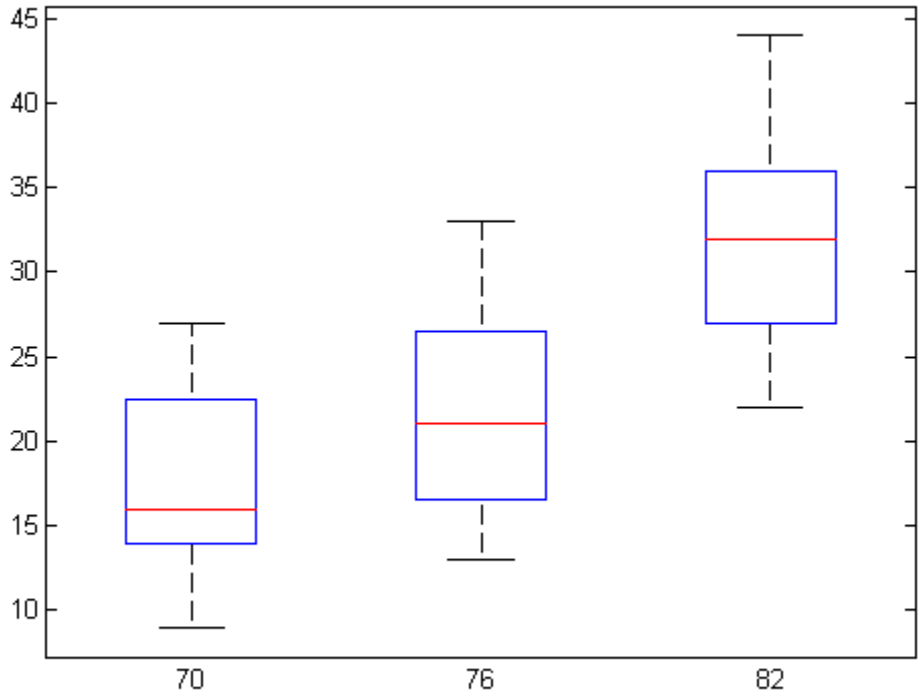
Use Levene's test to test the null hypothesis that the variances in miles per gallon (`MPG`) are equal across different model years.

```
p = vartestn(MPG,Model_Year,'TestType','LeveneAbsolute')
```

```
p =

    0.6320
```

Group Summary Table

Group	Count	Mean	Std Dev
70	29	17.6897	5.33923
76	34	21.5735	5.8893
82	31	31.7097	5.39255
Pooled	94	23.7181	5.562
Levene's statistic (absolute)	0.46126		
Degrees of freedom	2, 91		
p-value	0.63195		



The high *p*-value, `p = 0.63195`, indicates that `vartestn` does not reject the null hypothesis that the variances in miles per gallon (`MPG`) are equal across different model years.

Test for Equal Variances Using the Brown-Forsythe Test

Load the sample data.

```
load examgrades;
```

Test the null hypothesis that the variances are equal across the five columns of data in the students' exam grades matrix, `grades`, using the Brown-Forsythe test. Suppress the display of the summary table of statistics and the box plot.

```
[p,stats] = vartestn(grades,'TestType','BrownForsythe','Display','off')

p =

   1.3121e-06


stats =

    fstat: 8.4160
       df: [4 595]
```

The small *p*-value, `p = 1.3121e-06`, indicates that `vartestn` rejects the null hypothesis that the variances are equal across all five columns, in favor of the alternative hypothesis that at least one column has a different variance.

Input Arguments

x — Sample data

matrix | vector

Sample data, specified as a matrix or vector. If a grouping variable group is specified, x must be a vector. If a grouping variable is not specified, x must be a matrix. In either case, `vartestn` treats `NaN` values as missing values and ignores them.

Data Types: `single` | `double`

group — Grouping variable

categorical array | logical or numeric vector | cell array of strings

Grouping variable, specified as a categorical array, logical or numeric vector, or cell array of strings with one row for each element of x. Each unique value in a grouping variable defines a group.

For example, if `Gender` is a cell array of strings with values `'Male'` and `'Female'`, you can use `Gender` as a grouping variable to test your data by gender.

Example: `Gender`

Data Types: `single` | `double` | `logical` | `cell` | `char`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'TestType','BrownForsythe','Display','off'` specifies a Brown-Forsythe test and omits the plot of the results.

`'Display'` — Display settings for test results

`'on'` (default) | `'off'`

Display settings for test results, specified as the comma-separated pair consisting of `'Display'` and one of the following.

`'on'`	Display a box plot and table of summary statistics.
`'off'`	Do not display a box plot and table of summary statistics.

Example: `'display','off'`

`'TestType'` — Type of hypothesis test

`'Bartlett'` (default) | `'LeveneQuadratic'` | `'LeveneAbsolute'` | `'BrownForsythe'` | `'OBrien'`

Type of hypothesis test to perform, specified as the comma-separated pair consisting of `'TestType'` and one of the following.

`'Bartlett'`	Bartlett's test.
`'LeveneQuadratic'`	Levene's test computed by performing ANOVA on the squared deviations of the data values from their group means.
`'LeveneAbsolute'`	Levene's test computed by performing ANOVA on the absolute deviations of the data values from their group means.
`'BrownForsythe'`	Brown-Forsythe test computed by performing ANOVA on the absolute deviations of the data values from the group medians.
`'OBrien'`	O'Brien's modification of Levene's test with `W` = 0.5.

Example: `'TestType','OBrien'`

Output Arguments

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

stats — Test statistics

structure

Test statistics for the hypothesis test, returned as a structure containing:

- `chistat`: Value of the test statistic.
- `df`: Degrees of freedom of the test.

More About

Bartlett's Test

Bartlett's test is used to test whether multiple data samples have equal variances, against the alternative that at least two of the data samples do not have equal variances.

The test statistic is

$$T = \frac{(N-k)\ln {s_p}^2 - \sum_{i=1}^{k}(N_i-1)\ln {s_i}^2}{1+\left(1/\left(3(k-1)\right)\right)\left(\left(\sum_{i=1}^{k}1/(N_i-1)\right)-1/(N-k)\right)},$$

where ${s_i}^2$ is the variance of the ith group, N is the total sample size, N_i is the sample size of the ith group, k is the number of groups, and ${s_p}^2$ is the pooled variance. The pooled variance is defined as

$$s_p{}^2 = \sum_{i=1}^{k}(N_i - 1)s_i{}^2 / (N - k).$$

The test statistic has a chi-square distribution with $k - 1$ degrees of freedom under the null hypothesis.

Bartlett's test is sensitive to departures from normality. If your data comes from a nonnormal distribution, Levene's test could provide a more accurate result.

Levene, Brown-Forsythe, and O'Brien Tests

The Levene, Brown-Forsythe, and O'Brien tests are used to test if multiple data samples have equal variances, against the alternative that at least two of the data samples do not have equal variances.

The test statistic is

$$W = \frac{(N-k)\sum_{i=1}^{k} N_i\left(\bar{Z}_{i.} - \bar{Z}_{..}\right)^2}{(k-1)\sum_{i=1}^{k}\sum_{j=1}^{N_i}\left(Z_{ij} - \bar{Z}_{i.}\right)^2},$$

where N_i is the sample size of the ith group, and k is the number of groups. Depending on the type of test specified with the `TestType` name-value pair arguments, Z_{ij} can have one of four definitions:

- If you specify `LeveneAbsolute`, `vartestn` uses $Z_{ij} = \left|Y_{ij} - \bar{Y}_{i.}\right|$, where $\bar{Y}_{i.}$ is the mean of the ith subgroup.
- If you specify `LeveneQuadratic`, `vartestn` uses $Z_{ij}{}^2 = \left(Y_{ij} - \bar{Y}_{i.}\right)^2$, where $\bar{Y}_{i.}$ is the mean of the ith subgroup.
- If you specify `BrownForsythe`, `vartestn` uses $Z_{ij} = \left|Y_{ij} - \tilde{Y}_{i.}\right|$, where $\tilde{Y}_{i.}$ is the median of the ith subgroup.
- If you specify `OBrien`, `vartestn` uses

$$Z_{ij} = \frac{(0.5 + n_i - 2) n_i \left(y_{ij} - \bar{y}_i \right)^2 - 0.5(n_i - 1)\sigma_i{}^2}{(n_i - 1)(n_i - 2)},$$

where n_i is the size of the ith group, σ_i^2 is its sample variance.

In all cases, the test statistic has an F-distribution with $k - 1$ numerator degrees of freedom, and $N - k$ denominator degrees of freedom.

The Levene, Brown-Forsythe, and O'Brien tests are less sensitive to departures from normality than Bartlett's test, so they are useful alternatives if you suspect the samples come from nonnormal distributions.

See Also

`anova1` | `vartest` | `vartest2`

vertcat

Class: dataset

Vertical concatenation for dataset arrays

Compatibility

The `dataset` data type might be removed in a future release. To work with heterogeneous data, use the MATLAB `table` data type instead. See MATLAB `table` documentation for more information.

Syntax

```
ds = vertcat(ds1, ds2, ...)
```

Description

`ds = vertcat(ds1, ds2, ...)` vertically concatenates the dataset arrays `ds1, ds2, ...`. Observation names, when present, must be unique across datasets. `vertcat` fills in default observation names for the output when some of the inputs have names and some do not.

Variable names for all dataset arrays must be identical except for order. `vertcat` concatenates by matching variable names. `vertcat` assigns values for the "per-variable" properties (e.g., `Units` and `VarDescription`) in `ds` from the corresponding property values in `ds1`.

See Also

`cat` | `horzcat`

view

Class: classregtree

Plot tree

Compatibility

`classregtree` will be removed in a future release. See `fitctree`, `fitrtree`, `ClassificationTree`, or `RegressionTree` instead.

Syntax

```
view(t)
view(t,param1,val1,param2,val2,...)
```

Description

`view(t)` displays the decision tree `t` as computed by `classregtree` in a figure window. Each branch in the tree is labeled with its decision rule, and each terminal node is labeled with the predicted value for that node. Click any node to get more information about it. The information displayed is specified by the **Click to display** pop-up menu at the top of the figure.

`view(t,param1,val1,param2,val2,...)` specifies optional parameter name/value pairs:

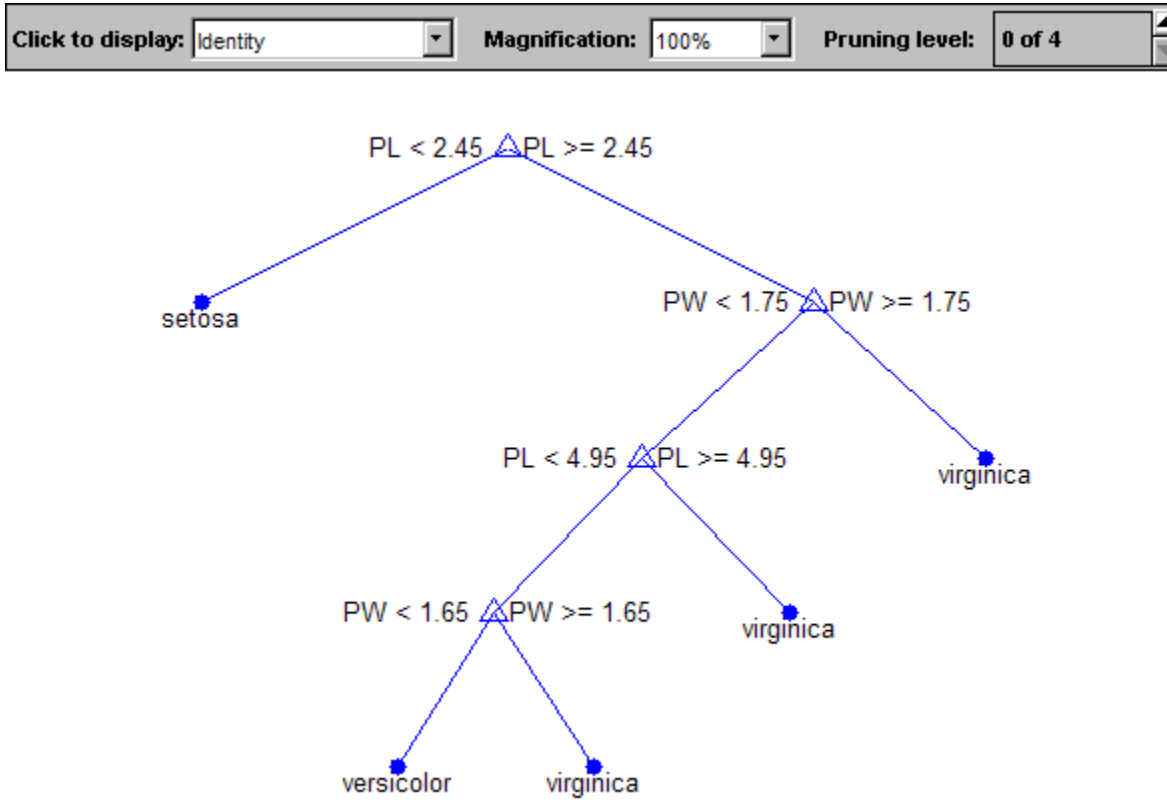
- `'names'` — A cell array of names for the predictor variables, in the order in which they appear in the matrix `X` from which the tree was created. (See `classregtree`.)
- `'prunelevel'` — Initial pruning level to display.

For each branch node, the left child node corresponds to the points that satisfy the condition, and the right child node corresponds to the points that do not satisfy the condition.

Examples

Create a classification tree for Fisher's iris data:

```
load fisheriris;

t = classregtree(meas,species,...
                 'names',{'SL' 'SW' 'PL' 'PW'})
t =
Decision tree for classification
1  if PL<2.45 then node 2 elseif PL>=2.45 then node 3 else setosa
2  class = setosa
3  if PW<1.75 then node 4 elseif PW>=1.75 then node 5 else versicolor
4  if PL<4.95 then node 6 elseif PL>=4.95 then node 7 else versicolor
5  class = virginica
6  if PW<1.65 then node 8 elseif PW>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(t)
```



References

[1] Breiman, L., J. Friedman, R. Olshen, and C. Stone. *Classification and Regression Trees*. Boca Raton, FL: CRC Press, 1984.

See Also

`classregtree` | `prune` | `test` | `eval`

compact

Class: clustering.evaluation.ClusterCriterion
Package: clustering.evaluation

Compact clustering evaluation object

Syntax

```
c = compact(eva)
```

Description

`c = compact(eva)` returns a compact clustering evaluation object, which contains a subset of information about the clustering solution in eva. Compacting a clustering evaluation object reduces the memory requirements of the object, which is useful when clustering a large data set.

Input Arguments

eva — Clustering evaluation data

clustering evaluation object

Clustering evaluation data, specified as a clustering evaluation object. Create a clustering evaluation object using `evalclusters`.

Output Arguments

c — Compact clustering evaluation object

clustering evaluation object

Compact clustering evaluation object, returned as a clustering evaluation object. The compact object includes the clustering evaluation results, In the compact object, the properties for the input data `X`, optimal clustering solution `OptimalY`, and the list of excluded data `Missing` are empty.

Examples

Create a Compact Clustering Evaluation Object

Create a compact clustering evaluation object from a full clustering evaluation object.

Load the sample data.

```
load fisheriris;
```

The data contains length and width measurements from the sepals and petals of three species of iris flowers.

Create a clustering evaluation object. Cluster the data using `kmeans`, and evaluate the optimal number of clusters using the gap criterion.

```
rng('default');  % For reproducibility
eva = evalclusters(meas,'kmeans','Gap','KList',[1:6])
```

```
eva =

  GapEvaluation with properties:

    NumObservations: 150
       InspectecedK: [1 2 3 4 5 6]
    CriterionValues: [0.0747 0.5906 0.8737 1.0055 1.0466 0.9848]
           OptimalK: 4
```

Create a compact clustering evaluation object from `eva`.

```
c = compact(eva)
```

```
c =

  GapEvaluation with properties:

    NumObservations: 150
       InspectecedK: [1 2 3 4 5 6]
    CriterionValues: [0.0747 0.5906 0.8737 1.0055 1.0466 0.9848]
           OptimalK: 4
```

The displayed output of the compact object `c` is the same as the original object `eva`, but some properties not shown in the display are different. For example, in the compact object, the properties `x`, `OptimalY`, and `Missing` are empty.

Display the optimal clustering solution `OptimalY` for `c`.

```
c.OptimalY
```

```
ans =

     []
```

See Also

`evalclusters`

view

Class: CompactClassificationTree

View tree

Syntax

```
view(tree)
view(tree,Name,Value)
```

Description

`view(tree)` returns a text description of `tree`, a decision tree.

`view(tree,Name,Value)` describes `tree` with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

A classification tree or compact classification tree created by `fitctree` or `compact`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Mode'`

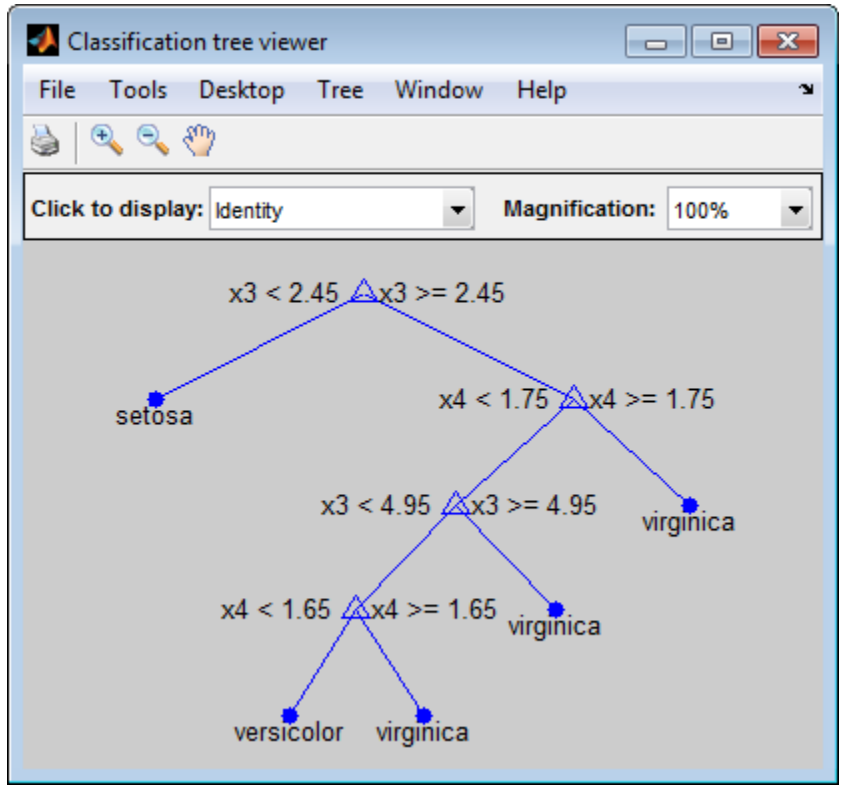
String describing the display of tree, either `'graph'` or `'text'`. `'graph'` opens a user interface displaying `tree`, and containing controls for querying the tree. `'text'` sends output to the Command Window describing `tree`.

Default: `'text'`

Examples

View the classification tree for Fisher's iris model in both textual and graphical displays:

```
load fisheriris
tree = fitctree(meas,species);
view(tree)

Decision tree for classification
1  if x3<2.45 then node 2 elseif x3>=2.45 then node 3 else setosa
2  class = setosa
3  if x4<1.75 then node 4 elseif x4>=1.75 then node 5 else versicolor
4  if x3<4.95 then node 6 elseif x3>=4.95 then node 7 else versicolor
5  class = virginica
6  if x4<1.65 then node 8 elseif x4>=1.65 then node 9 else versicolor
7  class = virginica
8  class = versicolor
9  class = virginica

view(tree,'Mode','graph')
```



See Also

`ClassificationTree` | `fitctree`

view

Class: CompactRegressionTree

View tree

Syntax

```
view(tree)
view(tree,Name,Value)
```

Description

`view(tree)` returns a text description of `tree`, a decision tree.

`view(tree,Name,Value)` describes `tree` with additional options specified by one or more Name,Value pair arguments.

Input Arguments

`tree`

A regression tree or compact regression tree created by `fitrtree` or `compact`.

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single quotes (`' '`). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

`'Mode'`

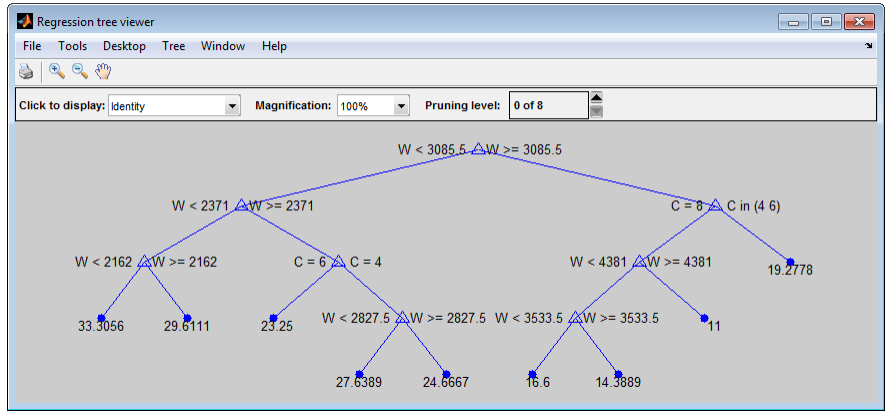
String describing the display of tree, either `'graph'` or `'text'`. `'graph'` opens a GUI displaying `tree`, and containing controls for querying the tree. `'text'` sends output to the Command Window describing `tree`.

Default: `'text'`

Examples

View a regression tree for the `carsmall` data in both textual and graphical displays:

```
load carsmall
tree = fitrtree([Weight, Cylinders],MPG,...
                'categoricalpredictors',2,'MinParent',20,...
                'PredictorNames',{'W','C'});
view(tree)

Decision tree for regression
 1  if W<3085.5 then node 2 elseif W>=3085.5 then node 3 else 23.7181
 2  if W<2371 then node 4 elseif W>=2371 then node 5 else 28.7931
 3  if C=8 then node 6 elseif C in {4 6} then node 7 else 15.5417
 4  if W<2162 then node 8 elseif W>=2162 then node 9 else 32.0741
 5  if C=6 then node 10 elseif C=4 then node 11 else 25.9355
 6  if W<4381 then node 12 elseif W>=4381 then node 13 else 14.2963
 7  fit = 19.2778
 8  fit = 33.3056
 9  fit = 29.6111
10  fit = 23.25
11  if W<2827.5 then node 14 elseif W>=2827.5 then node 15 else 27.2143
12  if W<3533.5 then node 16 elseif W>=3533.5 then node 17 else 14.8696
13  fit = 11
14  fit = 27.6389
15  fit = 24.6667
16  fit = 16.6
17  fit = 14.3889

view(tree,'Mode','graph')
```



See Also

`RegressionTree` | `fitrtree`

wblcdf

Weibull cumulative distribution function

Syntax

```
p = wblcdf(x,a,b)
[p,plo,pup] = wblcdf(x,a,b,pcov,alpha)
[p,plo,pup] = wblcdf( ___ ,'upper')
```

Description

`p = wblcdf(x,a,b)` returns the cdf of the Weibull distribution with scale parameter `a` and shape parameter `b`, at each value in `x`. `x`, `a`, and `b` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `a` and `b` are both `1`. The parameters `a` and `b` must be positive.

`[p,plo,pup] = wblcdf(x,a,b,pcov,alpha)` returns confidence bounds for `p` when the input parameters `a` and `b` are estimates. `pcov` is the 2-by-2 covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies 100(1 - `alpha`)% confidence bounds. `plo` and `pup` are arrays of the same size as `p` containing the lower and upper confidence bounds.

`[p,plo,pup] = wblcdf( ___ ,'upper')` returns the complement of the Weibull cdf for each value in `x`, using an algorithm that more accurately computes the extreme upper tail probabilities. You can use `'upper'` with any of the previous syntaxes.

The function `wblcdf` computes confidence bounds for `p` using a normal approximation to the distribution of the estimate

$$\hat{b}\left(\log x - \log \hat{a}\right)$$

and then transforms those bounds to the scale of the output `p`. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `pcov` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The Weibull cdf is

$$p = F(x \mid a,b) = \int_0^x b a^{-b} t^{b-1} e^{-\left(\frac{t}{a}\right)^b} dt = 1 - e^{-\left(\frac{x}{a}\right)^b} I_{(0,\infty)}(x)$$

Examples

Weibull Distribution cdf

What is the probability that a value from a Weibull distribution with parameters `a = 0.15` and `b = 0.8` is less than 0.5?

```
probability = wblcdf(0.5, 0.15, 0.8)
```

```
probability =
  0.9272
```

How sensitive is this result to small changes in the parameters?

```
[A, B] = meshgrid(0.1:0.05:0.2,0.2:0.05:0.3);
probability = wblcdf(0.5, A, B)
```

```
probability =
  0.7484  0.7198  0.6991
  0.7758  0.7411  0.7156
  0.8022  0.7619  0.7319
```

More About

- “Weibull Distribution” on page B-172

See Also

`cdf` | `wblpdf` | `wblinv` | `wblstat` | `wblfit` | `wbllike` | `wblrnd`

wblfit

Weibull parameter estimates

Syntax

```
parmhat = wblfit(data)
[parmhat,parmci] = wblfit(data)
[parmhat,parmci] = wblfit(data,alpha)
[...] = wblfit(data,alpha,censoring)
[...] = wblfit(data,alpha,censoring,freq)
[...] = wblfit(...,options)
```

Description

`parmhat = wblfit(data)` returns the maximum likelihood estimates, `parmhat`, of the parameters of the Weibull distribution given the values in the vector `data`, which must be positive. `parmhat` is a two-element row vector: `parmhat(1)` estimates the Weibull parameter a, and `parmhat(2)` estimates the Weibull parameter b, in the pdf

$$y = f\left(x \mid a,b\right) = ba^{-b}x^{b-1}e^{-\left(\frac{x}{a}\right)^{b}}I_{(0,\infty)}\left(x\right)$$

`[parmhat,parmci] = wblfit(data)` returns 95% confidence intervals for the estimates of a and b in the 2-by-2 matrix `parmci`. The first row contains the lower bounds of the confidence intervals for the parameters, and the second row contains the upper bounds of the confidence intervals.

[`[parmhat,parmci] = wblfit(data,alpha)` returns 100(1 - `alpha`)% confidence intervals for the parameter estimates.

`[...] = wblfit(data,alpha,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is `1` for observations that are right-censored and `0` for observations that are observed exactly.

`[...] = wblfit(data,alpha,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. The vector `freq` typically contains integer frequencies for the

corresponding elements in `data`, but can contain any non-negative values. Pass in `[]` for `alpha`, `censoring`, or `freq` to use their default values.

`[...] = wblfit(...,options)` accepts a structure, `options`, that specifies control parameters for the iterative algorithm the function uses to compute maximum likelihood estimates. The Weibull fit function accepts an `options` structure that can be created using the function `statset`. Enter `statset ('wblfit')` to see the names and default values of the parameters that `lognfit` accepts in the `options` structure. See the reference page for `statset` for more information about these options.

Examples

```
data = wblrnd(0.5,0.8,100,1);
[parmhat, parmci] = wblfit(data)
parmhat =
  0.5861  0.8567
parmci =
  0.4606  0.7360
  0.7459  0.9973
```

More About

- "Weibull Distribution" on page B-172

See Also

`mle` | `wbllike` | `wblpdf` | `wblcdf` | `wblinv` | `wblstat` | `wblrnd`

wblinv

Weibull inverse cumulative distribution function

Syntax

```
X = wblinv(P,A,B)
[X,XLO,XUP] = wblinv(P,A,B,PCOV,alpha)
```

Description

`X = wblinv(P,A,B)` returns the inverse cumulative distribution function (cdf) for a Weibull distribution with scale parameter `A` and shape parameter `B`, evaluated at the values in `P`. `P`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The default values for `A` and `B` are both `1`.

`[X,XLO,XUP] = wblinv(P,A,B,PCOV,alpha)` returns confidence bounds for `X` when the input parameters `A` and `B` are estimates. `PCOV` is a 2-by-2 matrix containing the covariance matrix of the estimated parameters. `alpha` has a default value of 0.05, and specifies 100(1 - `alpha`)% confidence bounds. `XLO` and `XUP` are arrays of the same size as `X` containing the lower and upper confidence bounds.

The function `wblinv` computes confidence bounds for `X` using a normal approximation to the distribution of the estimate

$$\log a + \frac{\log q}{b}$$

where q is the `P`th quantile from a Weibull distribution with scale and shape parameters both equal to 1. The computed bounds give approximately the desired confidence level when you estimate `mu`, `sigma`, and `PCOV` from large samples, but in smaller samples other methods of computing the confidence bounds might be more accurate.

The inverse of the Weibull cdf is

$$x = F^{-1}(p \mid a,b) = -a\left[\ln(1-p)\right]^{1/b} I_{[0,1]}(p)$$

Examples

The lifetimes (in hours) of a batch of light bulbs has a Weibull distribution with parameters a = 200 and b = 6.

Find the median lifetime of the bulbs:

```
life = wblinv(0.5, 200, 6)
life =
 188.1486
```

Generate 100 random values from this distribution, and estimate the 90th percentile (with confidence bounds) from the random sample

```
x = wblrnd(200,6,100,1);
p = wblfit(x)
[nlogl,pcov] = wbllike(p,x)
[q90,q90lo,q90up] = wblinv(0.9,p(1),p(2),pcov)
p =

  204.8918    6.3920


nlogl =

  496.8915


pcov =

   11.3392    0.5233
    0.5233    0.2573


q90 =

  233.4489


q90lo =

  226.0092
```

```
q90up =

  241.1335
```

More About

- "Weibull Distribution" on page B-172

See Also

`icdf` | `wblcdf` | `wblpdf` | `wblstat` | `wblfit` | `wbllike` | `wblrnd`

wbllike

Weibull negative log-likelihood

Syntax

```
nlogL = wbllike(params,data)
[logL,AVAR] = wbllike(params,data)
[...] = wbllike(params,data,censoring)
[...] = wbllike(params,data,censoring,freq)
```

Description

`nlogL = wbllike(params,data)` returns the Weibull log-likelihood. `params(1)` is the scale parameter, `A`, and `params(2)` is the shape parameter, `B`.

`[logL,AVAR] = wbllike(params,data)` also returns `AVAR`, which is the asymptotic variance-covariance matrix of the parameter estimates if the values in `params` are the maximum likelihood estimates. `AVAR` is the inverse of Fisher's information matrix. The diagonal elements of `AVAR` are the asymptotic variances of their respective parameters.

`[...] = wbllike(params,data,censoring)` accepts a Boolean vector, `censoring`, of the same size as `data`, which is 1 for observations that are right-censored and 0 for observations that are observed exactly.

`[...] = wbllike(params,data,censoring,freq)` accepts a frequency vector, `freq`, of the same size as `data`. `freq` typically contains integer frequencies for the corresponding elements in `data`, but can contain any nonnegative values. Pass in `[]` for `censoring` to use its default value.

The Weibull negative log-likelihood for uncensored data is

$$(-\log L) = -\log \prod_{i=1} f(a,b \mid x_i) = -\sum_{i=1}^{n} \log f(a,b \mid x_i)$$

where f is the Weibull pdf.

`wbllike` is a utility function for maximum likelihood estimation.

Examples

This example continues the example from `wblfit`.

```
r = wblrnd(0.5,0.8,100,1);
[logL, AVAR] = wbllike(wblfit(r),r)
logL =
  47.3349
AVAR =
  0.0048  0.0014
  0.0014  0.0040
```

More About

- "Weibull Distribution" on page B-172

References

[1] Patel, J. K., C. H. Kapadia, and D. B. Owen. *Handbook of Statistical Distributions*. New York: Marcel Dekker, 1976.

See Also

`wblfit` | `wblpdf` | `wblcdf` | `wblinv` | `wblstat` | `wblrnd`

wblpdf

Weibull probability density function

Syntax

```
Y = wblpdf(X,A,B)
```

Description

`Y = wblpdf(X,A,B)` computes the Weibull pdf at each of the values in `X` using the corresponding scale parameter, `A` and shape parameter, `B`. `X`, `A`, and `B` can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other inputs. The parameters in `A` and `B` must be positive.

The Weibull pdf is

$$f(x \mid a,b) = \frac{b}{a}\left(\frac{x}{a}\right)^{b-1} e^{-(x/a)^b}.$$

Some references refer to the Weibull distribution with a single parameter. This corresponds to `wblpdf` with `A = 1`.

Examples

The exponential distribution is a special case of the Weibull distribution.

```
lambda = 1:6;
y = wblpdf(0.1:0.1:0.6,lambda,1)
y =
  0.9048   0.4524   0.3016   0.2262   0.1810   0.1508

y1 = exppdf(0.1:0.1:0.6,lambda)
y1 =
  0.9048   0.4524   0.3016   0.2262   0.1810   0.1508
```

More About

- `wblfit`
- `wblinv`
- `wbllike`
- `wblplot`
- `wblrnd`
- `wblstat`
- "Weibull Distribution" on page B-172

References

[1] Devroye, L. *Non-Uniform Random Variate Generation*. New York: Springer-Verlag, 1986.

See Also

`pdf` | `wblcdf`

wblplot

Weibull probability plot

Syntax

```
wblplot(X)
h = wblplot(X)
```

Description

`wblplot(X)` displays a Weibull probability plot of the data in `X`. If `X` is a matrix, `wblplot` displays a plot for each column.

`h = wblplot(X)` returns handles to the plotted lines.

The purpose of a Weibull probability plot is to graphically assess whether the data in `X` could come from a Weibull distribution. If the data are Weibull the plot will be linear. Other distribution types might introduce curvature in the plot. `wblplot` uses midpoint probability plotting positions. Use `probplot` when the data included censored observations.

Examples

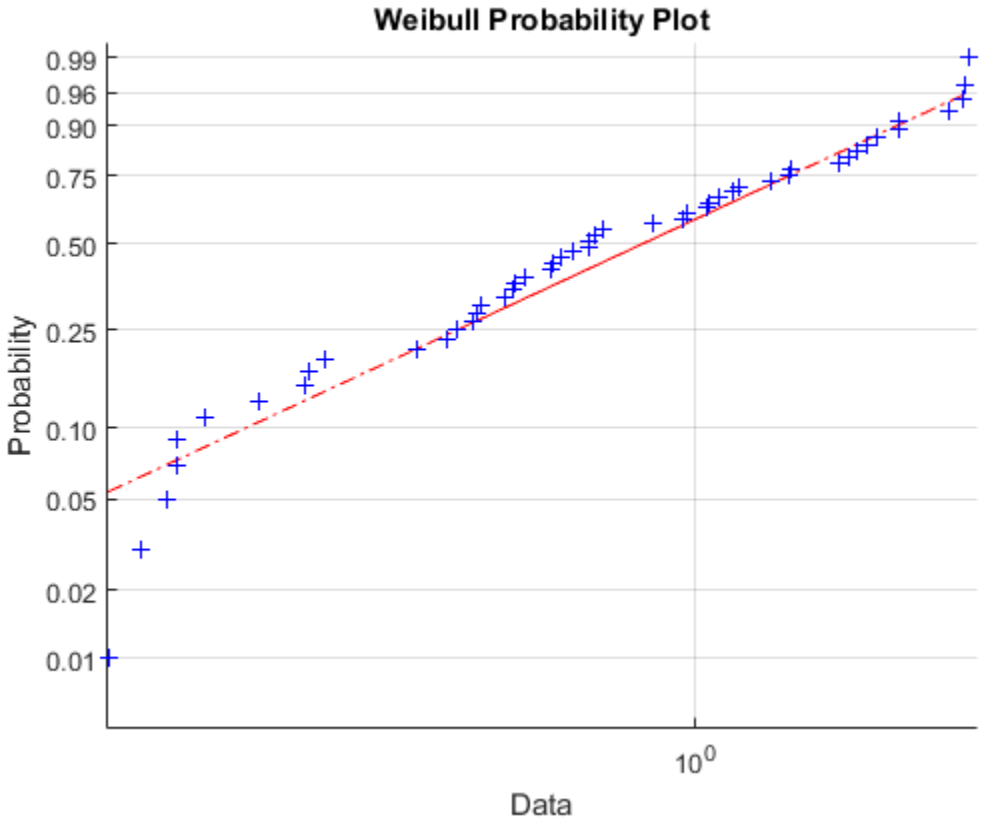
Create a Weibull Probability Plot

Generate a vector `r` containing 50 random numbers from a Weibull distribution with parameters `A = 1.2` and `B = 1.5`.

```
rng default;  % For reproducibility
r = wblrnd(1.2,1.5,50,1);
```

Create a Weibull probability plot to visually determine if the data comes from a Weibull distribution.

```
figure;
wblplot(r)
```



The plot indicates that the data likely comes from a Weibull distribution.

More About

- `wblfit`
- `wblinv`
- `wbllike`
- `wblpdf`
- `wblrnd`
- `wblstat`

- “Weibull Distribution” on page B-172

See Also

`probplot` | `normplot` | `wblcdf`

wblrnd

Weibull random numbers

Syntax

```
R = wblrnd(A,B)
R = wblrnd(A,B,m,n,...)
R = wblrnd(A,B,[m,n,...])
```

Description

`R = wblrnd(A,B)` generates random numbers for the Weibull distribution with scale parameter, `A` and shape parameter, `B`. The input arguments `A` and `B` can be either scalars or matrices. `A` and `B`, can be vectors, matrices, or multidimensional arrays that all have the same size. A scalar input is expanded to a constant array of the same size as the other input.

`R = wblrnd(A,B,m,n,...)` or `R = wblrnd(A,B,[m,n,...])` generates an `m`-by-`n`-by-... array. The `A`, `B` parameters can each be scalars or arrays of the same size as `R`.

Devroye [1] refers to the Weibull distribution with a single parameter; this is `wblrnd` with A = `1`.

Examples

```
n1 = wblrnd(0.5:0.5:2,0.5:0.5:2)
n1 =
  0.0178  0.0860  2.5216  0.9124

n2 = wblrnd(1/2,1/2,[1 6])
n2 =
  0.0046  1.7214  2.2108  0.0367  0.0531  0.0917
```

More About

- "Weibull Distribution" on page B-172

References

[1] Devroye, L. *Non-Uniform Random Variate Generation*. New York: Springer-Verlag, 1986.

See Also

`random` | `wblpdf` | `wblcdf` | `wblinv` | `wblstat` | `wblfit` | `wbllike`

wblstat

Weibull mean and variance

Syntax

```
[M,V] = wblstat(A,B)
```

Description

`[M,V] = wblstat(A,B)` returns the mean of and variance for the Weibull distribution with scale parameter, `A` and shape parameter, `B`. Vector or matrix inputs for `A` and `B` must have the same size, which is also the size of `M` and `V`. A scalar input for `A` or `B` is expanded to a constant matrix with the same dimensions as the other input.

The mean of the Weibull distribution with parameters a and b is

$$a\left[\Gamma\left(1+b^{-1}\right)\right]$$

and the variance is

$$a^2\left[\Gamma\left(1+2b^{-1}\right)-\Gamma\left(1+b^{-1}\right)^2\right]$$

Examples

```
[m,v] = wblstat(1:4,1:4)
m =
  1.0000  1.7725  2.6789  3.6256
v =
  1.0000  0.8584  0.9480  1.0346

wblstat(0.5,0.7)
ans =
  0.6329
```

More About

- "Weibull Distribution" on page B-172

See Also

`wblpdf` | `wblcdf` | `wblinv` | `wblfit` | `wbllike` | `wblrnd`

prob.WeibullDistribution class

Package: prob
Superclasses: prob.ToolboxFittableParametricDistribution

Weibull probability distribution object

Description

`prob.WeibullDistribution` is an object consisting of parameters, a model description, and sample data for a Weibull probability distribution.

Create a probability distribution object with specified parameter values using `makedist`. Alternatively, fit a distribution to data using `fitdist` or the Distribution Fitting app.

Construction

`pd = makedist('Weibull')` creates a Weibull probability distribution object using the default parameter values.

`pd = makedist('Weibull','a',a,'b',b)` creates a Weibull probability distribution object using the specified parameter values.

Input Arguments

a — Scale parameter

1 (default) | positive scalar value

Scale parameter of the Weibull distribution, specified as a positive scalar value.

Data Types: `single` | `double`

b — Shape parameter

1 (default) | positive scalar value

Shape parameter of the Weibull distribution, specified as a positive scalar value.

Data Types: `single` | `double`

Properties

a — Scale parameter
positive scalar value

Scale parameter of the Weibull distribution, stored as a positive scalar value.

Data Types: `single | double`

b — Shape parameter
positive scalar value

Shape parameter of the Weibull distribution, stored as a positive scalar value.

Data Types: `single | double`

`DistributionName` — Probability distribution name
probability distribution name string

Probability distribution name, stored as a valid probability distribution name string. This property is read-only.

Data Types: `char`

`InputData` — Data used for distribution fitting
structure

Data used for distribution fitting, stored as a structure containing the following:

- `data`: Data vector used for distribution fitting.
- `cens`: Censoring vector, or empty if none.
- `freq`: Frequency vector, or empty if none.

This property is read-only.

Data Types: `struct`

`IsTruncated` — Logical flag for truncated distribution
`0 | 1`

Logical flag for truncated distribution, stored as a logical value. If `IsTruncated` equals `0`, the distribution is not truncated. If `IsTruncated` equals `1`, the distribution is truncated. This property is read-only.

Data Types: `logical`

`NumParameters` — Number of parameters

positive integer value

Number of parameters for the probability distribution, stored as a positive integer value. This property is read-only.

Data Types: `single | double`

`ParameterCovariance` — Covariance matrix of the parameter estimates

matrix of scalar values

Covariance matrix of the parameter estimates, stored as a p-by-p matrix, where p is the number of parameters in the distribution. The (`i`,`j`) element is the covariance between the estimates of the `i`th parameter and the `j`th parameter. The (`i`,`i`) element is the estimated variance of the `i`th parameter. If parameter `i` is fixed rather than estimated by fitting the distribution to data, then the (`i`,`i`) elements of the covariance matrix are 0. This property is read-only.

Data Types: `single | double`

`ParameterDescription` — Distribution parameter descriptions

cell array of strings

Distribution parameter descriptions, stored as a cell array of strings. Each cell contains a short description of one distribution parameter. This property is read-only.

Data Types: `char`

`ParameterIsFixed` — Logical flag for fixed parameters

array of logical values

Logical flag for fixed parameters, stored as an array of logical values. If `0`, the corresponding parameter in the `ParameterNames` array is not fixed. If `1`, the corresponding parameter in the `ParameterNames` array is fixed. This property is read-only.

Data Types: `logical`

`ParameterNames` — Distribution parameter names

cell array of strings

Distribution parameter names, stored as a cell array of strings. This property is read-only.

Data Types: `char`

`ParameterValues` — Distribution parameter values

vector of scalar values

Distribution parameter values, stored as a vector. This property is read-only.

Data Types: `single` | `double`

`Truncation` — Truncation interval

vector of scalar values

Truncation interval for the probability distribution, stored as a vector containing the lower and upper truncation boundaries. This property is read-only.

Data Types: `single` | `double`

Methods

Inherited Methods

cdf	Cumulative distribution function of probability distribution object
icdf	Inverse cumulative distribution function of probability distribution object
iqr	Interquartile range of probability distribution object
median	Median of probability distribution object
pdf	Probability density function of probability distribution object
random	Generate random numbers from probability distribution object
truncate	Truncate probability distribution object

mean	Mean of probability distribution object
negloglik	Negative log likelihood of probability distribution object
paramci	Confidence intervals for probability distribution parameters
proflik	Profile likelihood function for probability distribution object
std	Standard deviation of probability distribution object
var	Variance of probability distribution object

Definitions

Weibull Distribution

The Weibull distribution is used in reliability and lifetime modeling, and to model the breaking strength of materials.

The Weibull distribution uses the following parameters.

Parameter	Description	Support
a	Scale parameter	$a > 0$
b	Shape parameter	$b > 0$

The probability density function (pdf) is

$$f(x \mid a,b) = \frac{b}{a}\left(\frac{x}{a}\right)^{b-1} \exp\left\{-\left(\frac{x}{a}\right)^{b}\right\} \quad ; \quad x \geq 0 \, .$$

Examples

Create a Weibull Distribution Object Using Default Parameters

Create a Weibull distribution object using the default parameter values.

```
pd = makedist('Weibull')
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 1
    B = 1
```

Create a Weibull Distribution Object Using Specified Parameter Values

Create a Weibull distribution object by specifying the parameter values.

```
pd = makedist('Weibull','a',2,'b',5)
```

```
pd =

  WeibullDistribution

  Weibull distribution
    A = 2
    B = 5
```

Compute the mean of the distribution.

```
m = mean(pd)
```

```
m =

    1.8363
```

See Also

`dfittool` | `fitdist` | `makedist`

More About

- "Weibull Distribution"

- Class Attributes
- Property Attributes

wishrnd

Wishart random numbers

Syntax

```
W = wishrnd(Sigma,df)
W = wishrnd(Sigma,df,D)
[W,D] = wishrnd(Sigma,df)
```

Description

`W = wishrnd(Sigma,df)` generates a random matrix `W` having the Wishart distribution with covariance matrix `Sigma` and with `df` degrees of freedom. The inverse of `W` has the Inverse Wishart distribution with parameters `Tau = inv(Sigma)` and `df` degrees of freedom.

`W = wishrnd(Sigma,df,D)` expects `D` to be the Cholesky factor of `Sigma`. If you call `wishrnd` multiple times using the same value of `Sigma`, it's more efficient to supply `D` instead of computing it each time.

`[W,D] = wishrnd(Sigma,df)` returns `D` so you can provide it as input in future calls to `wishrnd`.

This function defines the parameter `Sigma` so that the mean of the output matrix is `Sigma*df`

More About

- “Wishart Distribution” on page B-175

See Also

`iwishrnd`

X property

Class: TreeBagger

X data used to create ensemble

Description

The `X` property is a numeric matrix of size `Nobs`-by-`Nvars`, where `Nobs` is the number of observations (rows) and `Nvars` is the number of variables (columns) in the training data. This matrix contains the predictor (or feature) values.

xptread

Create table from data stored in SAS XPORT format file

Syntax

```
data = xptread
data = xptread(filename)
[data,missing] = xptread(filename)
xptread(...,'ReadObsNames',true)
```

Description

`data = xptread` displays a dialog box for selecting a file, then reads data from the file into a table. The file must be in the `SAS XPORT` format.

`data = xptread(filename)` retrieves data from a `SAS XPORT` format file `filename`. The `XPORT` format allows for 28 missing data types, represented in the file by an upper case letter, `'.'` or `'_'`. `xptread` converts all missing data to `NaN` values in `data`. However, if you need the specific missing types then you can recover this information by specifying a second output.

`[data,missing] = xptread(filename)` returns a nominal array, `missing`, of the same size as `data` containing the missing data type information from the `xport` format file. The entries are undefined for values that are not present and are one of `'.'`, `'_'`, `'A'`,...,`'Z'` for missing values.

`xptread(...,'ReadObsNames',true)` treats the first variable in the file as observation names. The default value is false.

`xptread` only supports single data sets per file. `xptread` does not support compressed files.

Examples

Read In SAS XPORT Data

Read in `SAS XPORT` format data.

```
data = xptread('sample.xpt');
```

See Also

table

x2fx

Convert predictor matrix to design matrix

Syntax

```
D = x2fx(X,model)
D = x2fx(X,model,categ)
D = x2fx(X,model,categ,catlevels)
```

Description

`D = x2fx(X,model)` converts a matrix of predictors `X` to a design matrix `D` for regression analysis. Distinct predictor variables should appear in different columns of `X`.

The optional input `model` controls the regression model. By default, `x2fx` returns the design matrix for a linear additive model with a constant term. `model` is one of the following strings:

- `'linear'` — Constant and linear terms. This is the default.
- `'interaction'` — Constant, linear, and interaction terms
- `'quadratic'` — Constant, linear, interaction, and squared terms
- `'purequadratic'` — Constant, linear, and squared terms

If `X` has n columns, the order of the columns of `D` for a full quadratic model is:

1. The constant term
2. The linear terms (the columns of `X`, in order 1, 2, ..., n)
3. The interaction terms (pairwise products of the columns of `X`, in order (1, 2), (1, 3), ..., (1, n), (2, 3), ..., (n–1, n))
4. The squared terms (in order 1, 2, ..., n)

Other models use a subset of these terms, in the same order.

Alternatively, `model` can be a matrix specifying polynomial terms of arbitrary order. In this case, `model` should have one column for each column in `X` and one row for each term in the model. The entries in any row of `model` are powers for the corresponding columns of `X`. For example, if `X` has columns `X1`, `X2`, and `X3`, then a row `[0 1 2]` in

model specifies the term `(X1.^0).*(X2.^1).*(X3.^2)`. A row of all zeros in *model* specifies a constant term, which can be omitted.

`D = x2fx(X,model,categ)` treats columns with numbers listed in the vector `categ` as categorical variables. Terms involving categorical variables produce dummy variable columns in `D`. Dummy variables are computed under the assumption that possible categorical levels are completely enumerated by the unique values that appear in the corresponding column of `X`.

`D = x2fx(X,model,categ,catlevels)` accepts a vector `catlevels` the same length as `categ`, specifying the number of levels in each categorical variable. In this case, values in the corresponding column of `X` must be integers in the range from 1 to the specified number of levels. Not all of the levels need to appear in `X`.

Examples

Example 1

The following converts 2 predictors `X1` and `X2` (the columns of `X`) into a design matrix for a full quadratic model with terms `constant`, `X1`, `X2`, `X1.*X2`, `X1.^2`, and `X2.^2`.

```
X = [1 10
     2 20
     3 10
     4 20
     5 15
     6 15];

D = x2fx(X,'quadratic')
D =
     1     1    10    10     1   100
     1     2    20    40     4   400
     1     3    10    30     9   100
     1     4    20    80    16   400
     1     5    15    75    25   225
     1     6    15    90    36   225
```

Example 2

The following converts 2 predictors `X1` and `X2` (the columns of `X`) into a design matrix for a quadratic model with terms `constant`, `X1`, `X2`, `X1.*X2`, and `X1.^2`.

```
X = [1 10
     2 20
     3 10
     4 20
     5 15
     6 15];
model = [0 0
         1 0
         0 1
         1 1
         2 0];

D = x2fx(X,model)
D =
     1     1    10    10     1
     1     2    20    40     4
     1     3    10    30     9
     1     4    20    80    16
     1     5    15    75    25
     1     6    15    90    36
```

See Also

regstats | rstool | candexch | candgen | cordexch | rowexch

Y property

Class: TreeBagger

Y data used to create ensemble

Description

The Y property is an array of true class labels for classification, or response values for regression. Y can be a numeric column vector, a character matrix, or a cell array of strings.

zscore

Standardized *z*-scores

Syntax

```
Z = zscore(X)
Z = zscore(X,flag)
Z = zscore(X,flag,dim)
[Z,mu,sigma] = zscore( ___ )
```

Description

`Z = zscore(X)` returns the *z*-score for each element of `X` such that columns of `X` are centered to have mean 0 and scaled to have standard deviation 1. `Z` is the same size as `X`.

- If `X` is a vector, then `Z` is a vector of *z*-scores.
- If `X` is a matrix, then `Z` is a matrix of the same size as `X`, and each column of `Z` has mean 0 and standard deviation 1.
- For multidimensional arrays, *z*-scores in `Z` are computed along the first nonsingleton dimension of `X`.

`Z = zscore(X,flag)` scales `X` using the standard deviation indicated by `flag`.

- If `flag` is 0 (default), then `zscore` scales `X` using the sample standard deviation, with $n - 1$ in the denominator of the standard deviation formula. `zscore(X,0)` is the same as `zscore(X)`.
- If `flag` is 1, then `zscore` scales `X` using the population standard deviation, with n in the denominator of standard deviation formula.

`Z = zscore(X,flag,dim)` standardizes `X` along dimension `dim`. For example, for a matrix `X`, if `dim` = 1, then `zscore` uses the means and standard deviations along the columns of `X`, if `dim` = 2, then `zscore` uses the means and standard deviations along the rows of `X`.

`[Z,mu,sigma] = zscore( ___ )` also returns the means and standard deviations used for centering and scaling, `mu` and `sigma`, respectively. You can use any of the input arguments in the previous syntaxes.

Examples

Z-Scores of Two Data Vectors

Compute and plot the *z*-scores of two data vectors, and then compare the results.

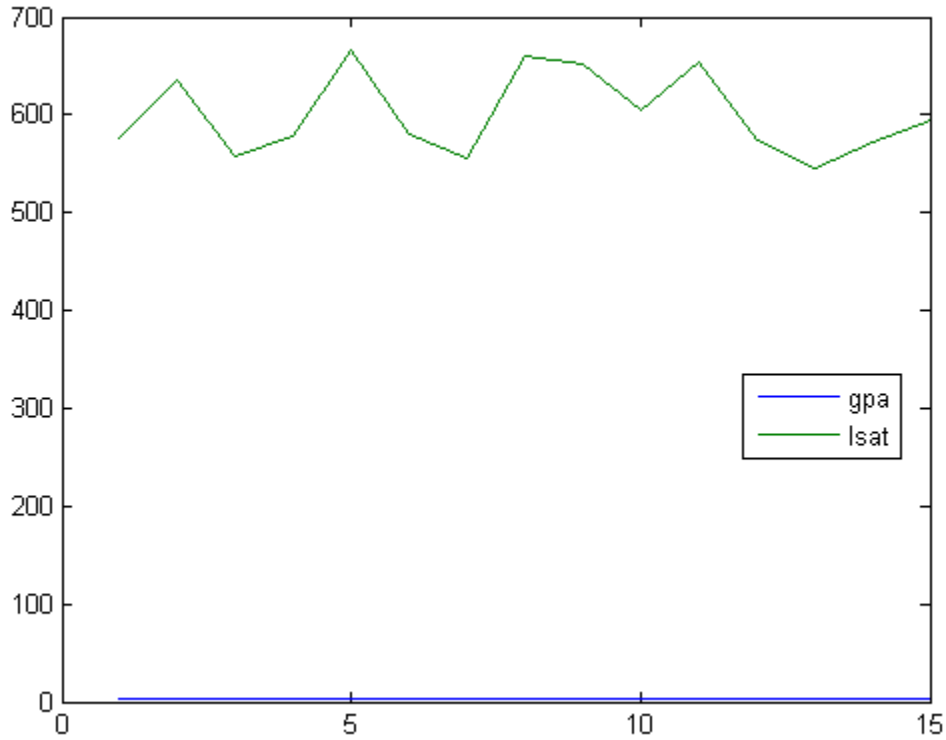
Load the sample data.

```
load('lawdata.mat')
```

Two variables load into the workspace: `gpa` and `lsat`.

Plot both variables on the same axes.

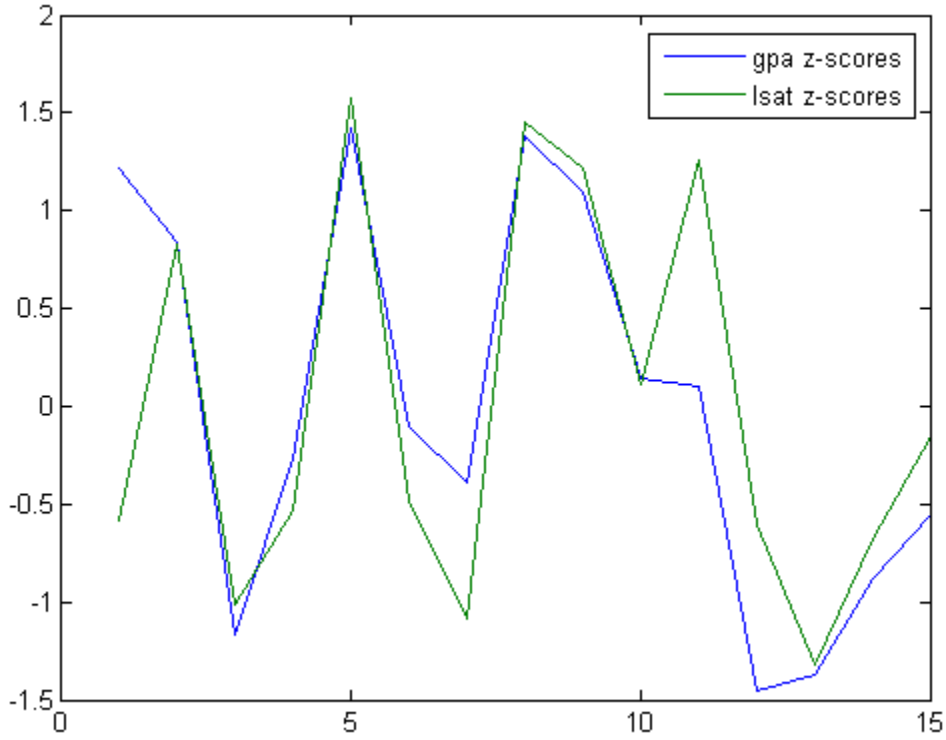
```
plot([gpa,lsat])
legend('gpa','lsat','Location','East')
```



It is difficult to compare these two measures because they are on a very different scale.

Plot the *z*-scores of `gpa` and `lsat` on the same axes.

```
Zgpa = zscore(gpa);
Zlsat = zscore(lsat);
plot([Zgpa, Zlsat])
legend('gpa z-scores','lsat z-scores','Location','Northeast')
```



Now, you can see the relative performance of individuals with respect to both their `gpa` and `lsat` results. For example, the third individual's `gpa` and `lsat` results are both one standard deviation below the sample mean. The eleventh individual's `gpa` is around the sample mean but has an `lsat` score almost 1.25 standard deviations above the sample average.

Check the mean and standard deviation of the *z*-scores you created.

```
mean([Zgpa,Zlsat])
```

```
ans =

   1.0e-14 *
```

```
   -0.1088    0.0357

 std([Zgpa,Zlsat])

ans =

     1     1
```

By definition, *z*-scores of `gpa` and `lsat` have mean 0 and standard deviation 1.

Z-Scores for a Population vs. Sample

Load the sample data.

```
load('lawdata.mat')
```

Two variables load into the workspace: `gpa` and `lsat`.

Compute the *z*-scores of `gpa` using the population formula for standard deviation.

```
Z1 = zscore(gpa,1); % population formula
Z0 = zscore(gpa,0); % sample formula
disp([Z1 Z0])

 1.2554    1.2128
 0.8728    0.8432
-1.2100   -1.1690
-0.2749   -0.2656
 1.4679    1.4181
-0.1049   -0.1013
-0.4024   -0.3888
 1.4254    1.3771
 1.1279    1.0896
 0.1502    0.1451
 0.1077    0.1040
-1.5076   -1.4565
-1.4226   -1.3743
-0.9125   -0.8815
-0.5724   -0.5530
```

For a sample from a population, the population standard deviation formula with n in the denominator corresponds to the maximum likelihood estimate of the population standard

deviation, and might be biased. The sample standard deviation formula, on the other hand, is the unbiased estimator of the population standard deviation for a sample.

Z-Scores of a Data Matrix

Compute *z*-scores using the mean and standard deviation computed along the columns or rows of a data matrix.

Load the sample data.

```
load('flu.mat')
```

The dataset array `flu` is loaded in the workplace. `flu` has 52 observations on 11 variables. The first variable contains dates (in weeks). The other variables contain the flu estimates for different regions in the U.S.

Convert the dataset array to a data matrix.

```
flu2 = double(flu(:,2:end));
```

The new data matrix, `flu2`, is a 52-by-10 double data matrix. The rows correspond to the weeks and the columns correspond to the U.S. regions in the data set array `flu`.

Standardize the flu estimate for each region (the *columns* of `flu2`).

```
Z1 = zscore(flu2,[ ],1);
```

You can see the *z*-scores in the variable editor by double-clicking on the matrix `Z1` created in the workspace.

Standardize the flu estimate for each week (the *rows* of `flu2`).

```
Z2 = zscore(flu2,[ ],2);
```

Z-Scores, Mean, and Standard Deviation

Return the mean and standard deviation used to compute the *z*-scores.

Load the sample data.

```
load('lawdata.mat')
```

Two variables load into the workspace: `gpa` and `lsat`.

Return the *z*-scores, mean, and standard deviation of `gpa`.

```
[Z,gpamean,gpastdev] = zscore(gpa)
```

```
Z =

    1.2128
    0.8432
   -1.1690
   -0.2656
    1.4181
   -0.1013
   -0.3888
    1.3771
    1.0896
    0.1451
    0.1040
   -1.4565
   -1.3743
   -0.8815
   -0.5530

gpamean =

    3.0947

gpastdev =

    0.2435
```

Input Arguments

`X` — Input data

vector | matrix | multidimensional array

Input data, specified as a vector, matrix, or multidimensional array.

Data Types: `double` | `single`

`flag` — Indicator for the standard deviation

0 (default) | 1

Indicator for the standard deviation used to compute the *z*-scores, specified as 0 or 1.

- If `flag` is 0 (default), then `zscore` scales `X` using the sample standard deviation. `zscore(X,0)` is the same as `zscore(X)`.
- If `flag` is 1, then `zscore` scales `X` using the population standard deviation.

`dim` — Dimension
1 (default) | positive integer

Dimension along which to calculate the *z*-scores of `X`, specified as a positive integer. For example, for a matrix `X`, if `dim` = 1, then `zscore` uses the means and standard deviations along the columns of `X`, if `dim` = 2, then `zscore` uses the means and standard deviations along the rows of `X`.

Output Arguments

`Z` — *z*-scores
vector | matrix | multidimensional array

z-scores, returned as a vector, matrix, or multidimensional array. A vector of *z*-scores has mean 0 and variance 1.

- If `X` is a vector, then `Z` is a vector of *z*-scores.
- If `X` is an array, then `zscore` is an array, with each column or row standardized to have mean 0 and variance 1 (depending on `dim`). If `dim` is not specified, `zscore` standardizes along the first nonsingleton dimension of `X`.

`mu` — Mean
scalar | vector

Mean of `X` used to compute the *z*-scores, returned as a scalar or vector.

- If `X` is a vector, then `mu` is a scalar.
- If `X` is a matrix, then `mu` is a row vector if `zscore` calculates the means along the columns of `X` (`dim` = 1), and a column vector if `zscore` calculates the means along the rows of `X` (`dim` = 2).

`sigma` — Standard deviation
scalar | vector

Standard deviation of `X` used to compute the *z*-scores, returned as a scalar or vector.

- If `X` is a vector, then `sigma` is a scalar.
- If `X` is a matrix, then `sigma` is a row vector if `zscore` calculates the standard deviations along the columns of `X` (`dim` = 1), and a column vector if `zscore` calculates the standard deviations along the rows of `X` (`dim` = 2).

More About

Z-Score

For a random variable X with mean μ and standard deviation σ, the z-score of a value x is

$$z = \frac{(x - \mu)}{\sigma}.$$

For sample data with mean $\bar{X}$ and standard deviation S, the z-score of a data point x is

$$z = \frac{\left(x - \bar{X}\right)}{S}.$$

z-scores measure the distance of a data point from the mean in terms of the standard deviation. This is also called *standardization* of data. The standardized data set has mean 0 and standard deviation 1, and retains the shape properties of the original data set (same skewness and kurtosis).

You can use z-scores to put data on the same scale before further analysis. This lets you to compare two or more data sets with different units.

Multidimensional Array

A *multidimensional array* is an array with more than two dimensions. For example, if X is a 1-by-3-by-4 array, then `X` is a three-dimensional array.

First Nonsingleton Dimension

A *first nonsingleton dimension* is the first dimension of an array whose size is not equal to 1. For example, if `X` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `X`.

Sample Standard Deviation

The *sample standard deviation*, S, is given by

$$S = \sqrt{\frac{\sum_{i=1}^{n}\left(x_i - \bar{X}\right)^2}{n-1}}.$$

S is the square root of an unbiased estimator of the variance of the population from which `X` is drawn, as long as `X` consists of independent, identically distributed samples.

Notice that the denominator in this variance formula is $n - 1$.

Population Standard Deviation

If the data is the entire population of values, then you can use the *population standard deviation*,

$$\sigma = \sqrt{\frac{\sum_{i=1}^{n}\left(x_i - \mu\right)^2}{n}}.$$

If `X` is a random sample from a population, then μ is estimated by the sample mean, and σ is the biased maximum likelihood estimator of the population standard deviation.

Notice that the denominator in this variance formula is n.

Algorithms

`zscore` returns `NaN`s for any sample containing `NaN`s.

`zscore` returns `0`s for any sample that is constant (all values are the same). For example, if `X` is a vector of the same numeric value, then `Z` is a vector of `0`s. If `X` is a matrix with a column of consisting of the same value, then that column of `Z` consists of `0`s.

See Also

`mean` | `std`

ztest

z-test

Syntax

```
h = ztest(x,m,sigma)
h= ztest(x,m,sigma,Name,Value)
[h,p] = ztest(___)
[h,p,ci,zval] = ztest(___)
```

Description

`h = ztest(x,m,sigma)` returns a test decision for the null hypothesis that the data in the vector x comes from a normal distribution with mean m and a standard deviation sigma, using the *z*-test. The alternative hypothesis is that the mean is not m. The result h is `1` if the test rejects the null hypothesis at the 5% significance level, and `0` otherwise.

`h= ztest(x,m,sigma,Name,Value)` returns a test decision for the *z*-test with additional options specified by one or more name-value pair arguments. For example, you can change the significance level or conduct a one-sided test.

`[h,p] = ztest(___)` also returns the *p*-value of the test, using any of the input arguments from previous syntaxes.

`[h,p,ci,zval] = ztest(___)` also returns the confidence interval of the population mean, ci, and the value of the test statistic, zval.

Examples

Test for a Hypothesized Mean

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
```

```
x = grades(:,1);
```

Test the null hypothesis that the data comes from a normal distribution with mean `m = 75` and standard deviation `sigma = 10`.

```
[h,p,ci,zval] = ztest(x,75,10)
```

```
h =
     0

p =
    0.9927

ci =
   73.2191
   76.7975

zval =
    0.0091
```

The returned value of `h = 0` indicates that `ztest` does not reject the null hypothesis at the default 5% significance level.

One-Sided Hypothesis Test

Load the sample data. Create a vector containing the first column of the students' exam grades data.

```
load examgrades;
x = grades(:,1);
```

Test the null hypothesis that the data comes from a normal distribution with mean `m = 65` and standard deviation `sigma = 10`, against the alternative that the mean is greater than 65.

```
[h,p] = ztest(x,65,10,'Tail','right')
```

```
h =
     1

p =
   2.8596e-28
```

The returned value of `h = 1` indicates that `ztest` rejects the null hypothesis at the default 5% significance level, in favor of the alternative hypothesis that the population mean is greater than 65.

Input Arguments

`x` — Sample data

vector | matrix | multidimensional array

Sample data, specified as a vector, matrix, or multidimensional array.

- If x is specified as a vector, `ztest` returns a single value for each output argument.
- If x is specified as a matrix, `ztest` performs a separate *z*-test along each column of x and returns a vector of results.
- If x is specified as a multidimensional array, `ztest` works along the first nonsingleton dimension of x.

In all cases, `ztest` treats `NaN` values as missing data and ignores them.

Data Types: `single` | `double`

`m` — Hypothesized mean

scalar value

Hypothesized mean, specified as a scalar value.

Data Types: `single` | `double`

`sigma` — Population standard deviation

scalar value

Population standard deviation, specified as a scalar value.

Data Types: `single` | `double`

Name-Value Pair Arguments

Specify optional comma-separated pairs of Name,Value arguments. `Name` is the argument name and `Value` is the corresponding value. `Name` must appear inside single

quotes (' '). You can specify several name and value pair arguments in any order as `Name1,Value1,...,NameN,ValueN`.

Example: `'Tail','right','Alpha',0.01` specifies a right-tailed hypothesis test at the 1% significance level.

`'Alpha'` — Significance level

`0.05` (default) | scalar value in the range (0,1)

Significance level of the hypothesis test, specified as the comma-separated pair consisting of `'Alpha'` and a scalar value in the range (0,1).

Example: `'Alpha',0.01`

Data Types: `single` | `double`

`'Dim'` — Dimension

first nonsingleton dimension (default) | positive integer value

Dimension of the input matrix along which to test the means, specified as the comma-separated pair consisting of `'Dim'` and a positive integer value. For example, specifying `'Dim',1` tests the column means, while `'Dim',2` tests the row means.

Example: `'Dim',2`

Data Types: `single` | `double`

`'Tail'` — Type of alternative hypothesis

`'both'` (default) | `'right'` | `'left'`

Type of alternative hypothesis to evaluate, specified as the comma-separated pair consisting of `'Tail'` and one of the following.

`'both'`	Test the alternative hypothesis that the population mean is not equal to `m`.
`'right'`	Test the alternative hypothesis that the population mean is greater than `m`.
`'left'`	Test the alternative hypothesis that the population mean is less than `m`.

Example: `'Tail','right'`

Output Arguments

h — Hypothesis test result

1 | 0

Hypothesis test result, returned as a logical value.

- If h = 1, this indicates the rejection of the null hypothesis at the Alpha significance level.
- If h = 0, this indicates a failure to reject the null hypothesis at the Alpha significance level.

p — *p*-value

scalar value in the range [0,1]

p-value of the test, returned as a scalar value in the range [0,1]. p is the probability of observing a test statistic as extreme as, or more extreme than, the observed value under the null hypothesis. Small values of p cast doubt on the validity of the null hypothesis.

ci — Confidence interval

vector

Confidence interval for the true population mean, returned as a two-element vector containing the lower and upper boundaries of the 100 × (1 – Alpha)% confidence interval.

zval — Test statistic

nonnegative scalar value

Test statistic, returned as a nonnegative scalar value.

More About

z-Test

The *z*-test is a parametric hypothesis test used to determine whether a sample data set comes from a population with a particular mean. The test assumes the sample data comes from a population with a normal distribution and a known standard deviation.

The test statistic is

$$z = \frac{\bar{x} - \mu}{\sigma / \sqrt{n}},$$

where $\bar{x}$ is the sample mean, μ is the population mean, σ is the population standard deviation, and n is the sample size. Under the null hypothesis, the test statistic has a standard normal distribution.

Multidimensional Array

A multidimensional array has more than two dimensions. For example, if `x` is a 1-by-3-by-4 array, then `x` is a three-dimensional array.

First Nonsingleton Dimension

The first nonsingleton dimension is the first dimension of an array whose size is not equal to 1. For example, if `x` is a 1-by-2-by-3-by-4 array, then the second dimension is the first nonsingleton dimension of `x`.

See Also

`ttest` | `ttest2`

Classification Learner

Train models to classify data using supervised machine learning

Description

The Classification Learner app trains models to classify data. Using this app, you can explore supervised machine learning using various classifiers. Classification types include decision trees, support vector machines, nearest neighbors, and ensemble classification. You can perform supervised machine learning by supplying a known set of input data (observations or examples) and known responses to the data (e.g., labels or classes). You use the data to train a model that generates predictions for the response to new data. To use the model with new data, or to learn about programmatic classification, you can export the model to the workspace or generate MATLAB code to recreate the trained model.

Required Products

- MATLAB
- Statistics and Machine Learning Toolbox

Open the Classification Learner App

- Open from the Apps tab of the MATLAB Toolstrip, in the Math, Statistics and Optimization group
- Alternatively, start it from the MATLAB command prompt using `classificationLearner`.

Examples

- "Explore Classification Models Interactively"
- "Choose a Classifier"
- "Explore Decision Trees Interactively"
- "Explore Support Vector Machines Interactively"
- "Explore Nearest Neighbor Classification Interactively"

- “Explore Ensemble Classification Interactively”

More About

- “Classification Trees and Regression Trees”

Parameters

Import Data

Open a dialog to select data from the workspace. Importing new data starts a new app session and discards any previous data and trained models.

1. The app tries to select a suitable response variable. Change the selections if needed to specify the response, predictors and any variables you do not want to import.

   Response variables can be a categorical array, cell array of strings, character array, logical vector, or a numeric vector the same size as the input predictor data.
2. (Optionally) Choose a validation method to examine the predictive accuracy of the fitted models, or try the default settings.

For details, see “Select Data and Validation for Classification Problem”.

Feature Selection

Open the Feature Selection dialog box to specify predictors to include in the model.

Use the check boxes to try including different features in the model. See if you can improve the model by removing features with low predictive power.

Classifier Choice

Specify the classifier to train by clicking an option in the **Classifier** toolstrip section. To see all available classifier options, on the far right of the **Classifier** section, click the arrow to expand the list of classifiers. The options in the **Classifier** gallery are starting points with different settings.

For help, see “Choose a Classifier”.

Tip After you choose a classifier type (e.g., Support Vector Machines), try training each of the options in the **Classifier** gallery. The options in the **Classifier** gallery are starting points with different settings. Try them all to see which option produces the best model with your data.

Decision Trees

Decision trees are easy to interpret, fast for fitting and prediction, and low on memory usage, but they can have low predictive accuracy. Try to grow shallower trees to prevent overfitting. Control the depth with the Minimum leaf size setting.

For details, see “Choose a Classifier”.

Tip Try training each of the decision tree options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to further improve your model, try feature selection, and then (optionally) try changing some advanced options.

Support Vector Machines

Support vector machines have high predictive accuracy, medium fitting speed, and can have good prediction speed and memory usage with few support vectors. Linear SVM is easy to interpret, but other kernel functions are less easy to interpret.

For details, see “Choose a Classifier”.

Tip Try training each of the support vector machine options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to further improve your model, try feature selection, and then (optionally) try changing some advanced options.

Nearest Neighbor Classifiers

Nearest Neighbor Classifiers has good predictive accuracy in low dimensions, but not in high dimensions. They have fast fitting speed, medium prediction speed, high memory usage, and are not easy to interpret.

For details, see “Choose a Classifier”.

Tip Try training each of the nearest neighbor options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to further improve your model, try feature selection, and then (optionally) try changing some advanced options.

Ensemble Classifiers

Ensemble Classifiers meld results from many weak learners into one high-quality ensemble predictor. Qualities depend on the choice of algorithm.

Note: All ensemble classifiers tend to be slow to fit because they often need many learners. They are not easy to interpret.

For details, see “Choose a Classifier”.

Tip Try training each of the ensemble classifier options in the **Classifier** gallery. Train them all to see which settings produce the best model with your data. Select the best model in the History list. To try to further improve your model, try feature selection, and then (optionally) try changing some advanced options.

Generate Code

After you create classification models interactively in Classification Learner app, you can generate MATLAB code for your best model. You can then use the code to train the model with new data.

The app generates code from the model you select in the History list, and displays the file in the MATLAB Editor. The file includes the predictors and response and the classifier training methods. View the generated code to learn how to programmatically create a trained model using the classifier and validation options you selected in the app.

To retrain your classifier model, call the file from the command line with your original data as input arguments. You also can call the file with new data.

For details, see “Export Classification Model to Predict New Data”.

Export Model

After you create classification models interactively in Classification Learner app, you can export your best model to the workspace. You can then use the trained model to make predictions with new data. Export the currently selected classifier in the History list to the workspace as a classification object. For example, a `ClassificationTree`, or `CompactClassificationTree`. Compact classification objects do not include the training data.

For details, see “Export Classification Model to Predict New Data”.

Settings

If you do not want to include the data used for training the tree, select the **Export compacted** option. This exports the model as a compact classification object that does not include the data (e.g., `CompactClassificationTree`). You cannot perform some tasks with a compact classification object, such as cross validation. Use a compact classification tree for making predictions (classifications) of new data.

See Also

Functions

`fitcecoc` | `fitcknn` | `fitcsvm` | `fitctree` | `fitensemble`

Introduced in R2015a

Distribution Fitting

Fit probability distributions to data

Description

The Distribution Fitting app interactively fits probability distributions to data imported from the MATLAB workspace. You can choose from 22 built-in probability distributions or create your own custom distribution. The app displays plots of the fitted distribution superimposed on a histogram of the data. Available plots include probability density function (pdf), cumulative distribution function (cdf), probability plots, and survivor functions. You can export the fitted parameter values to the workspace as a probability distribution object, and use object functions to perform further analyses. For more information on working with these objects, see "Working with Probability Distributions" on page 5-3. For the programmatic work flow of the Distribution Fitting app, see `dfittool`.

Required Products

- MATLAB
- Statistics and Machine Learning Toolbox

Open the Distribution Fitting App

- On the MATLAB toolstrip, click the Apps tab. In the Math, Statistics and Optimization group, open the **Distribution Fitting** app.
- Alternatively, at the command prompt, enter `dfittool`.

Examples

- "Fit a Distribution Using the Distribution Fitting App" on page 5-101

Parameters

Data

To select data from the workspace, open a dialog box.

1. From the **Data** drop-down list, select your variable of interest. If the variable is a matrix, the app imports the first column of the matrix by default. To select a different column or row of the matrix, click **Select Column or Row**. Alternatively, you can enter any valid MATLAB expression in the **Data** field.
2. (Optionally) From the **Censoring** and **Frequency** drop-down lists, select variables containing censoring and frequency data . If the variable is a matrix, the app imports the first column of the matrix by default. To select a different column or row of the matrix, click **Select Column or Row**.
3. In the **Dataset name** field, name the data set or accept the default name, and then click **Create Data Set**. The name of the new data set appears in the **Manage data sets** pane. Click the buttons below this pane to view the data (**View**), set the bin rules (**Set Bin Rules**), rename the data set (**Rename**), or delete the data set (**Delete**).

New Fit

To fit a probability distribution to an imported data set, open a dialog box.

1. In the **Fit name** field, name the data set or accept the default name.
2. From the **Data** drop-down list, select the data set to fit.
3. From the **Distribution** drop-down list, select the type of distribution to fit.
4. (Optionally) In the **Exclusion rule** drop-down list, specify a rule to exclude some data values. To populate this drop-down list, you must first define exclusion rules by clicking **Exclude** in the main window of the app.
5. Click **Apply** to fit the distribution to the data. The Distribution Fitting app displays a plot of the distribution, along with the corresponding data.

Manage Fits

To display a table of the available fits, open a dialog box.

1. Select **Plot** to specify which fits to plot in the main window. Clearing the **Plot** check box removes the fit from the plot.
2. If you select **Plot** for a particular fit, you can select **Conf bounds** to also display the confidence bounds for that fit on the plot in the main window. Clearing the **Conf bounds** check box removes the confidence intervals from the plot. The Distribution Fitting app displays confidence bounds only if the Display Type in the main window is set to `Cumulative probability (CDF)`, `Quantile (inverse CDF)`, `Survivor function`, or `Cumulative hazard`.
3. (Optionally) Click **New Fit** to open a **New Fit** window
4. (Optionally) Click **Copy** to create a copy of the selected fit.
5. (Optionally) Click **Edit** to open an **Edit Fit** window, where you can edit the fit.
6. (Optionally) Click **Save to workspace** to save the selected fit as a probability distribution object in the MATLAB workspace.
7. (Optionally) Click **Delete** to delete the selected fit.

Evaluate

To evaluate a fit at whatever data points you choose, open a dialog box. Available probability functions include the probability density function (pdf), cumulative distribution function (cdf), quantile (inverse cdf), survival function, cumulative hazard, and hazard rate.

1. In the **Fit** pane, select one or more fits to evaluate.
2. From the **Function** drop-down list, select the type of probability function to evaluate.
3. In the **At x =** field, specify the values at which to evaluate the function. If you specify **Function** as `Quantile (inverse CDF)`, this field name changes to **At p =** and you enter a vector of probability values.
4. (Optionally) Select **Compute confidence bounds** to compute the confidence bounds for the selected fit. This check box is enabled only if you specify **Function** as `Cumulative probability (CDF)`, `Quantile (inverse CDF)`, `Survivor function`, or `Cumulative hazard`. In the **Level** field, set the level for the confidence bounds or accept the default value.
5. (Optionally) Select **Plot function** to display a plot of the distribution function, evaluated at the points that you enter in the **At x =** field, in a new window.
6. To apply these settings to the selected fit, click **Apply**. The results appear on the right side of the **Evaluate** window.

7 (Optionally) Click **Export to Workspace** to export a matrix containing the results to the MATLAB workspace.

Exclude

To define data exclusion rules to apply to the fit, open a dialog box.

1 In the **Exclusion rule name** field, specify a name for the exclusion rule.

2 In the **Exclude sections** pane, define the exclusion rule. In the **Lower limits exclude data** and **Upper limits exclude data** fields, you can numerically specify limits. Alternatively, in the **Exclude graphically** pane, you can define the exclusion rule graphically. From the **Select data** drop-down list, select the data set and click **Exclude Graphically**. An interactive plot opens where you can add lower or upper limits by clicking and dragging a boundary on the plot.

3 Click **Create Exclusion Rule**.

4 (Optionally) You can copy, view, rename, or delete exclusion rules. Select the rule from the **Existing exclusion rules** field on the right of the **Exclude** window and click the appropriate button.

Programmatic Use

`dfittool` opens the Distribution Fitting app, or brings focus to the app if it is already open.

`dfittool(y)` opens the Distribution Fitting app populated with the data specified by the vector y.

`dfittool(y,cens)` uses the vector cens to specify whether the observation `y(j)` is censored, `(cens(j)==1)`, or observed exactly, `(cens(j)==0)`. If cens is omitted or empty, then no y values are censored.

`dfittool(y,cens,freq)` uses the vector freq to specify the frequency of each element contained in y. If freq is omitted or empty, then all values in y have a frequency of 1.

`dfittool(y,cens,freq,dsname)` creates a data set with the name dsname using the data vector, y, censoring indicator, cens, and frequency vector, freq. Specify dsname as a string enclosed in single quotes, for example, `'mydata'`.

See Also

Functions

`dfittool` | `fitdist` | `makedist`

More About

- "Model Data Using the Distribution Fitting App" on page 5-74
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

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Sample Data Sets

Statistics and Machine Learning Toolbox software includes the sample data sets in the following table.

To load a data set into the MATLAB workspace, type:

```
load filename
```

where *filename* is one of the files listed in the table.

Data sets contain individual data variables, description variables with references, and dataset arrays encapsulating the data set and its description, as appropriate.

File	Description of Data Set
acetylene.mat	Chemical reaction data with correlated predictors
arrhythmia.mat	Cardiac arrhythmia data from the UCI machine learning repository
carbig.mat	Measurements of cars, 1970–1982
carsmall.mat	Subset of carbig.mat. Measurements of cars, 1970, 1976, 1982
cereal.mat	Breakfast cereal ingredients
cities.mat	Quality of life ratings for U.S. metropolitan areas
discrim.mat	A version of cities.mat used for discriminant analysis
examgrades.mat	Exam grades on a scale of 0–100
fisheriris.mat	Fisher's 1936 iris data
flu.mat	Google Flu Trends estimated ILI (influenza-like illness) percentage for various regions of the US, and CDC weighted ILI percentage based on sentinel provider reports
gas.mat	Gasoline prices around the state of Massachusetts in 1993
hald.mat	Heat of cement vs. mix of ingredients
hogg.mat	Bacteria counts in different shipments of milk
hospital.mat	Simulated hospital data
imports-85.mat	1985 Auto Imports Database from the UCI repository
ionosphere.mat	Ionosphere dataset from the UCI machine learning repository

File	Description of Data Set
kmeansdata.mat	Four-dimensional clustered data
lawdata.mat	Grade point average and LSAT scores from 15 law schools
mileage.mat	Mileage data for three car models from two factories
moore.mat	Biochemical oxygen demand on five predictors
morse.mat	Recognition of Morse code distinctions by non-coders
ovariancancer.mat	Grouped observations on 4000 predictors
parts.mat	Dimensional run-out on 36 circular parts
polydata.mat	Sample data for polynomial fitting
popcorn.mat	Popcorn yield by popper type and brand
reaction.mat	Reaction kinetics for Hougen-Watson model
sat.dat	Scholastic Aptitude Test averages by gender and test (table)
sat2.dat	Scholastic Aptitude Test averages by gender and test (csv)
spectra.mat	NIR spectra and octane numbers of 60 gasoline samples
stockreturns.mat	Simulated stock returns

B

Distribution Reference

Bernoulli Distribution

In this section...

Overview

The Bernoulli distribution is a discrete probability distribution with the only two possible values for the random variable. Each instance of an event with a Bernoulli distribution is called a Bernoulli trial.

Parameters

The Bernoulli distribution uses the following parameter.

Parameter	Description	Support
p	Probability of success	$0 \le p \le 1$

Probability Mass Function

The probability mass function (pmf) is

$$f(x \mid p) = \begin{cases} 1-p & , \quad x = 0, \\ p & , \quad x = 1 \end{cases}.$$

Mean and Variance

The mean is

$$\text{mean} = p\,.$$

The variance is

$$\text{var} = p(1-p).$$

Relationship to Other Distributions

The Bernoulli distribution is a special case of the binomial distribution, with the number of trials $n = 1$. The geometric distribution models the number of Bernoulli trials before the first success (or first failure).

More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Beta Distribution

In this section...

Overview

The beta distribution describes a family of curves that are unique in that they are nonzero only on the interval (0 1). A more general version of the function assigns parameters to the endpoints of the interval.

Statistics and Machine Learning Toolbox provides several ways to work with the beta distribution. You can use the following approaches to estimate parameters from sample data, compute the pdf, cdf, and icdf, generate random numbers, and more.

- Fit a probability distribution object to sample data, or create a probability distribution object with specified parameter values. See `Using BetaDistribution Objects` for more information.
- Work with data input from matrices, tables, and dataset arrays using probability distribution functions. See “Supported Distributions” on page 5-17 for a list of beta distribution functions.
- Interactively fit, explore, and generate random numbers from the distribution using an app or user interface.

For more information on each of these options, see “Working with Probability Distributions” on page 5-3.

Parameters

The beta distribution uses the following parameters.

Parameter	Description	Support
a	First shape parameter	$\alpha > 0$

Parameter	Description	Support
b	Second shape parameter	$b > 0$

Probability Density Function

Definition

The probability density function (pdf) of the beta distribution is

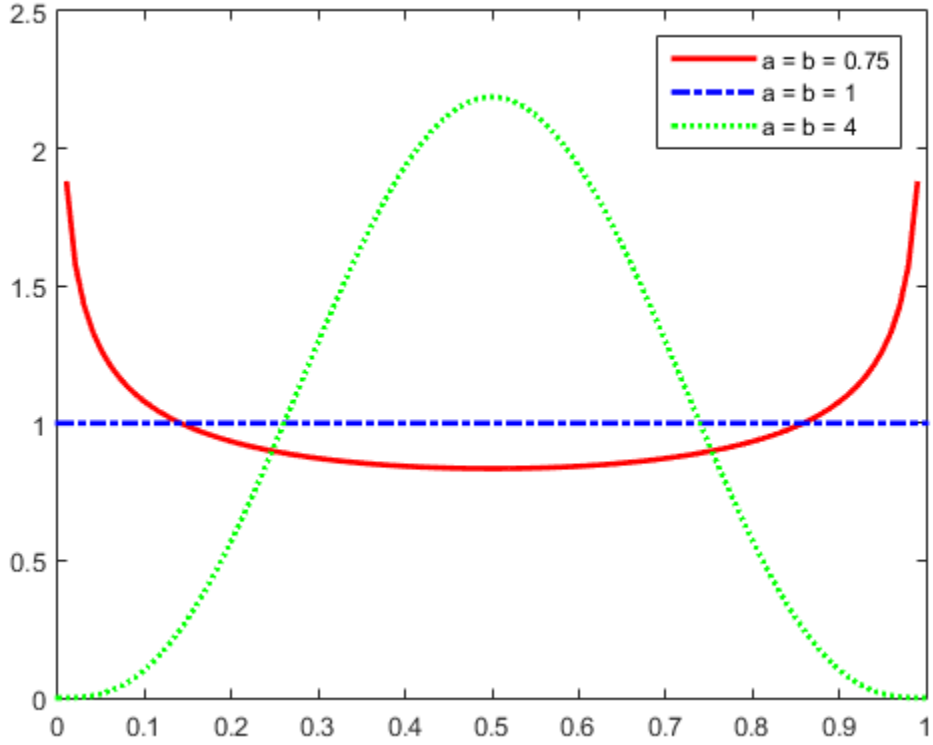
$$y = f(x \mid a,b) = \frac{1}{B(a,b)} x^{a-1}(1-x)^{b-1} I_{(0,1)}(x)$$

where $B(\cdot)$ is the Beta function. The indicator function $I_{(0,1)}(x)$ ensures that only values of x in the range (0,1) have nonzero probability.

Plot

This plot shows how changing the value of the parameters alters the shape of the pdf. The constant pdf (the flat line) shows that the standard uniform distribution is a special case of the beta distribution, which occurs when `a = b = 1`.

```
X = 0:.01:1;
y1 = betapdf(X,0.75,0.75);
y2 = betapdf(X,1,1);
y3 = betapdf(X,4,4);

figure
plot(X,y1,'Color','r','LineWidth',2)
hold on
plot(X,y2,'LineStyle','-.','Color','b','LineWidth',2)
plot(X,y3,'LineStyle',':','Color','g','LineWidth',2)
legend({'a = b = 0.75','a = b = 1','a = b = 4'},'Location','NorthEast');
hold off
```



Relationship to Other Distributions

The beta distribution has a functional relationship with the t distribution. If Y is an observation from Student's t distribution with ν degrees of freedom, then the following transformation generates X, which is beta distributed.

$$X = \frac{1}{2} + \frac{1}{2}\frac{Y}{\sqrt{\nu + Y^2}}$$

If $Y \sim t(\upsilon)$, then $X \sim \beta\left(\frac{\nu}{2}, \frac{\nu}{2}\right)$

This relationship is used to compute values of the t cdf and inverse function as well as generating t distributed random numbers.

Cumulative Distribution Function

The beta cdf is the same as the incomplete beta function.

Example

Suppose you are collecting data that has hard lower and upper bounds of zero and one respectively. Parameter estimation is the process of determining the parameters of the beta distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the beta pdf. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. Maximum likelihood estimation (MLE) involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `betafit` returns the MLEs and confidence intervals for the parameters of the beta distribution. Here is an example using random numbers from the beta distribution with `a = 5` and`b = 0.2`.

```
rng default  % For reproducibility
r = betarnd(5,0.2,100,1);
[phat, pci] = betafit(r)
```

```
phat =

    7.4911    0.2135


pci =

    5.0861    0.1744
   11.0334    0.2614
```

The MLE for parameter `a` is 7.4911, compared to the true value of 5. The 95% confidence interval for `a` goes from 2.8051 to 6.2610, which does not include the true value. While

this is an unlikely result, it does sometimes happen when estimating distribution parameters.

Similarly the MLE for parameter b is 0.2135, compared to the true value of 0.2. The 95% confidence interval for b goes from 0.1771 to 0.2832, which does include the true value. In this made-up example you know the "true value." In experimentation you do not.

More About

- Using BetaDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Binomial Distribution

In this section...

Overview

The binomial distribution models the total number of successes in repeated trials from an infinite population under the following conditions:

- Only two outcomes are possible on each of n trials.
- The probability of success for each trial is constant.
- All trials are independent of each other.

Parameters

The binomial distribution uses the following parameters.

Parameter	Description	Support
`N`	Number of trials	positive integer
`p`	Probability of success	$0 \le p \le 1$

Probability Density Function

The probability density function (pdf) is

$$f(x \mid N, p) = \binom{N}{x} p^x (1-p)^{N-x} \quad ; \quad x = 0, 1, 2, \ldots, N,$$

where x is the number of successes in n trials of a Bernoulli process with probability of success p.

Mean and Variance

The mean is

$$\text{mean} = np .$$

The variance is

$$\text{var} = np(1-p) .$$

Relationship to Other Distributions

The binomial distribution is a generalization of the Bernoulli distribution, allowing for a number of trials n greater than 1. The binomial distribution generalizes to the multinomial distribution when there are more than two possible outcomes for each trial.

Example

Suppose you are collecting data from a widget manufacturing process, and you record the number of widgets within specification in each batch of 100. You might be interested in the probability that an individual widget is within specification. Parameter estimation is the process of determining the parameter, p, of the binomial distribution that fits this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the binomial pdf above. But for the pdf, the parameters (n and p) are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the value of p that give the highest likelihood given the particular set of data.

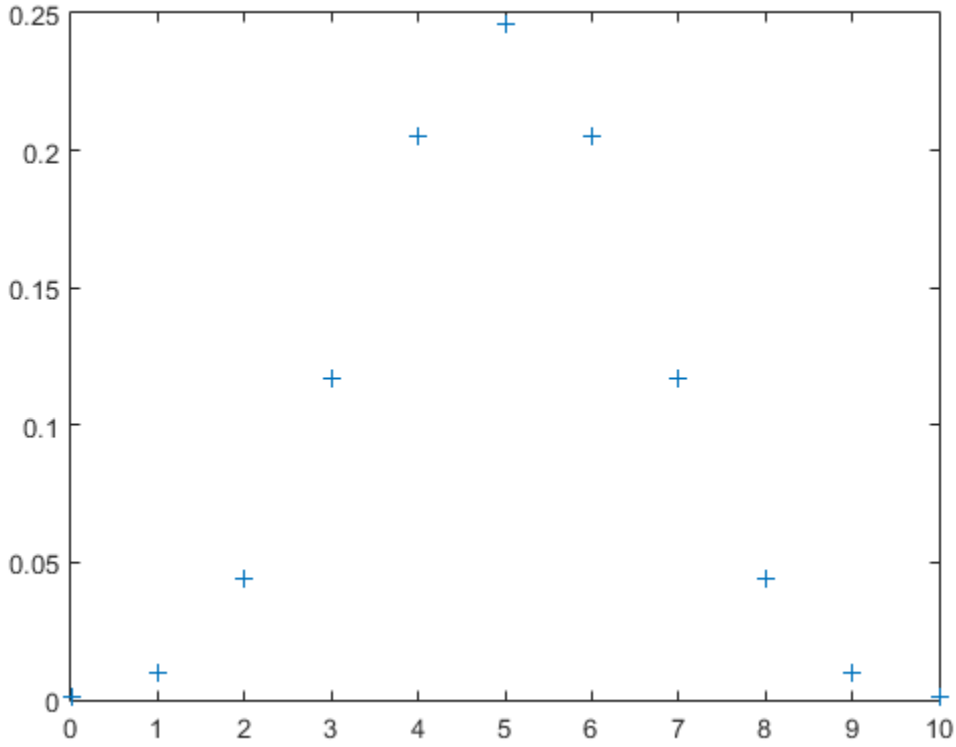
The function `binofit` returns the MLEs and confidence intervals for the parameters of the binomial distribution. Here is an example using random numbers from the binomial distribution with $n = 100$ and $p = 0.9$.

```
rng default;  % for reproducibility
r = binornd(100,0.9)
[phat, pci] = binofit(r,100)


r =

    85


phat =

    0.8500


pci =

    0.7647    0.9135
```

The MLE for parameter p is 0.8800, compared to the true value of 0.9. The 95% confidence interval for p goes from 0.7998 to 0.9364, which includes the true value. In this made-up example you know the "true value" of p. In experimentation you do not.

The following commands generate a plot of the binomial pdf for $n = 10$ and $p = 1/2$.

```
x = 0:10;
y = binopdf(x,10,0.5);
plot(x,y,'+')
```



More About

- Using BinomialDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Birnbaum-Saunders Distribution

In this section...

Definition

The Birnbaum-Saunders distribution has the density function

$$\frac{1}{\sqrt{2\pi}}\exp\left\{-\frac{\left(\sqrt{x/\beta}-\sqrt{\beta/x}\right)^2}{2\gamma^2}\right\}\left(\frac{\left(\sqrt{x/\beta}+\sqrt{\beta/x}\right)}{2\gamma x}\right)$$

with scale parameter ß > 0 and shape parameter $\gamma > 0$, for $x > 0$.

If x has a Birnbaum-Saunders distribution with parameters ß and γ, then

$$\frac{\left(\sqrt{x/\beta}-\sqrt{\beta/x}\right)}{\gamma}$$

has a standard normal distribution.

Background

The Birnbaum-Saunders distribution was originally proposed as a lifetime model for materials subject to cyclic patterns of stress and strain, where the ultimate failure of the material comes from the growth of a prominent flaw. In materials science, Miner's Rule suggests that the damage occurring after n cycles, at a stress level with an expected lifetime of N cycles, is proportional to n / N. Whenever Miner's Rule applies, the Birnbaum-Saunders model is a reasonable choice for a lifetime distribution model.

Parameters

To estimate distribution parameters, us `mle` or the Distribution Fitting app.

More About

- Using BirnbaumSaundersDistribution Objects
- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

Burr Type XII Distribution

In this section...

Definition

The Burr type XII distribution is a three-parameter family of distributions on the positive real line. The cumulative distribution function (cdf) of the Burr distribution is

$$F(x \mid \alpha, c, k) = 1 - \frac{1}{\left(1 + \left(\frac{x}{\alpha}\right)^c\right)^k}, \quad x > 0,\ \alpha > 0,\ c > 0,\ k > 0,$$

where c and k are the shape parameters and α is the scale parameter. The probability density function (pdf) is

$$f(x \mid \alpha, c, k) = \frac{\frac{kc}{\alpha}\left(\frac{x}{\alpha}\right)^{c-1}}{\left(1 + \left(\frac{x}{\alpha}\right)^c\right)^{k+1}}, \quad x > 0, \alpha > 0, c > 0, k > 0\,.$$

The density of the Burr type XII distribution is L-shaped if $c \le 1$ and unimodal, otherwise.

Background

Burr distribution was first discussed by Burr (1942) as a two-parameter family. An additional scale parameter was introduced by Tadikamalla (1980). It is a very flexible distribution family that can express a wide range of distribution shapes. The Burr distribution includes, overlaps, or has as a limiting case, many commonly used distributions such as gamma, lognormal, loglogistic, bell-shaped, and J-shaped beta distributions (but not U-shaped). Some compound distributions also correspond to the Burr distribution. For example, compounding a Weibull distribution with a gamma distribution for its scale parameter results in a Burr distribution. Similarly, compounding an exponential distribution with a gamma distribution for its rate parameter, 1/μ, also yields a Burr distribution. The Burr distribution also has two asymptotic limiting cases: Weibull and Pareto Type I.

The Burr distribution can fit a wide range of empirical data. Different values of its parameters cover a broad set of skewness and kurtosis. Hence, it is used in various fields such as finance, hydrology, and reliability to model a variety of data types. Examples of data modeled by the Burr distribution are household income, crop prices, insurance risk, travel time, flood levels, and failure data.

The survival and hazard functions of Burr type XII distribution are, respectively,

$$S(x\mid\alpha,c,k)=\frac{1}{\left[1+\left(\frac{x}{\alpha}\right)^{c}\right]^{k}}$$

and

$$h(x\mid\alpha,c,k)=\frac{\frac{kc}{\alpha}\left(\frac{x}{\alpha}\right)^{c-1}}{1+\left(\frac{x}{\alpha}\right)^{c}}.$$

If $c > 1$, the hazard function h(x) is non-monotonic with a mode at $x = \alpha(c-1)^{1/c}$.

Parameters

The three-parameter Burr distribution is defined by its scale parameter α and shape parameters c and k. You can estimate the parameters using `mle` or `fitdist`. Both functions support censored data for Burr distribution.

Generate sample data from a Burr distribution with scale parameter 0.5 and shape parameters 2 and 5.

```
rng('default')
R = random('burr',0.5,2,5,1000,1);
```

Estimate the parameters and the confidence intervals.

```
[phat,pci] = mle(R,'distribution','burr')
```

```
phat =

    0.4154    2.1217    4.0550


pci =

    0.2985    1.9560    2.4079
    0.5782    2.3014    6.8288
```

The default 95% confidence intervals for the parameters include the true parameter values.

The three-parameter Burr distribution converges asymptotically to one of the two limiting forms as its parameters diverge:

- If $k \to 0$, $c \to \infty$, $ck = \lambda$, then the Burr distribution reduces to a two-parameter Pareto distribution with the cdf

$$F_P = 1 - \left(\frac{x}{\alpha}\right)^{-\lambda}, x \geq \alpha.$$

- If $k \to \infty$, $\alpha \to \infty$, $\alpha/k^{1/c} = \theta$, then the Burr distribution reduces to a two-parameter Weibull distribution with the cdf

$$F_W(x \mid c,\theta) = 1 - \exp\left[-\left(\frac{x}{\theta}\right)^c\right].$$

If `mle` or `fitdist` detects such divergence, it returns an error message, but informs you of the limiting distribution and corresponding parameter estimates for that distribution.

Fit a Burr Distribution and Draw the cdf

This example shows how to fit a Burr distribution to data, draw the cdf, and construct a histogram with a Burr distribution fit.

1. Load the sample data.

```
load('arrhythmia.mat')
```

The fifth column in `X` contains a measurement obtained from electrocardiograms, called QRS duration.

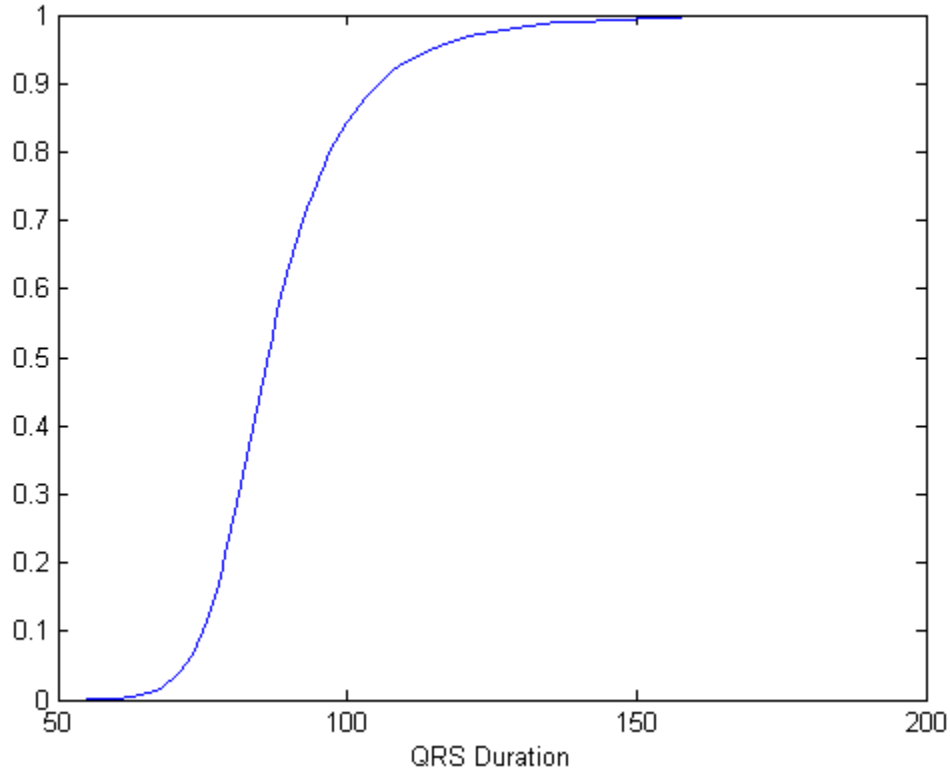
2. Fit a Burr distribution to the QRS duration data, and get the parameter estimates.

```
PD = fitdist(X(:,5),'burr');
```

`PD` has the maximum likelihood estimates of the Burr distribution parameters in the property `Param`. The estimates are $\alpha = 80.4515$, $c = 18.9251$, $k = 0.4492$.

3. Plot the cdf of the QRS duration data.

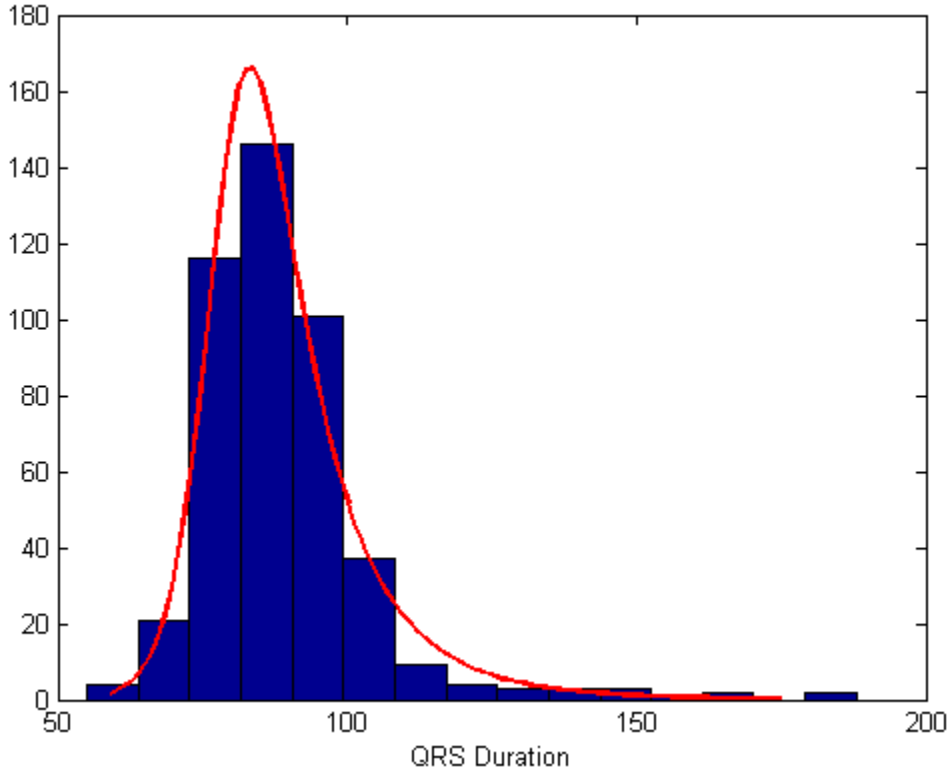
```
QRScdf=cdf('burr',sortrows(X(:,5)),80.4515,18.9251,0.4492);
plot(sortrows(X(:,5)),QRScdf)
xlabel('QRS Duration')
```



cdf of QRS duration data

4. Draw the histogram of QRS duration data with 15 bins and the pdf of the Burr distribution fit.

```
histfit(X(:,5),15,'burr')
xlabel('QRS Duration')
```



Histogram of QRS data with a Burr distribution fit

Compare Lognormal and Burr pdfs

This example shows how to compare the lognormal pdf to the Burr pdf using income data generated from a lognormal distribution.

1. Generate the income data.

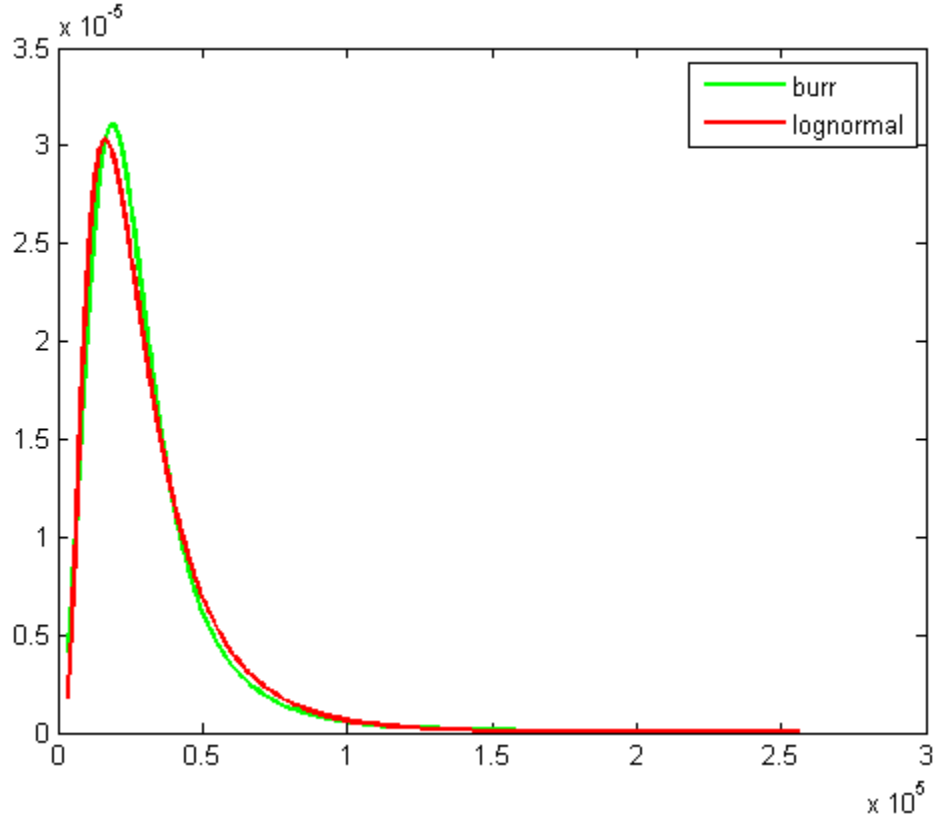
```
rng('default') % for reproducibility
y = random('logn',log(25000),0.65,500,1);
```

2. Fit a Burr distribution.

```
pd = fitdist(y,'burr');
```

3. Plot both the Burr and lognormal pdfs of income data on the same axis.

```
p = pdf('burr',sortrows(y),26007,2.6374,1.0966);
p2 = pdf('logn',sortrows(y),log(25000),0.65);
plot(sortrows(y),p,'g',sortrows(y),p2,'r','LineWidth',2)
legend('burr','lognormal')
```



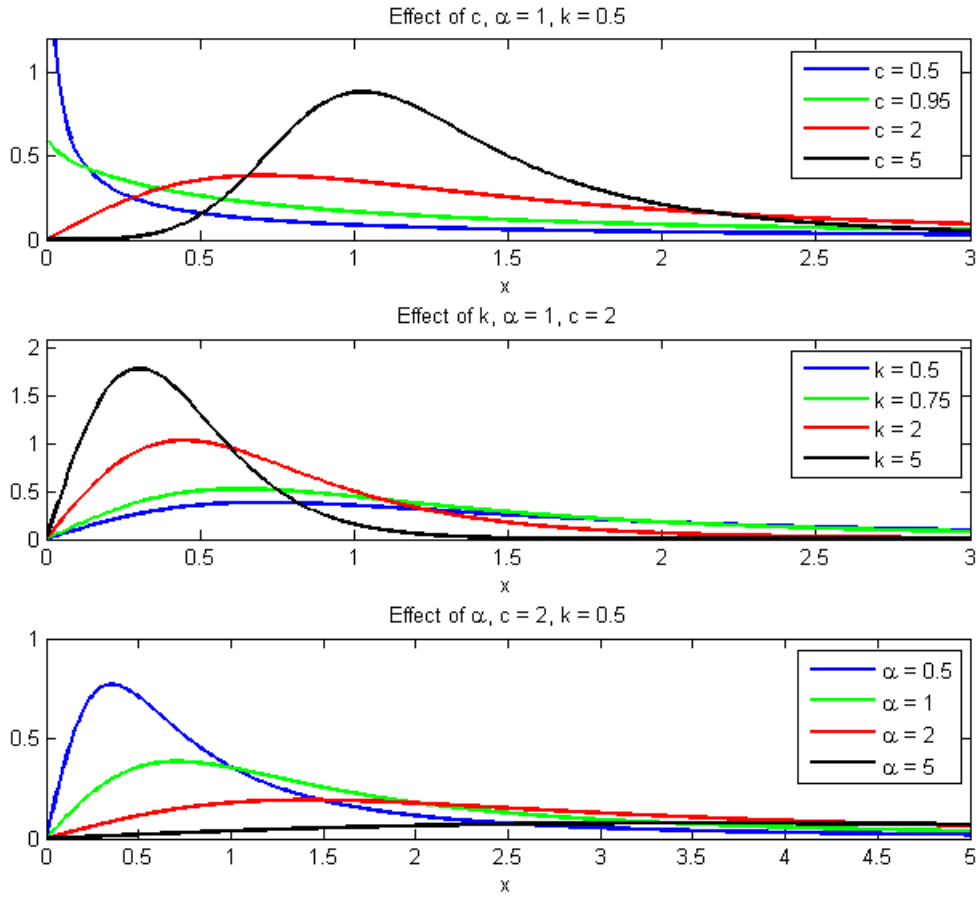
Burr and Lognormal pdfs fitted to income data

Burr pdf for Various Parameters

This example shows how to create a variety of shapes for probability density functions of the Burr distribution.

```
X = 0:0.01:5;
c = [0.5 0.95 2 5];
k = [0.5 0.75 2 5];
alpha = [0.5 1 2 5];
colors = ['b';'g';'r';'k']'
```

```
figure
for i = 1:1:4
pdf1(i,:) = pdf('burr',X,1,c(i),0.5);
pdf2(i,:) = pdf('burr',X,1,2,k(i));
pdf3(i,:) = pdf('burr',X,alpha(i),2,0.5);

axC = subplot(3,1,1);
pC(i) = plot(X,pdf1(i,:),colors(i),'LineWidth',2);
title('Effect of c, \alpha = 1, k = 0.5'),xlabel('x')
hold on

axK = subplot(3,1,2);
pK(i) = plot(X,pdf2(i,:),colors(i),'LineWidth',2);
title('Effect of k, \alpha = 1, c = 2'),xlabel('x')
hold on

axAlpha = subplot(3,1,3);
pAlpha(i) = plot(X,pdf3(i,:),colors(i),'LineWidth',2);
title('Effect of \alpha, c = 2, k = 0.5'),xlabel('x')
hold on
end

set(axC,'XLim',[0 3],'YLim',[0 1.2]);
set(axK,'XLim',[0 3],'YLim',[0 2.1]);
set(axAlpha,'XLim',[0 5],'YLim',[0 1]);

legend(axC,'c=0.5','c=0.95','c=2','c=5');
legend(axK,'k=0.5','k=0.75','k=2','k=5');
legend(axAlpha,'\alpha=0.5','\alpha=1','\alpha=2','\alpha=5');
```



This figure illustrates how the shape and scale of the Burr distribution changes for different values of its parameters.

Survival and Hazard Functions of Burr Distribution

This example shows how to find and plot the survival and hazard functions for a sample coming from a Burr distribution.

1. Generate the data.

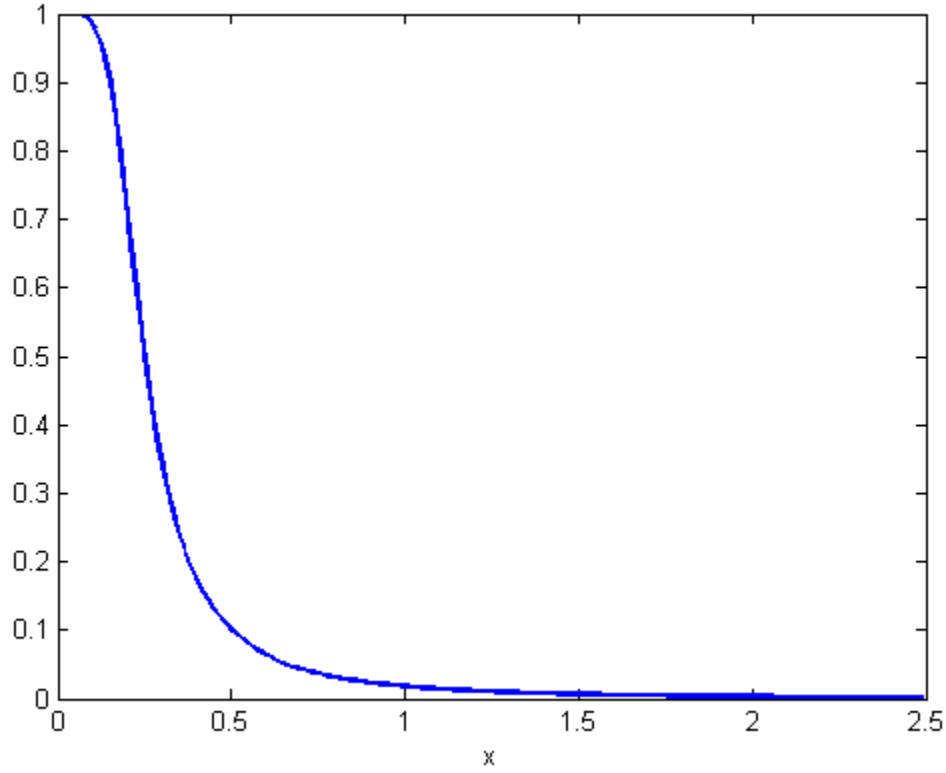
```
X = 0:0.015:2.5;
```

2. Evaluate the pdf and cdf of data in X.

```
Xpdf = pdf('burr',X,0.2,5,0.5);
Xcdf = cdf('burr',X,0.2,5,0.5);
```

3. Evaluate and plot the survival function of data in X.

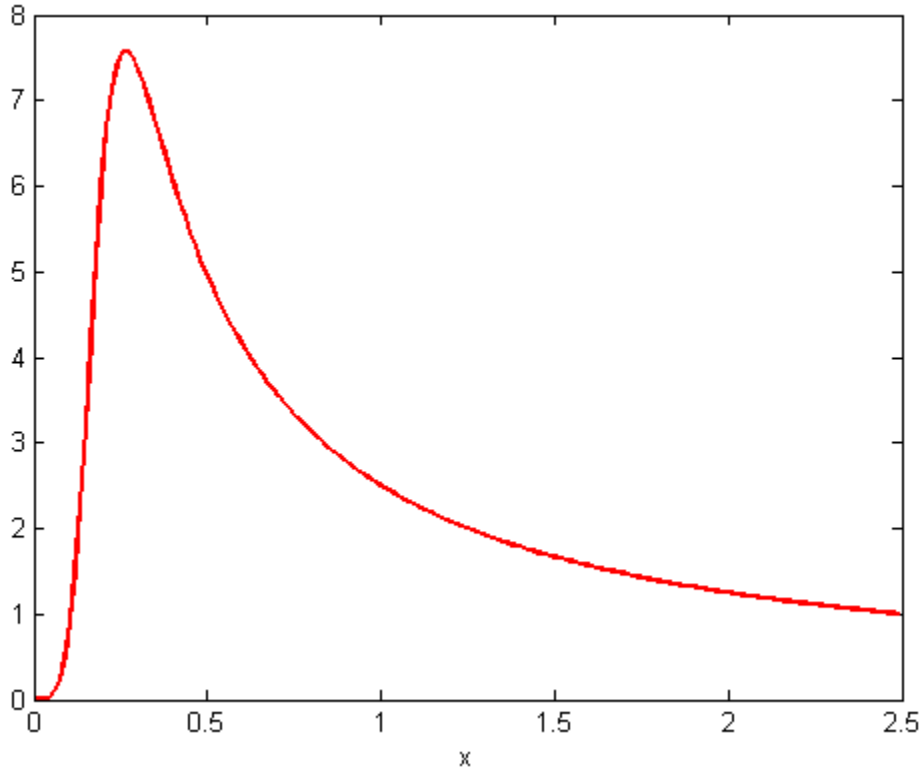
```
S = 1.-Xcdf; % survival function
plot(X,S,'LineWidth',2)
xlabel('x')
```



Survival function

4. Evaluate and plot the hazard function of data in X.

```
H = Xpdf./S; % hazard function
plot(X,H,'r','LineWidth',2)
xlabel('x')
```



Hazard function

Divergence of Parameter Estimates

This example shows how to interpret the display when the parameter estimates diverge when fitting a Burr distribution to input data.

1. Generate sample data from the Weibull distribution with parameters 0.5 and 2.

```
rng('default') % for reproducibility
X = wblrnd(0.5,2,100,1);
```

2. Fit a Burr distribution.

```
PD = fitdist(X,'burr');
```

```
Error using addburr>burrfit (line 566)
The data are not fit by a Burr distribution with finite
parameters. The maximum likelihood fit is provided by the
k->Inf, alpha->Inf limiting form of the Burr distribution: a
Weibull distribution with the parameters below.
 a (scale): 0.476817
 b (shape): 1.96219

Error in fitdata (line 24)
        p = F(x,fixedparams{:},0.05,opts{:});

Error in ProbDistUnivParam.fit (line 94)
pd = fitdata(pd,spec,x,cens,freq,fixedparams,options);

Error in fitdist (line 124)
        pd =
        ProbDistUnivParam.fit(x,distname,'cens',cens,'freq',freq,args{:});
```

The error message tells you that the Weibull family seems to fit the data better and gives you the parameter estimates from a Weibull fit. You can use those estimates directly. If you need covariance estimates for the parameters or other information about the fit, you can refit a Weibull distribution to the data.

3. Fit a Weibull distribution to the data and find the confidence intervals for the parameter estimates.

```
PD = fitdist(X,'weibull');
paramci(PD)
```

```
ans =

    0.4291    1.6821
    0.5298    2.2890
```

These are the 95% confidence intervals of the parameter estimates for the Weibull distribution fit.

References

[1] Burr, Irving W. "Cumulative frequency functions." *The Annals of Mathematical Statistics*, Vol. 13, Number 2, 1942, pp. 215–232.

[2] Tadikamalla, Pandu R. "A look at the Burr and related distributions." *International Statistical Review*, Vol. 48, Number 3, 1980, pp. 337–344.

[3] Rodriguez, Robert N. "A guide to the Burr type XII distributions." *Biometrika*, Vol. 64, Number 1, 1977, pp. 129–134.

[4] AL-Hussaini, Essam K. "A characterization of the Burr type XII distribution". *Appl. Math. Lett.* Vol. 4, Number 1, 1991, pp. 59–61.

[5] Grammig, Joachim and Kai-Oliver Maurer. "Non-monotonic hazard functions and the autoregressive conditional duration model." *Econometrics Journal*, Vol. 3, 2000, pp. 16–38.

More About

- Using BurrDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Chi-Square Distribution

In this section...

Overview

The chi-square distribution is commonly used in hypothesis testing, particularly the chi-squared test for goodness of fit.

Parameters

The chi-square distribution uses the following parameter.

Parameter	Description	Support
v	Degrees of freedom	v is a nonnegative integer value

Probability Density Function

The probability density function (pdf) is

$$y = f(x \mid v) = \frac{x^{(v-2)/2} e^{-x/2}}{2^{\frac{v}{2}} \Gamma(v/2)}$$

where $\Gamma(\cdot)$ is the Gamma function, v is the degrees of freedom, and $x \geq 0$.

Cumulative Distribution Function

The cumulative distribution function (cdf) is

$$p = F(x \mid \nu) = \int_0^x \frac{t^{(\nu-2)/2} e^{-t/2}}{2^{\nu/2}\Gamma(\nu/2)} dt$$

where $\Gamma(\cdot)$ is the Gamma function, v is the degrees of freedom, and $x \geq 0$.

Descriptive Statistics

The mean is v.

The variance is 2v.

Relationship to Other Distributions

The χ^2 distribution is a special case of the gamma distribution where $b = 2$ in the equation for gamma distribution below.

$$y = f(x \mid a, b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{x}{b}}$$

The χ^2 distribution gets special attention because of its importance in normal sampling theory. If a set of n observations is normally distributed with variance σ^2, and s^2 is the sample standard deviation, then

$$\frac{(n-1)s^2}{\sigma^2} \sim \chi^2(n-1)$$

This relationship is used to calculate confidence intervals for the estimate of the normal parameter σ^2 in the function `normfit`.

Examples

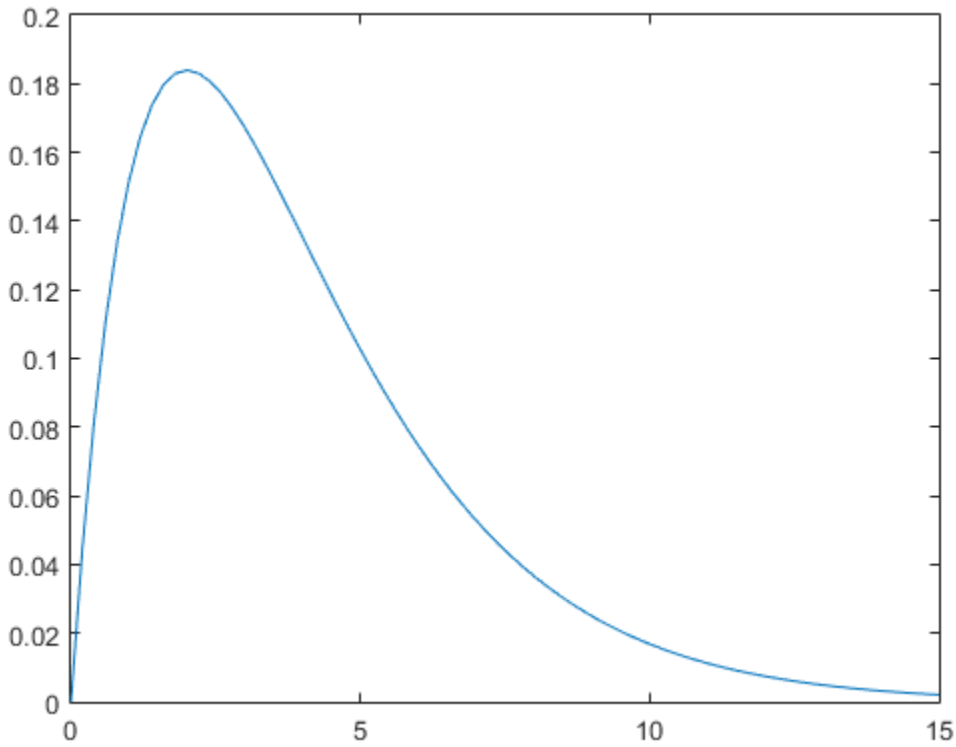
Compute Chi-Square Distribution pdf

Compute the pdf of a chi-square distribution with 4 degrees of freedom.

```
x = 0:0.2:15;
y = chi2pdf(x,4);
```

Plot the pdf.

```
figure;
plot(x,y)
```



The chi-square distribution is skewed to the right, especially for few degrees of freedom.

More About

- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

Copulas

See “Copulas: Generate Correlated Samples” on page 5-160.

Custom Distributions

User-defined custom distributions, created using files and function handles, are supported by the Statistics and Machine Learning Toolbox functions `pdf`, `cdf`, `icdf`, and `mle`, and the Statistics and Machine Learning Toolbox Distribution Fitting app.

Exponential Distribution

In this section...

Definition

The exponential pdf is

$$y = f(x \mid \mu) = \frac{1}{\mu} e^{\frac{-x}{\mu}}$$

Background

Like the chi-square distribution, the exponential distribution is a special case of the gamma distribution (obtained by setting $a = 1$)

$$y = f(x \mid a, b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{x}{b}}$$

where $\Gamma(\cdot)$ is the Gamma function.

The exponential distribution is special because of its utility in modeling events that occur randomly over time. The main application area is in studies of lifetimes.

Parameters

Suppose you are stress testing light bulbs and collecting data on their lifetimes. You assume that these lifetimes follow an exponential distribution. You want to know how long you can expect the average light bulb to last. Parameter estimation is the process of determining the parameters of the exponential distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the exponential pdf above. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `expfit` returns the MLEs and confidence intervals for the parameters of the exponential distribution. Here is an example using random numbers from the exponential distribution with $\mu = 700$.

```
lifetimes = exprnd(700,100,1);
[muhat, muci] = expfit(lifetimes)
```

```
muhat =

  672.8207

muci =

  547.4338
  810.9437
```

The MLE for parameter μ is 672, compared to the true value of 700. The 95% confidence interval for μ goes from 547 to 811, which includes the true value.

In the life tests you do not know the true value of μ so it is nice to have a confidence interval on the parameter to give a range of likely values.

Examples

Exponentially Distributed Lifetime Data

For exponentially distributed lifetimes, the probability that an item will survive an extra unit of time is independent of the current age of the item. The example shows a specific case of this special property.

```
l = 10:10:60;
lpd = l+0.1;
deltap = (expcdf(lpd,50)-expcdf(l,50))./(1-expcdf(l,50))
```

```
deltap =
    0.0020    0.0020    0.0020    0.0020    0.0020    0.0020
```

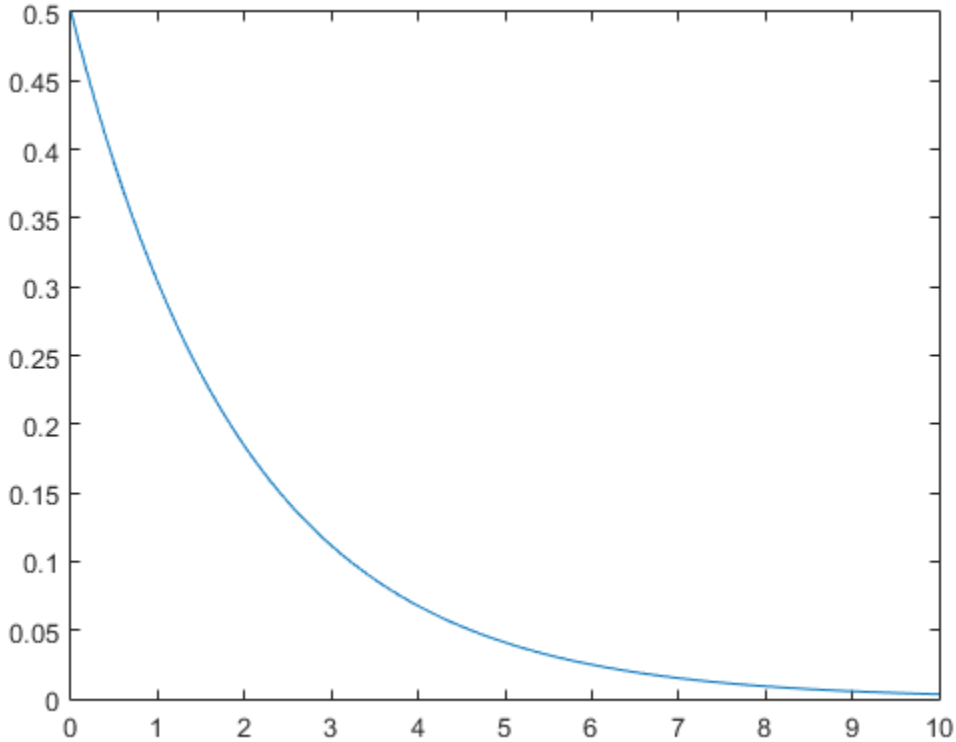
Compute the Exponential Distribution pdf

Compute the pdf of an exponential distribution with parameter `mu = 2`.

```
x = 0:0.1:10;
y = exppdf(x,2);
```

Plot the pdf.

```
figure;
plot(x,y)
```



More About

- Using ExponentialDistribution Objects

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Extreme Value Distribution

In this section...

Definition

The probability density function for the extreme value distribution with location parameter μ and scale parameter σ is

$$y = f\left(x \mid \mu,\sigma\right) = \sigma^{-1}\exp\left(\frac{x-\mu}{\sigma}\right)\exp\left(-\exp\left(\frac{x-\mu}{\sigma}\right)\right)$$

This form of the probability density function is suitable for modeling the minimum value. To model the maximum value, use the negative of the original values.

If T has a Weibull distribution with parameters a and b, then $\log T$ has an extreme value distribution with parameters $\mu = \log a$ and $\sigma = 1/b$.

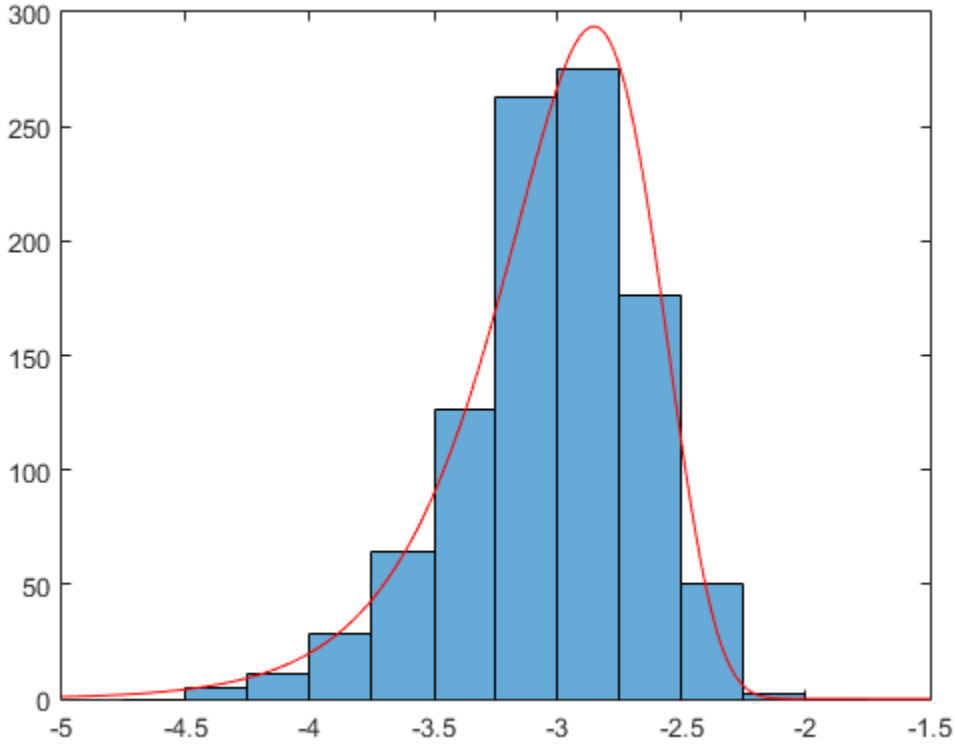
Background

Extreme value distributions are often used to model the smallest or largest value among a large set of independent, identically distributed random values representing measurements or observations. The extreme value distribution is appropriate for modeling the smallest value from a distribution whose tails decay exponentially fast, for example, the normal distribution. It can also model the largest value from a distribution, such as the normal or exponential distributions, by using the negative of the original values.

For example, the following fits an extreme value distribution to minimum values taken over 1000 sets of 500 observations from a normal distribution.

```
rng default;  % For reproducibility
```

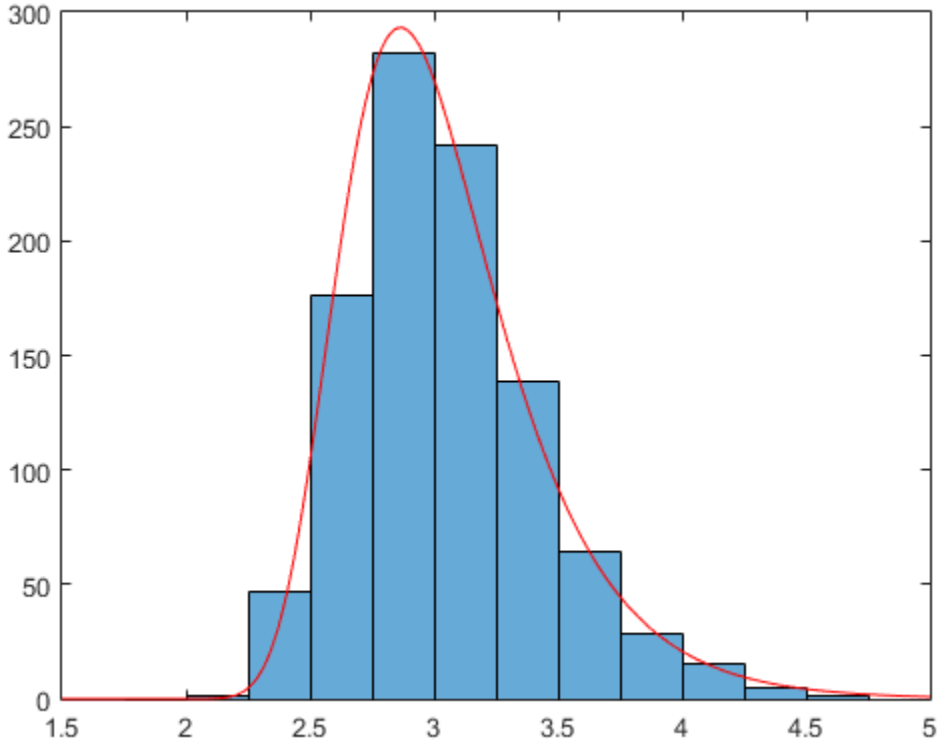
```
xMinima = min(randn(1000,500), [], 2);
paramEstsMinima = evfit(xMinima);
y = linspace(-5,-1.5,1001);
histogram(xMinima,-4.75:.25:-1.75);
p = evpdf(y,paramEstsMinima(1),paramEstsMinima(2));
line(y,.25*length(xMinima)*p,'color','r')
```



The following fits an extreme value distribution to the maximum values in each set of observations.

```
rng default;  % For reproducibility
xMaxima = max(randn(1000,500), [], 2);
paramEstsMaxima = evfit(-xMaxima);
y = linspace(1.5,5,1001);
```

```
histogram(xMaxima,1.75:.25:4.75);
p = evpdf(-y,paramEstsMaxima(1),paramEstsMaxima(2));
line(y,.25*length(xMaxima)*p,'color','r')
```



Although the extreme value distribution is most often used as a model for extreme values, you can also use it as a model for other types of continuous data. For example, extreme value distributions are closely related to the Weibull distribution. If `T` has a Weibull distribution, then `log(T)` has a type 1 extreme value distribution.

Parameters

The function `evfit` returns the maximum likelihood estimates (MLEs) and confidence intervals for the parameters of the extreme value distribution. The following example

shows how to fit some sample data using `evfit`, including estimates of the mean and variance from the fitted distribution.

Suppose you want to model the size of the smallest washer in each batch of 1000 from a manufacturing process. If you believe that the sizes are independent within and between each batch, you can fit an extreme value distribution to measurements of the minimum diameter from a series of eight experimental batches. The following code returns the MLEs of the distribution parameters as `parmhat` and the confidence intervals as the columns of `parmci`.

```
x = [19.774 20.141 19.44 20.511 21.377 19.003 19.66 18.83];
[parmhat, parmci] = evfit(x)
```

```
parmhat =
   20.2506    0.8223

parmci =
   19.644 0.49861
   20.857 1.3562
```

You can find mean and variance of the extreme value distribution with these parameters using the function `evstat`.

```
[meanfit, varfit] = evstat(parmhat(1),parmhat(2))
```

```
meanfit =
   19.776

varfit =
   1.1123
```

Examples

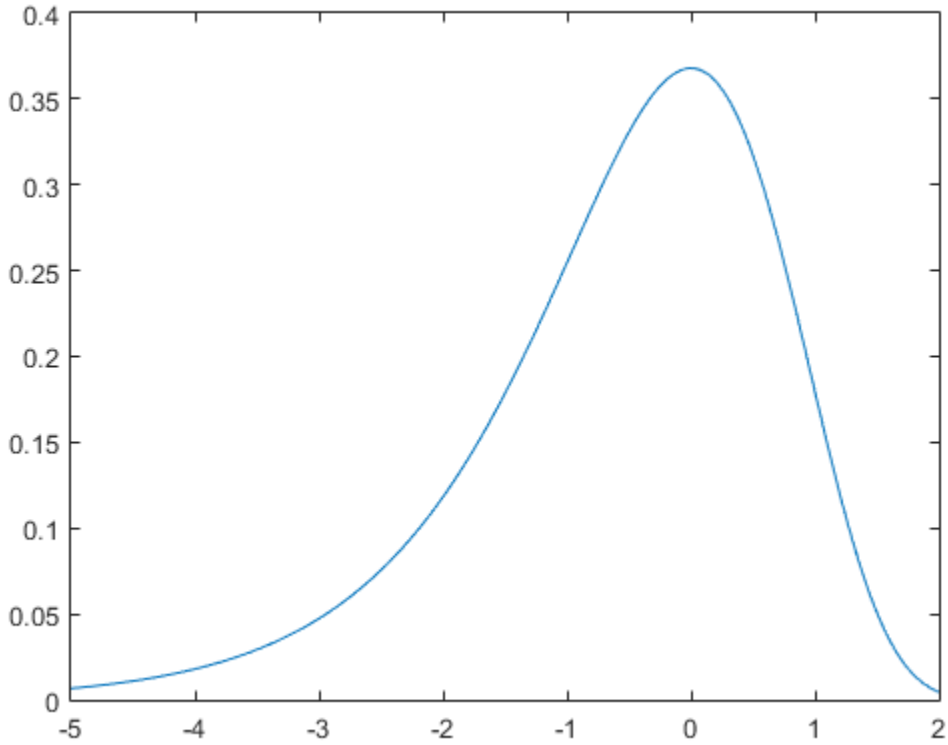
Compute the Extreme Value Distribution pdf

Compute the pdf of an extreme value distribution.

```
t = [-5:.01:2];
y = evpdf(t);
```

Plot the pdf.

```
figure;
plot(t,y)
```

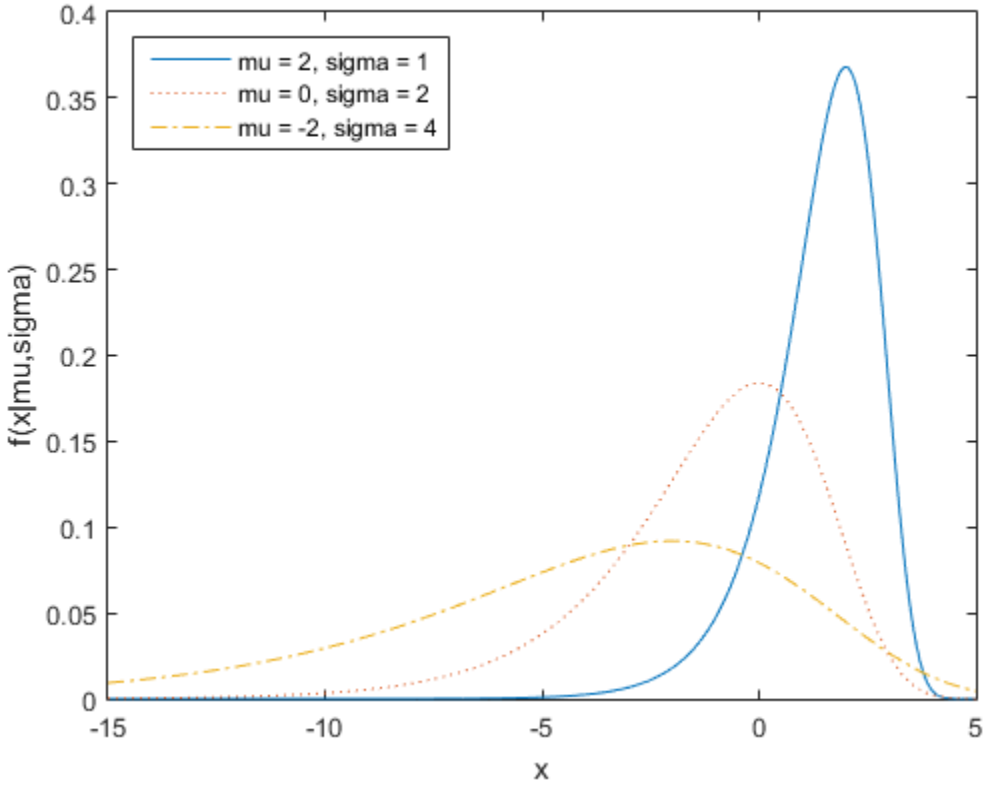


The extreme value distribution is skewed to the left, and its general shape remains the same for all parameter values. The location parameter, `mu`, shifts the distribution along the real line, and the scale parameter, `sigma`, expands or contracts the distribution.

The following plots the probability function for different combinations of `mu` and `sigma`.

```
x = -15:.01:5;
plot(x,evpdf(x,2,1),'-', ...
     x,evpdf(x,0,2),':', ...
     x,evpdf(x,-2,4),'-.');
legend({'mu = 2, sigma = 1', ...
        'mu = 0, sigma = 2', ...
        'mu = -2, sigma = 4'}, ...
       'Location','NW')
```

```
xlabel('x')
ylabel('f(x|mu,sigma)')
```



More About

- Using ExtremeValueDistribution Objects
- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

F Distribution

In this section...

Definition

The pdf for the F distribution is

$$y = f\left(x \mid \nu_1, \nu_2\right) = \frac{\Gamma\left[\frac{\left(\nu_1 + \nu_2\right)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{x^{\frac{\nu_1 - 2}{2}}}{\left[1 + \left(\frac{\nu_1}{\nu_2}\right)x\right]^{\frac{\nu_1 + \nu_2}{2}}}$$

where $\Gamma(\cdot)$ is the Gamma function.

Background

The F distribution has a natural relationship with the chi-square distribution. If χ_1 and χ_2 are both chi-square with ν_1 and ν_2 degrees of freedom respectively, then the statistic F below is F-distributed.

$$F\left(\nu_1, \nu_2\right) = \frac{\chi_1 / \nu_1}{\chi_2 / \nu_2}$$

The two parameters, ν_1 and ν_2, are the numerator and denominator degrees of freedom. That is, ν_1 and ν_2 are the number of independent pieces of information used to calculate χ_1 and χ_2, respectively.

Examples

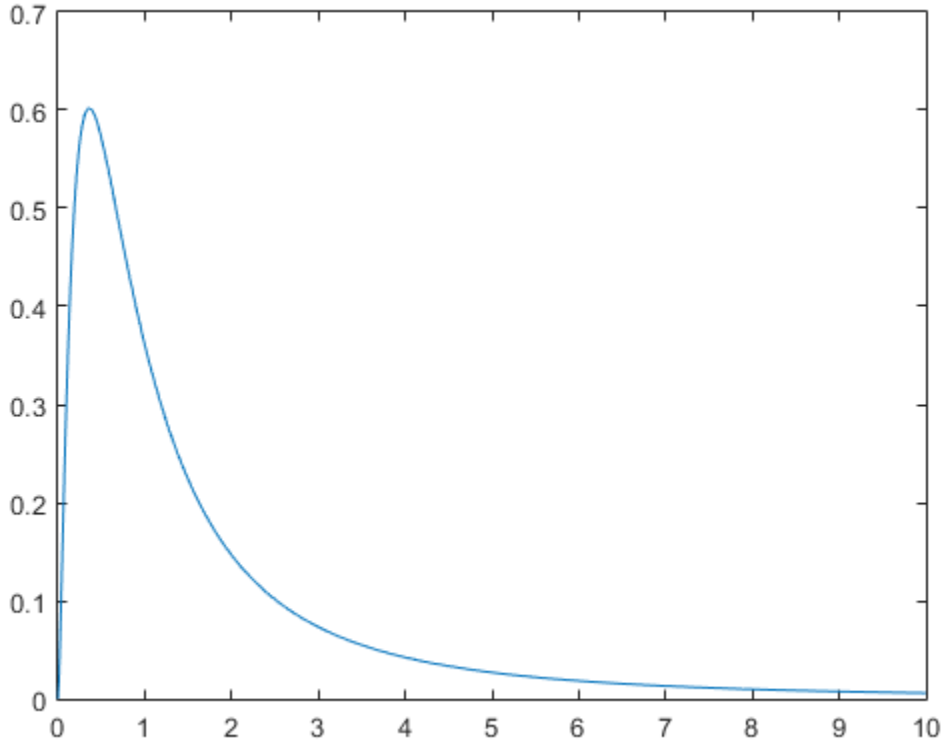
Compute the *F* Distribution pdf

Compute the pdf of an F distibution with 5 numerator degrees of freedom and 3 denominator degrees of freedom.

```
x = 0:0.01:10;
y = fpdf(x,5,3);
```

Plot the pdf.

```
figure;
plot(x,y)
```



The plot shows that the *F* distribution exists on positive real numbers and is skewed to the right.

More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Gamma Distribution

In this section...

Definition

The gamma pdf is

$$y = f(x \mid a,b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{\frac{-x}{b}}$$

where $\Gamma(\cdot)$ is the Gamma function.

Background

The gamma distribution models sums of exponentially distributed random variables.

The gamma distribution family is based on two parameters. The chi-square and exponential distributions, which are children of the gamma distribution, are one-parameter distributions that fix one of the two gamma parameters.

The gamma distribution has the following relationship with the incomplete Gamma function.

$$f(x \mid a,b) = \text{gammainc}\left(\frac{x}{b}, a\right)$$

When a is large, the gamma distribution closely approximates a normal distribution with the advantage that the gamma distribution has density only for positive real numbers.

Parameters

Suppose you are stress testing computer memory chips and collecting data on their lifetimes. You assume that these lifetimes follow a gamma distribution. You want to know how long you can expect the average computer memory chip to last. Parameter estimation is the process of determining the parameters of the gamma distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the gamma pdf above. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the x's) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `gamfit` returns the MLEs and confidence intervals for the parameters of the gamma distribution. Here is an example using random numbers from the gamma distribution with $a = 10$ and $b = 5$.

```
lifetimes = gamrnd(10,5,100,1);
[phat, pci] = gamfit(lifetimes)

phat =

    10.9821    4.7258

pci =

    7.4001    3.1543
   14.5640    6.2974
```

Note `phat(1)` = $\hat{a}$ and `phat(2)` = $\hat{b}$. The MLE for parameter a is 10.98, compared to the true value of 10. The 95% confidence interval for a goes from 7.4 to 14.6, which includes the true value.

Similarly the MLE for parameter b is 4.7, compared to the true value of 5. The 95% confidence interval for b goes from 3.2 to 6.3, which also includes the true value.

In the life tests you do not know the true value of a and b so it is nice to have a confidence interval on the parameters to give a range of likely values.

Examples

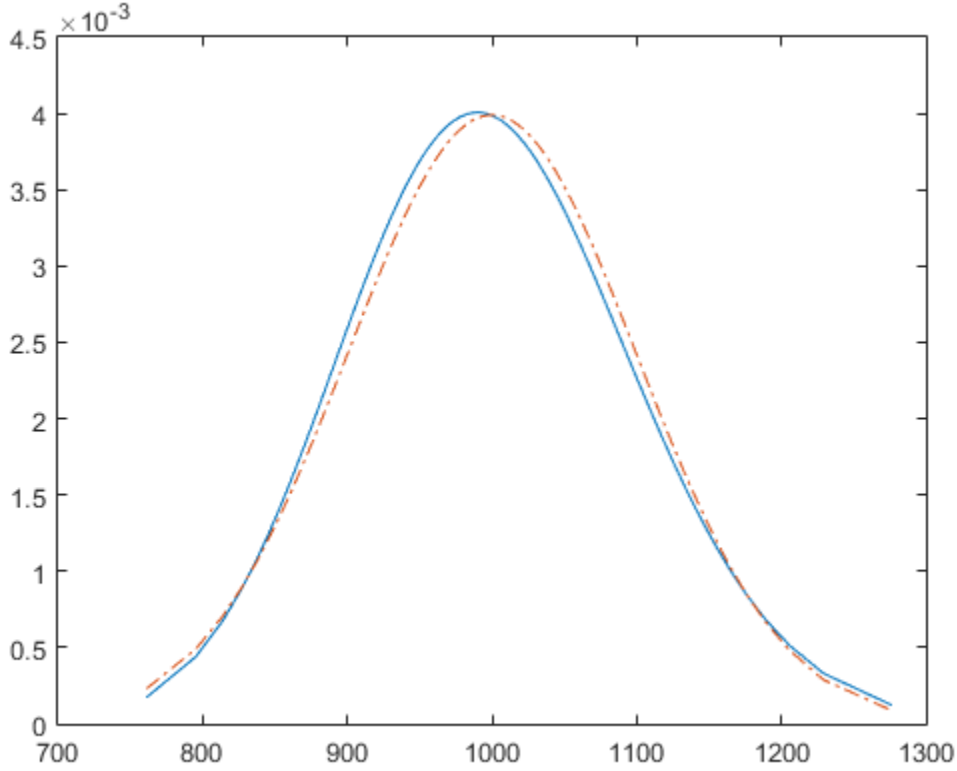
Compute the Gamma Distribution pdf

Compute the pdf of a gamma distribution with parameters `A = 100` and `B = 10`. For comparison, also compute the pdf of a normal distribution with parameters `mu = 1000` and `sigma = 100`.

```
x = gaminv((0.005:0.01:0.995),100,10);
y = gampdf(x,100,10);
y1 = normpdf(x,1000,100);
```

Plot the pdfs of the gamma distribution and the normal distribution on the same figure.

```
figure;
plot(x,y,'-',x,y1,'-.')
```



More About

- Using GammaDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Gaussian Distribution

See “Normal Distribution” on page B-130.

Gaussian Mixture Distributions

See the discussion of the `gmdistribution` class in "Gaussian Mixture Models" on page 5-150.

Generalized Extreme Value Distribution

In this section...

Definition

The probability density function for the generalized extreme value distribution with location parameter μ, scale parameter σ, and shape parameter $k \neq 0$ is

$$y = f(x \mid k, \mu, \sigma) = \left(\frac{1}{\sigma}\right) \exp\left(-\left(1 + k\frac{(x-\mu)}{\sigma}\right)^{-\frac{1}{k}}\right)\left(1 + k\frac{(x-\mu)}{\sigma}\right)^{-1-\frac{1}{k}}$$

for

$$1 + k\frac{(x-\mu)}{\sigma} > 0$$

$k > 0$ corresponds to the Type II case, while $k < 0$ corresponds to the Type III case. For $k = 0$, corresponding to the Type I case, the density is

$$y = f(x \mid 0, \mu, \sigma) = \left(\frac{1}{\sigma}\right) \exp\left(-\exp\left(-\frac{(x-\mu)}{\sigma}\right) - \frac{(x-\mu)}{\sigma}\right)$$

Background

Like the extreme value distribution, the generalized extreme value distribution is often used to model the smallest or largest value among a large set of independent, identically distributed random values representing measurements or observations. For example, you might have batches of 1000 washers from a manufacturing process. If you record the

size of the largest washer in each batch, the data are known as block maxima (or minima if you record the smallest). You can use the generalized extreme value distribution as a model for those block maxima.

The generalized extreme value combines three simpler distributions into a single form, allowing a continuous range of possible shapes that includes all three of the simpler distributions. You can use any one of those distributions to model a particular dataset of block maxima. The generalized extreme value distribution allows you to "let the data decide" which distribution is appropriate.

The three cases covered by the generalized extreme value distribution are often referred to as the Types I, II, and III. Each type corresponds to the limiting distribution of block maxima from a different class of underlying distributions. Distributions whose tails decrease exponentially, such as the normal, lead to the Type I. Distributions whose tails decrease as a polynomial, such as Student's *t*, lead to the Type II. Distributions whose tails are finite, such as the beta, lead to the Type III.

Types I, II, and III are sometimes also referred to as the Gumbel, Frechet, and Weibull types, though this terminology can be slightly confusing. The Type I (Gumbel) and Type III (Weibull) cases actually correspond to the mirror images of the usual Gumbel and Weibull distributions, for example, as computed by the functions `evcdf` and `evfit` , or `wblcdf` and `wblfit`, respectively. Finally, the Type II (Frechet) case is equivalent to taking the reciprocal of values from a standard Weibull distribution.

Parameters

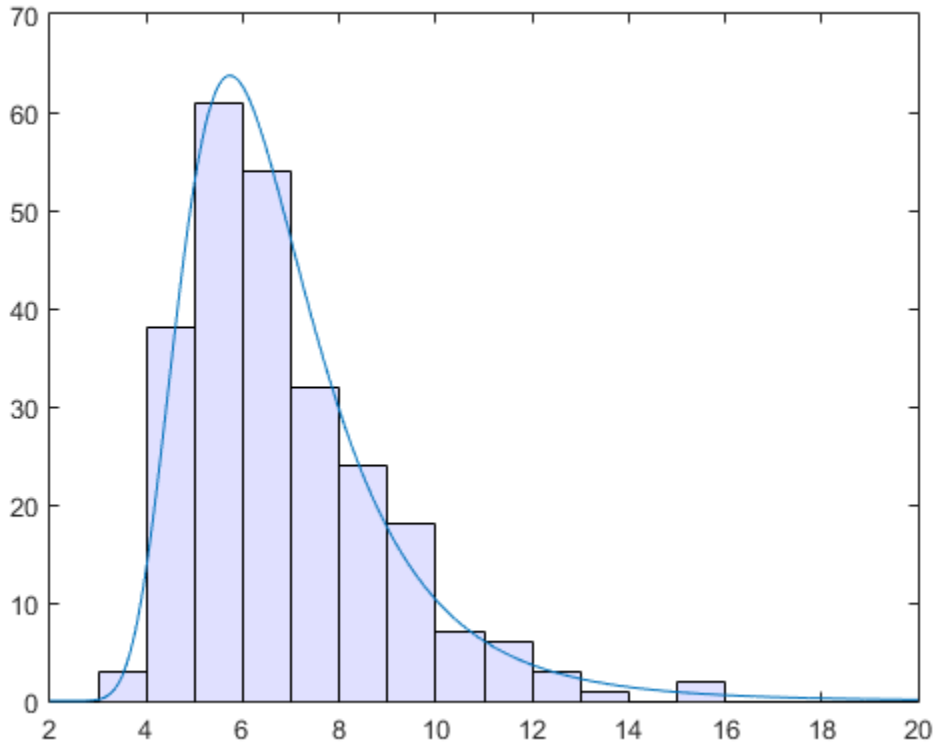
If you generate 250 blocks of 1000 random values drawn from Student's *t* distribution with 5 degrees of freedom, and take their maxima, you can fit a generalized extreme value distribution to those maxima.

```
blocksize = 1000;
nblocks = 250;
rng default  % For reproducibility
t = trnd(5,blocksize,nblocks);
x = max(t); % 250 column maxima
paramEsts = gevfit(x)
```

```
paramEsts =

    0.1185    1.4530    5.8929
```

Notice that the shape parameter estimate (the first element) is positive, which is what you would expect based on block maxima from a Student's t distribution.

```
histogram(x,2:20,'FaceColor',[.8 .8 1]);
xgrid = linspace(2,20,1000);
line(xgrid,nblocks*...
     gevpdf(xgrid,paramEsts(1),paramEsts(2),paramEsts(3)));
```

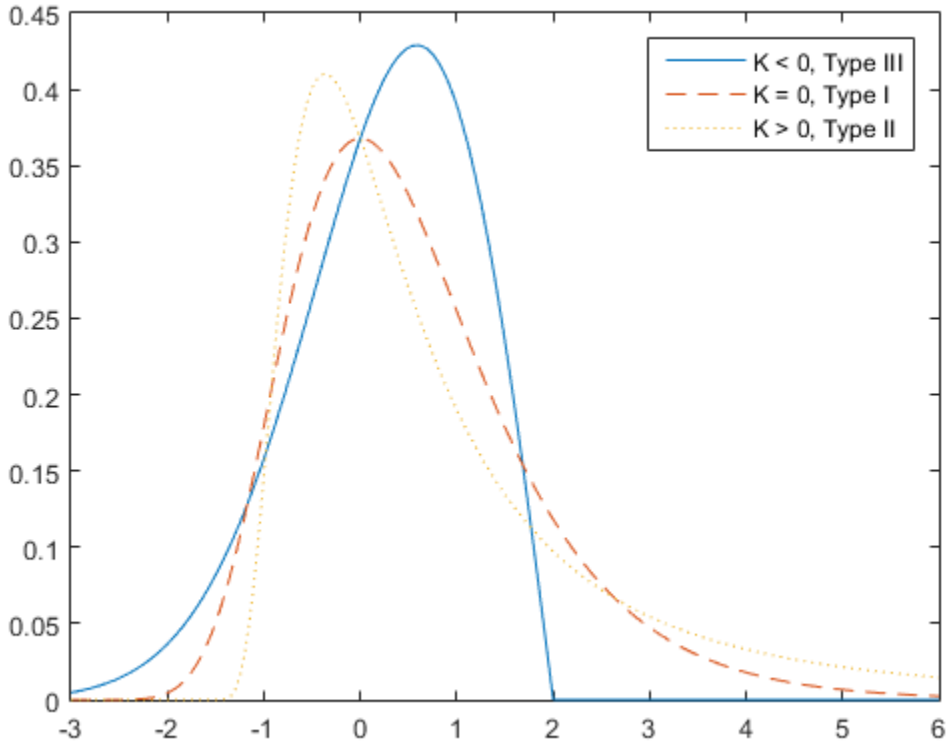


Examples

Compute the Generalized Extreme Value Distribution pdf

Generate examples of probability density functions for the three basic forms of the generalized extreme value distribution.

```
x = linspace(-3,6,1000);
y1 = gevpdf(x,-.5,1,0);
y2 = gevpdf(x,0,1,0);
y3 = gevpdf(x,.5,1,0);
plot(x,y1,'-', x,y2,'--', x,y3,':')
legend({'K < 0, Type III' 'K = 0, Type I' 'K > 0, Type II'})
```



Notice that for `k = 0`, the distribution has zero probability density for `x` such that $x < -\sigma/k + \mu$.

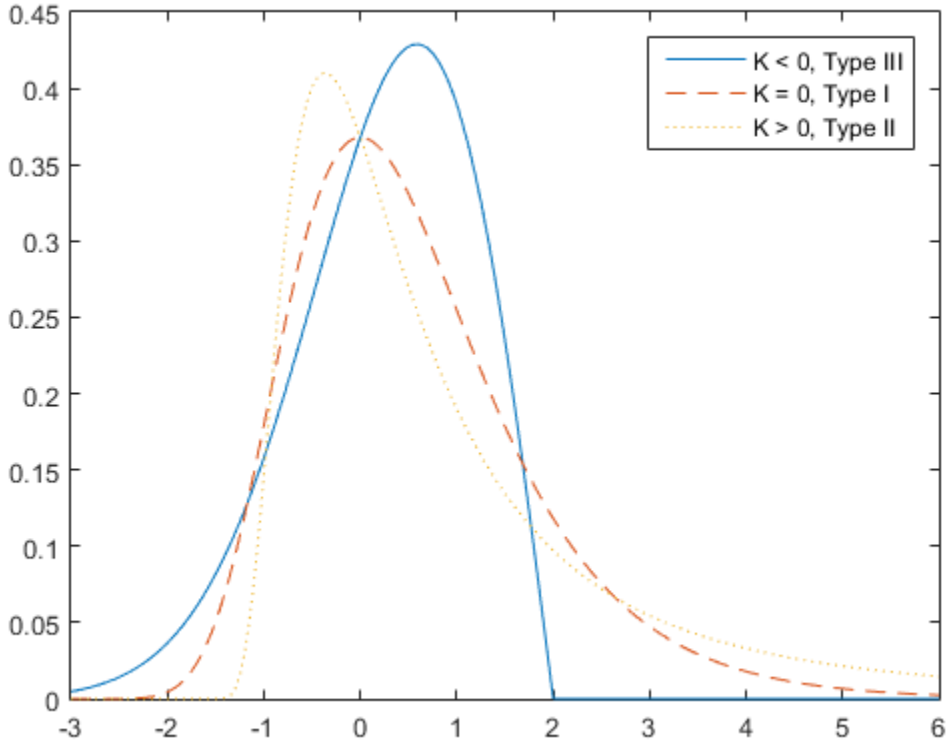
For `k = 0`, the distribution has zero probability density for $x > -\sigma/k + \mu$.

For `k = 0`, there is no upper or lower bound.

Compute the Generalized Extreme Value Distribution pdf

Generate examples of probability density functions for the three basic forms of the generalized extreme value distribution.

```
x = linspace(-3,6,1000);
y1 = gevpdf(x,-.5,1,0);
y2 = gevpdf(x,0,1,0);
y3 = gevpdf(x,.5,1,0);
plot(x,y1,'-', x,y2,'--', x,y3,':')
legend({'K < 0, Type III' 'K = 0, Type I' 'K > 0, Type II'})
```



Notice that for `k = 0`, the distribution has zero probability density for `x` such that $x < -\sigma/k + \mu$.

For `k = 0`, the distribution has zero probability density for $x > -\sigma/k + \mu$.

For `k = 0`, there is no upper or lower bound.

More About

- Using GeneralizedExtremeValueDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Generalized Pareto Distribution

In this section...

Definition

The probability density function for the generalized Pareto distribution with shape parameter $k \neq 0$, scale parameter σ, and threshold parameter θ, is

$$y = f(x \mid k,\sigma,\theta) = \left(\frac{1}{\sigma}\right)\left(1 + k\frac{(x-\theta)}{\sigma}\right)^{-1-\frac{1}{k}}$$

for $\theta < x$, when $k > 0$, or for $\theta < x < \theta - \sigma/k$ when $k < 0$.

For $k = 0$, the density is

$$y = f(x \mid 0,\sigma,\theta) = \left(\frac{1}{\sigma}\right)e^{-\frac{(x-\theta)}{\sigma}}$$

for $\theta < x$.

If $k = 0$ and $\theta = 0$, the generalized Pareto distribution is equivalent to the exponential distribution. If $k > 0$ and $\theta = \sigma/k$, the generalized Pareto distribution is equivalent to the Pareto distribution with a scale parameter equal to σ/k and a shape parameter equal to $1/k$.

Background

Like the exponential distribution, the generalized Pareto distribution is often used to model the tails of another distribution. For example, you might have washers from a manufacturing process. If random influences in the process lead to differences in the sizes of the washers, a standard probability distribution, such as the normal, could be used to model those sizes. However, while the normal distribution might be a good model near its mode, it might not be a good fit to real data in the tails and a more complex

model might be needed to describe the full range of the data. On the other hand, only recording the sizes of washers larger (or smaller) than a certain threshold means you can fit a separate model to those tail data, which are known as *exceedences*. You can use the generalized Pareto distribution in this way, to provide a good fit to extremes of complicated data.

The generalized Pareto distribution allows a continuous range of possible shapes that includes both the exponential and Pareto distributions as special cases. You can use either of those distributions to model a particular dataset of exceedences. The generalized Pareto distribution allows you to "let the data decide" which distribution is appropriate.

The generalized Pareto distribution has three basic forms, each corresponding to a limiting distribution of exceedence data from a different class of underlying distributions.

- Distributions whose tails decrease exponentially, such as the normal, lead to a generalized Pareto shape parameter of zero.
- Distributions whose tails decrease as a polynomial, such as Student's *t*, lead to a positive shape parameter.
- Distributions whose tails are finite, such as the beta, lead to a negative shape parameter.

The generalized Pareto distribution is used in the tails of distribution fit objects of the `paretotails` class.

Parameters

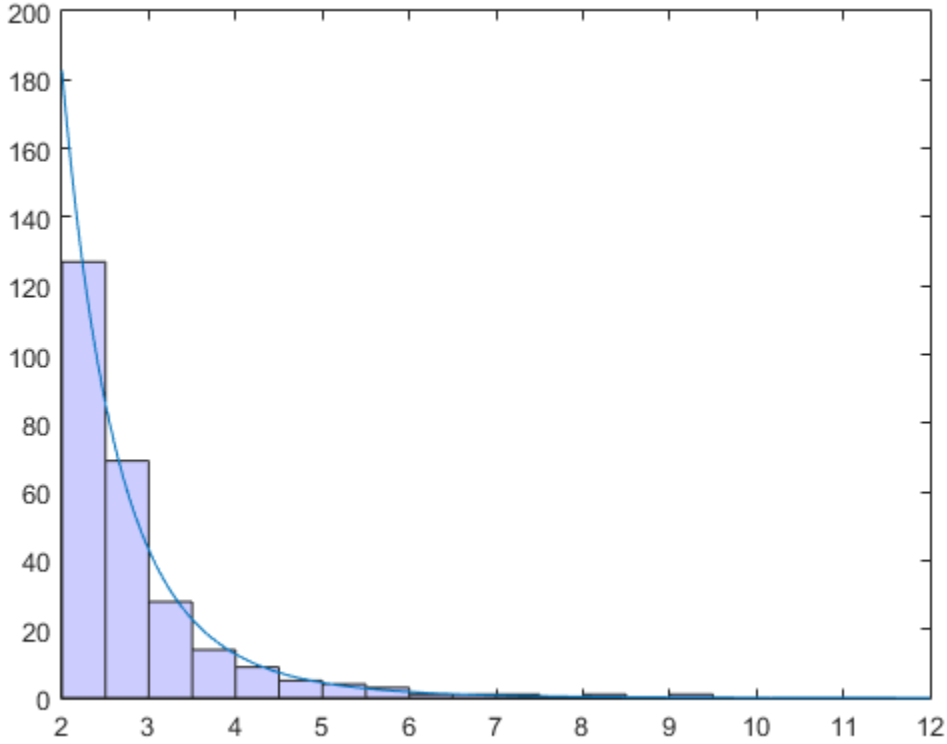
If you generate a large number of random values from a Student's *t* distribution with 5 degrees of freedom, and then discard everything less than 2, you can fit a generalized Pareto distribution to those exceedences.

```
rng default  % For reproducibility
t = trnd(5,5000,1);
y = t(t > 2) - 2;
paramEsts = gpfit(y)
```

```
paramEsts =

    0.1445    0.7225
```

Notice that the shape parameter estimate (the first element) is positive, which is what you would expect based on exceedences from a Student's *t* distribution.

```
hist(y+2,2.25:.5:11.75);
h = findobj(gca,'Type','patch');
h.FaceColor = [.8 .8 1];
xgrid = linspace(2,12,1000);
line(xgrid,.5*length(y)*...
     gppdf(xgrid,paramEsts(1),paramEsts(2),2));
```



Examples

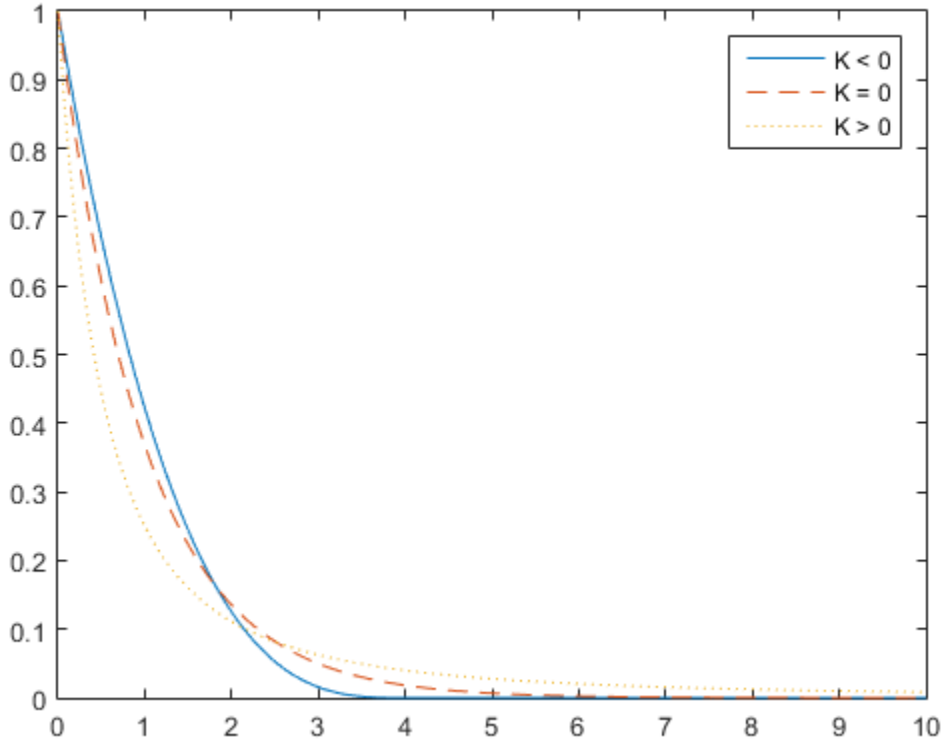
Compute Generalized Pareto Distribution pdf

Compute the pdf of three generalized Pareto distributions. The first has shape parameter `k = -0.25`, the second has `k = 0`, and the third has `k = 1`.

```
x = linspace(0,10,1000);
y1 = gppdf(x,-.25,1,0);
y2 = gppdf(x,0,1,0);
y3 = gppdf(x,1,1,0);
```

Plot the three pdfs on the same figure.

```
figure;
plot(x,y1,'-', x,y2,'--', x,y3,':')
legend({'K < 0' 'K = 0' 'K > 0'});
```



Related Examples

- “Fit a Nonparametric Distribution with Pareto Tails” on page 5-61

More About

- Using GeneralizedParetoDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Geometric Distribution

In this section...

Overview

The geometric distribution models the number of failures before one success in a series of independent trials, where each trial results in either success or failure, and the probability of success in any individual trial is constant. For example, if you toss a coin, the geometric distribution models the number of tails observed before getting a heads. The geometric distribution is discrete, existing only on the nonnegative integers.

Parameters

The geometric distribution uses the following parameter.

Parameter	Description
$0 \le p \le 1$	Probability of success

Probability Distribution Function

Definition

The probability distribution function (pdf) of the geometric distribution is

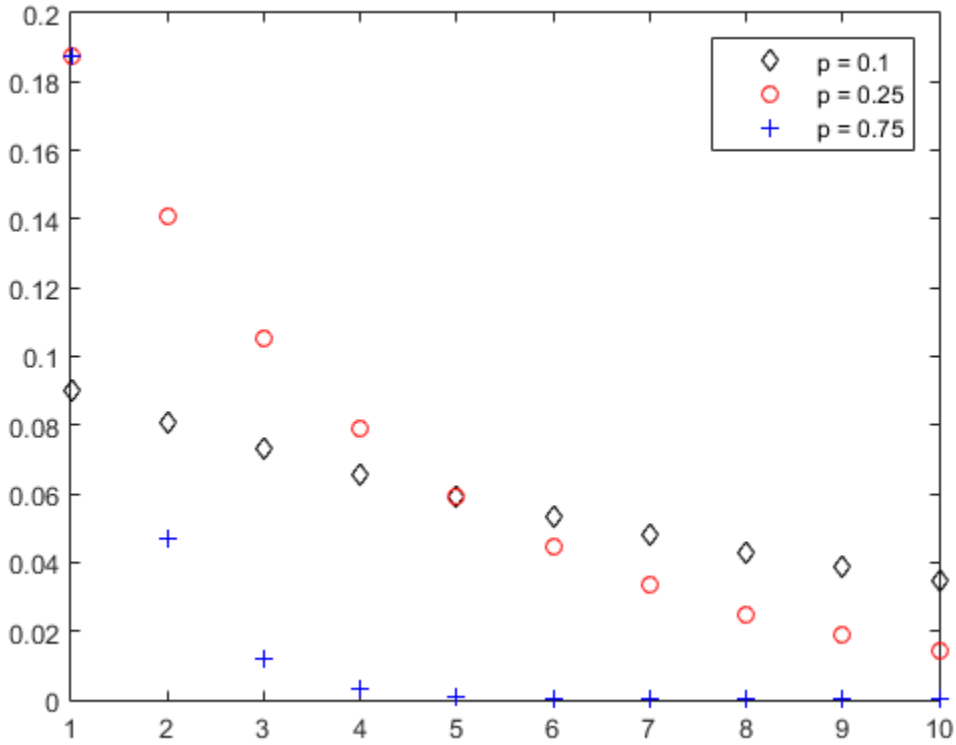
$$y = f(x \mid p) = p(1-p)^x \quad ; \quad x = 0,1,2,\ldots,$$

where p is the probability of success, and x is the number of failures before the first success. The result y is the probability of observing exactly x trials before a success, when the probability of success in any given trial is p. For discrete distributions, the probability distribution function is also known as the probability mass function (pmf).

Plot

This plot shows how changing the value of the probability parameter p alters the shape of the pdf. Use `geopdf` to compute the pdf for values at x equals 1 through 10, for three different values of p. Then plot all three pdfs on the same figure for a visual comparison.

```
x = [1:10];
y1 = geopdf(x,0.1);   % For p = 0.1
y2 = geopdf(x,0.25);  % For p = 0.25
y3 = geopdf(x,0.75);  % For p = 0.75

figure;
plot(x,y1,'kd')
hold on
plot(x,y2,'ro')
plot(x,y3,'b+')
legend({'p = 0.1','p = 0.25','p = 0.75'})
hold off
```



In this plot, the value of y is the probability of observing exactly x trials before a success. When the probability of success p is large, y decreases rapidly as x increases, and the probability of observing a large number of failures before a success quickly becomes small. But when the probability of success p is small, y decreases slowly as x increases. The probability of observing a large number of failures before a success still decreases as the number of trials increases, but at a much slower rate.

Random Number Generation

A random number generated from a geometric distribution represents the number of failures observed before a success in a single experiment, given the probability of success p for each independent trial. Use `geornd` to generate random numbers from the

geometric distribution. For example, the following generates a random number from a geometric distribution with probability of success p equal to 0.1.

```
p = 0.1;
r = geornd(p)


r =

     1
```

The returned random number represents the number of failures observed before a success in a series of independent trials.

Relationship to Other Distributions

The geometric distribution is a special case of the negative binomial distribution, with the specified number of successes parameter r equal to 1.

Cumulative Distribution Function

Definition

The cumulative distribution function (cdf) of the geometric distribution is

$$y = F(x \mid p) = 1 - (1-p)^{x+1} \; ; x = 0,1,2,\ldots,$$

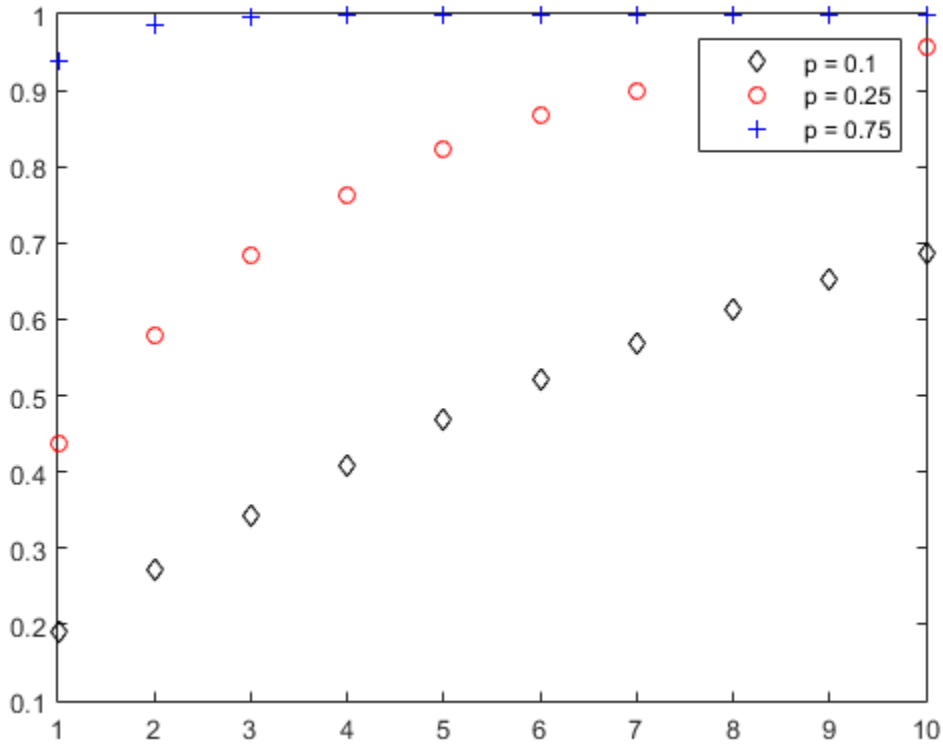
where p is the probability of success, and x is the number of failures before the first success. The result y is the probability of observing up to x trials before a success, when the probability of success in any given trial is p.

Plot

This plot shows how changing the value of the parameter p alters the shape of the cdf. Use `geocdf` to compute the cdf values at x equals 1 through 10, for three different values of p. Then plot all three cdfs on the same figure for a visual comparison.

```
x = [1:10];
y1 = geocdf(x,0.1);   % For p = 0.1
y2 = geocdf(x,0.25);  % For p = 0.25
```

```
y3 = geocdf(x,0.75);  % For p = 0.75

figure;
plot(x,y1,'kd')
hold on
plot(x,y2,'ro')
plot(x,y3,'b+')
legend({'p = 0.1','p = 0.25','p = 0.75'})
hold off
```



In this plot, the value of y is the probability of observing up to x trials before a success. When the probability of success p is large, y increases rapidly as x increases. The probability of observing a success quickly becomes very high, even for a small number of trials. But when the probability of success p is small, y increases slowly as x increases.

The probability of observing a success still increases as the number of trials increases, but at a much slower rate.

Inverse cdf

The inverse cdf of a geometric distribution determines the value of x that corresponds to a probability y of observing x successes in a row in independent trials. Use `geoinv` to compute the inverse cdf of the geometric distribution. For example, the following returns the smallest possible integer x such that the geometric cdf y evaluated at x is greater than or equal to 0.1 , when the probability of success for each independent trial p is 0.03.

```
y = 0.1;
p = 0.03;
x = geoinv(y,p)
```

```
x =

     3
```

Mean and Variance

The mean of the geometric distribution is

$$\text{mean} = \frac{1-p}{p},$$

and the variance of the geometric distribution is

$$\text{var} = \frac{1-p}{p^2},$$

where p is the probability of success.

Use `geostat` to compute the mean and variance of a geometric distribution. For example, the following computes the mean m and variance v of a geometric distribution with probability parameter p equal to 0.25.

```
p = 0.25;
```

```
[m,v] = geostat(p)

m =

     3

v =

    12
```

Example

Compute Geometric Distribution Probabilities

Suppose the probability of a five-year-old car battery not starting in cold weather is 0.03. What is the probability of the car starting for 25 consecutive days during a long cold snap?

Model the scenario using a geometric distribution. In this case, the "failure" event is the car starting, and the "success" event is the car not starting. We want to determine the probability of observing 25 failures (the car starting) without observing a single success (the car not starting). The probability of success for each trial (the car not starting in any single attempt) is `P = 0.03`.

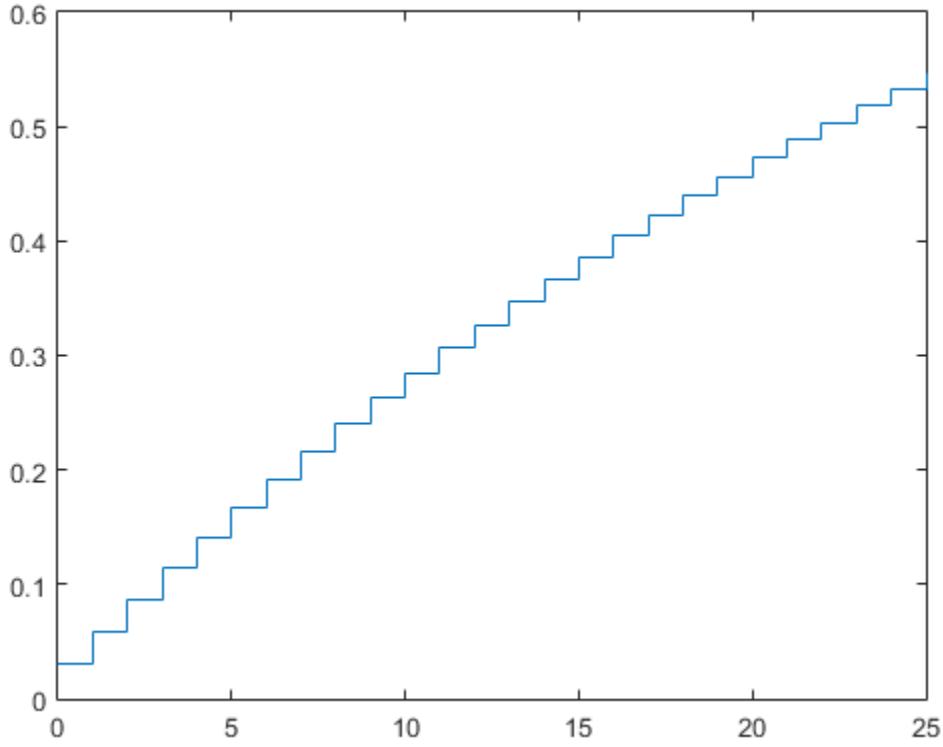
To solve, first compute the cumulative distribution function (cdf) for `x = 25` trials. This returns the probability of observing success (the car not starting) in up to 25 trials. Then subtract this result from `1` to determine the probability of *not* observing success in up to 25 trials - in other words, the probability that the car starts at every one of the 25 attempts.

```
pstart = 1 - geocdf(25,0.03)

pstart =

    0.4530
```

The returned result `pstart = 0.4530` is the probability that the car will start every day for 25 days in a row during a cold snap.

This plot of the cdf for this scenario shows that, as the number of trials (`x`) increases, the probability of success (`y`) also increases. In the context of this example, it means that the more times you attempt to start the car, the greater the probability that it does not start on at least one of those occasions.

```
figure;
x = 0:25;
y = geocdf(x,0.03);
stairs(x,y)
```



More About

- “Working with Probability Distributions” on page 5-3

- “Supported Distributions” on page 5-17

Hypergeometric Distribution

In this section...

Definition

The hypergeometric pdf is

$$y = f(x \mid M, K, n) = \frac{\binom{K}{x}\binom{M-K}{n-x}}{\binom{M}{n}}$$

Background

The hypergeometric distribution models the total number of successes in a fixed-size sample drawn without replacement from a finite population.

The distribution is discrete, existing only for nonnegative integers less than the number of samples or the number of possible successes, whichever is greater. The hypergeometric distribution differs from the binomial only in that the population is finite and the sampling from the population is without replacement.

The hypergeometric distribution has three parameters that have direct physical interpretations.

- M is the size of the population.
- K is the number of items with the desired characteristic in the population.
- n is the number of samples drawn.

Sampling "without replacement" means that once a particular sample is chosen, it is removed from the relevant population for all subsequent selections.

Examples

Compute and Plot Hypergeometric Distribution CDF

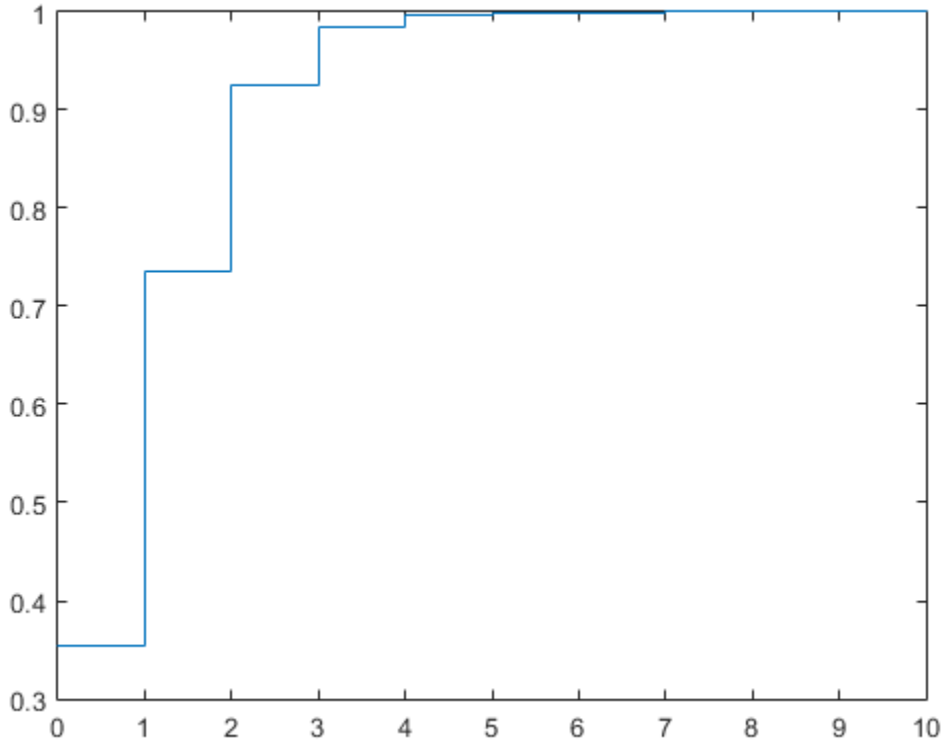
This example shows how to compute and plot the cdf of a hypergeometric distribution.

Compute the cdf of a hypergeometric distribution that draws 20 samples from a group of 1000 items, when the group contains 50 items of the desired type.

```
x = 0:10;
y = hygecdf(x,1000,50,20);
```

Plot the cdf.

```
stairs(x,y)
```



The x-axis of the plot shows the number of items drawn that are of the desired type. The y-axis shows the corresponding cdf values.

More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Inverse Gaussian Distribution

In this section...

Definition

The inverse Gaussian distribution has the density function

$$\sqrt{\frac{\lambda}{2\pi x^3}}\exp\left\{-\frac{\lambda}{2\mu^2 x}(x-\mu)^2\right\}$$

Background

Also known as the Wald distribution, the inverse Gaussian is used to model nonnegative positively skewed data. The distribution originated in the theory of Brownian motion, but has been used to model diverse phenomena. Inverse Gaussian distributions have many similarities to standard Gaussian (normal) distributions, which lead to applications in inferential statistics.

Parameters

To estimate distribution parameters, use `mle` or the Distribution Fitting app.

More About

- Using InverseGaussianDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Inverse Wishart Distribution

Definition

The probability density function of the d-dimensional Inverse Wishart distribution is given by

$$y = f(\mathrm{X}, \Sigma, \nu) = \frac{|T|^{(\nu/2)} e^{\left(-\frac{1}{2}\mathrm{trace}\left(TX^{-1}\right)\right)}}{2^{(\nu d)/2} \pi^{(d(d-1))/4} |X|^{(\nu+d+1)/2} \Gamma(\nu/2)\ldots\Gamma(\nu-(d-1))/2},$$

where X and T are d-by-d symmetric positive definite matrices, and ν is a scalar greater than or equal to d. While it is possible to define the Inverse Wishart for singular T, the density cannot be written as above.

If a random matrix has a Wishart distribution with parameters T^{-1} and ν, then the inverse of that random matrix has an inverse Wishart distribution with parameters T and ν. The mean of the distribution is given by

$$\frac{1}{\nu - d - 1} T$$

where d is the number of rows and columns in T.

Only random matrix generation is supported for the inverse Wishart, including both singular and nonsingular T.

Background

The inverse Wishart distribution is based on the Wishart distribution. In Bayesian statistics it is used as the conjugate prior for the covariance matrix of a multivariate normal distribution.

Example

Notice that the sampling variability is quite large when the degrees of freedom is small.

```
Tau = [1 .5; .5 2];
df = 10; S1 = iwishrnd(Tau,df)*(df-2-1)

S1 =
       1.7959      0.64107
      0.64107       1.5496

df = 1000; S2 = iwishrnd(Tau,df)*(df-2-1)

S2 =
       0.9842      0.50158
      0.50158       2.1682
```

See Also

"Wishart Distribution" on page B-175

More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Johnson System

See “Pearson and Johnson Systems” on page 6-26.

Kernel Distribution

In this section...

Overview

A kernel distribution is a nonparametric representation of the probability density function (pdf) of a random variable. You can use a kernel distribution when a parametric distribution cannot properly describe the data, or when you want to avoid making assumptions about the distribution of the data. This distribution is defined by a smoothing function and a bandwidth value that controls the smoothness of the resulting density curve.

Kernel Density Estimator

The kernel density estimator is the estimated probability density function (pdf) of the random variable. Its formula is given by the equation

$$\hat{f}_h(x) = \frac{1}{nh}\sum_{i=1}^{n} K\left(\frac{x - x_i}{h}\right) \quad ; \quad -\infty < x < \infty ,$$

where n is the sample size, $K(\bullet)$ is the kernel smoothing function, h is the bandwidth.

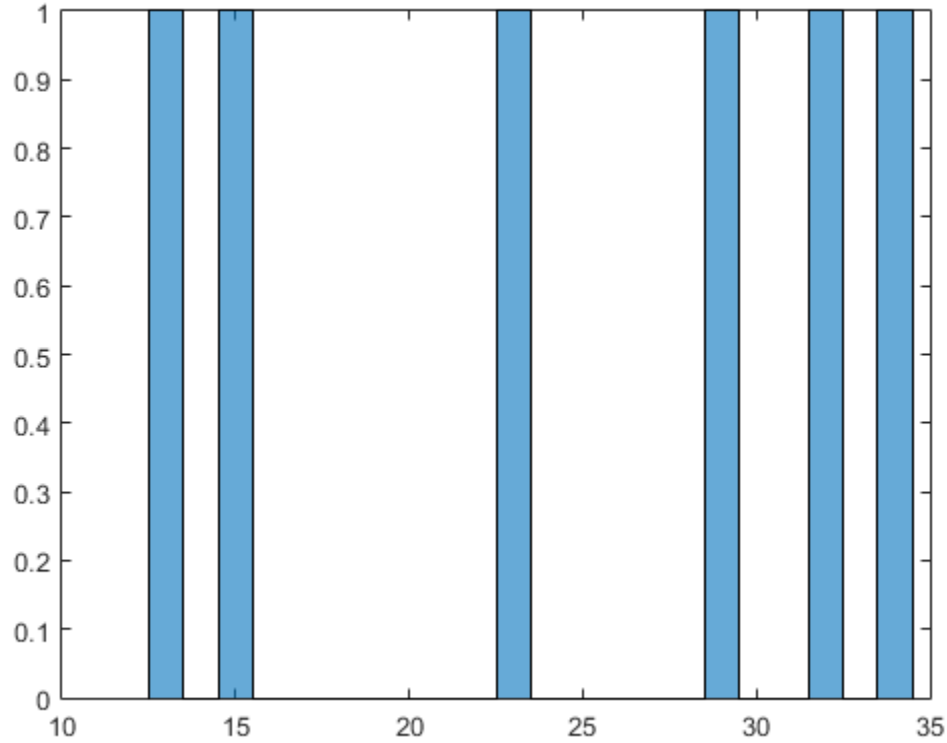
Kernel Smoothing Function

The kernel smoothing function defines the shape of the curve used to generate the pdf. Similar to a histogram, the kernel distribution builds a function to represent the probability distribution using the sample data. But unlike a histogram, which places the values into discrete bins, a kernel distribution sums the component smoothing functions for each data value to produce a smooth, continuous probability curve. The following

plots show a visual comparison of a histogram and a kernel distribution generated from the same sample data.

A histogram represents the probability distribution by establishing bins and placing each data value in the appropriate bin.

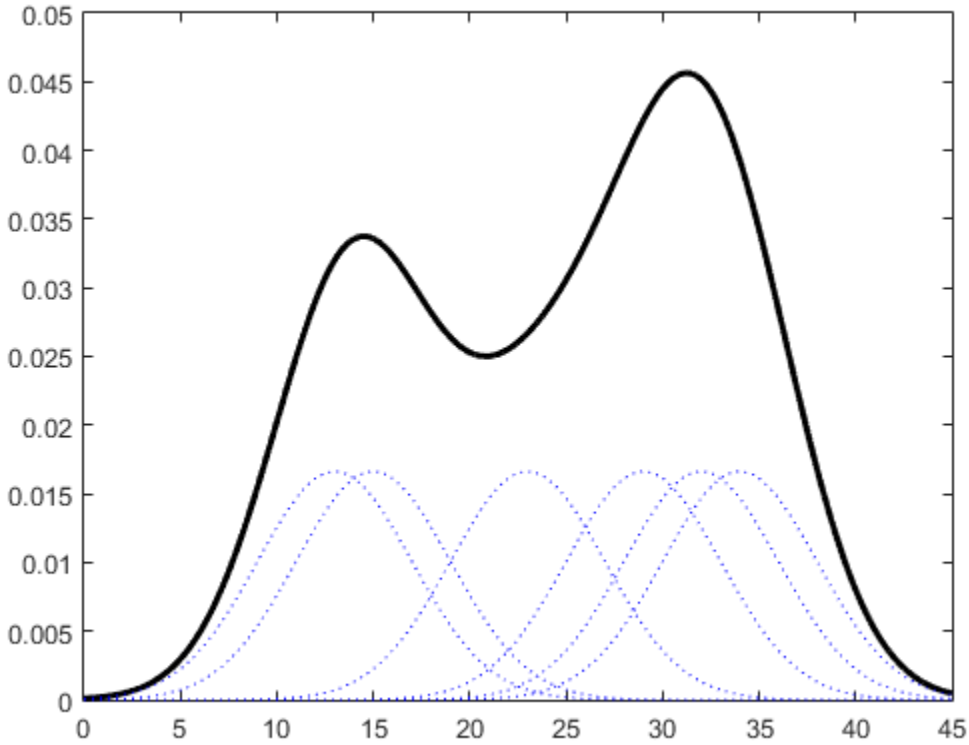
```
SixMPG = [13;15;23;29;32;34];
figure;
histogram(SixMPG)
```



Because of this bin count approach, the histogram produces a discrete probability density function. This might be unsuitable for certain applications, such as generating random numbers from a fitted distribution.

Alternatively, the kernel distribution builds the pdf by creating an individual probability density curve for each data value, then summing the smooth curves. This approach creates one smooth, continuous probability density function for the data set.

```
figure;
pdSix = fitdist(SixMPG,'Kernel','BandWidth',4);
x = 0:.1:45;
ySix = pdf(pdSix,x);
plot(x,ySix,'k-','LineWidth',2);

% Plot each individual pdf and scale its appearance on the plot
hold on;
for i=1:6
    pd = makedist('Normal','mu',SixMPG(i),'sigma',4);
    y = pdf(pd,x);
    y = y/6;
    plot(x,y,'b:');
end
hold off;
```



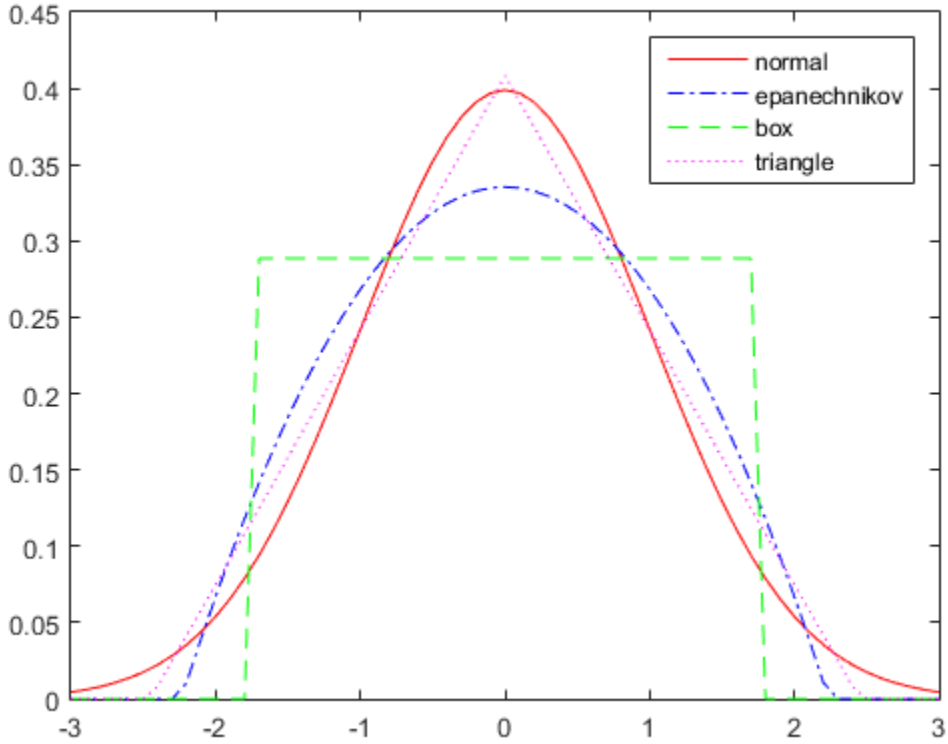
The smaller dashed curves are the probability distributions for each value in the sample data, scaled to fit the plot. The larger solid curve is the overall kernel distribution of the `SixMPG` data. The kernel smoothing function refers to the shape of those smaller component curves, which have a normal distribution in this example.

You can choose one of several options for the kernel smoothing function. This plot shows the shapes of the available smoothing functions.

Set plot specifications

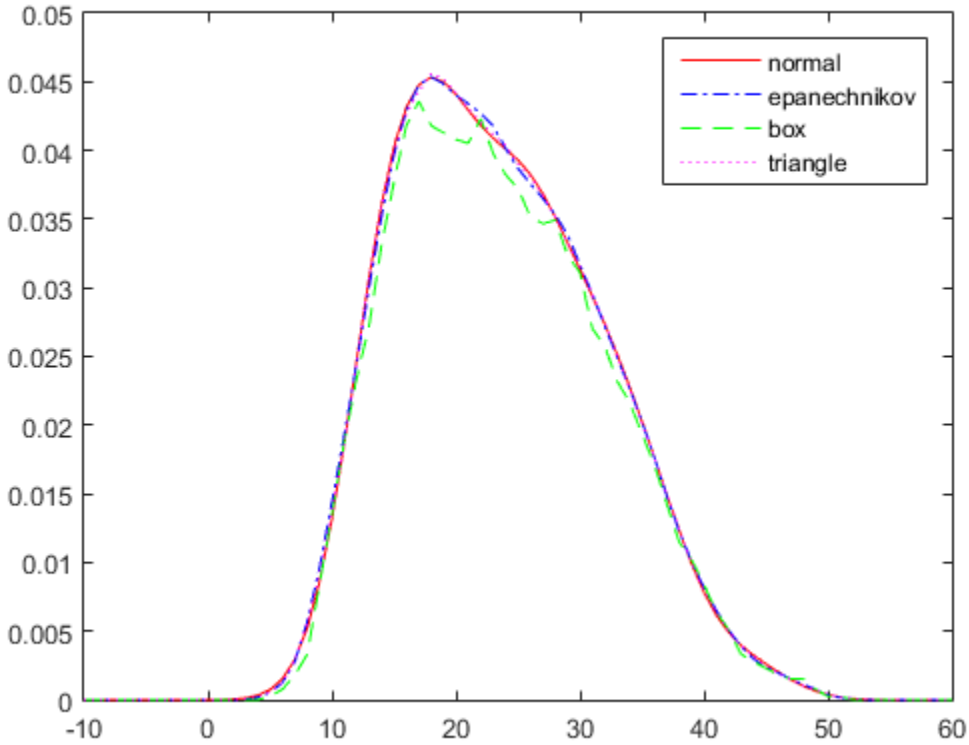
```
hname = {'normal' 'epanechnikov' 'box' 'triangle'};
colors = {'r' 'b' 'g' 'm'};
lines = {'-','-.','--',':'};
```

```
% Generate a sample of each kernel smoothing function and plot
data = [0];
figure;
for j=1:4
    pd = fitdist(data,'kernel','Kernel',hname{j});
    x = -3:.1:3;
    y = pdf(pd,x);
    plot(x,y,'Color',colors{j},'LineStyle',lines{j});
    hold on;
end
legend(hname{:});
hold off;
```



To understand the effect of different kernel smoothing functions on the shape of the resulting pdf estimate, compare plots of the mileage data (MPG) from `carbig.mat` using each available kernel function.

```
load carbig;
% Set plot specifications
hname = {'normal' 'epanechnikov' 'box' 'triangle'};
colors = {'r' 'b' 'g' 'm'};
lines = {'-','-.','--',':'};

% Generate kernel distribution objects and plot
figure;
for j=1:4
    pd = fitdist(MPG,'kernel','Kernel',hname{j});
    x = -10:1:60;
    y = pdf(pd,x);
    plot(x,y,'Color',colors{j},'LineStyle',lines{j});
    hold on;
end
legend(hname{:});
hold off;
```



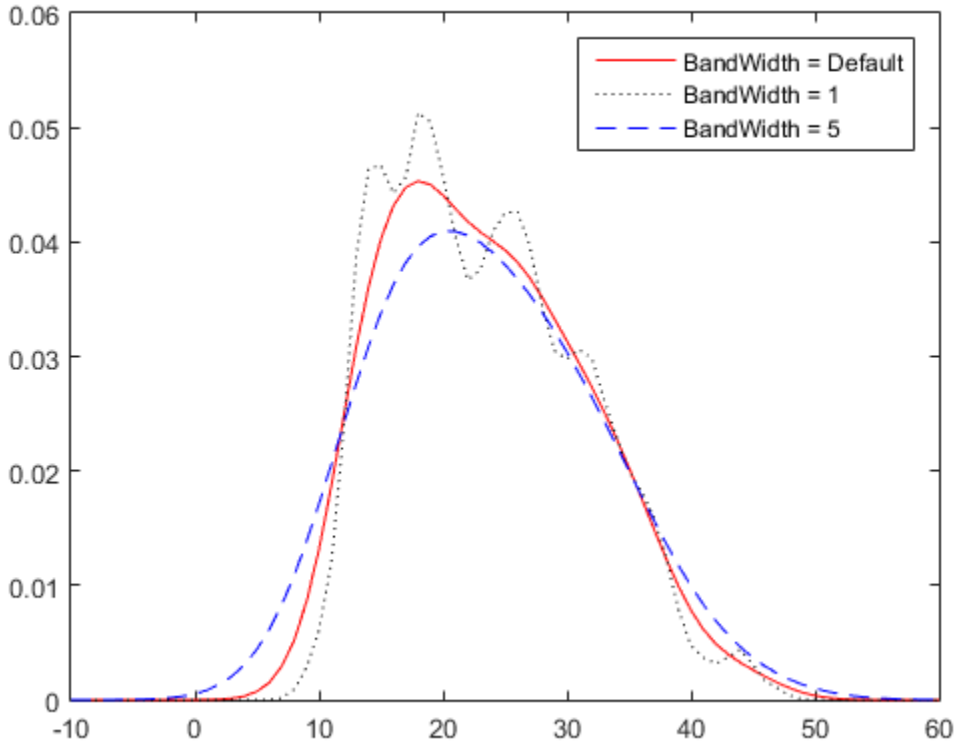
Each density curve uses the same input data, but applies a different kernel smoothing function to generate the pdf. The density estimates are roughly comparable, but the shape of each curve varies slightly. For example, the box kernel produces a density curve that is less smooth than the others.

Bandwidth

The choice of bandwidth value controls the smoothness of the resulting probability density curve. This plot shows the density estimate for the same `MPG` data, using a normal kernel smoothing function with three different bandwidths.

Create kernel distribution objects

```
pd1 = fitdist(MPG,'kernel');
pd2 = fitdist(MPG,'kernel','BandWidth',1);
pd3 = fitdist(MPG,'kernel','BandWidth',5);

% Compute each pdf
x = -10:1:60;
y1 = pdf(pd1,x);
y2 = pdf(pd2,x);
y3 = pdf(pd3,x);

% Plot each pdf
plot(x,y1,'Color','r','LineStyle','-');
hold on;
plot(x,y2,'Color','k','LineStyle',':');
plot(x,y3,'Color','b','LineStyle','--');
legend({'BandWidth = Default','BandWidth = 1','BandWidth = 5'});
hold off;
```



The default bandwidth, which is theoretically optimal for estimating densities for the normal distribution, produces a reasonably smooth curve. Specifying a smaller bandwidth produces a very rough curve, but reveals that there might be two major peaks in the data. Specifying a larger bandwidth produces a curve nearly identical to the kernel function, and is so smooth that it obscures potentially important features of the data.

See Also

`ksdensity`

Related Examples

- “Fit Kernel Distribution Object to Data” on page 5-49

- "Fit Kernel Distribution Using ksdensity" on page 5-54
- "Fit Distributions to Grouped Data Using ksdensity" on page 5-57

More About

- Using KernelDistribution Objects
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Logistic Distribution

In this section...

Overview

The logistic distribution is used for growth models and in logistic regression. It has longer tails and a higher kurtosis than the normal distribution.

Parameters

The logistic distribution uses the following parameters.

Parameter	Description	Support
`mu`	Mean	$-\infty < \mu < \infty$
`sigma`	Scale parameter	$\sigma \geq 0$

Probability Density Function

The probability density function (pdf) is

$$f(x \mid \mu,\sigma) = \frac{\exp\left\{\frac{x-\mu}{\sigma}\right\}}{\sigma\left(1+\exp\left\{\frac{x-\mu}{\sigma}\right\}\right)^2} \quad ; \quad -\infty < x < \infty.$$

Relationship to Other Distributions

The loglogistic distribution is closely related to the logistic distribution. If x is distributed loglogistically with parameters μ and σ, then $\log(x)$ is distributed logistically with mean and standard deviation.

More About

- Using LogisticDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Loglogistic Distribution

In this section...

Overview

The loglogistic distribution is a probability distribution whose logarith has a logistic distribution. This distribution is often used in survival analysis to model events that experience an initial rate increase, followed by a rate decrease. It is also known as the Fisk distribution in economics applications.

Parameters

The loglogistic distribution uses the following parameters.

Parameter	Description	Support
`mu`	Log mean	$\mu > 0$
`sigma`	Log scale parameter	$\sigma > 0$

Probability Density Function

The probability density function (pdf) is

$$f(x \mid \mu,\sigma) = \frac{1}{\sigma}\frac{1}{x}\frac{e^z}{\left(1+e^z\right)^2} \quad ; \quad x \geq 0,$$

where $z = \dfrac{\log(x) - \mu}{\sigma}$.

Relationship to Other Distributions

The loglogistic distribution is closely related to the logistic distribution. If x is distributed loglogistically with parameters μ and σ, then $\log(x)$ is distributed logistically with mean and standard deviation. The relationship is similar to that between the lognormal and normal distribution.

More About

- Using LoglogisticDistribution Objects
- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

Lognormal Distribution

In this section...

Overview

The lognormal distribution is a probability distribution whose logarithm has a normal distribution. It is sometimes called the Galton distribution. The lognormal distribution is applicable when the quantity of interest must be positive, since log(x) exists only when x is positive.

Parameters

The lognormal distribution uses the following parameters.

Parameter	Description	Support
`mu`	Log mean	$-\infty < \mu < \infty$
`sigma`	Log standard deviation	$\sigma \geq 0$

Probability Density Function

The probability density function (pdf) of the lognormal distribution is

$$f(x \mid \mu,\sigma) = \frac{1}{x\sigma\sqrt{2\pi}} \exp\left\{\frac{-(\ln x - \mu)^2}{2\sigma^2}\right\} \quad ; \quad x > 0 .$$

Descriptive Statistics

The mean is

$$\text{mean} = \exp\left(\mu + \frac{\sigma^2}{2}\right).$$

The variance is

$$\text{var} = \exp\left(2\mu + \sigma^2\right)\left(\exp\left(\sigma^2\right) - 1\right).$$

You can compute these descriptive statistics using the `lognstat` function.

Relationship to Other Distributions

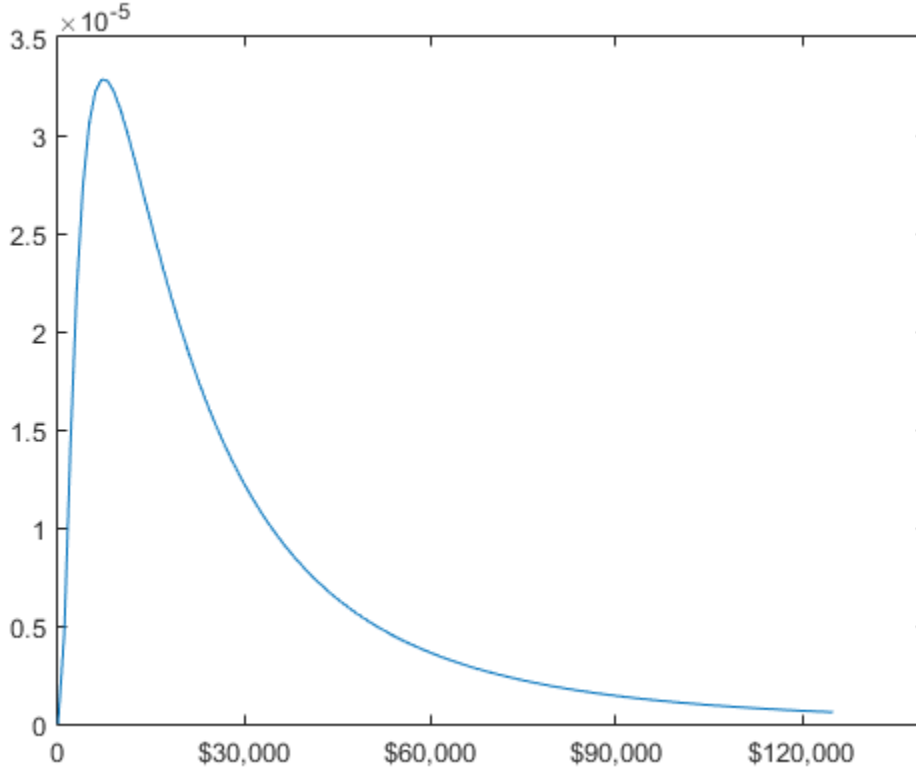
The lognormal distribution is closely related to the normal distribution. If x is distributed lognormally with parameters μ and σ, then $\log(x)$ is distributed normally with mean μ and standard deviation σ. The lognormal distribution is applicable when the quantity of interest must be positive, since $\log(x)$ exists only when x is positive.

Examples

Compute the Lognormal Distribution pdf

Suppose the income of a family of four in the United States follows a lognormal distribution with `mu = log(20,000)` and `sigma = 1`. Compute and plot the income density.

```
x = (10:1000:125010)';
y = lognpdf(x,log(20000),1.0);

figure;
plot(x,y)
h = gca;
h.XTick = [0 30000 60000 90000 120000];
h.XTickLabel = {'0','$30,000','$60,000',...
                    '$90,000','$120,000'};
```



More About

- Using LognormalDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Multinomial Distribution

In this section...

Overview

Multinomial distribution models the probability of each combination of successes in a series of independent trials. Use this distribution when there are more than two possible mutually exclusive outcomes for each trial, and each outcome has a fixed probability of success.

Parameter

Multinomial distribution uses the following parameter.

Parameter	Description	Constraints
`probabilities`	Outcome probabilities	$0 \le probabilities(i) \le 1;\ \sum_{all(i)} probabilities(i) = 1$

Probability Density Function

The multinomial pdf is

$$f(x \mid n, p) = \frac{n!}{x_1! \cdots x_k!} p_1^{x_1} \cdots p_k^{x_k},$$

where k is the number of possible mutually exclusive outcomes for each trial, and n is the total number of trials. The vector $x = (x_1 \ldots x_k)$ is the number of observations of each k outcome, and contains nonnegative integer components that sum to n. The vector p

= (p_1...p_k) is the fixed probability of each k outcome, and contains nonnegative scalar components that sum to 1.

Descriptive Statistics

The expected number of observations of outcome i in n trials is

$$\mathrm{E}\{x_i\} = np_i \ ,$$

where p_i is the fixed probability of outcome i.

The variance is of outcome i is

$$\mathrm{var}\left(x_i\right) = np_i\left(1 - p_i\right).$$

The covariance of outcomes i and j is

$$\mathrm{cov}(x_i, x_j) = -np_i p_j \ , i \neq j.$$

Relationship to Other Distributions

The multinomial distribution is a generalization of the binomial distribution. While the binomial distribution gives the probability of the number of "successes" in n independent trials of a two-outcome process, the multinomial distribution gives the probability of each combination of outcomes in n independent trials of a k-outcome process. The probability of each outcome in any one trial is given by the fixed probabilities p_1,..., p_k.

More About

- Using MultinomialDistribution Objects
- "Multinomial Probability Distribution Objects" on page 5-128
- "Multinomial Probability Distribution Functions" on page 5-132
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Multivariate Gaussian Distribution

See “Multivariate Normal Distribution” on page B-101.

Multivariate Normal Distribution

In this section...

Definition

The probability density function of the d-dimensional multivariate normal distribution is given by

$$y = f(x,\mu,\Sigma) = \frac{1}{\sqrt{|\Sigma|(2\pi)^d}} e^{-\frac{1}{2}(x-\mu)'\Sigma^{-1}(x-\mu)}$$

where x and μ are 1-by-d vectors and Σ is a d-by-d symmetric positive definite matrix. While it is possible to define the multivariate normal for singular Σ, the density cannot be written as above. Only random vector generation is supported for the singular case. Note that while most textbooks define the multivariate normal with x and μ oriented as column vectors, for the purposes of data analysis software, it is more convenient to orient them as row vectors, and Statistics and Machine Learning Toolbox software uses that orientation.

Background

The multivariate normal distribution is a generalization of the univariate normal to two or more variables. It is a distribution for random vectors of correlated variables, each element of which has a univariate normal distribution. In the simplest case, there is no correlation among variables, and elements of the vectors are independent univariate normal random variables.

The multivariate normal distribution is parameterized with a mean vector, μ, and a covariance matrix, Σ. These are analogous to the mean μ and variance σ^2 parameters of a univariate normal distribution. The diagonal elements of Σ contain the variances for each variable, while the off-diagonal elements of Σ contain the covariances between variables.

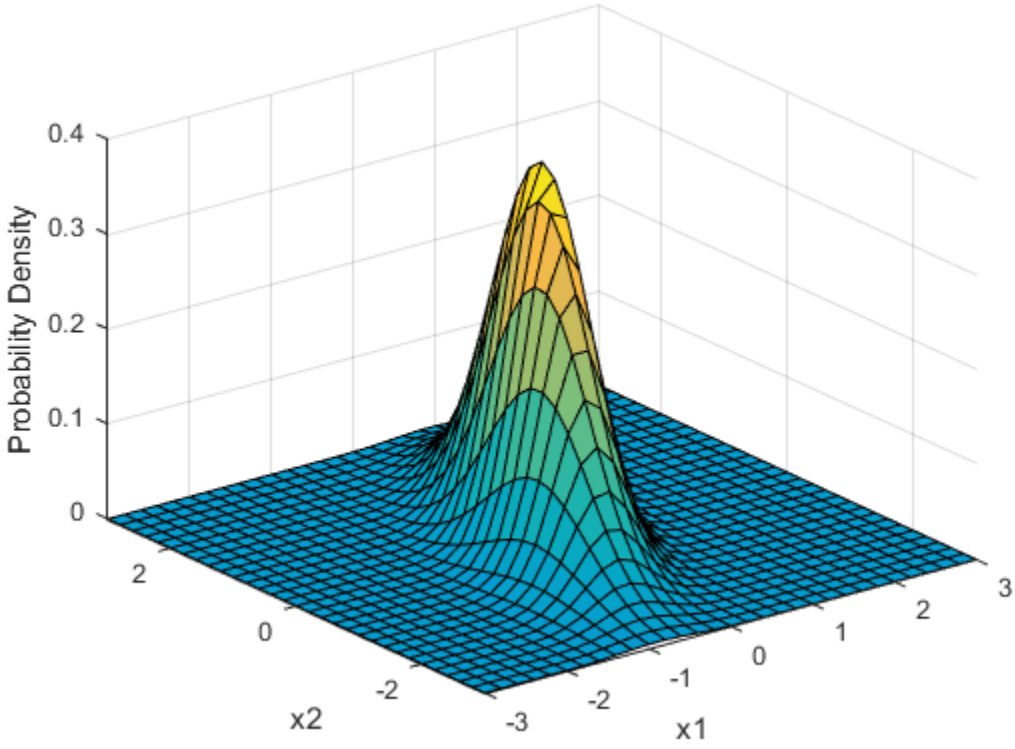
The multivariate normal distribution is often used as a model for multivariate data, primarily because it is one of the few multivariate distributions that is tractable to work with.

Examples

Compute the Multivariate Normal pdf

Compute and plot the pdf of a multivariate normal distribution.

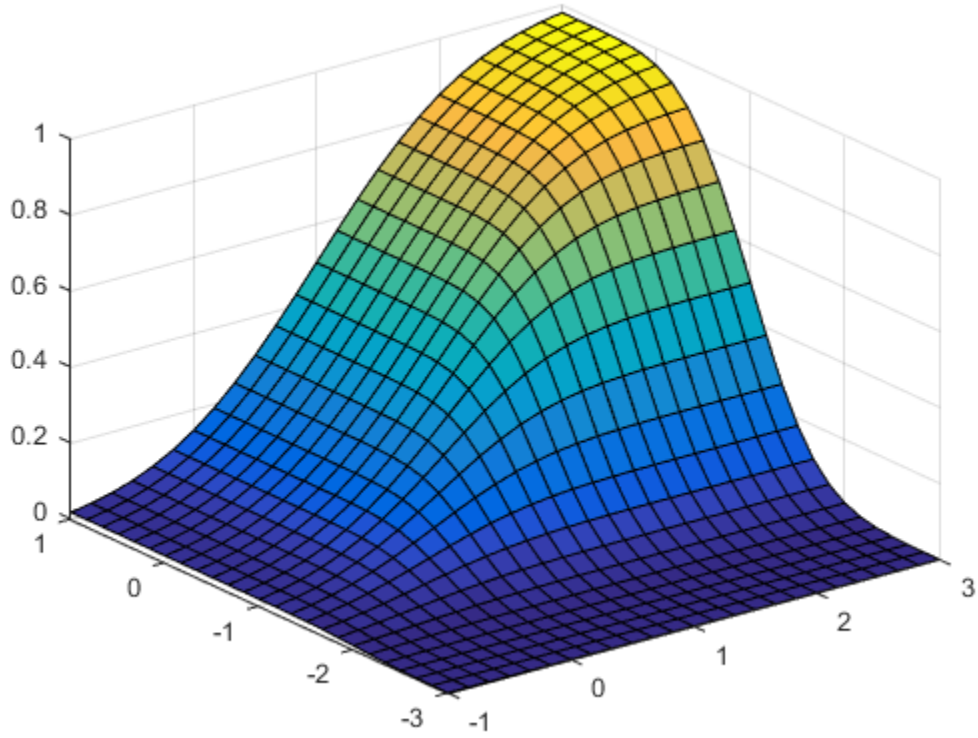
```
mu = [0 0];
Sigma = [.25 .3; .3 1];
x1 = -3:.2:3; x2 = -3:.2:3;
[X1,X2] = meshgrid(x1,x2);
F = mvnpdf([X1(:) X2(:)],mu,Sigma);
F = reshape(F,length(x2),length(x1));
surf(x1,x2,F);
caxis([min(F(:))-.5*range(F(:)),max(F(:))]);
axis([-3 3 -3 3 0 .4])
xlabel('x1'); ylabel('x2'); zlabel('Probability Density');
```



Compute the Multivariate Normal cdf

Compute and plot the cdf of a multivariate normal distribution with parameters `mu = [1 -1]` and `SIGMA = [.9 .4; .4 .3]`.

```
mu = [1 -1];
SIGMA = [.9 .4; .4 .3];
figure;
[X1,X2] = meshgrid(linspace(-1,3,25)',linspace(-3,1,25)');
X = [X1(:) X2(:)];
p = mvncdf(X,mu,SIGMA);
surf(X1,X2,reshape(p,25,25));
```



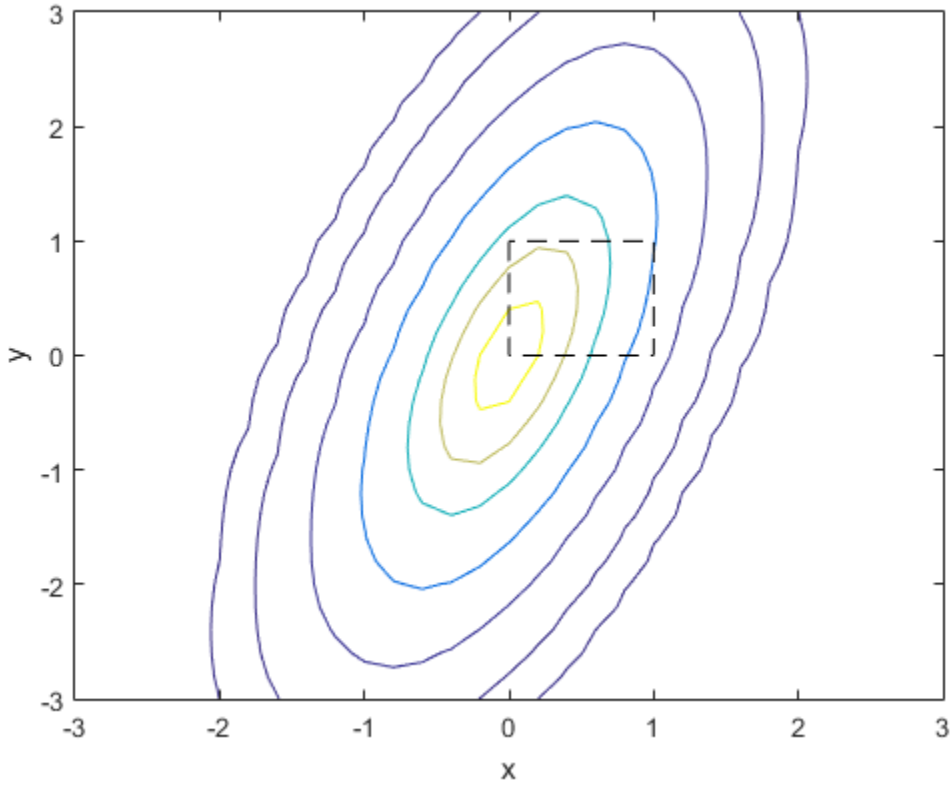
Compute Cumulative Probabilities Over Regions

Since the bivariate normal distribution is defined on the plane, you can also compute cumulative probabilities over rectangular regions.

Compute the probability contained within the unit square, and create a contour plot of the results.

```
mu = [0 0];
Sigma = [.25 .3; .3 1];
x1 = -3:.2:3; x2 = -3:.2:3;
[X1,X2] = meshgrid(x1,x2);
F = mvnpdf([X1(:) X2(:)],mu,Sigma);
F = reshape(F,length(x2),length(x1));
```

```
mvncdf([0 0],[1 1],mu,Sigma);
contour(x1,x2,F,[.0001 .001 .01 .05:.1:.95 .99 .999 .9999]);
xlabel('x'); ylabel('y');
line([0 0 1 1 0],[1 0 0 1 1],'linestyle','--','color','k');
```



Computing a multivariate cumulative probability requires significantly more work than computing a univariate probability. By default, the `mvncdf` function computes values to less than full machine precision, and returns an estimate of the error as an optional second output.

```
[F,err] = mvncdf([0 0],[1 1],mu,Sigma)
```

```
F =

    0.2097

err =

   1.0000e-08
```

Multivariate *t* Distribution

In this section...

Definition

The probability density function of the d-dimensional multivariate Student's t distribution is given by

$$f(x,\Sigma,\nu) = \frac{1}{|\Sigma|^{1/2}} \frac{1}{\sqrt{(\nu\pi)^d}} \frac{\Gamma((\nu+d)/2)}{\Gamma(\nu/2)} \left(1 + \frac{x' \Sigma^{-1} x}{\nu}\right)^{-(\nu+d)/2}.$$

where x is a 1-by-d vector, Σ is a d-by-d symmetric, positive definite matrix, and ν is a positive scalar. While it is possible to define the multivariate Student's t for singular Σ, the density cannot be written as above. For the singular case, only random number generation is supported. Note that while most textbooks define the multivariate Student's t with x oriented as a column vector, for the purposes of data analysis software, it is more convenient to orient x as a row vector, and Statistics and Machine Learning Toolbox software uses that orientation.

Background

The multivariate Student's t distribution is a generalization of the univariate Student's t to two or more variables. It is a distribution for random vectors of correlated variables, each element of which has a univariate Student's t distribution. In the same way as the univariate Student's t distribution can be constructed by dividing a standard univariate normal random variable by the square root of a univariate chi-square random variable, the multivariate Student's t distribution can be constructed by dividing a multivariate normal random vector having zero mean and unit variances by a univariate chi-square random variable.

The multivariate Student's t distribution is parameterized with a correlation matrix, Σ, and a positive scalar degrees of freedom parameter, ν. ν is analogous to the degrees of freedom parameter of a univariate Student's t distribution. The off-diagonal elements of Σ contain the correlations between variables. Note that when Σ is the identity matrix, variables are uncorrelated; however, they are not independent.

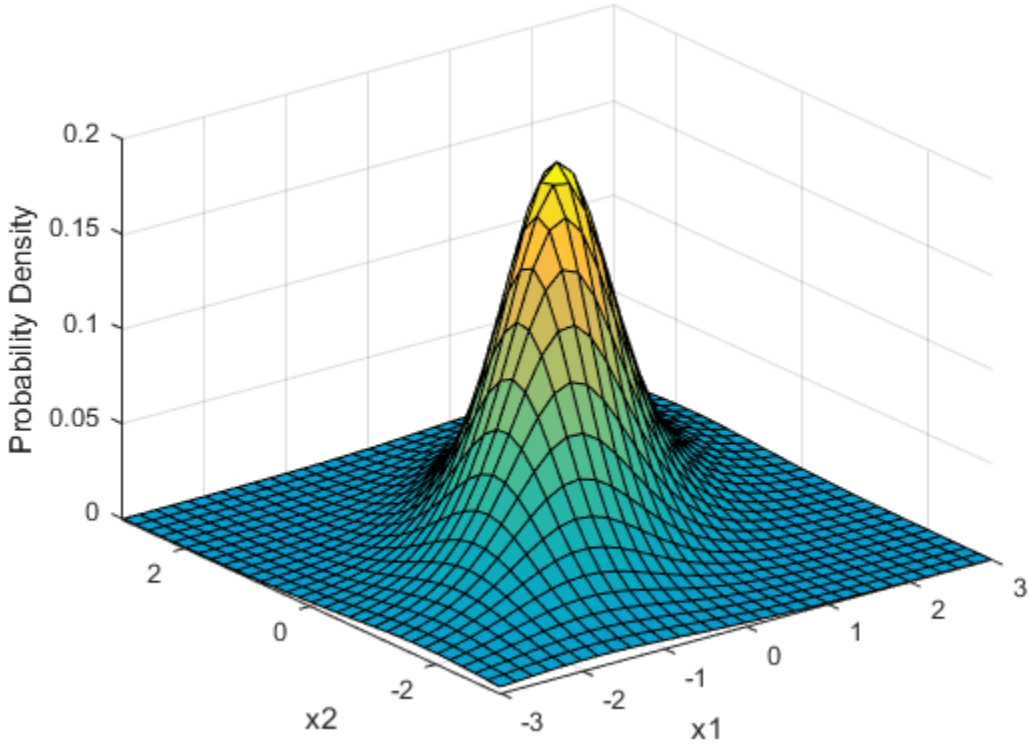
The multivariate Student's t distribution is often used as a substitute for the multivariate normal distribution in situations where it is known that the marginal distributions of the individual variables have fatter tails than the normal.

Example

Plot PDF and CDF of Multivariate *t*-Distribution

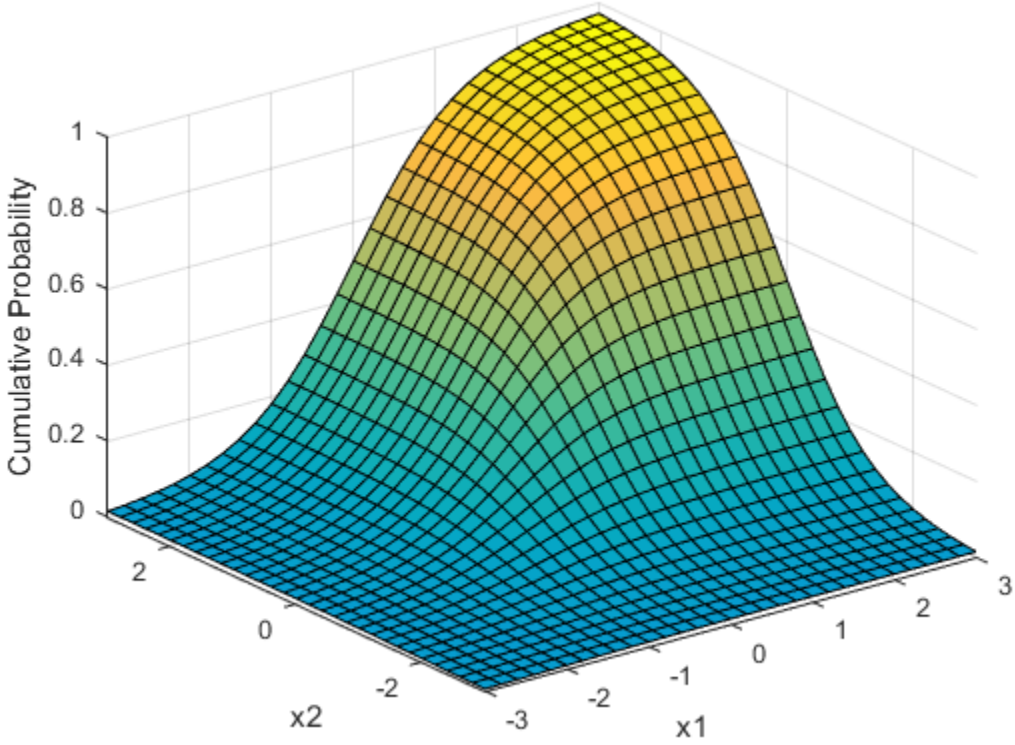
Plot the pdf of a bivariate Student's t distribution. You can use this distribution for a higher number of dimensions as well, although visualization is not easy.

```
Rho = [1 .6; .6 1];
nu = 5;
x1 = -3:.2:3; x2 = -3:.2:3;
[X1,X2] = meshgrid(x1,x2);
F = mvtpdf([X1(:) X2(:)],Rho,nu);
F = reshape(F,length(x2),length(x1));
surf(x1,x2,F);
caxis([min(F(:))-.5*range(F(:)),max(F(:))]);
axis([-3 3 -3 3 0 .2])
xlabel('x1'); ylabel('x2'); zlabel('Probability Density');
```



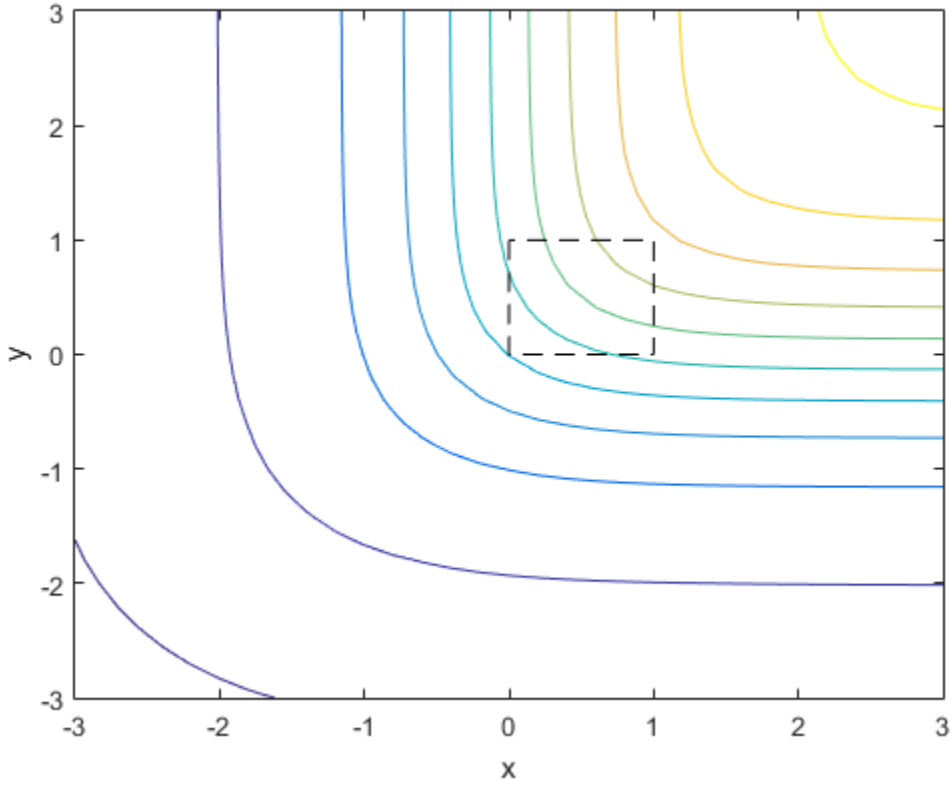
Plot the cdf of a bivariate Student's t distribution.

```
F = mvtcdf([X1(:) X2(:)],Rho,nu);
F = reshape(F,length(x2),length(x1));
surf(x1,x2,F);
caxis([min(F(:))-.5*range(F(:)),max(F(:))]);
axis([-3 3 -3 3 0 1])
xlabel('x1'); ylabel('x2'); zlabel('Cumulative Probability');
```



Since the bivariate Student's *t* distribution is defined on the plane, you can also compute cumulative probabilities over rectangular regions. For example, this contour plot illustrates the computation that follows, of the probability contained within the unit square shown in the figure.

```
contour(x1,x2,F,[.0001 .001 .01 .05:.1:.95 .99 .999 .9999]);
xlabel('x'); ylabel('y');
line([0 0 1 1 0],[1 0 0 1 1],'linestyle','--','color','k');
```



Compute the value of the probability contained within the unit square.

```
F = mvtcdf([0 0],[1 1],Rho,nu)
```

```
F =

    0.1401
```

Computing a multivariate cumulative probability requires significantly more work than computing a univariate probability. By default, the `mvtcdf` function computes values to less than full machine precision and returns an estimate of the error, as an optional second output.

```
[F,err] = mvtcdf([0 0],[1 1],Rho,nu)

F =

    0.1401

err =

   1.0000e-08
```

Nakagami Distribution

In this section...

Definition

The Nakagami distribution has the density function

$$2\left(\frac{\mu}{\omega}\right)^{\mu}\frac{1}{\Gamma(\mu)}x^{(2\mu-1)}e^{\frac{-\mu}{\omega}x^2}$$

with shape parameter μ and scale parameter $\omega > 0$, for $x > 0$. If x has a Nakagami distribution with parameters μ and ω, then x^2 has a gamma distribution with shape parameter μ and scale parameter ω/μ.

Background

In communications theory, Nakagami distributions, Rician distributions, and Rayleigh distributions are used to model scattered signals that reach a receiver by multiple paths. Depending on the density of the scatter, the signal will display different fading characteristics. Rayleigh and Nakagami distributions are used to model dense scatters, while Rician distributions model fading with a stronger line-of-sight. Nakagami distributions can be reduced to Rayleigh distributions, but give more control over the extent of the fading.

Parameters

To estimate distribution parameters, use `mle` or the Distribution Fitting app.

More About

- Using NakagamiDistribution Objects
- "Working with Probability Distributions" on page 5-3

- “Supported Distributions” on page 5-17

Negative Binomial Distribution

In this section...

Definition

When the r parameter is an integer, the negative binomial pdf is

$$y = f(x \mid r, p) = \binom{r + x - 1}{x} p^r q^x I_{(0,1,\ldots)}(x)$$

where $q = 1 - p$. When r is not an integer, the binomial coefficient in the definition of the pdf is replaced by the equivalent expression

$$\frac{\Gamma(r + x)}{\Gamma(r)\Gamma(x + 1)}$$

Background

In its simplest form (when r is an integer), the negative binomial distribution models the number of failures x before a specified number of successes is reached in a series of independent, identical trials. Its parameters are the probability of success in a single trial, p, and the number of successes, r. A special case of the negative binomial distribution, when $r = 1$, is the geometric distribution, which models the number of failures before the first success.

More generally, r can take on non-integer values. This form of the negative binomial distribution has no interpretation in terms of repeated trials, but, like the Poisson distribution, it is useful in modeling count data. The negative binomial distribution is more general than the Poisson distribution because it has a variance that is greater than its mean, making it suitable for count data that do not meet the assumptions of the Poisson distribution. In the limit, as r increases to infinity, the negative binomial distribution approaches the Poisson distribution.

Parameters

Suppose you are collecting data on the number of auto accidents on a busy highway, and would like to be able to model the number of accidents per day. Because these are count data, and because there are a very large number of cars and a small probability of an accident for any specific car, you might think to use the Poisson distribution. However, the probability of having an accident is likely to vary from day to day as the weather and amount of traffic change, and so the assumptions needed for the Poisson distribution are not met. In particular, the variance of this type of count data sometimes exceeds the mean by a large amount. The data below exhibit this effect: most days have few or no accidents, and a few days have a large number.

```
accident = [2  3  4  2  3  1  12  8  14  31  23  1  10  7  0];
m = mean(accident)
v = var(accident)
```

```
m =

    8.0667


v =

   79.3524
```

The negative binomial distribution is more general than the Poisson, and is often suitable for count data when the Poisson is not. The function `nbinfit` returns the maximum likelihood estimates (MLEs) and confidence intervals for the parameters of the negative binomial distribution. Here are the results from fitting the `accident` data:

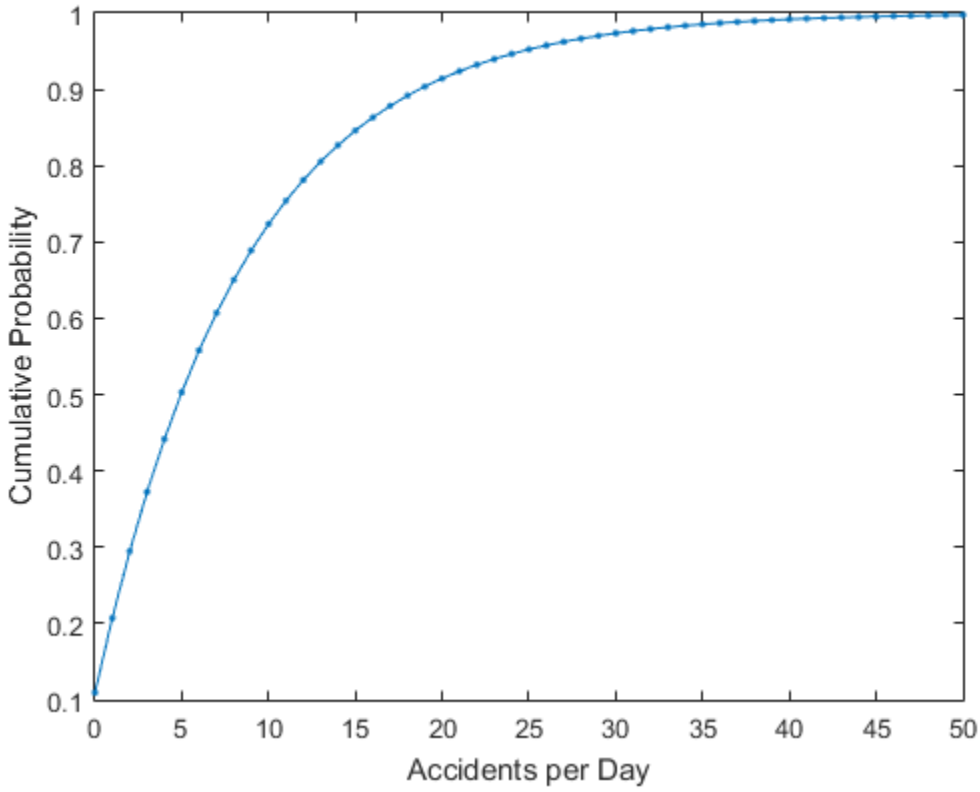
```
[phat,pci] = nbinfit(accident)
```

```
phat =

    1.0060    0.1109


pci =

    0.2152    0.0171
```

```
    1.7968    0.2046
```

It is difficult to give a physical interpretation in this case to the individual parameters. However, the estimated parameters can be used in a model for the number of daily accidents. For example, a plot of the estimated cumulative probability function shows that while there is an estimated 10% chance of no accidents on a given day, there is also about a 10% chance that there will be 20 or more accidents.

```
plot(0:50,nbincdf(0:50,phat(1),phat(2)),'.-');
xlabel('Accidents per Day')
ylabel('Cumulative Probability')
```

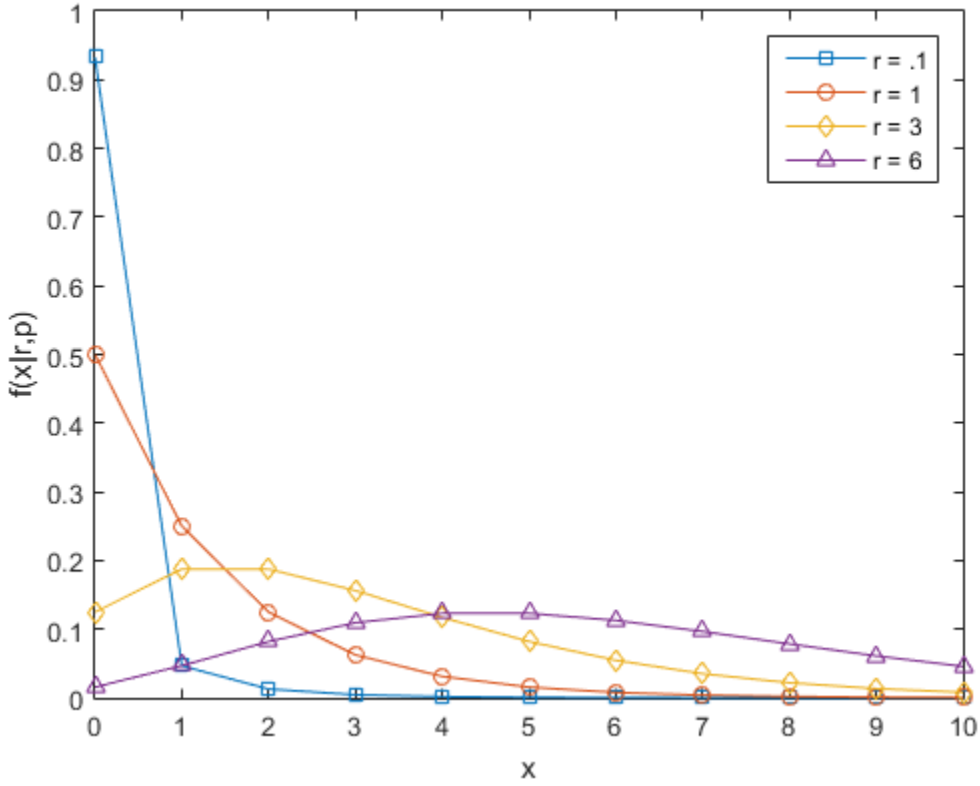


Example

Compute and Plot Negative Binomial Distribution PDF

Compute and plot the pdf using four different values for the parameter `r`, the desired number of successes: `.1`, `1`, `3`, and `6`. In each case, the probability of success `p` is `.5`.

```
x = 0:10;
plot(x,nbinpdf(x,.1,.5),'s-', ...
     x,nbinpdf(x,1,.5),'o-', ...
     x,nbinpdf(x,3,.5),'d-', ...
     x,nbinpdf(x,6,.5),'^-');
legend({'r = .1' 'r = 1' 'r = 3' 'r = 6'})
xlabel('x')
ylabel('f(x|r,p)')
```



The plot shows that the negative binomial distribution can take on a variety of shapes, ranging from very skewed to nearly symmetric, depending on the value of `r`.

More About

- Using NegativeBinomialDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Noncentral Chi-Square Distribution

In this section...

Definition

There are many equivalent formulas for the noncentral chi-square distribution function. One formulation uses a modified Bessel function of the first kind. Another uses the generalized Laguerre polynomials. The cumulative distribution function is computed using a weighted sum of χ^2 probabilities with the weights equal to the probabilities of a Poisson distribution. The Poisson parameter is one-half of the noncentrality parameter of the noncentral chi-square

$$F(x \mid \nu, \delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!} e^{\frac{-\delta}{2}} \right) \Pr\left[\chi^2_{\nu+2j} \le x \right]$$

where δ is the noncentrality parameter.

Background

The χ^2 distribution is actually a simple special case of the noncentral chi-square distribution. One way to generate random numbers with a χ^2 distribution (with ν degrees of freedom) is to sum the squares of ν standard normal random numbers (mean equal to zero.)

What if the normally distributed quantities have a mean other than zero? The sum of squares of these numbers yields the noncentral chi-square distribution. The noncentral chi-square distribution requires two parameters: the degrees of freedom and the noncentrality parameter. The noncentrality parameter is the sum of the squared means of the normally distributed quantities.

The noncentral chi-square has scientific application in thermodynamics and signal processing. The literature in these areas may refer to it as the "Rician Distribution" on page B-144 or generalized "Rayleigh Distribution" on page B-141.

Examples

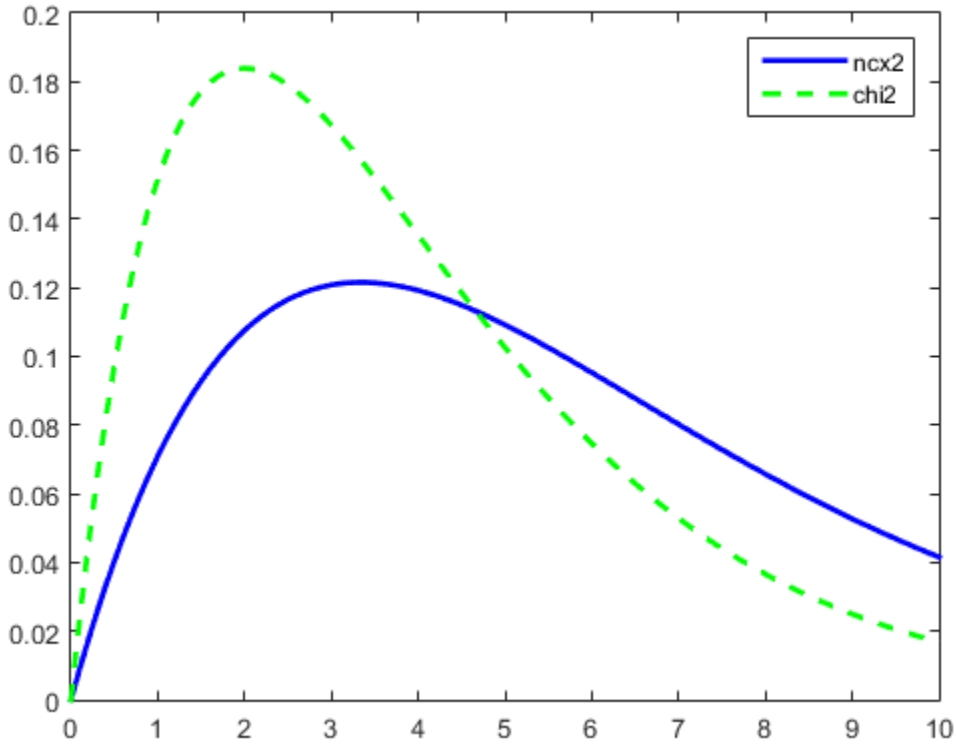
Compute Noncentral Chi-Square Distribution pdf

Compute the pdf of a noncentral chi-square distribution with degrees of freedom `V = 4` and noncentrality parameter `DELTA = 2`. For comparison, also compute the pdf of a chi-square distribution with the same degrees of freedom.

```
x = (0:0.1:10)';
ncx2 = ncx2pdf(x,4,2);
chi2 = chi2pdf(x,4);
```

Plot the pdf of the noncentral chi-square distribution on the same figure as the pdf of the chi-square distribution.

```
figure;
plot(x,ncx2,'b-','LineWidth',2)
hold on
plot(x,chi2,'g--','LineWidth',2)
legend('ncx2','chi2')
```



More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Noncentral F Distribution

In this section...

Definition

Similar to the noncentral χ^2 distribution, the toolbox calculates noncentral F distribution probabilities as a weighted sum of incomplete beta functions using Poisson probabilities as the weights.

$$F(x \mid \nu_1,\nu_2,\delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!} e^{\frac{-\delta}{2}} \right) I\left(\frac{\nu_1 \cdot x}{\nu_2 + \nu_1 \cdot x} \middle| \frac{\nu_1}{2} + j, \frac{\nu_2}{2} \right)$$

$I(x \mid a,b)$ is the incomplete beta function with parameters a and b, and δ is the noncentrality parameter.

Background

As with the χ^2 distribution, the F distribution is a special case of the noncentral F distribution. The F distribution is the result of taking the ratio of χ^2 random variables each divided by its degrees of freedom.

If the numerator of the ratio is a noncentral chi-square random variable divided by its degrees of freedom, the resulting distribution is the noncentral F distribution.

The main application of the noncentral F distribution is to calculate the power of a hypothesis test relative to a particular alternative.

Examples

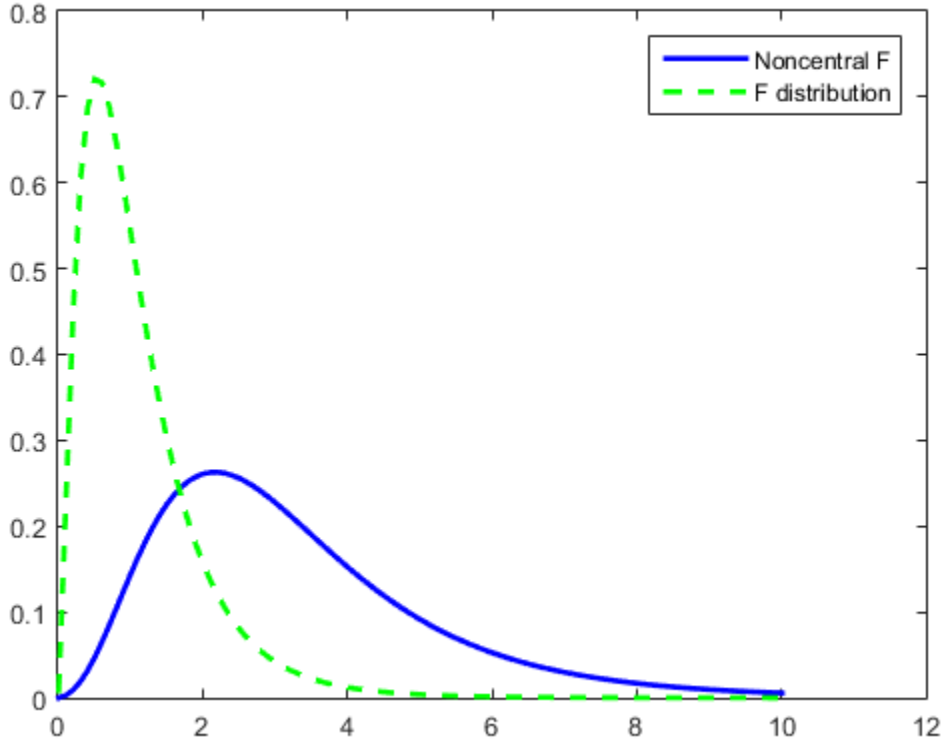
Compute Noncentral *F* Distribution pdf

Compute the pdf of a noncentral F distribution with degrees of freedom `NU1 = 5` and `NU2 = 20`, and noncentrality parameter `DELTA = 10`. For comparison, also compute the pdf of an F distribution with the same degrees of freedom.

```
x = (0.01:0.1:10.01)';
p1 = ncfpdf(x,5,20,10);
p = fpdf(x,5,20);
```

Plot the pdf of the noncentral F distribution and the pdf of the F distribution on the same figure.

```
figure;
plot(x,p1,'b-','LineWidth',2)
hold on
plot(x,p,'g--','LineWidth',2)
legend('Noncentral F','F distribution')
```



More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Noncentral t Distribution

In this section...

Definition

The most general representation of the noncentral t distribution is quite complicated. Johnson and Kotz [60] give a formula for the probability that a noncentral t variate falls in the range $[-u, u]$.

$$P(-u < x < u \mid \nu,\delta) = \sum_{j=0}^{\infty}\left(\frac{\left(\frac{1}{2}\delta^2\right)^j}{j!}e^{\frac{-\delta^2}{2}}\right) I\left(\frac{u^2}{\nu+u^2}\middle|\frac{1}{2}+j,\frac{\nu}{2}\right)$$

$I(x \mid \nu,\delta)$ is the incomplete beta function with parameters ν and δ. δ is the noncentrality parameter, and ν is the number of degrees of freedom.

Background

The noncentral t distribution is a generalization of Student's t distribution.

Student's t distribution with $n - 1$ degrees of freedom models the t-statistic

$$t = \frac{\bar{x} - \mu}{s / \sqrt{n}}$$

where $\bar{x}$ is the sample mean and s is the sample standard deviation of a random sample of size n from a normal population with mean μ. If the population mean is actually μ_0, then the t-statistic has a noncentral t distribution with noncentrality parameter

$$\delta = \frac{\mu_0 - \mu}{\sigma / \sqrt{n}}$$

The noncentrality parameter is the normalized difference between μ_0 and μ.

The noncentral t distribution gives the probability that a t test will correctly reject a false null hypothesis of mean μ when the population mean is actually μ_0; that is, it gives the power of the t test. The power increases as the difference $\mu_0 - \mu$ increases, and also as the sample size n increases.

Examples

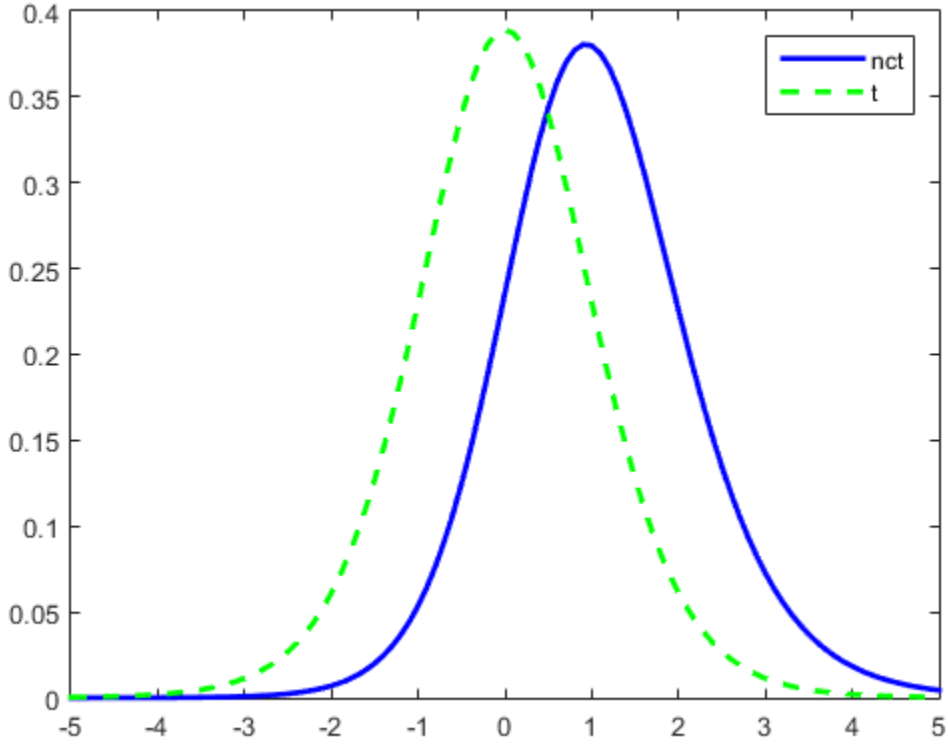
Compute Noncentral *t* Distribution pdf

Compute the pdf of a noncentral t distribution with degrees of freedom `V = 10` and noncentrality parameter `DELTA = 1`. For comparison, also compute the pdf of a t distribution with the same degrees of freedom.

```
x = (-5:0.1:5)';
nct = nctpdf(x,10,1);
t = tpdf(x,10);
```

Plot the pdf of the noncentral t distribution and the pdf of the t distribution on the same figure.

```
plot(x,nct,'b-','LineWidth',2)
hold on
plot(x,t,'g--','LineWidth',2)
legend('nct','t')
```



More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Normal Distribution

In this section...

Definition

The normal pdf is

$$y = f(x \mid \mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

Background

The normal distribution is a two-parameter family of curves. The first parameter, μ, is the mean. The second, σ, is the standard deviation. The standard normal distribution (written $\Phi(x)$) sets μ to 0 and σ to 1.

$\Phi(x)$ is functionally related to the error function, *erf*.

$$erf\left(x\right) = 2\Phi\left(x\sqrt{2}\right) - 1$$

The first use of the normal distribution was as a continuous approximation to the binomial.

The usual justification for using the normal distribution for modeling is the Central Limit Theorem, which states (roughly) that the sum of independent samples from any distribution with finite mean and variance converges to the normal distribution as the sample size goes to infinity.

Parameters

To use statistical parameters such as mean and standard deviation reliably, you need to have a good estimator for them. The maximum likelihood estimates (MLEs) provide

one such estimator. However, an MLE might be biased, which means that its expected value of the parameter might not equal the parameter being estimated. For example, an MLE is biased for estimating the variance of a normal distribution. An unbiased estimator that is commonly used to estimate the parameters of the normal distribution is the *minimum variance unbiased estimator* (*MVUE*). The MVUE has the minimum variance of all unbiased estimators of a parameter.

The MVUEs of parameters μ and σ^2 for the normal distribution are the sample mean and variance. The sample mean is also the MLE for μ. The following are two common formulas for the variance.

$$s^2 = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2$$

$$s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2$$

where

$$\bar{x} = \sum_{i=1}^{n}\frac{x_i}{n}$$

Equation 1 is the maximum likelihood estimator for σ^2, and equation 2 is the MVUE.

As an example, suppose you want to estimate the mean, μ, and the variance, σ^2, of the heights of all fourth grade children in the United States. The function `normfit` returns the MVUE for μ, the square root of the MVUE for σ^2, and confidence intervals for μ and σ^2. Here is a playful example modeling the heights in inches of a randomly chosen fourth grade class.

```
rng default;  % For reproducibility
height = normrnd(50,2,30,1);  % Simulate heights
[mu,s,muci,sci] = normfit(height)
```

```
mu =
```

```
   51.1038


s =

    2.6001


muci =

   50.1329
   52.0747


sci =

    2.0707
    3.4954
```

Note that `s^2` is the MVUE of the variance.

```
s^2


ans =

    6.7605
```

Examples

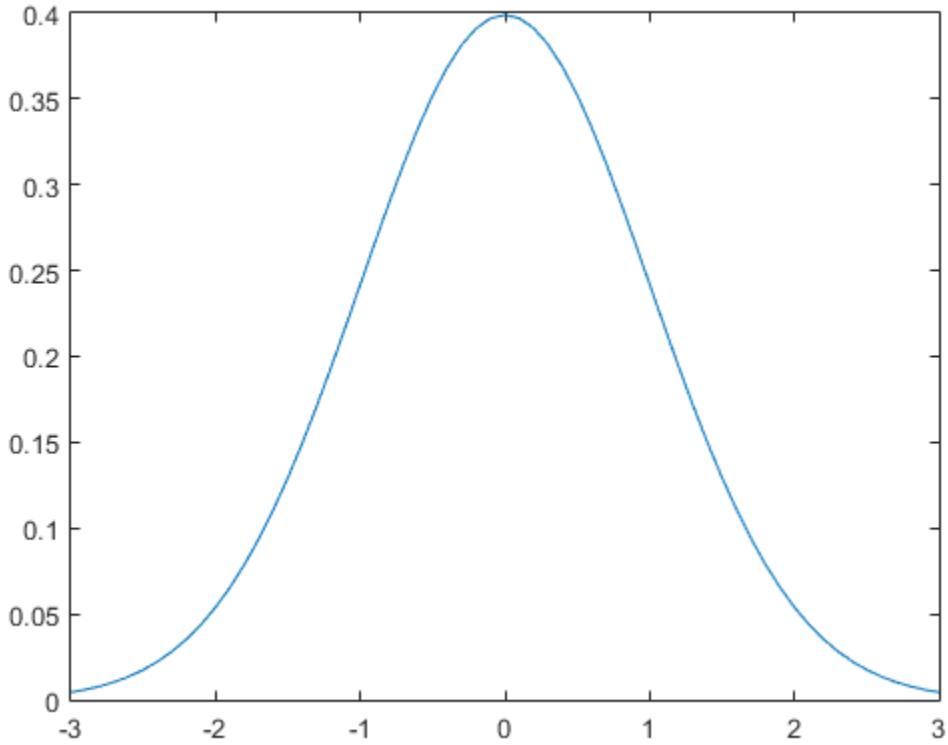
Compute and Plot the Normal Distribution pdf

Compute the pdf of a standard normal distribution, with parameters μ equal to 0 and σ equal to 1.

```
x = [-3:.1:3];
norm = normpdf(x,0,1);
```

Plot the pdf.

```
figure;
plot(x,norm)
```



More About

- Using NormalDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Pareto Distribution

See “Generalized Pareto Distribution” on page B-60.

Pearson System

See “Pearson and Johnson Systems” on page 6-26.

Piecewise Linear Distribution

In this section...

Overview

The piecewise linear distribution creates a nonparametric representation of the cumulative distribution function (cdf) by linearly connecting the known cdf values from the sample data.

Parameters

The piecewise linear distribution uses the following parameters.

Parameter	Description
`x`	Vector of x values at which the cdf changes slope
`Fx`	Vector of cdf values that correspond to each value in `x`

Cumulative Distribution Function

The piecewise linear distribution constructs a continuous cumulative distribution function (cdf) by connecting the empirical cdf values such that the cdf increases linearly between `x`(j) and `x`(j + 1).

Relationship to Other Distributions

The piecewise linear distribution is a continuous version of the discrete empirical cumulative distribution function (ecdf).

More About

- Using PiecewiseLinearDistribution Objects
- "Nonparametric and Empirical Probability Distributions" on page 5-40
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Poisson Distribution

In this section...

Definition

The Poisson pdf is

$$f(x \mid \lambda) = \frac{\lambda^x}{x!} e^{-\lambda}; x = 0, 1, 2, \ldots, \infty .$$

Background

The Poisson distribution is appropriate for applications that involve counting the number of times a random event occurs in a given amount of time, distance, area, etc. Sample applications that involve Poisson distributions include the number of Geiger counter clicks per second, the number of people walking into a store in an hour, and the number of flaws per 1000 feet of video tape.

The Poisson distribution is a one-parameter discrete distribution that takes nonnegative integer values. The parameter, λ, is both the mean and the variance of the distribution. Thus, as the size of the numbers in a particular sample of Poisson random numbers gets larger, so does the variability of the numbers.

The Poisson distribution is the limiting case of a binomial distribution where N approaches infinity and p goes to zero while $Np = \lambda$.

The Poisson and exponential distributions are related. If the number of counts follows the Poisson distribution, then the interval between individual counts follows the exponential distribution.

Parameters

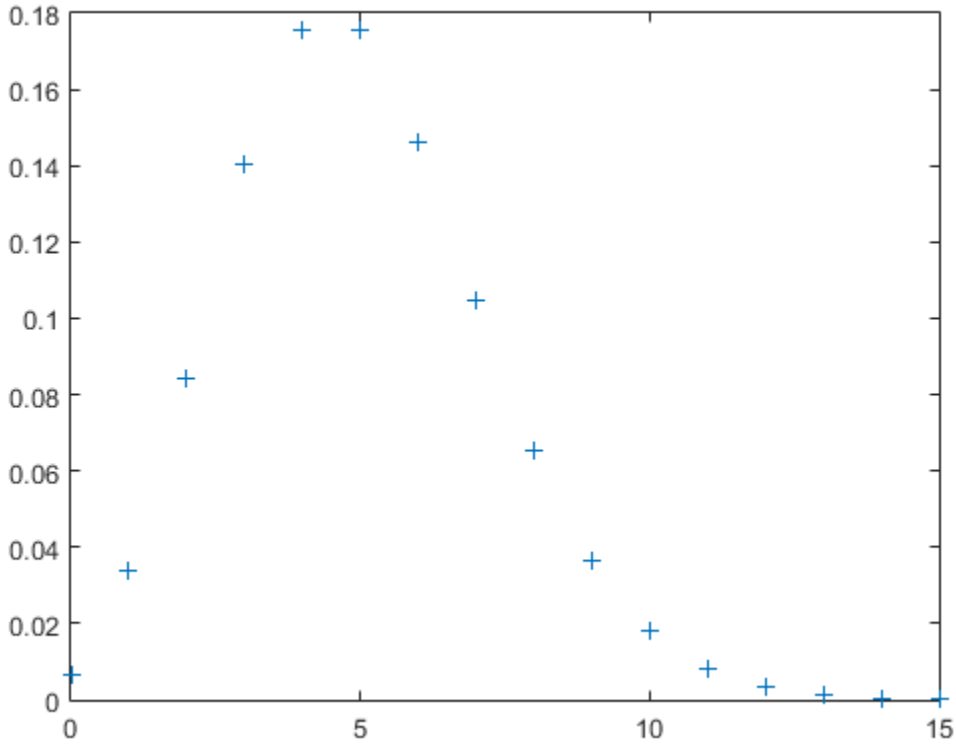
The MLE and the MVUE of the Poisson parameter, λ, is the sample mean. The sum of independent Poisson random variables is also Poisson distributed with the parameter equal to the sum of the individual parameters. This is used to calculate confidence intervals λ. As λ gets large the Poisson distribution can be approximated by a normal distribution with $\mu = \lambda$ and $\sigma^2 = \lambda$. This approximation is used to calculate confidence intervals for values of λ greater than 100.

Examples

Compute and Plot Poisson Distribution PDF

Compute and plot the pdf of a Poisson distribution with parameter `lambda = 5`.

```
x = 0:15;
y = poisspdf(x,5);
plot(x,y,'+')
```



More About

- Using PoissonDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Rayleigh Distribution

In this section...

Definition

The Rayleigh pdf is

$$y = f(x \mid b) = \frac{x}{b^2} e^{\left(\frac{-x^2}{2b^2}\right)}$$

Background

The Rayleigh distribution is a special case of the Weibull distribution. If A and B are the parameters of the Weibull distribution, then the Rayleigh distribution with parameter b is equivalent to the Weibull distribution with parameters $A = \sqrt{2}b$ and $B = 2$.

If the component velocities of a particle in the x and y directions are two independent normal random variables with zero means and equal variances, then the distance the particle travels per unit time is distributed Rayleigh.

In communications theory, Nakagami distributions, Rician distributions, and Rayleigh distributions are used to model scattered signals that reach a receiver by multiple paths. Depending on the density of the scatter, the signal will display different fading characteristics. Rayleigh and Nakagami distributions are used to model dense scatters, while Rician distributions model fading with a stronger line-of-sight. Nakagami distributions can be reduced to Rayleigh distributions, but give more control over the extent of the fading.

Parameters

The `raylfit` function returns the MLE of the Rayleigh parameter. This estimate is

$$b = \sqrt{\frac{1}{2n}\sum_{i=1}^{n} x_i^2}$$

Examples

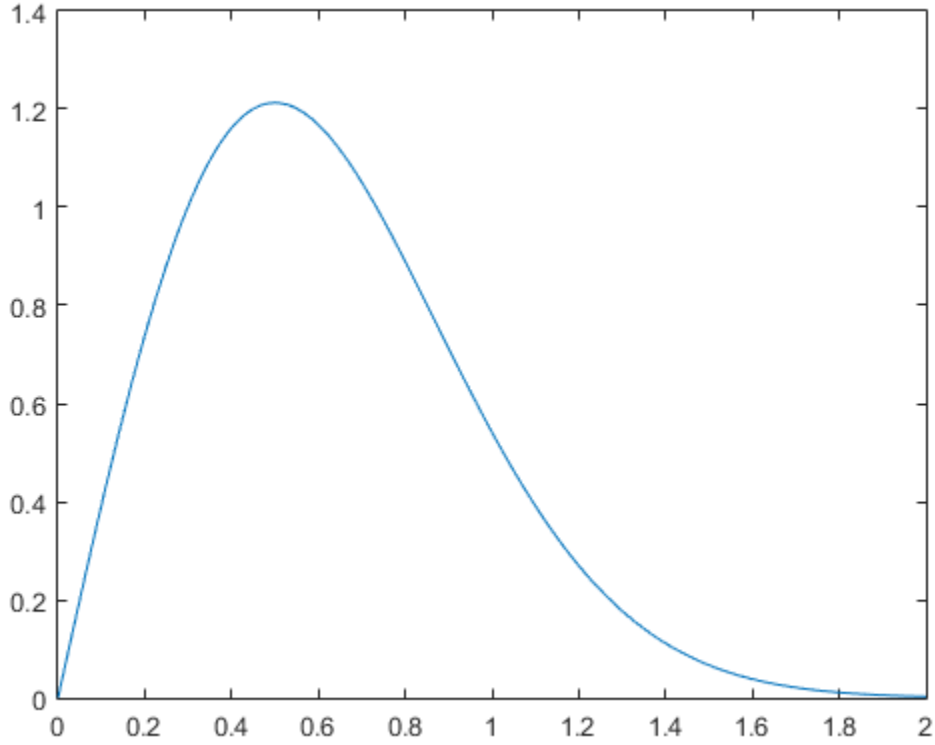
Compute and Plot Rayleigh Distribution pdf

Compute the pdf of a Rayleigh distribution with parameter `B = 0.5`.

```
x = [0:0.01:2];
p = raylpdf(x,0.5);
```

Plot the pdf.

```
figure;
plot(x,p)
```



More About

- Using RayleighDistribution Objects
- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

Rician Distribution

In this section...

Definition

The Rician distribution has the density function

$$I_0\left(\frac{xs}{\sigma^2}\right)\frac{x}{\sigma^2}e^{-\left(\frac{x^2+s^2}{2\sigma^2}\right)}$$

with noncentrality parameter $s \geq 0$ and scale parameter $\sigma > 0$, for $x > 0$. I_0 is the zero-order modified Bessel function of the first kind. If x has a Rician distribution with parameters s and σ, then $(x/\sigma)^2$ has a noncentral chi-square distribution with two degrees of freedom and noncentrality parameter $(s/\sigma)^2$.

Background

In communications theory, Nakagami distributions, Rician distributions, and Rayleigh distributions are used to model scattered signals that reach a receiver by multiple paths. Depending on the density of the scatter, the signal will display different fading characteristics. Rayleigh and Nakagami distributions are used to model dense scatters, while Rician distributions model fading with a stronger line-of-sight. Nakagami distributions can be reduced to Rayleigh distributions, but give more control over the extent of the fading.

Parameters

To estimate distribution parameters, use `mle` or the Distribution Fitting app.

More About

- Using RicianDistribution Objects

- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

Student's t Distribution

In this section...

Overview

The Student's t distribution is a family of curves depending on a single parameter ν (the degrees of freedom).

Parameters

The Student's t distribution uses the following parameter.

Parameter	Description
ν = 1, 2, 3,...	Degrees of freedom

Probability Density Function

Definition

The probability density function (pdf) of the Student's t distribution is

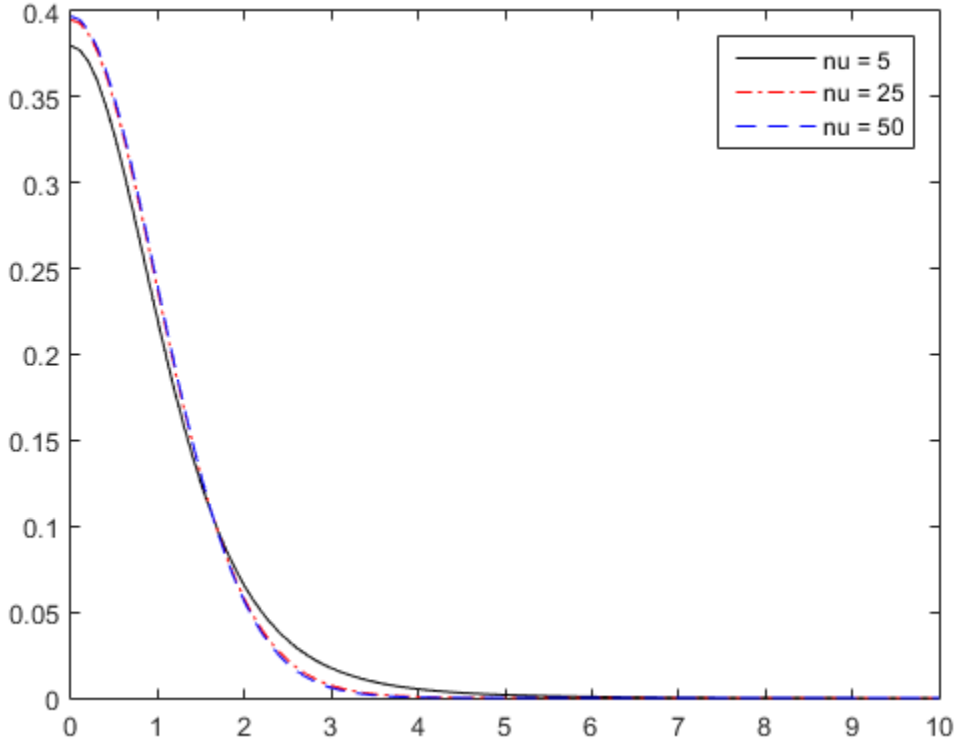
$$y = f(x|\nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{x^2}{\nu}\right)^{\frac{\nu+1}{2}}}$$

where ν is the degrees of freedom and $\Gamma(\cdot)$ is the Gamma function. The result y is the probability of observing a particular value of x from a Student's t distribution with ν degrees of freedom.

Plot

This plot shows how changing the value of the degrees of freedom parameter ν alters the shape of the pdf. Use `tpdf` to compute the pdf for values x equals 0 through 10, for three different values of ν. Then plot all three pdfs on the same figure for a visual comparison.

```
x = [0:.1:10];
y1 = tpdf(x,5);   % For nu = 5
y2 = tpdf(x,25);  % For nu = 25
y3 = tpdf(x,50);  % For nu = 50

figure;
plot(x,y1,'Color','black','LineStyle','-')
hold on
plot(x,y2,'Color','red','LineStyle','-.')
plot(x,y3,'Color','blue','LineStyle','--')
legend({'nu = 5','nu = 25','nu = 50'})
hold off
```



Random Number Generation

Use `trnd` to generate random numbers from the Student's t distribution. For example, the following generates a random number from a Student's t distribution with degrees of freedom ν equal to 10.

```
nu = 10;
r = trnd(nu)
```

```
r =

    1.0585
```

Relationship to Other Distributions

As the degrees of freedom ν goes to infinity, the t distribution approaches the standard normal distribution.

If x is a random sample of size n from a normal distribution with mean μ, then the statistic

$$t = \frac{\bar{x} - \mu}{s / \sqrt{n}}$$

where $\bar{x}$ is the sample mean and s is the sample standard deviation, has Student's t distribution with $n - 1$ degrees of freedom.

The Cauchy distribution is a Student's t distribution with degrees of freedom νequal to 1. The Cauchy distribution has an undefined mean and variance.

Cumulative Distribution Function

Definition

The cumulative distribution function (cdf) of Student's t distribution is

$$p = F(x \mid \nu) = \int_{-\infty}^{x} \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1 + \frac{t^2}{\nu}\right)^{\frac{\nu+1}{2}}} dt$$

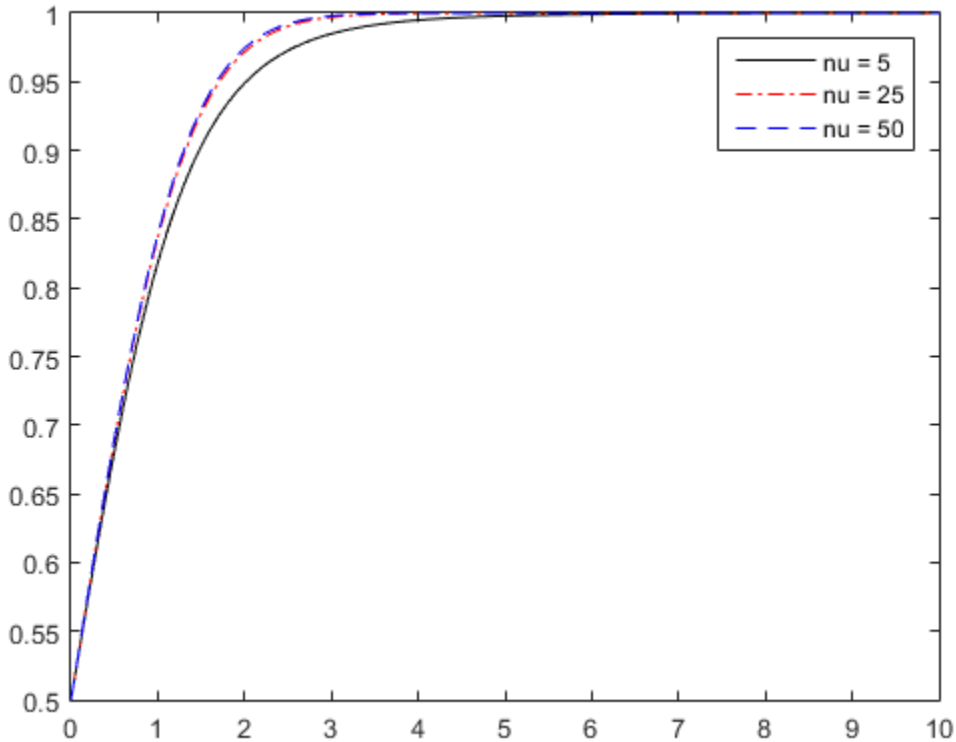
where ν is the degrees of freedom and $\Gamma(\cdot)$ is the Gamma function. The result p is the probability that a single observation from the t distribution with ν degrees of freedom will fall in the interval $[-\infty, x]$.

Plot

This plot shows how changing the value of the parameter ν alters the shape of the cdf. Use `tcdf` to compute the cdf for values x equals 0 through 10, for three different values of ν. Then plot all three cdfs on the same figure for a visual comparison.

```
x = [0:.1:10];
y1 = tcdf(x,5);   % For nu = 5
```

```
y2 = tcdf(x,25);  % For nu = 25
y3 = tcdf(x,50);  % For nu = 50

figure;
plot(x,y1,'Color','black','LineStyle','-')
hold on
plot(x,y2,'Color','red','LineStyle','-.')
plot(x,y3,'Color','blue','LineStyle','--')
legend({'nu = 5','nu = 25','nu = 50'})
hold off
```



Inverse cdf

Use `tinv` to compute the inverse cdf of the Student's t distribution.

```
p = .95;
nu = 50;
x = tinv(p,nu)


x =

    1.6759
```

Mean and Variance

The mean of the Student's t distribution is

$$\text{mean} = 0$$

for degrees of freedom ν greater than 1. If ν equals 1, then the mean is undefined.

The variance of the Student's t distribution is

$$\text{var} = \frac{\nu}{\nu - 2}$$

for degrees of freedom ν greater than 2. If ν is less than or equal to 2, then the variance is undefined.

Use `tstat` to compute the mean and variance of a Student's t distribution. For example, the following computes the mean and variance of a Student's t distribution with degrees of freedom ν equal to 10.

```
nu = 10;
[m,v] = tstat(nu)


m =

     0
```

```
v =

    1.2500
```

Example

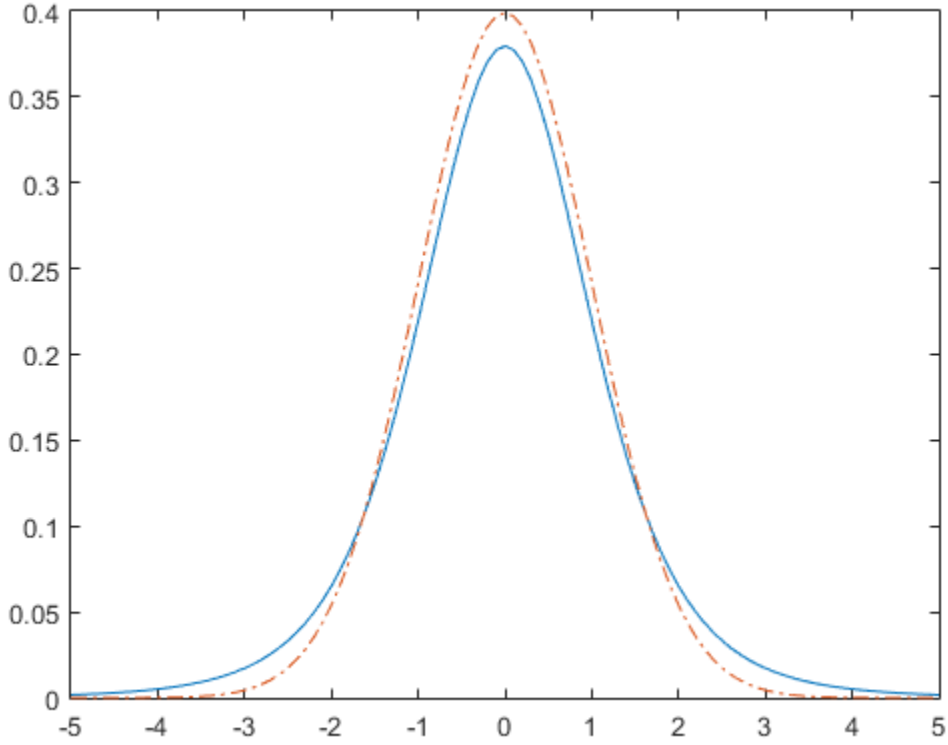
Compare Student's *t* and Normal Distribution pdfs

Compute the pdf for a Student's *t* distribution with parameter `nu = 5`, and for a standard normal distribution.

```
x = -5:0.1:5;
y = tpdf(x,5);
z = normpdf(x,0,1);
```

Plot the Student's *t* and standard normal pdfs on the same figure. The standard normal pdf (dashed line) has shorter tails than the Student's *t* pdf (solid line).

```
figure;
plot(x,y,'-',x,z,'-.')
```



Related Examples

- "Generate Cauchy Random Numbers Using Student's *t*" on page 5-142

More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

t Location-Scale Distribution

In this section...

Overview

The *t* location-scale distribution is useful for modeling data distributions with heavier tails (more prone to outliers) than the normal distribution. It approaches the normal distribution as ν approaches infinity, and smaller values of ν yield heavier tails.

Parameters

The *t* location-scale distribution uses the following parameters.

Parameter	Description	Support
μ	Location parameter	$-\infty < \mu < \infty$
σ	Scale parameter	$\sigma > 0$
ν	Shape parameter	$\nu > 0$

To estimate distribution parameters, use `mle`. Alternatively, fit a `prob.tLocationScaleDistribution` object to data using `fitdist` or the Distribution Fitting app, `disttool`.

Probability Density Function

The probability density function (pdf) of the *t* location-scale distribution is

$$\frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\sigma\sqrt{\nu\pi}\Gamma\left(\frac{\nu}{2}\right)}\left[\frac{\nu+\left(\frac{x-\mu}{\sigma}\right)^2}{\nu}\right]^{-\left(\frac{\nu+1}{2}\right)}$$

where $\Gamma(\cdot)$ is the gamma function, μ is the location parameter, σ is the scale parameter, and ν is the shape parameter .

To compute the probability density function, use `pdf`. Alternatively, you can create a `prob.tLocationScaleDistribution` object using `fitdist` or `makedist`, then use the `pdf` method to work with the object.

Cumulative Distribution Function

To compute the probability density function, use `cdf`. Alternatively, you can create a `prob.tLocationScaleDistribution` object using `fitdist` or `makedist`, then use the `cdf` method to work with the object.

Descriptive Statistics

The mean of the *t* location-scale distribution is

$$\text{mean} = \mu ,$$

where μ is the location parameter. The mean is only defined for shape parameter values $\nu > 1$. For other values of ν, the mean is undefined.

The variance of the *t* location-scale distribution is

$$\text{var} = \sigma^2 \frac{\nu}{\nu-2},$$

where μ is the location parameter and ν is the shape parameter. The variance is only defined for values of $\nu > 2$. For other values of ν, the variance is undefined.

To compute the mean and variance, create a `prob.tLocationScaleDistribution` object using `fitdist` or `makedist`. You can also use the Distribution Fitting app, `disttool`.

Relationship to Other Distributions

If x has a t location-scale distribution, with parameters μ, σ, and ν, then

$$\frac{x-\mu}{\sigma}$$

has a Student's t distribution with ν degrees of freedom.

More About

- Using tLocationScaleDistribution Objects
- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

Triangular Distribution

In this section...

Overview

The triangular distribution provides a simplistic representation of the probability distribution when limited sample data is available. Its parameters are the minimum, maximum, and peak of the data. Common applications include business and economic simulations, project management planning, natural phenomena modeling, and audio dithering.

Parameters

The triangular distribution uses the following parameters.

Parameter	Description	Constraints
a	Lower limit	$a \le b$
b	Peak location	$a \le b \le c$
c	Upper limit	$c \ge b$

Parameter Estimation

Typically, you estimate triangular distribution parameters using subjectively reasonable values based on the sample data. You can estimate the lower and upper limit parameters a and c using the minimum and maximum values of the sample data, respectively. You can estimate the peak location parameter b using the sample mean, median, mode, or any other subjectively reasonable estimate of the population mode.

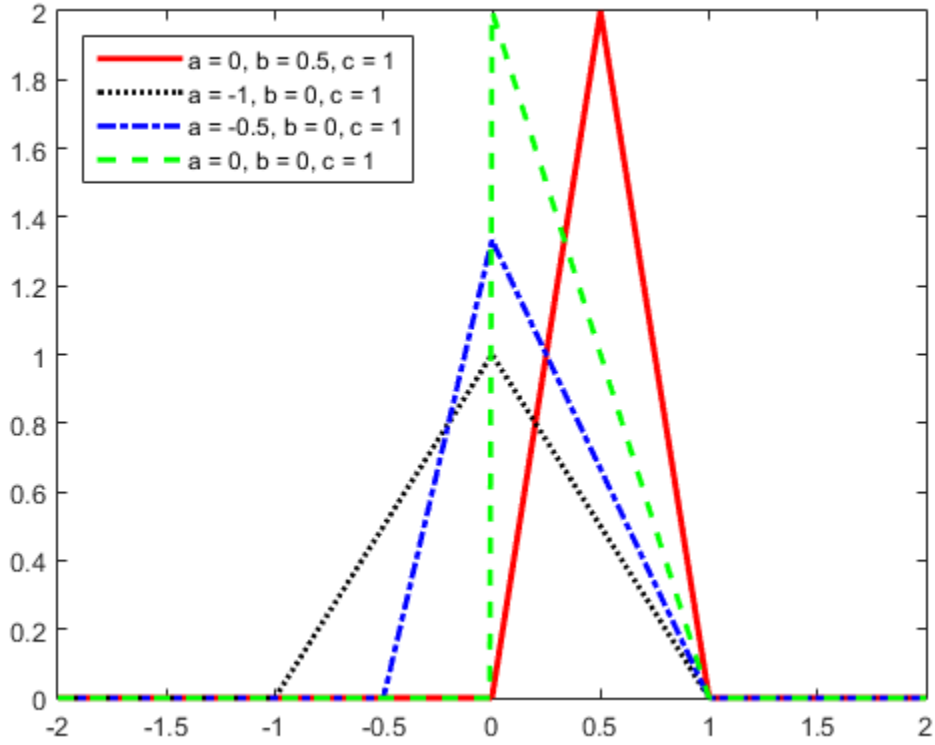
Probability Density Function

The probability density function (pdf) of the triangular distribution is

$$f(x \mid a,b,c) = \begin{cases} \dfrac{2(x-a)}{(c-a)(b-a)} & ; \quad a \le x \le b \\ \dfrac{2(c-x)}{(c-a)(c-b)} & ; \quad b < x \le c \\ 0 & ; \quad x < a \,,\, x > c \end{cases} .$$

This plot shows how changing the value of the parameters a, b, and c alters the shape of the pdf.

```
% Create four distribution objects with different parameters
pd1 = makedist('Triangular');
pd2 = makedist('Triangular','a',-1,'b',0,'c',1);
pd3 = makedist('Triangular','a',-.5,'b',0,'c',1);
pd4 = makedist('Triangular','a',0,'b',0,'c',1);

% Compute the pdfs
x = -2:.01:2;
pdf1 = pdf(pd1,x);
pdf2 = pdf(pd2,x);
pdf3 = pdf(pd3,x);
pdf4 = pdf(pd4,x);

% Plot the pdfs
figure;
plot(x,pdf1,'r','LineWidth',2)
hold on;
plot(x,pdf2,'k:','LineWidth',2);
plot(x,pdf3,'b-.','LineWidth',2);
plot(x,pdf4,'g--','LineWidth',2);
legend({'a = 0, b = 0.5, c = 1','a = -1, b = 0, c = 1',...
    'a = -0.5, b = 0, c = 1','a = 0, b = 0, c = 1'},'Location','NW');
hold off;
```



As the distance between a and c increases, the density at any particular value within the distribution boundaries decreases. Because the density function integrates to 1, the height of the pdf plot decreases as its width increases. The location of the peak parameter b determines whether the pdf skews right or left, or if it is symmetrical.

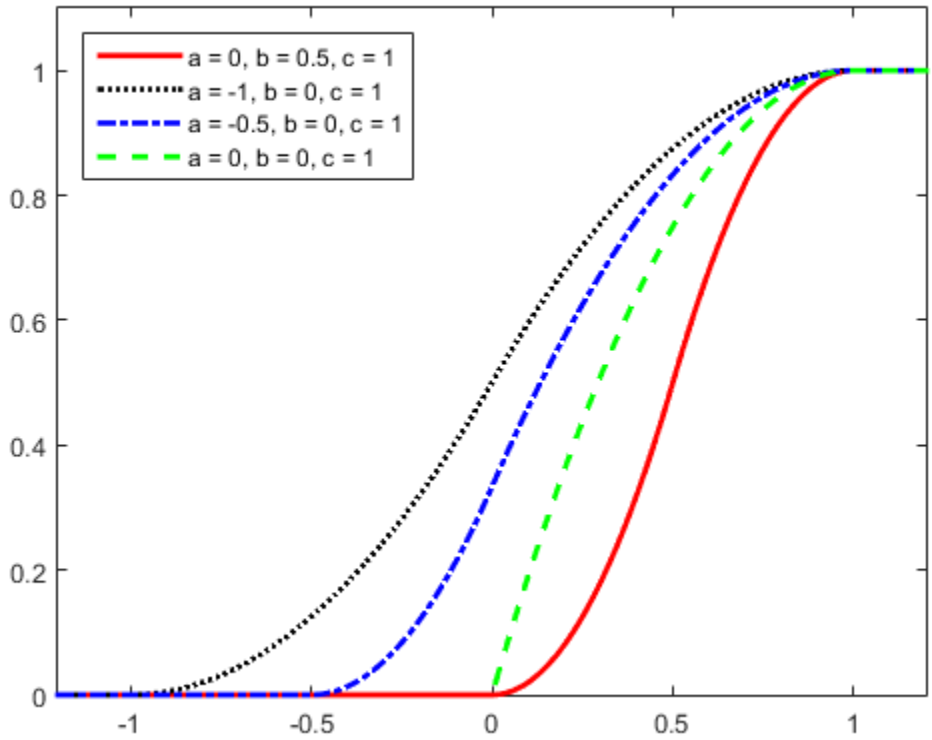
Cumulative Distribution Function

The cumulative distribution function (cdf) of the triangular distribution is

$$F(x \mid a,b,c) = \begin{cases} 0 & , \quad x < a \\ \dfrac{(x-a)^2}{(c-a)(b-a)} & , \quad a \le x \le b \\ 1 - \dfrac{(c-x)^2}{(c-a)(c-b)} & , \quad b < x \le c \\ 1 & , \quad x > c \end{cases}.$$

This plot shows how changing the value of the parameters a, b, and c alters the shape of the cdf.

```
% Create four distribution objects with different parameters
pd1 = makedist('Triangular');
pd2 = makedist('Triangular','a',-1,'b',0,'c',1);
pd3 = makedist('Triangular','a',-.5,'b',0,'c',1);
pd4 = makedist('Triangular','a',0,'b',0,'c',1);

% Compute the cdfs
x = -1.2:.01:1.2;
cdf1 = cdf(pd1,x);
cdf2 = cdf(pd2,x);
cdf3 = cdf(pd3,x);
cdf4 = cdf(pd4,x);

% Plot the cdfs
figure;
plot(x,cdf1,'r','LineWidth',2)
xlim([-1.2 1.2]);
ylim([0 1.1]);hold on;
plot(x,cdf2,'k:','LineWidth',2);
plot(x,cdf3,'b-.','LineWidth',2);
plot(x,cdf4,'g--','LineWidth',2);
legend({'a = 0, b = 0.5, c = 1','a = -1, b = 0, c = 1',...
    'a = -0.5, b = 0, c = 1','a = 0, b = 0, c = 1'},'Location','NW');
hold off;
```



Descriptive Statistics

The mean and variance of the triangular distribution are related to the parameters a, b, and c.

The mean is

$$\text{mean} = \left(\frac{a + b + c}{3} \right).$$

The variance is

$$\text{var} = \left(\frac{a^2 + b^2 + c^2 - ab - ac - bc}{18} \right).$$

Related Examples

- "Generate Random Numbers Using the Triangular Distribution" on page 5-66

More About

- Using TriangularDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Uniform Distribution (Continuous)

In this section...

Overview

The uniform distribution (also called the rectangular distribution) is notable because it has a constant probability distribution function (pdf) between its two bounding parameters. It is appropriate for representing the distribution of round-off errors in values tabulated to a particular number of decimal places, and is used in random number generating techniques such as the inversion method.

Parameters

The uniform distribution uses the following parameters.

Parameter	Description	Constraints
`lower`	Lower limit	$-\infty < lower < upper$
`upper`	Upper limit	$lower < upper < \infty$

Parameter Estimation

The maximum likelihood estimator (MLE) for *lower* is the sample minimum. The MLE for *upper* is the sample maximum.

Probability Density Function

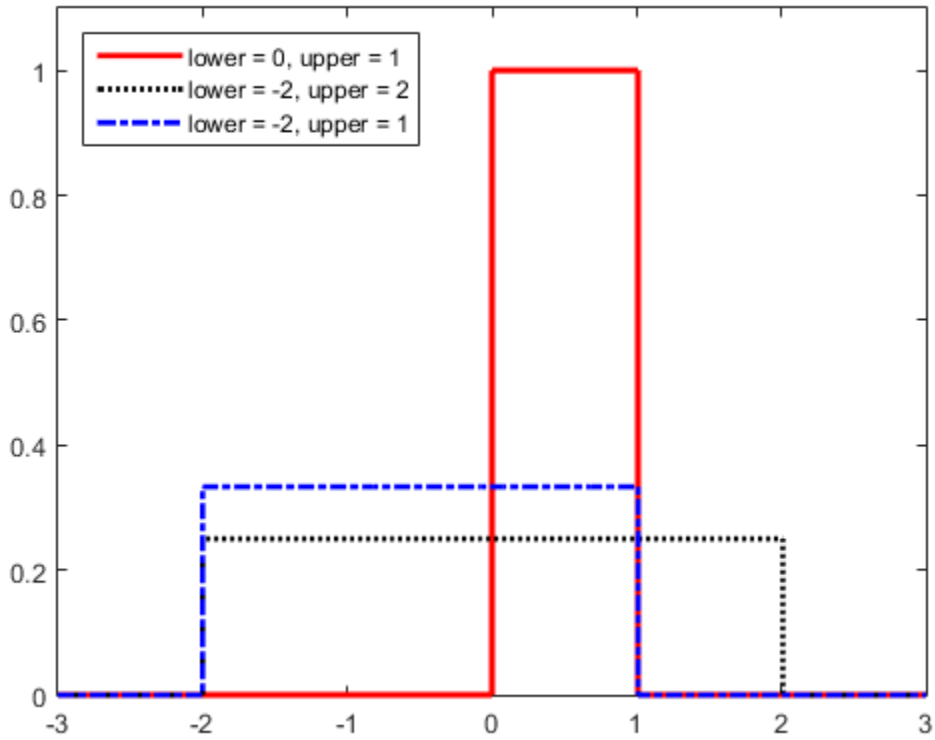
The probability density function (pdf) of the continuous uniform distribution is

$$f(x \mid lower, upper) = \begin{cases} \left(\frac{1}{upper - lower}\right) & ; \quad lower \le x \le upper \\ 0 & ; \quad otherwise \end{cases} .$$

The pdf is constant between *lower* and *upper*.

This plot illustrates how changing the value of the parameters *lower* and *upper* affects the shape of the pdf.

```
% Create three distribution objects with different parameters
pd1 = makedist('Uniform');
pd2 = makedist('Uniform','lower',-2,'upper',2);
pd3 = makedist('Uniform','lower',-2,'upper',1);

% Compute the pdfs
x = -3:.01:3;
pdf1 = pdf(pd1,x);
pdf2 = pdf(pd2,x);
pdf3 = pdf(pd3,x);

% Plot the pdfs
figure;
stairs(x,pdf1,'r','LineWidth',2);
hold on;
stairs(x,pdf2,'k:','LineWidth',2);
stairs(x,pdf3,'b-.','LineWidth',2);
ylim([0 1.1]);
legend({'lower = 0, upper = 1','lower = -2, upper = 2',...
    'lower = -2, upper = 1'},'Location','NW');
hold off;
```



As the distance between *lower* and *upper* increases, the density at any particular value within the distribution boundaries decreases. Because the density function integrates to 1, the height of the pdf plot decreases as its width increases.

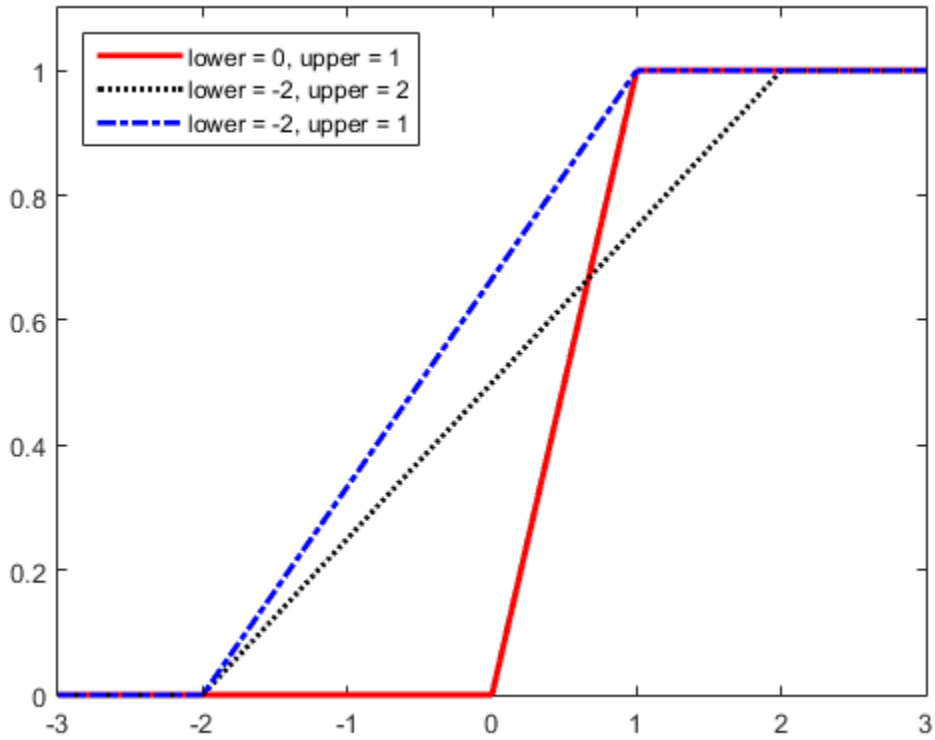
Cumulative Distribution Function

The cumulative distribution function (cdf) of the continuous uniform distribution is

$$F(x \mid lower, upper) = \begin{cases} 0 & ; \quad x < lower \\ \dfrac{x - lower}{upper - lower} & ; \quad lower \le x < upper \\ 1 & ; \quad x \ge upper \end{cases}.$$

This plot illustrates how changing the value of the parameters *lower* and *upper* affects the shape of the cdf.

```
% Create three distribution objects with different parameters
pd1 = makedist('Uniform');
pd2 = makedist('Uniform','lower',-2,'upper',2);
pd3 = makedist('Uniform','lower',-2,'upper',1);

% Compute the cdfs
x = -3:.01:3;
cdf1 = cdf(pd1,x);
cdf2 = cdf(pd2,x);
cdf3 = cdf(pd3,x);

% Plot the cdfs
figure;
plot(x,cdf1,'r','LineWidth',2);
hold on;
plot(x,cdf2,'k:','LineWidth',2);
plot(x,cdf3,'b-.','LineWidth',2);
ylim([0 1.1]);
legend({'lower = 0, upper = 1','lower = -2, upper = 2',...
    'lower = -2, upper = 1'},'Location','NW');
hold off;
```



Descriptive Statistics

The mean and variance of the continuous uniform distribution are related to the parameters *lower* and *upper*.

The mean is

$$\text{mean} = \frac{1}{2}(lower + upper) .$$

The variance is

$$\text{var} = \frac{1}{12}(upper - lower)^2 .$$

Relationship to Other Distributions

The standard uniform distribution (`lower = 0` and `upper = 1`) is a special case of the beta distribution obtained by setting the beta distribution parameters `a = 1` and `b = 1`.

The inversion method uses the continuous standard uniform distribution to generate random numbers for any other continuous distribution. The inversion method relies on the principle that continuous cumulative distribution functions (cdfs) range uniformly over the open interval (0,1). If u is a uniform random number on (0,1), then $x = \mathtt{F}^{-1}(u)$ generates a random number x from any continuous distribution with the specified cdf `F`.

Related Examples

- "Generate Random Numbers Using Uniform Distribution Inversion" on page 5-135

More About

- Using UniformDistribution Objects
- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Uniform Distribution (Discrete)

In this section...

Definition

The discrete uniform pdf is

$$y = f(x \mid N) = \frac{1}{N} I_{(1,\ldots,N)}(x)$$

Background

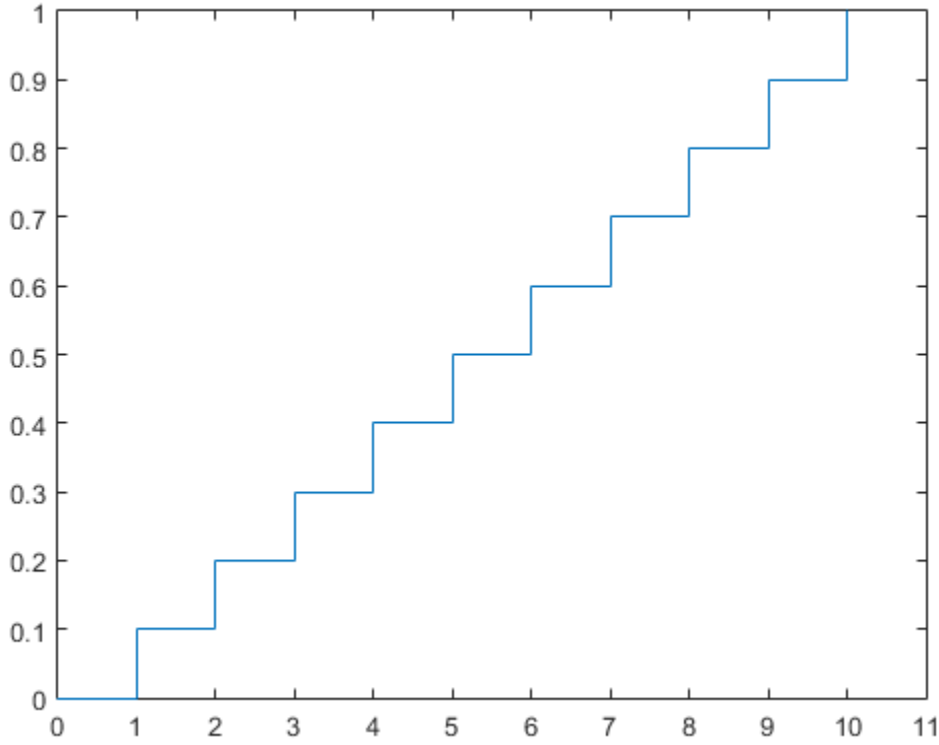
The discrete uniform distribution is a simple distribution that puts equal weight on the integers from one to *N*.

Examples

Plot a Discrete Uniform Distribution cdf

As for all discrete distributions, the cdf is a step function. The plot shows the discrete uniform cdf for $N = 10$.

```
x = 0:10;
y = unidcdf(x,10);
figure;
stairs(x,y)
h = gca;
h.XLim = [0 11];
```



Generate Discrete Uniform Random Numbers

Pick a random sample of 10 from a list of 553 items.

```
rng default;  % for reproducibility
numbers = unidrnd(553,1,10)
```

```
numbers =

   451   501    71   506   350    54   155   303   530   534
```

More About

- "Working with Probability Distributions" on page 5-3
- "Supported Distributions" on page 5-17

Weibull Distribution

In this section...

Definition

The Weibull pdf is positive only for positive values of x, and is zero otherwise. For strictly positive values of the shape parameter b and scale parameter a, the density is

$$f(x \mid a,b) = \frac{b}{a}\left(\frac{x}{a}\right)^{b-1} e^{-(x/a)^b}.$$

Background

Waloddi Weibull offered the distribution that bears his name as an appropriate analytical tool for modeling the breaking strength of materials. Current usage also includes reliability and lifetime modeling. The Weibull distribution is more flexible than the exponential for these purposes.

To see why, consider the hazard rate function (instantaneous failure rate). If $f(t)$ and $F(t)$ are the pdf and cdf of a distribution, then the hazard rate is

$$h(t) = \frac{f(t)}{1 - F(t)}$$

Substituting the pdf and cdf of the exponential distribution for $f(t)$ and $F(t)$ above yields a constant. The example below shows that the hazard rate for the Weibull distribution can vary.

Parameters

Suppose you want to model the tensile strength of a thin filament using the Weibull distribution. The function `wblfit` gives maximum likelihood estimates and confidence intervals for the Weibull parameters.

```
rng('default');  % For reproducibility
strength = wblrnd(0.5,2,100,1);  % Simulated strengths
[p,ci] = wblfit(strength)
```

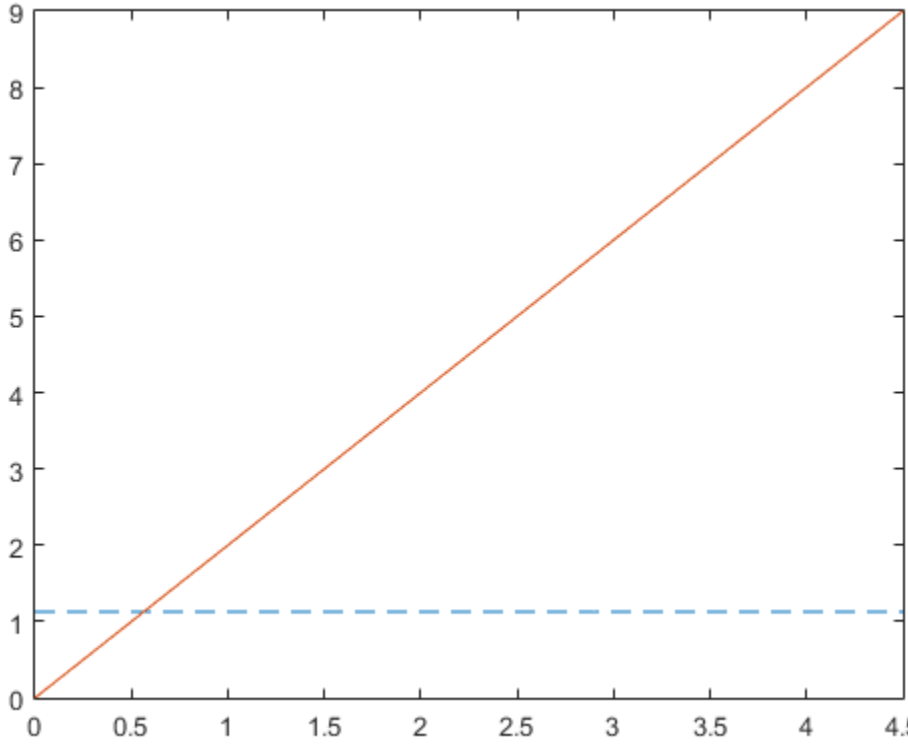
```
p =

    0.4768    1.9622


ci =

    0.4291    1.6821
    0.5298    2.2890
```

The default 95% confidence interval for each parameter contains the true value.

Example

The exponential distribution has a constant hazard function, which is not generally the case for the Weibull distribution. The plot shows the hazard function for exponential (dashed line) and Weibull (solid line) distributions having the same mean life. The Weibull hazard rate here increases with age (a reasonable assumption).

```
t = 0:0.1:4.5;
h1 = exppdf(t,0.8862) ./ (1-expcdf(t,0.8862));
h2 = wblpdf(t,1,2) ./ (1-wblcdf(t,1,2));
plot(t,h1,'--',t,h2,'-')
```



More About

- Using WeibullDistribution Objects
- “Working with Probability Distributions” on page 5-3
- “Supported Distributions” on page 5-17

Wishart Distribution

In this section...

Overview

The Wishart distribution is a generalization of the univariate chi-square distribution to two or more variables. It is a distribution for symmetric positive semidefinite matrices, typically covariance matrices, the diagonal elements of which are each chi-square random variables. In the same way as the chi-square distribution can be constructed by summing the squares of independent, identically distributed, zero-mean univariate normal random variables, the Wishart distribution can be constructed by summing the inner products of independent, identically distributed, zero-mean multivariate normal random vectors. The Wishart distribution is often used as a model for the distribution of the sample covariance matrix for multivariate normal random data, after scaling by the sample size.

Only random matrix generation is supported for the Wishart distribution, including both singular and nonsingular Σ.

Parameters

The Wishart distribution is parameterized with a symmetric, positive semidefinite matrix, Σ, and a positive scalar degrees of freedom parameter, v. v is analogous to the degrees of freedom parameter of a univariate chi-square distribution, and Σv is the mean of the distribution.

Probability Density Function

The probability density function of the d-dimensional Wishart distribution is given by

$$y = f(X, \Sigma, \nu) = \frac{|X|^{((\nu-d-1)/2)} e^{\left(-\frac{1}{2}\mathrm{trace}\left(\Sigma^{-1}X\right)\right)}}{2^{(\nu d)/2}\pi^{(d(d-1))/4}|\Sigma|^{\nu/2}\Gamma(\nu/2)\ldots\Gamma(\nu-(d-1))/2}$$

where X and Σ are d-by-d symmetric positive definite matrices, and ν is a scalar greater than $d - 1$. While it is possible to define the Wishart for singular Σ, the density cannot be written as above.

Example

If x is a bivariate normal random vector with mean zero and covariance matrix

$$\Sigma = \begin{pmatrix} 1 & .5 \\ .5 & 2 \end{pmatrix}$$

then you can use the Wishart distribution to generate a sample covariance matrix without explicitly generating x itself. Notice how the sampling variability is quite large when the degrees of freedom is small.

```
Sigma = [1 .5; .5 2];
df = 10; S1 = wishrnd(Sigma,df)/df

S1 =
       1.7959       0.64107
      0.64107        1.5496

df = 1000; S2 = wishrnd(Sigma,df)/df

S2 =
       0.9842       0.50158
      0.50158        2.1682
```

See Also

`wishrnd`

More About

- "Inverse Wishart Distribution" on page B-78
- "Supported Distributions" on page 5-17

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